SEQUENCE LISTING

<110> Fred Hutchinson Cancer Research Center
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Greenberg, Philip D.

<120> IMMUNOMODULATORY FUSION PROTEINS AND
USES THEREOF

<130> 360056.433WO

<140> PCT
<141> 2016-03-04

<150> US 62/128,979
<151> 2015-03-05

<160> 178

<170> FastSEQ for Windows Version 4.0

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<223> huCD200Rtm-CD28 construct

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<220>
<223> huCD200R entire extracellular domain

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tgctggccga agtgaacacc agctggcccg tgaagatggc caccaacgcc gtgctgtgct 180
gccctcctat cgccctgcgg aacctgatca tcatcacctg ggagatcatc ctgcggggcc 240
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<210> 3
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<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R transmembrane domain

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ctg 63

<210> 4
<211> 81
<212> DNA
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<220>
<223> CD28 transmembrane domain

<400> 4
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gccttcatca tcttttgggt c 81

<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 intracellular domain

<400> 5
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agc 123

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

<220>
<223> huCD200R-CD28tm construct

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<210> 7
<211> 942

<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-9aas-CD28Cys construct

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tgccctccta tcgccctgcg gaacctgatc atcatcacct gggagatcat cctgcggggc 240
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atccccgagg gcgattgcgc caccaagcag gaatactggt ccaacggcac cgtgaccgtg 600
aagtccacct gtcactggga ggtgcacaac gtgtccaccg tgacatgcca cgtgtcccac 660
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<210> 8
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-9aas portion of extracellular domain

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tgccctccta tcgccctgcg gaacctgatc atcatcacct gggagatcat cctgcggggc 240
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ttccaccggg gataccatct gcaggtgctc gtgacccccg aagtgaccct gttccagaac 480
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atccccgagg gcgattgcgc caccaagcag gaatactggt ccaacggcac cgtgaccgtg 600
aagtccacct gtcactggga ggtgcacaac gtgtccaccg tgacatgcca cgtgtcccac 660
ctgaccggca acaagagcct gtacatcgag ctgctgcctg tg 702

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28Cys multimerization domain

<400> 9
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<210> 10
<211> 933
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-12aas-CD28Cys construct

<400> 10
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<210> 11
<211> 693
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-12aas portion of extracellular domain

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<210> 12
<211> 945
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-9aas-CD28Cys tm-41BBic construct

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<210> 13
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular component

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gagctg 126

<210> 14
<211> 936
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-12aas-CD28Cys tm-41BBic construct

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<210> 15
<211> 1059
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-12aas-CD28Cys tm ic-41BBic construct

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tgcagattcc ccgaggaaga agaaggcggc tgcgagctg 1059

<210> 16
<211> 1305
<212> DNA
<213> Artificial Sequence

<220>

<223> huSIRPalphatm-CD28 construct

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<210> 17
<211> 1119
<212> DNA
<213> Artificial Sequence

<220>
<223> huSIRP alpha entire extracellular domain

<400> 17
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gcctcttgtg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgac 120
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aacatggact tcagcatccg gatcggcaac atcacccctg ccgatgccgg cacctactac 360
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gccgccgaga acaccggcag caacgagcgg aacatctac 1119

<210> 18
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> huSIRP alpha transmembrane domain

<400> 18
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gtg 63

<210> 19

<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> huSIRP alpha-CD28tm construct

<400> 19
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gcctcttgtg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgac 120
aagagcgtgc tggtggccgc tggcgaaacc gccaccctga gatgtacagc caccagcctg 180
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aacatggact tcagcatccg gatcggcaac atcacccctg ccgatgccgg cacctactac 360
tgcgtgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc 420
gagctgagcg tgcgggctaa accttctgcc cctgtggtgt ctggacctgc cgccagagct 480
acacctcagc acaccgtgtc ttttacctgc gagagccacg gcttcagccc cagagacatc 540
accctgaagt ggttcaagaa cggcaacgag ctgtccgact tccagaccaa cgtggaccct 600
gtgggcgaga gcgtgtccta cagcatccac agcaccgcca aggtggtgct gacccgcgaa 660
gatgtgcaca gccaagtgat ctgcgaggtg gcccacgtga cactgcaggg cgatcctctg 720
agaggaaccg ccaacctgtc cgagacaatc agagtgcccc ccaccctgga agtgacccag 780
cagcctgtgc gggccgagaa ccaagtgaac gtgacctgcc aagtgcggaa gttctacccc 840
cagcggctgc agctgacctg gctggaaaac ggcaatgtgt cccggaccga gacagccagc 900
accgtgaccg agaacaagga tggcacctac aattggatga gctggctgct cgtgaacgtg 960
tccgcccacc gggacgatgt gaagctgaca tgccaggtgg aacacgacgg ccagcctgcc 1020
gtgtccaaga gccacgatct gaaggtgtca gcccatccca aagagcaggg ctccaacaca 1080
gccgccgaga acaccggcag caacgagcgg aacatctact tctgggtgct ggtggtggtc 1140
ggaggcgtgc tggcctgcta cagcctgctg gtcaccgtgg ccttcatcat cttttgggtc 1200
cgcagcaagc ggagcagagg cggccacagc gactacatga acatgacccc tagacggcct 1260
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agc 1323

<210> 20
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> huSIRP alpha 12aas-CD28Cys construct

<400> 20
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aagagcgtgc tggtggccgc tggcgaaacc gccaccctga gatgtacagc caccagcctg 180
atccccgtgg gccccatcca gtggtttaga ggcgctggcc ctggcagaga gctgatctac 240
aaccagaaag agggccactt ccccagagtg accaccgtgt ccgacctgac caagcggaac 300
aacatggact tcagcatccg gatcggcaac atcacccctg ccgatgccgg cacctactac 360
tgcgtgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc 420
gagctgagcg tgcgggctaa accttctgcc cctgtggtgt ctggacctgc cgccagagct 480
acacctcagc acaccgtgtc ttttacctgc gagagccacg gcttcagccc cagagacatc 540
accctgaagt ggttcaagaa cggcaacgag ctgtccgact tccagaccaa cgtggaccct 600
gtgggcgaga gcgtgtccta cagcatccac agcaccgcca aggtggtgct gacccgcgaa 660
gatgtgcaca gccaagtgat ctgcgaggtg gcccacgtga cactgcaggg cgatcctctg 720
agaggaaccg ccaacctgtc cgagacaatc agagtgcccc ccaccctgga agtgacccag 780
cagcctgtgc gggccgagaa ccaagtgaac gtgacctgcc aagtgcggaa gttctacccc 840
cagcggctgc agctgacctg gctggaaaac ggcaatgtgt cccggaccga gacagccagc 900
accgtgaccg agaacaagga tggcacctac aattggatga gctggctgct cgtgaacgtg 960
tccgcccacc gggacgatgt gaagctgaca tgccaggtgg aacacgacgg ccagcctgcc 1020
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gcctgtccca gccctctgtt tcccggccct agcaagcctt tctgggtgct ggtggtggtc 1140
ggaggcgtgc tggcctgcta cagcctgctg gtcaccgtgg ccttcatcat cttttgggtc 1200
cgcagcaagc ggagcagagg cggccacagc gactacatga acatgacccc tagacggcct 1260
ggccccacca gaaagcacta ccagccctac gcccctcccc gggactttgc cgcctacaga 1320
agc 1323

<210> 21
<211> 1083
<212> DNA

<213> Artificial Sequence

<220>
<223> huSIRP alpha 12aas portion of extracellular domain

<400> 21
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aagagcgtgc tggtggccgc tggcgaaacc gccaccctga gatgtacagc caccagcctg 180
atccccgtgg gccccatcca gtggtttaga ggcgctggcc ctggcagaga gctgatctac 240
aaccagaaag agggccactt ccccagagtg accaccgtgt ccgacctgac caagcggaac 300
aacatggact tcagcatccg gatcggcaac atcacccctg ccgatgccgg cacctactac 360
tgcgtgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc 420
gagctgagcg tgcgggctaa accttctgcc cctgtggtgt ctggacctgc cgccagagct 480
acacctcagc acaccgtgtc ttttacctgc gagagccacg gcttcagccc cagagacatc 540
accctgaagt ggttcaagaa cggcaacgag ctgtccgact tccagaccaa cgtggaccct 600
gtgggcgaga gcgtgtccta cagcatccac agcaccgcca aggtggtgct gacccgcgaa 660
gatgtgcaca gccaagtgat ctgcgaggtg gcccacgtga cactgcaggg cgatcctctg 720
agaggaaccg ccaacctgtc cgagacaatc agagtgcccc ccaccctgga agtgacccag 780
cagcctgtgc gggccgagaa ccaagtgaac gtgacctgcc aagtgcggaa gttctacccc 840
cagcggctgc agctgacctg gctggaaaac ggcaatgtgt cccggaccga gacagccagc 900
accgtgaccg agaacaagga tggcacctac aattggatga gctggctgct cgtgaacgtg 960
tccgcccacc gggacgatgt gaagctgaca tgccaggtgg aacacgacgg ccagcctgcc 1020
gtgtccaaga gccacgatct gaaggtgtca gcccatccca aagagcaggg ctccaacaca 1080
gcc 1083

<210> 22
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> huSIRP alpha-12aas-CD28Cys tm-41BBic construct

<400> 22
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aagagcgtgc tggtggccgc tggcgaaacc gccaccctga gatgtacagc caccagcctg 180
atccccgtgg gccccatcca gtggtttaga ggcgctggcc ctggcagaga gctgatctac 240
aaccagaaag agggccactt ccccagagtg accaccgtgt ccgacctgac caagcggaac 300
aacatggact tcagcatccg gatcggcaac atcacccctg ccgatgccgg cacctactac 360
tgcgtgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc 420
gagctgagcg tgcgggctaa accttctgcc cctgtggtgt ctggacctgc cgccagagct 480
acacctcagc acaccgtgtc ttttacctgc gagagccacg gcttcagccc cagagacatc 540
accctgaagt ggttcaagaa cggcaacgag ctgtccgact tccagaccaa cgtggaccct 600
gtgggcgaga gcgtgtccta cagcatccac agcaccgcca aggtggtgct gacccgcgaa 660
gatgtgcaca gccaagtgat ctgcgaggtg gcccacgtga cactgcaggg cgatcctctg 720
agaggaaccg ccaacctgtc cgagacaatc agagtgcccc ccaccctgga agtgacccag 780
cagcctgtgc gggccgagaa ccaagtgaac gtgacctgcc aagtgcggaa gttctacccc 840
cagcggctgc agctgacctg gctggaaaac ggcaatgtgt cccggaccga gacagccagc 900
accgtgaccg agaacaagga tggcacctac aattggatga gctggctgct cgtgaacgtg 960
tccgcccacc gggacgatgt gaagctgaca tgccaggtgg aacacgacgg ccagcctgcc 1020
gtgtccaaga gccacgatct gaaggtgtca gcccatccca aagagcaggg ctccaacaca 1080
gcctgtccca gccctctgtt tcccggccct agcaagcctt tctgggtgct ggtggtggtc 1140
ggaggcgtgc tggcctgcta cagcctgctg gtcaccgtgg ccttcatcat cttttgggtc 1200
aagcggggca gaaagaagct gctgtacatc ttcaagcagc ctttcatgcg gcccgtgcag 1260
accacccagg aagaggacgg ctgctcctgc agattccccg aggaagaaga aggcggctgc 1320
gagctg 1326

<210> 23
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> huSIRP alpha-12aas-CD28Cys tm ic-41BBic construct

<400> 23

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gcctcttgtg cttggagcgg agtggctggc gaagaggaac tgcaagtgat ccagcccgac     120
aagagcgtgc tggtggccgc tggcgaaacc gccaccctga gatgtacagc caccagcctg     180
atccccgtgg gccccatcca gtggtttaga ggcgctggcc ctggcagaga gctgatctac     240
aaccagaaag agggccactt ccccagagtg accaccgtgt ccgacctgac caagcggaac     300
aacatggact tcagcatccg gatcggcaac atcacccctg ccgatgccgg cacctactac     360
tgcgtgaagt tccggaaggg cagccccgac gacgtggaat tcaaaagcgg agccggcacc     420
gagctgagcg tgcgggctaa accttctgcc cctgtggtgt ctggacctgc cgccagagct     480
acacctcagc acaccgtgtc ttttacctgc gagagccacg gcttcagccc cagagacatc     540
accctgaagt ggttcaagaa cggcaacgag ctgtccgact tccagaccaa cgtggaccct     600
gtgggcgaga gcgtgtccta cagcatccac agcaccgcca aggtggtgct gacccgcgaa     660
gatgtgcaca gccaagtgat ctgcgaggtg gcccacgtga cactgcaggg cgatcctctg     720
agaggaaccg ccaacctgtc cgagacaatc agagtgcccc ccaccctgga agtgacccag     780
cagcctgtgc gggccgagaa ccaagtgaac gtgacctgcc aagtgcggaa gttctacccc     840
cagcggctgc agctgacctg gctggaaaac ggcaatgtgt cccggaccga gacagccagc     900
accgtgaccg agaacaagga tggcacctac aattggatga gctggctgct cgtgaacgtg     960
tccgcccacc gggacgatgt gaagctgaca tgccaggtgg aacacgacgg ccagcctgcc    1020
gtgtccaaga gccacgatct gaaggtgtca gcccatccca aagagcaggg ctccaacaca    1080
gcctgtccca gccctctgtt tcccggccct agcaagcctt tctgggtgct ggtggtggtc    1140
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cgcagcaagc ggagcagagg cggccacagc gactacatga acatgacccc tagacggcct    1260
ggccccacca gaaagcacta ccagccctac gcccctcccc gggactttgc cgcctacaga    1320
agcaagcggg gcagaaagaa gctgctgtac atcttcaagc agcctttcat gcggcccgtg    1380
cagaccaccc aggaagagga cggctgctcc tgcagattcc ccgaggaaga agaaggcggc    1440
tgcgagctg                                                            1449

<210> 24
<211> 305
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200Rtm-CD28 protein

<400> 24
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1               5                  10                  15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20                  25                  30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35                  40                  45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50                  55                  60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65                  70                  75                  80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85                  90                  95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100                 105                 110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115                 120                 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130                 135                 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145                 150                 155                 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165                 170                 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180                 185                 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195                 200                 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210                 215                 220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys Ser
225                 230                 235                 240
Ala Lys Leu Tyr Ile Pro Tyr Ile Ile Leu Thr Ile Ile Ile Leu Thr
                245                 250                 255
Ile Val Gly Phe Ile Trp Leu Leu Arg Ser Lys Arg Ser Arg Gly Gly
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260 265 270
His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
275 280 285
Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
290 295 300
Ser
305

<210> 25
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R entire extracellular domain

<400> 25
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1 5 10 15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
20 25 30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
35 40 45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
50 55 60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65 70 75 80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
85 90 95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
100 105 110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
115 120 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
130 135 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145 150 155 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
165 170 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
180 185 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
195 200 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
210 215 220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys Ser
225 230 235 240
Ala Lys Leu

<210> 26
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R transmembrane domain

<400> 26
Tyr Ile Pro Tyr Ile Ile Leu Thr Ile Ile Ile Leu Thr Ile Val Gly
1 5 10 15
Phe Ile Trp Leu Leu
20

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

<220>
<223> CD28 transmembrane domain protein

<400> 27
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1   5   10   15
Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
            20   25

<210> 28
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 intracellular domain protein

<400> 28
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
 1   5   10   15
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            20   25   30
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        35   40

<210> 29
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-CD28tm protein

<400> 29
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1   5   10   15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20   25   30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35   40   45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50   55   60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65   70   75   80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85   90   95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100   105   110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115   120   125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130   135   140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145   150   155   160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165   170   175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180   185   190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195   200   205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210   215   220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys Ser
225   230   235   240
Ala Lys Leu Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
                245   250   255
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser

260 265 270
Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg
275 280 285
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
290 295 300
Asp Phe Ala Ala Tyr Arg Ser
305 310

<210> 30
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-9aas-CD28Cys protein

<400> 30
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1 5 10 15
Thr Ile Phe Leu Val Ala Ala Ser Ser Leu Cys Met Asp Glu Lys
20 25 30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
35 40 45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
50 55 60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65 70 75 80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
85 90 95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
100 105 110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
115 120 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
130 135 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145 150 155 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
165 170 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
180 185 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
195 200 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
210 215 220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Cys Pro Ser Pro Leu Phe
225 230 235 240
Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
245 250 255
Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
260 265 270
Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met
275 280 285
Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
290 295 300
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
305 310

<210> 31
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-9aas protein

<400> 31
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu

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 1               5                  10                  15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20                  25                  30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35                  40                  45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50                  55                  60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65                  70                  75                  80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85                  90                  95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100                 105                 110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115                 120                 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130                 135                 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145                 150                 155                 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165                 170                 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180                 185                 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195                 200                 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210                 215                 220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val
225                 230
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<210> 32
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28Cys (extracellular portion) protein

<400> 32

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Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
 1               5                  10
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<210> 33
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-12aas-CD28Cys protein

<400> 33

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Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1               5                  10                  15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20                  25                  30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35                  40                  45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50                  55                  60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65                  70                  75                  80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85                  90                  95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100                 105                 110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115                 120                 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
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130 135 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145 150 155 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
165 170 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
180 185 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
195 200 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
210 215 220
Lys Ser Leu Tyr Ile Glu Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
225 230 235 240
Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
245 250 255
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
260 265 270
Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg
275 280 285
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
290 295 300
Asp Phe Ala Ala Tyr Arg Ser
305 310

<210> 34
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-12aas protein

<400> 34
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1 5 10 15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
20 25 30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
35 40 45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
50 55 60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65 70 75 80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
85 90 95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
100 105 110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
115 120 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
130 135 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145 150 155 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
165 170 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
180 185 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
195 200 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
210 215 220
Lys Ser Leu Tyr Ile Glu Leu
225 230

<210> 35
<211> 315
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-9aas-CD28Cys tm-41BBic protein

<400> 35
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1   5   10   15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20   25   30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35   40   45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50   55   60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65   70   75   80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85   90   95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100   105   110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115   120   125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130   135   140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145   150   155   160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165   170   175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180   185   190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195   200   205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210   215   220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Cys Pro Ser Pro Leu Phe
225   230   235   240
Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
                245   250   255
Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
            260   265   270
Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
        275   280   285
Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
    290   295   300
Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
305   310   315

<210> 36
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular component protein

<400> 36
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 1   5   10   15
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
            20   25   30
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
        35   40

<210> 37
<211> 312
<212> PRT
<213> Artificial Sequence

<220>

<223> huCD200R-12aas-CD28Cys tm-41BBic protein

<400> 37
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1   5   10   15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20   25   30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35   40   45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50   55   60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65   70   75   80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85   90   95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100   105   110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115   120   125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130   135   140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145   150   155   160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165   170   175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180   185   190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195   200   205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210   215   220
Lys Ser Leu Tyr Ile Glu Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
225   230   235   240
Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
                245   250   255
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Lys Arg
            260   265   270
Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
        275   280   285
Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
    290   295   300
Glu Glu Glu Gly Gly Cys Glu Leu
305   310

<210> 38
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-12aas-CD28Cys tm ic-41BBic protein

<400> 38
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1   5   10   15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20   25   30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35   40   45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50   55   60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65   70   75   80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85   90   95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100   105   110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly

```
        115                 120                 125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130                 135                 140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145                 150                 155                 160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165                 170                 175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180                 185                 190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195                 200                 205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210                 215                 220
Lys Ser Leu Tyr Ile Glu Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
225                 230                 235                 240
Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
                245                 250                 255
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
            260                 265                 270
Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg
        275                 280                 285
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
    290                 295                 300
Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
305                 310                 315                 320
Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
                325                 330                 335
Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
            340                 345                 350
Leu
```

<210> 39
<211> 435
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha tm-CD28 protein

<400> 39

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Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1               5                  10                  15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
            20                  25                  30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
        35                  40                  45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
    50                  55                  60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65                  70                  75                  80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
                85                  90                  95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
            100                 105                 110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
        115                 120                 125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
    130                 135                 140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145                 150                 155                 160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
                165                 170                 175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
            180                 185                 190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
        195                 200                 205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
```

210 215 220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350
Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365
Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
370 375 380
Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ser Lys Arg Ser Arg
385 390 395 400
Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
405 410 415
Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
420 425 430
Tyr Arg Ser
435

<210> 40
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha entire extracellular domain protein

<400> 40
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu

225 230 235 240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350
Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365
Glu Arg Asn Ile Tyr
370

<210> 41
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha transmembrane domain protein

<400> 41
Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala Leu Leu Met Ala
1 5 10 15
Ala Leu Tyr Leu Val
20

<210> 42
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha -CD28tm protein

<400> 42
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser

195 200 205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350
Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
355 360 365
Glu Arg Asn Ile Tyr Phe Trp Val Leu Val Val Val Gly Gly Val Leu
370 375 380
Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
385 390 395 400
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
405 410 415
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
420 425 430
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
435 440

<210> 43
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha-12aas-CD28Cys protein

<400> 43
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser

210 215 220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350
Pro Lys Glu Gln Gly Ser Asn Thr Ala Cys Pro Ser Pro Leu Phe Pro
355 360 365
Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu
370 375 380
Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
385 390 395 400
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
405 410 415
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
420 425 430
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
435 440

<210> 44
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha-12aas protein

<400> 44
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu

225 230 235 240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
325 330 335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
340 345 350
Pro Lys Glu Gln Gly Ser Asn Thr Ala
355 360

<210> 45
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha-12aas-CD28Cys tm-41BBic protein

<400> 45
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
35 40 45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
85 90 95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
130 135 140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
180 185 190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
195 200 205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
210 215 220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225 230 235 240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
245 250 255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
260 265 270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
275 280 285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
290 295 300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305 310 315 320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp

                325   330   335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
            340   345   350
Pro Lys Glu Gln Gly Ser Asn Thr Ala Cys Pro Ser Pro Leu Phe Pro
        355   360   365
Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu
    370   375   380
Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
385   390   395   400
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
                405   410   415
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
            420   425   430
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
        435   440

<210> 46
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> huSIRP alpha-12aas-CD28Cys tm ic-41BBic protein

<400> 46
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
 1   5   10   15
Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
            20   25   30
Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
        35   40   45
Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
    50   55   60
Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65   70   75   80
Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
                85   90   95
Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
            100   105   110
Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
        115   120   125
Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
    130   135   140
Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145   150   155   160
Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
                165   170   175
Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser
            180   185   190
Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
        195   200   205
Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser
    210   215   220
Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
225   230   235   240
Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
                245   250   255
Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
            260   265   270
Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
        275   280   285
Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
    290   295   300
Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
305   310   315   320
Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
                325   330   335
Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His

```
            340                 345                 350
Pro Lys Glu Gln Gly Ser Asn Thr Ala Cys Pro Ser Pro Leu Phe Pro
        355                 360                 365
Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu
    370                 375                 380
Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
385                 390                 395                 400
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
                405                 410                 415
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            420                 425                 430
Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu
        435                 440                 445
Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
    450                 455                 460
Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
465                 470                 475                 480
Cys Glu Leu
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<210> 47
<211> 900
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200Rtm-CD28

<400> 47

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acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc     180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc     240
agctgcacaa tcgcctacaa ggtggacacc aagaccaacg agacaagctg cctgggcaga     300
aacatcacct gggccagcac cccagaccac agccctgagc tgcagatcag cgccgtgaca     360
ctgcagcacg agggcaccta cacatgcgag acagtgaccc ccgagggcaa cttcgagaag     420
aactacgatc tgcaggtgct ggtgcccccc gaagtgacct acttccccga gaagaataga     480
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ggcgactgtg tgaccaccag cgagagccac agcaacggca cagtgaccgt gcggagcacc     600
tgtcactggg agcagaacaa cgtgtccgac gtgtcctgca tcgtgtccca cctgaccggc     660
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ccttacatca tccccagcat catcatcctg atcatcatcg gctgcatctg cctgctgaac     780
agcagaagaa acagaggcgg ccagagcgac tacatgaaca tgaccccag aaggcctggc     840
ctgaccagaa agccctacca gccttacgcc cctgccagag acttcgccgc ctacagacct     900
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<210> 48
<211> 918
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-CD28tm

<400> 48

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acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc     180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc     240
agctgcacaa tcgcctacaa ggtggacacc aagaccaacg agacaagctg cctgggcaga     300
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aactacgatc tgcaggtgct ggtgcccccc gaagtgacct acttccccga gaagaataga     480
agcgccgtgt gcgaggccat ggctggcaaa cctgccgccc agatctcttg gagccctgac     540
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gccctggtgg tggtggccgg cgtgctgttt tgttacggcc tgctcgtgac cgtggccctg     780
tgcgtgatct ggaccaacag cagaagaaac agaggcggcc agagcgacta catgaacatg     840
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ttcgccgcct acagacct 918

<210> 49
<211> 945
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-CD28Cys

<400> 49
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gccggcagca gctgcaccga caagaaccag accacccaga acaacagcag cagccccctg 120
acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc 180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc 240
agctgcacaa tcgcctacaa ggtggacacc aagaccaacg agacaagctg cctgggcaga 300
aacatcacct gggccagcac cccagaccac agccctgagc tgcagatcag cgccgtgaca 360
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aactacgatc tgcaggtgct ggtgccccca gaagtgacct acttccccga gaagaataga 480
agcgccgtgt gcgaggccat ggctggcaaa cctgccgccc agatctcttg gagccctgac 540
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<210> 50
<211> 936
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-3aas-CD28Cys

<400> 50
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gccggcagca gctgcaccga caagaaccag accacccaga acaacagcag cagccccctg 120
acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc 180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc 240
agctgcacaa tcgcctacaa ggtggacacc aagaccaacg agacaagctg cctgggcaga 300
aacatcacct gggccagcac cccagaccac agccctgagc tgcagatcag cgccgtgaca 360
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aactacgatc tgcaggtgct ggtgccccca gaagtgacct acttccccga gaagaataga 480
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tacgcccctg ccagagactt cgccgcctac agacct 936

<210> 51
<211> 918
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-9aas-CD28Cys

<400> 51
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agcgccgtgt gcgaggccat ggctggcaaa cctgccgccc agatctcttg gagccctgac 540
ggcgactgtg tgaccaccag cgagagccac agcaacggca cagtgaccgt gcggagcacc 600
tgtcactggg agcagaacaa cgtgtccgac gtgtcctgca tcgtgtccca cctgaccggc 660
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gccctggtgg tggtggccgg cgtgctgttt tgttacggcc tgctcgtgac cgtggccctg 780
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ttcgccgcct acagacct 918

<210> 52
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-9aas-CD28Cys tm-41BBic

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acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc 180
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cagcccttca agaaaaccac cggcgctgcc caggaagagg acgcctgcag ctgtagatgc 900
cctcaggaag aagaaggcgg cggaggcggc tacgagctg 939

<210> 53
<211> 1062
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-9aas-CD28Cys tm ic-41BBic

<400> 53
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acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc 180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc 240
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aactacgatc tgcaggtgct ggtgcccccc gaagtgacct acttccccga gaagaataga 480
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tgtcactggg agcagaacaa cgtgtccgac gtgtcctgca tcgtgtccca cctgaccggc 660
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tgccctcagg aagaagaagg cggcggaggc ggctacgagc tg 1062

<210> 54

<211> 1305
<212> DNA
<213> Artificial Sequence

<220>
<223> muSIRP alpha tm-CD28

<400> 54
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aagtccgtgt ctgtggccgc tggcgacagc accgtgctga actgtaccct gaccagcctg 180
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taccagcctt acgcccctgc cagagacttc gccgcctaca gacct 1305

<210> 55
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> muSIRP alpha-CD28tm

<400> 55
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agcgccagct gtttctgtac cggcgccacc ggcaaagaac tgaaagtgac ccagcccgag 120
aagtccgtgt ctgtggccgc tggcgacagc accgtgctga actgtaccct gaccagcctg 180
ctgcccgtgg gccccatcag atggtataga ggcgtgggcc ctagcagact gctgatctac 240
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aacatggact tcagcatcag gatcagcaac gtgacccctg ccgacgccgg catctactac 360
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cagcagagcc ccaccagcat gaaccaagtg aacctgacct gcagagccga gagattctac 840
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cct 1323

<210> 56
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> muSIRP alpha-CD28cys

<400> 56
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aagtccgtgt ctgtggccgc tggcgacagc accgtgctga actgtaccct gaccagcctg 180
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accgaggtgt acgtgctggc taagcccagc cctcctgagg tgtccggccc tgctgataga 480
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aagctgttct gggctctggt ggtggtggcc ggcgtgctgt tttgttacgg cctgctcgtg 1200
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tacatgaaca tgacccccag aaggcctggc ctgacccgga agccttacca gccttacgcc 1320
cctgccagag acttcgccgc ctacagacct 1350

<210> 57
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> muSIRP alpha -6aas-CD28cys

<400> 57
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aagtccgtgt ctgtggccgc tggcgacagc accgtgctga actgtaccct gaccagcctg 180
ctgcccgtgg gccccatcag atggtataga ggcgtgggcc ctagcagact gctgatctac 240
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aacatggact tcagcatcag gatcagcaac gtgacccctg ccgacgccgg catctactac 360
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atctggacca acagcagaag aaacagaggc ggccagagcg actacatgaa catgacccct 1260
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gcctacagac ct 1332

<210> 58
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>

<223> muSIRP alpha -9aas-CD28cys

<400> 58
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aagtccgtgt ctgtggccgc tggcgacagc accgtgctga actgtaccct gaccagcctg 180
ctgcccgtgg gccccatcag atggtataga ggcgtgggcc ctagcagact gctgatctac 240
agcttcgctg gcgagtacgt gcccagaatc agaaacgtgt ccgacaccac caagcggaac 300
aacatggact tcagcatcag gatcagcaac gtgacccctg ccgacgccgg catctactac 360
tgcgtgaagt tccagaaggg cagcagcgag cccgacaccg agattcagtc tggcggcgga 420
accgaggtgt acgtgctggc taagcccagc cctcctgagg tgtccggccc tgctgataga 480
ggcatccccg accagaaagt gaacttcaca tgcaagagcc acggcttcag ccccagaaac 540
atcaccctga agtggttcaa ggacggccag gaactgcacc ccctggaaac caccgtgaac 600
cccagcggca agaacgtgtc ctacaacatc agctccaccg tgcgggtggt gctgaacagc 660
atggacgtga acagcaaagt gatctgcgag gtggcccaca tcacactgga cagaagcccc 720
ctgagaggaa tcgccaacct gagcaacttc atcagagtgt ccccaaccgt gaaagtgaca 780
cagcagagcc ccaccagcat gaaccaagtg aacctgacct gcagagccga gagattctac 840
cccgaggacc tgcagctgat ctggctggaa aacggcaacg tgtccagaaa cgacaccccc 900
aagaacctga caaagaacac cgacggcacc tacaactaca cctccctgtt tctcgtgaac 960
tcctccgccc accgcgagga cgtggtgttc acgtgccaag tgaagcacga ccagcagccc 1020
gccatcacca gaaaccacac agtgctgggc ttcgcccaca gcagcgacca gggcagcatg 1080
cagaccttcc cctgccacac ccagagcagc cccaagctgt tctgggctct ggtggtggtg 1140
gccggcgtgc tgttttgtta cggcctgctc gtgaccgtgg ccctgtgcgt gatctggacc 1200
aacagcagaa gaaacagagg cggccagagc gactacatga acatgacccc cagaaggcct 1260
ggcctgaccc ggaagcctta ccagccttac gcccctgcca gagacttcgc cgcctacaga 1320
cct 1323

<210> 59
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<223> muSIRP alpha-23aas-CD28cys

<400> 59
atggaacctg ctggacctgc ccctggcaga ctgggacctc tgctgctgtg cctgctgctg 60
agcgccagct gtttctgtac cggcgccacc ggcaaagaac tgaaagtgac ccagcccgag 120
aagtccgtgt ctgtggccgc tggcgacagc accgtgctga actgtaccct gaccagcctg 180
ctgcccgtgg gccccatcag atggtataga ggcgtgggcc ctagcagact gctgatctac 240
agcttcgctg gcgagtacgt gcccagaatc agaaacgtgt ccgacaccac caagcggaac 300
aacatggact tcagcatcag gatcagcaac gtgacccctg ccgacgccgg catctactac 360
tgcgtgaagt tccagaaggg cagcagcgag cccgacaccg agattcagtc tggcggcgga 420
accgaggtgt acgtgctggc taagcccagc cctcctgagg tgtccggccc tgctgataga 480
ggcatccccg accagaaagt gaacttcaca tgcaagagcc acggcttcag ccccagaaac 540
atcaccctga agtggttcaa ggacggccag gaactgcacc ccctggaaac caccgtgaac 600
cccagcggca agaacgtgtc ctacaacatc agctccaccg tgcgggtggt gctgaacagc 660
atggacgtga acagcaaagt gatctgcgag gtggcccaca tcacactgga cagaagcccc 720
ctgagaggaa tcgccaacct gagcaacttc atcagagtgt ccccaaccgt gaaagtgaca 780
cagcagagcc ccaccagcat gaaccaagtg aacctgacct gcagagccga gagattctac 840
cccgaggacc tgcagctgat ctggctggaa aacggcaacg tgtccagaaa cgacaccccc 900
aagaacctga caaagaacac cgacggcacc tacaactaca cctccctgtt tctcgtgaac 960
tcctccgccc accgcgagga cgtggtgttc acgtgccaag tgaagcacga ccagcagccc 1020
gccatcacca gaaaccacac agtgctgggc tgccacaccc agagcagccc caagctgttc 1080
tgggctctgg tggtggtggc cggcgtgctg ttttgttacg gcctgctcgt gaccgtggcc 1140
ctgtgcgtga tctggaccaa cagcagaaga aacagaggcg gccagagcga ctacatgaac 1200
atgacccccа gaaggcctgg cctgacccgg aagccttacc agccttacgc ccctgccaga 1260
gacttcgccg cctacagacc t 1281

<210> 60
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD-1 ectodomain

<400> 60

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Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn
 1               5                  10                  15
Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu
            20                  25                  30
Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala
        35                  40                  45
Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val
    50                  55                  60
Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala
65                  70                  75                  80
Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala
                85                  90                  95
Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr
            100                 105                 110
Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg
        115                 120                 125
Ser Ala Gly Gln Phe Gln Thr Leu Val
    130                 135
```

<210> 61
<211> 627
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD2 entire extracellular domain

<400> 61

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atgagctttc catgtaaatt tgtagccagc ttccttctga ttttcaatgt ttcttccaaa      60
ggtgcagtct ccaaagagat tacgaatgcc ttggaaacct ggggtgcctt gggtcaggac     120
atcaacttgg acattcctag ttttcaaatg agtgatgata ttgacgatat aaaatgggaa     180
aaaacttcag acaagaaaaa gattgcacaa ttcagaaaag agaaagagac tttcaaggaa     240
aaagatacat ataagctatt taaaaatgga actctgaaaa ttaagcatct gaagaccgat     300
gatcaggata tctacaaggt atcaatatat gatacaaaag gaaaaaatgt gttggaaaaa     360
atatttgatt tgaagattca agagagggtc tcaaaaccaa agatctcctg gacttgtatc     420
aacacaaccc tgacctgtga ggtaatgaat ggaactgacc ccgaattaaa cctgtatcaa     480
gatgggaaac atctaaaact ttctcagagg gtcatcacac acaagtggac caccagcctg     540
agtgcaaaat tcaagtgcac agcagggaac aaagtcagca aggaatccag tgtcgagcct     600
gtcagctgtc cagagaaagg tctggac                                         627
```

<210> 62
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD2 entire extracellular domain

<400> 62

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Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
 1               5                  10                  15
Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
            20                  25                  30
Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
        35                  40                  45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
    50                  55                  60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65                  70                  75                  80
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
                85                  90                  95
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
            100                 105                 110
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
        115                 120                 125
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
    130                 135                 140
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
```

145 150 155 160
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
165 170 175
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
180 185 190
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
195 200 205
Asp

<210> 63
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD2 transmembrane domain

<400> 63
atctatctca tcattggcat atgtggagga ggcagcctct tgatggtctt tgtggcactg 60
ctcgttttct atatcacc 78

<210> 64
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD2 transmembrane domain

<400> 64
Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met Val
1 5 10 15
Phe Val Ala Leu Leu Val Phe Tyr Ile Thr
20 25

<210> 65
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD2tm-CD28 DNA

<400> 65
atgagctttc catgtaaatt tgtagccagc ttccttctga ttttcaatgt ttcttccaaa 60
ggtgcagtct ccaaagagat tacgaatgcc ttggaaacct ggggtgcctt gggtcaggac 120
atcaacttgg acattcctag ttttcaaatg agtgatgata ttgacgatat aaaatgggaa 180
aaaacttcag acaagaaaaa gattgcacaa ttcagaaaag agaaagagac tttcaaggaa 240
aaagatacat ataagctatt taaaaatgga actctgaaaa ttaagcatct gaagaccgat 300
gatcaggata tctacaaggt atcaatatat gatacaaaag gaaaaaatgt gttggaaaaa 360
atatttgatt tgaagattca agagagggtc tcaaaaccaa agatctcctg gacttgtatc 420
aacacaaccc tgacctgtga ggtaatgaat ggaactgacc ccgaattaaa cctgtatcaa 480
gatgggaaac atctaaaact ttctcagagg gtcatcacac acaagtggac caccagcctg 540
agtgcaaaat tcaagtgcac agcagggaac aaagtcagca aggaatccag tgtcgagcct 600
gtcagctgtc cagagaaagg tctggacatc tatctcatca ttggcatatg tggaggaggc 660
agcctcttga tggtctttgt ggcactgctc gttttctata tcacccgcag caagcggagc 720
agaggcggcc acagcgacta catgaacatg acccctagac ggcctggccc caccagaaag 780
cactaccagc cctacgcccc tccccgggac tttgccgcct acagaagc 828

<210> 66
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD2tm-CD28

<400> 66
Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
 1   5   10   15
Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
            20   25   30
Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
        35   40   45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
    50   55   60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65   70   75   80
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
                85   90   95
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
            100   105   110
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
        115   120   125
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
    130   135   140
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
145   150   155   160
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
                165   170   175
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
            180   185   190
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
        195   200   205
Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
    210   215   220
Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Arg Ser Lys Arg Ser
225   230   235   240
Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                245   250   255
Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            260   265   270
Ala Tyr Arg Ser
        275

<210> 67
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD2-CD28tm

<400> 67
atgagctttc catgtaaatt tgtagccagc ttccttctga ttttcaatgt ttcttccaaa 60
ggtgcagtct ccaaagagat tacgaatgcc ttggaaacct ggggtgcctt gggtcaggac 120
atcaacttgg acattcctag ttttcaaatg agtgatgata ttgacgatat aaaatgggaa 180
aaaacttcag acaagaaaaa gattgcacaa ttcagaaaag agaaagagac tttcaaggaa 240
aaagatacat ataagctatt taaaaatgga actctgaaaa ttaagcatct gaagaccgat 300
gatcaggata tctacaaggt atcaatatat gatacaaaag gaaaaaatgt gttggaaaaa 360
atatttgatt tgaagattca agagagggtc tcaaaaccaa agatctcctg gacttgtatc 420
aacacaaccc tgacctgtga ggtaatgaat ggaactgacc ccgaattaaa cctgtatcaa 480
gatgggaaac atctaaaact ttctcagagg gtcatcacac acaagtggac caccagcctg 540
agtgcaaaat tcaagtgcac agcagggaac aaagtcagca aggaatccag tgtcgagcct 600
gtcagctgtc cagagaaagg tctggacttc tgggtgctgg tggtggtcgg aggcgtgctg 660
gcctgctaca gcctgctggt caccgtggcc ttcatcatct tttgggtccg cagcaagcgg 720
agcagaggcg gccacagcga ctacatgaac atgaccccta gacggcctgg ccccaccaga 780
aagcactacc agccctacgc ccctccccgg gactttgccg cctacagaag c   831

<210> 68
<211> 277
<212> PRT
<213> Artificial Sequence

<220>

<223> huCD2-CD28tm

<400> 68

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Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
 1               5                  10                  15
Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
            20                  25                  30
Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
        35                  40                  45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
    50                  55                  60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65                  70                  75                  80
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
                85                  90                  95
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
            100                 105                 110
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
        115                 120                 125
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
    130                 135                 140
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
145                 150                 155                 160
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
                165                 170                 175
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
            180                 185                 190
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
        195                 200                 205
Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    210                 215                 220
Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
225                 230                 235                 240
Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                245                 250                 255
Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            260                 265                 270
Ala Ala Tyr Arg Ser
        275
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<210> 69
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD200R-CD28Cys

<400> 69

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atgctgtgcc cttggagaac cgccaacctg ggcctgctgc tgatcctgac catcttcctg      60
gtggccgcca gcagcagcct gtgcatggac gagaagcaga tcacccagaa ctacagcaag     120
gtgctggccg aagtgaacac cagctggccc gtgaagatgg ccaccaacgc cgtgctgtgc     180
tgccctccta tcgccctgcg gaacctgatc atcatcacct gggagatcat cctgcggggc     240
cagcccagct gtaccaaggc ctaccggaaa gagacaaacg agacaaaaga aacaaactgc     300
accgacgagc ggatcacatg ggtgtccaga cccgaccaga acagcgacct gcagatcaga     360
cccgtggcca tcacccacga cggctactac cggtgcatca tggtcacccc cgatggcaac     420
ttccaccggg gataccatct gcaggtgctc gtgacccccg aagtgaccct gttccagaac     480
cggaacagaa ccgccgtgtg caaggccgtg gccggaaaac ctgccgccca gatctcttgg     540
atccccgagg gcgattgcgc caccaagcag gaatactggt ccaacggcac cgtgaccgtg     600
aagtccacct gtcactggga ggtgcacaac gtgtccaccg tgacatgcca cgtgtcccac     660
ctgaccggca acaagagcct gtacatcgag ctgctgcctg tgcctggcgc caagaagtcc     720
gccaagctgt gtcccagccc tctgtttccc ggccctagca agcctttctg ggtgctggtg     780
gtggtcggag gcgtgctggc ctgctacagc ctgctggtca ccgtggcctt catcatcttt     840
tgggtccgca gcaagcggag cagaggcggc cacagcgact acatgaacat gacccctaga     900
cggcctggcc ccaccagaaa gcactaccag ccctacgccc ctccccggga ctttgccgcc     960
tacagaagc                                                             969
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<210> 70

<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD200R-CD28Cys

<400> 70
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
 1   5   10   15
Thr Ile Phe Leu Val Ala Ala Ser Ser Ser Leu Cys Met Asp Glu Lys
            20   25   30
Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr Ser
        35   40   45
Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro Ile
    50   55   60
Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg Gly
65   70   75   80
Gln Pro Ser Cys Thr Lys Ala Tyr Arg Lys Glu Thr Asn Glu Thr Lys
                85   90   95
Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro Asp
            100   105   110
Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Ala Ile Thr His Asp Gly
        115   120   125
Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg Gly
    130   135   140
Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln Asn
145   150   155   160
Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala Ala
                165   170   175
Gln Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu Tyr
            180   185   190
Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu Val
        195   200   205
His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly Asn
    210   215   220
Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys Ser
225   230   235   240
Ala Lys Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
                245   250   255
Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
            260   265   270
Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
        275   280   285
Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
    290   295   300
Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
305   310   315   320
Tyr Arg Ser

<210> 71
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> huFas entire extracellular domain

<400> 71
atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc   60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc   120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac   180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc   240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag   300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc   360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc   420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc   480

tccaacacaa agtgcaaaga ggaaggcagc agaagcaac 519

<210> 72
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> huFas entire extracellular domain

<400> 72
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1   5   10   15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
            20   25   30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35   40   45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50   55   60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65   70   75   80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85   90   95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100   105   110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115   120   125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130   135   140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145   150   155   160
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn
                165   170

<210> 73
<211> 498
<212> DNA
<213> Artificial Sequence

<220>
<223> huFas extracellular domain -7aas

<400> 73
atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc 60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc 120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac 180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc 240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag 300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc 360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc 420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc 480
tccaacacaa agtgcaaa 498

<210> 74
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> huFas extracellular domain -7aas

<400> 74
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1   5   10   15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
            20   25   30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35   40   45

```
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50                  55                  60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65                  70                  75                  80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85                  90                  95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130                 135                 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160
Ser Asn Thr Lys Cys Lys
                165
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<210> 75
<211> 483
<212> DNA
<213> Artificial Sequence

<220>
<223> huFas extracellular domain -12aas

<400> 75

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atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc      60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc     120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac     180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc     240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag     300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc     360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc     420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc     480
tcc                                                                  483
```

<210> 76
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> huFas extracellular domain -12aas

<400> 76

```
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1               5                  10                  15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
            20                  25                  30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35                  40                  45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50                  55                  60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65                  70                  75                  80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85                  90                  95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130                 135                 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160
Ser
```

<210> 77
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> huFas transmembrane domain

<400> 77
ctgggctggc tgtgcctcct gctgctgccc atccctctga tcgtgtgggt c 51

<210> 78
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> huFas transmembrane domain

<400> 78
Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp
1 5 10 15
Val

<210> 79
<211> 693
<212> DNA
<213> Artificial Sequence

<220>
<223> huFAStm-CD28

<400> 79
atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc 60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc 120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac 180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc 240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag 300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc 360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc 420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc 480
tccaacacaa agtgcaaaga ggaaggcagc agaagcaacc tgggctggct gtgcctcctg 540
ctgctgccca tccctctgat cgtgtgggtc cgcagcaagc ggagcagagg cggccacagc 600
gactacatga acatgacccc tagacggcct ggccccacca gaaagcacta ccagccctac 660
gcccctcccc gggactttgc cgcctacaga agc 693

<210> 80
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> huFAStm-CD28

<400> 80
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95

```
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130                 135                 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
                165                 170                 175
Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Arg Ser
            180                 185                 190
Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg
        195                 200                 205
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
    210                 215                 220
Asp Phe Ala Ala Tyr Arg Ser
225                 230
```

<210> 81
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> huFAS-CD28tm

<400> 81

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atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc      60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc     120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac     180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc     240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag     300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc     360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc     420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc     480
tccaacacaa agtgcaaaga ggaaggcagc agaagcaact tctgggtgct ggtggtggtc     540
ggaggcgtgc tggcctgcta cagcctgctg gtcaccgtgg ccttcatcat cttttgggtc     600
cgcagcaagc ggagcagagg cggccacagc gactacatga acatgacccc tagacggcct     660
ggccccacca gaaagcacta ccagccctac gcccctcccc gggactttgc cgcctacaga     720
agc                                                                  723
```

<210> 82
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> huFAS-CD28tm

<400> 82

```
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1               5                  10                  15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
            20                  25                  30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35                  40                  45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50                  55                  60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65                  70                  75                  80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85                  90                  95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
```

130 135 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Phe Trp Val
165 170 175
Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
180 185 190
Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly
195 200 205
His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
210 215 220
Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
225 230 235 240
Ser

<210> 83
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> huFAS-CD28Cys

<400> 83
atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc 60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc 120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac 180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc 240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag 300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc 360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc 420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg cacctgacc 480
tccaacacaa agtgcaaaga ggaaggcagc agaagcaact gtcccagccc tctgtttccc 540
ggccctagca agcctttctg ggtgctggtg gtggtcggag gcgtgctggc ctgctacagc 600
ctgctggtca ccgtggcctt catcatcttt tgggtccgca gcaagcggag cagaggcggc 660
cacagcgact acatgaacat gaccctaga cggcctggcc ccaccagaaa gcactaccag 720
ccctacgccc ctccccggga ctttgccgcc tacagaagc 759

<210> 84
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> huFAS-CD28Cys

<400> 84
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

```
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Cys Pro Ser
                165                 170                 175
Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
            180                 185                 190
Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
        195                 200                 205
Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr
    210                 215                 220
Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
225                 230                 235                 240
Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
                245                 250
```

<210> 85
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> huFAS-7aas-CD28Cys

<400> 85

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atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc      60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc     120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac     180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc     240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag     300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc     360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc     420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc     480
tccaacacaa agtgcaaatg tcccagccct ctgtttcccg gccctagcaa gcctttctgg     540
gtgctggtgg tggtcggagg cgtgctggcc tgctacagcc tgctggtcac cgtggccttc     600
atcatctttt gggtccgcag caagcggagc agaggcggcc acagcgacta catgaacatg     660
acccctagac ggcctggccc caccagaaag cactaccagc cctacgcccc tccccgggac     720
tttgccgcct acagaagc                                                   738
```

<210> 86
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> huFAS-7aas-CD28Cys

<400> 86

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Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1               5                  10                  15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
            20                  25                  30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35                  40                  45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50                  55                  60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65                  70                  75                  80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85                  90                  95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130                 135                 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160
Ser Asn Thr Lys Cys Lys Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser
                165                 170                 175
Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
```

```
            180                 185                 190
Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
        195                 200                 205
Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
    210                 215                 220
Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
225                 230                 235                 240
Phe Ala Ala Tyr Arg Ser
                245
```

<210> 87
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> FAS-12aas-CD28Cys

<400> 87
atgctgggca tctggaccct gctgcctctg gtgctgacaa gcgtggccag actgagcagc 60
aagagcgtga acgcccaagt gaccgacatc aacagcaagg gcctggaact gagaaagacc 120
gtgaccaccg tggaaaccca gaacctggaa ggcctgcacc acgacggcca gttctgccac 180
aagccttgtc cccctggcga gcggaaggcc agagactgta ctgtgaacgg cgacgagccc 240
gactgcgtgc cctgtcagga aggcaaagag tacaccgaca aggcccactt cagcagcaag 300
tgccggcggt gcagactgtg tgatgagggc cacggcctgg aagtggaaat caactgcacc 360
cggacccaga acaccaagtg cagatgcaag cccaacttct tctgcaacag caccgtgtgc 420
gagcactgcg acccctgtac caagtgcgaa cacggcatca tcaaagagtg caccctgacc 480
tcctgtccca gccctctgtt tcccggccct agcaagcctt tctgggtgct ggtggtggtc 540
ggaggcgtgc tggcctgcta cagcctgctg gtcaccgtgg ccttcatcat cttttgggtc 600
cgcagcaagc ggagcagagg cggccacagc gactacatga acatgacccc tagacggcct 660
ggccccacca gaaagcacta ccagccctac gcccctcccc gggactttgc cgcctacaga 720
agc 723

<210> 88
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> FAS-12aas-CD28Cys

<400> 88
```
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1               5                  10                  15
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
            20                  25                  30
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
        35                  40                  45
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
    50                  55                  60
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65                  70                  75                  80
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
                85                  90                  95
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
            100                 105                 110
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
        115                 120                 125
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
    130                 135                 140
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145                 150                 155                 160
Ser Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val
                165                 170                 175
Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
            180                 185                 190
Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly
        195                 200                 205
```

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
210 215 220
Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
225 230 235 240
Ser

<210> 89
<211> 510
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1 entire extracellular domain 2

<400> 89
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg 60
cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccaccctag cccatctcca 480
agacctgccg gccagttcca gacactggtc 510

<210> 90
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1 entire extracellular domain 2

<400> 90
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
35 40 45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160
Arg Pro Ala Gly Gln Phe Gln Thr Leu Val
165 170

<210> 91
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1 2 -12aas

<400> 91
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg 60

cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccaccctag ccca 474

<210> 92
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1 2 -12aas

<400> 92
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1   5   10   15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20   25   30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50   55   60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65   70   75   80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85   90   95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100   105   110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130   135   140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
145   150   155

<210> 93
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1 2 -15aas

<400> 93
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg 60
cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccac 465

<210> 94
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1 2 -15aas

<400> 94
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1   5   10   15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp

```
            20                  25                  30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35                  40                  45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50                  55                  60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65                  70                  75                  80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85                  90                  95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100                 105                 110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115                 120                 125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130                 135                 140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His
145                 150                 155

<210> 95
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1 2 -21aas

<400> 95
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg      60
cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc     120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc     180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc     240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg     300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca     360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc     420
gagctgagag tgaccgagag aagggcc                                         447

<210> 96
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1 2 -21aas

<400> 96
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1               5                  10                  15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20                  25                  30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35                  40                  45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50                  55                  60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65                  70                  75                  80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85                  90                  95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100                 105                 110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115                 120                 125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130                 135                 140
Thr Glu Arg Arg Ala
145

<210> 97
<211> 750
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<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1-CD28Cys

<400> 97
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg 60
cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccaccctag cccatctcca 480
agacctgccg gccagttcca gacactggtc tgtcccagcc ctctgtttcc cggccctagc 540
aagcctttct gggtgctggt ggtggtcgga ggcgtgctgg cctgctacag cctgctggtc 600
accgtggcct tcatcatctt ttgggtccgc agcaagcgga gcagaggcgg ccacagcgac 660
tacatgaaca tgacccctag acggcctggc cccaccagaa agcactacca gccctacgcc 720
cctccccggg actttgccgc ctacagaagc 750

<210> 98
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1-CD28Cys

<400> 98
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1   5   10   15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20   25   30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50   55   60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65   70   75   80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85   90   95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100   105   110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130   135   140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145   150   155   160
Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Cys Pro Ser Pro Leu Phe
                165   170   175
Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
            180   185   190
Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
        195   200   205
Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met
    210   215   220
Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
225   230   235   240
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
                245   250

<210> 99
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1-12aas-CD28Cys

<400> 99
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cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccaccctag cccatgtccc 480
agccctctgt ttcccggccc tagcaagcct ttctgggtgc tggtggtggt cggaggcgtg 540
ctggcctgct acagcctgct ggtcaccgtg gccttcatca tcttttgggt ccgcagcaag 600
cggagcagag gcggccacag cgactacatg aacatgaccc ctagacggcc tggccccacc 660
agaaagcact accagcccta cgcccctccc cgggactttg ccgcctacag aagc 714

<210> 100
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1-12aas-CD28Cys

<400> 100
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1   5   10   15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20   25   30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50   55   60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65   70   75   80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85   90   95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100   105   110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130   135   140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Cys Pro
145   150   155   160
Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
                165   170   175
Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
            180   185   190
Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp
        195   200   205
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
    210   215   220
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
225   230   235

<210> 101
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1-15aas-CD28Cys

<400> 101
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg 60
cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120

ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggccgaa gtgcctaccg cccactgtcc cagccctctg 480
tttcccggcc ctagcaagcc tttctgggtg ctggtggtgg tcggaggcgt gctggcctgc 540
tacagcctgc tggtcaccgt ggccttcatc atcttttggg tccgcagcaa gcggagcaga 600
ggcggccaca gcgactacat gaacatgacc cctagacggc ctggccccac cagaaagcac 660
taccagccct acgcccctcc ccgggacttt gccgcctaca gaagc 705

<210> 102
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1-15aas-CD28Cys

<400> 102
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1   5   10   15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20   25   30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50   55   60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65   70   75   80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85   90   95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100   105   110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130   135   140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Cys Pro Ser Pro Leu
145   150   155   160
Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
                165   170   175
Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
            180   185   190
Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn
        195   200   205
Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
    210   215   220
Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
225   230   235

<210> 103
<211> 687
<212> DNA
<213> Artificial Sequence

<220>
<223> huPD1-21aas-CD28Cys

<400> 103
atgcagatcc ctcaggcccc ttggcctgtc gtgtgggctg tgctgcagct gggatggcgg 60
cctggctggt ttctggacag ccccgacaga ccctggaacc cccctacatt ttcccctgcc 120
ctgctggtcg tgaccgaggg cgacaatgcc accttcacct gtagcttcag caacaccagc 180
gagagcttcg tgctgaactg gtacagaatg agccccagca accagaccga caagctggcc 240
gccttccccg aggatagatc tcagcccggc caggactgcc ggttcagagt gacccagctg 300
cccaacggcc gggacttcca catgtctgtc gtgcgggcca gacggaacga cagcggcaca 360
tatctgtgcg gcgccatcag cctggccccc aaggcccaga tcaaagagag cctgagagcc 420
gagctgagag tgaccgagag aagggcctgt cccagccctc tgtttcccgg ccctagcaag 480

cctttctggg tgctggtggt ggtcggaggc gtgctggcct gctacagcct gctggtcacc 540
gtggccttca tcatcttttg ggtccgcagc aagcggagca gaggcggcca cagcgactac 600
atgaacatga cccctagacg gcctggcccc accagaaagc actaccagcc ctacgccct 660
ccccgggact ttgccgccta cagaagc 687

<210> 104
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> huPD1-21aas-CD28Cys

<400> 104
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
 1   5   10   15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20   25   30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50   55   60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65   70   75   80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85   90   95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100   105   110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130   135   140
Thr Glu Arg Arg Ala Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
145   150   155   160
Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
                165   170   175
Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
            180   185   190
Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
        195   200   205
Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
    210   215   220
Ala Ala Tyr Arg Ser
225

<210> 105
<211> 810
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD2tm-CD28

<400> 105
atgaagtgca agttcctggg ctcattcttc ctgctgttca gcctgagcgg caagggcgcc 60
gactgcagag acaacgagac aatctggggc gtgctgggcc acggcatcac cctgaacatc 120
cccaacttcc agatgaccga cgacatcgac gaagtgcgct gggtgcgaag aggcacactg 180
gtggccgagt tcaagagaaa gaagccccca ttcctgatca gcgagacata cgaggtgctg 240
gccaacggca gcctgaagat caagaaaccc atgatgagaa acgacagcgg cacctacaac 300
gtgatggtgt acggcaccaa cggcatgacc agactggaaa aggacctgga cgtgcggatc 360
ctggaaaggg tgtccaagcc catgatccac tgggagtgcc ccaacaccac cctgacctgt 420
gctgtgctgc agggcaccga cttcgagctg aagctgtacc agggcgagac actgctgaac 480
tccctgcccc agaaaaacat gagctaccag tggaccaacc tgaacgcccc cttcaagtgc 540
gaggccatca accccgtgtc caaagaaagc aagatggaag tcgtgaactg ccccgagaag 600
ggcctgagct tctacgtgac agtgggcgtg ggagctggcg gactgctgct ggtgctgctg 660
gtggccctgt tcatcttctg catctgcaac agcagacgga acagaggcgg ccagagcgac 720
tacatgaaca tgacccccag aaggcctggc ctgaccagaa agccctacca gccttacgcc 780
cctgccagag acttcgccgc ctacagacct 810

<210> 106
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD2tm-CD28

<400> 106
Met Lys Cys Lys Phe Leu Gly Ser Phe Phe Leu Leu Phe Ser Leu Ser
 1   5   10   15
Gly Lys Gly Ala Asp Cys Arg Asp Asn Glu Thr Ile Trp Gly Val Leu
            20   25   30
Gly His Gly Ile Thr Leu Asn Ile Pro Asn Phe Gln Met Thr Asp Asp
        35   40   45
Ile Asp Glu Val Arg Trp Val Arg Arg Gly Thr Leu Val Ala Glu Phe
    50   55   60
Lys Arg Lys Lys Pro Pro Phe Leu Ile Ser Glu Thr Tyr Glu Val Leu
65   70   75   80
Ala Asn Gly Ser Leu Lys Ile Lys Lys Pro Met Met Arg Asn Asp Ser
                85   90   95
Gly Thr Tyr Asn Val Met Val Tyr Gly Thr Asn Gly Met Thr Arg Leu
            100   105   110
Glu Lys Asp Leu Asp Val Arg Ile Leu Glu Arg Val Ser Lys Pro Met
        115   120   125
Ile His Trp Glu Cys Pro Asn Thr Thr Leu Thr Cys Ala Val Leu Gln
    130   135   140
Gly Thr Asp Phe Glu Leu Lys Leu Tyr Gln Gly Glu Thr Leu Leu Asn
145   150   155   160
Ser Leu Pro Gln Lys Asn Met Ser Tyr Gln Trp Thr Asn Leu Asn Ala
                165   170   175
Pro Phe Lys Cys Glu Ala Ile Asn Pro Val Ser Lys Glu Ser Lys Met
            180   185   190
Glu Val Val Asn Cys Pro Glu Lys Gly Leu Ser Phe Tyr Val Thr Val
        195   200   205
Gly Val Gly Ala Gly Gly Leu Leu Leu Val Leu Leu Val Ala Leu Phe
    210   215   220
Ile Phe Cys Ile Cys Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp
225   230   235   240
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr
                245   250   255
Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
            260   265   270

<210> 107
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD2-CD28tm

<400> 107
atgaagtgca agttcctggg ctcattcttc ctgctgttca gcctgagcgg caagggcgcc   60
gactgcagag acaacgagac aatctggggc gtgctgggcc acggcatcac cctgaacatc   120
cccaacttcc agatgaccga cgacatcgac gaagtgcgct gggtgcgaag aggcacactg   180
gtggccgagt tcaagagaaa gaagccccca ttcctgatca gcgagacata cgaggtgctg   240
gccaacggca gcctgaagat caagaaaccc atgatgagaa acgacagcgg cacctacaac   300
gtgatggtgt acggcaccaa cggcatgacc agactggaaa aggacctgga cgtgcggatc   360
ctggaaaggg tgtccaagcc catgatccac tgggagtgcc ccaacaccac cctgacctgt   420
gctgtgctgc agggcaccga cttcgagctg aagctgtacc agggcgagac actgctgaac   480
tccctgcccc agaaaaacat gagctaccag tggaccaacc tgaacgcccc cttcaagtgc   540
gaggccatca accccgtgtc caaagaaagc aagatggaag tcgtgaactg ccccgagaag   600
ggcctgagct tctgggccct ggtggtggtg gccggcgtgc tgttttgtta cggcctgctc   660
gtgaccgtgg ccctgtgcgt gatctggacc aacagcagaa gaaacagagg cggccagagc   720
gactacatga acatgacccc cagaaggcct ggcctgacca gaaagcccta ccagccttac   780
gcccctgcca gagacttcgc cgcctacaga ccc   813

<210> 108
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD2-CD28tm

<400> 108
Met Lys Cys Lys Phe Leu Gly Ser Phe Phe Leu Leu Phe Ser Leu Ser
 1   5   10   15
Gly Lys Gly Ala Asp Cys Arg Asp Asn Glu Thr Ile Trp Gly Val Leu
            20   25   30
Gly His Gly Ile Thr Leu Asn Ile Pro Asn Phe Gln Met Thr Asp Asp
        35   40   45
Ile Asp Glu Val Arg Trp Val Arg Arg Gly Thr Leu Val Ala Glu Phe
    50   55   60
Lys Arg Lys Lys Pro Pro Phe Leu Ile Ser Glu Thr Tyr Glu Val Leu
65   70   75   80
Ala Asn Gly Ser Leu Lys Ile Lys Lys Pro Met Met Arg Asn Asp Ser
                85   90   95
Gly Thr Tyr Asn Val Met Val Tyr Gly Thr Asn Gly Met Thr Arg Leu
            100   105   110
Glu Lys Asp Leu Asp Val Arg Ile Leu Glu Arg Val Ser Lys Pro Met
        115   120   125
Ile His Trp Glu Cys Pro Asn Thr Thr Leu Thr Cys Ala Val Leu Gln
    130   135   140
Gly Thr Asp Phe Glu Leu Lys Leu Tyr Gln Gly Glu Thr Leu Leu Asn
145   150   155   160
Ser Leu Pro Gln Lys Asn Met Ser Tyr Gln Trp Thr Asn Leu Asn Ala
                165   170   175
Pro Phe Lys Cys Glu Ala Ile Asn Pro Val Ser Lys Glu Ser Lys Met
            180   185   190
Glu Val Val Asn Cys Pro Glu Lys Gly Leu Ser Phe Trp Ala Leu Val
        195   200   205
Val Val Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala
    210   215   220
Leu Cys Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser
225   230   235   240
Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro
                245   250   255
Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
            260   265   270

<210> 109
<211> 840
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD2-CD28Cys

<400> 109
atgaagtgca agttcctggg ctcattcttc ctgctgttca gcctgagcgg caagggcgcc   60
gactgcagag acaacgagac aatctggggc gtgctgggcc acggcatcac cctgaacatc   120
cccaacttcc agatgaccga cgacatcgac gaagtgcgct gggtgcgaag aggcacactg   180
gtggccgagt tcaagagaaa gaagccccca ttcctgatca gcgagacata cgaggtgctg   240
gccaacggca gcctgaagat caagaaaccc atgatgagaa acgacagcgg cacctacaac   300
gtgatggtgt acggcaccaa cggcatgacc agactggaaa aggacctgga cgtgcggatc   360
ctggaaaggg tgtccaagcc catgatccac tgggagtgcc ccaacaccac cctgacctgt   420
gctgtgctgc agggcaccga cttcgagctg aagctgtacc agggcgagac actgctgaac   480
tccctgcccc agaaaaacat gagctaccag tggaccaacc tgaacgcccc cttcaagtgc   540
gaggccatca accccgtgtc caaagaaagc aagatggaag tcgtgaactg ccccgagaag   600
ggcctgagct gccacaccca gagcagcccc aagctgttct gggccctggt ggtggtggcc   660
ggcgtgctgt tttgttacgg cctgctcgtg accgtggccc tgtgcgtgat ctggaccaac   720
agcagaagaa acagaggcgg ccagagcgac tacatgaaca tgacccccag aaggcctggc   780
ctgaccagaa agccctacca gccttacgcc cctgccagag acttcgccgc ctacagacct   840

<210> 110
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD2-CD28Cys

<400> 110
Met Lys Cys Lys Phe Leu Gly Ser Phe Phe Leu Leu Phe Ser Leu Ser
 1   5   10   15
Gly Lys Gly Ala Asp Cys Arg Asp Asn Glu Thr Ile Trp Gly Val Leu
            20   25   30
Gly His Gly Ile Thr Leu Asn Ile Pro Asn Phe Gln Met Thr Asp Asp
        35   40   45
Ile Asp Glu Val Arg Trp Val Arg Arg Gly Thr Leu Val Ala Glu Phe
    50   55   60
Lys Arg Lys Lys Pro Pro Phe Leu Ile Ser Glu Thr Tyr Glu Val Leu
65   70   75   80
Ala Asn Gly Ser Leu Lys Ile Lys Lys Pro Met Met Arg Asn Asp Ser
                85   90   95
Gly Thr Tyr Asn Val Met Val Tyr Gly Thr Asn Gly Met Thr Arg Leu
            100   105   110
Glu Lys Asp Leu Asp Val Arg Ile Leu Glu Arg Val Ser Lys Pro Met
        115   120   125
Ile His Trp Glu Cys Pro Asn Thr Thr Leu Thr Cys Ala Val Leu Gln
    130   135   140
Gly Thr Asp Phe Glu Leu Lys Leu Tyr Gln Gly Glu Thr Leu Leu Asn
145   150   155   160
Ser Leu Pro Gln Lys Asn Met Ser Tyr Gln Trp Thr Asn Leu Asn Ala
                165   170   175
Pro Phe Lys Cys Glu Ala Ile Asn Pro Val Ser Lys Glu Ser Lys Met
            180   185   190
Glu Val Val Asn Cys Pro Glu Lys Gly Leu Ser Cys His Thr Gln Ser
        195   200   205
Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe
    210   215   220
Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn
225   230   235   240
Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro
                245   250   255
Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala
            260   265   270
Arg Asp Phe Ala Ala Tyr Arg Pro
        275   280

<210> 111
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD2-CD28Cys-41BBic

<400> 111
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gactgcagag acaacgagac aatctggggc gtgctgggcc acggcatcac cctgaacatc   120
cccaacttcc agatgaccga cgacatcgac gaagtgcgct gggtgcgaag aggcacactg   180
gtggccgagt tcaagagaaa gaagccccca ttcctgatca gcgagacata cgaggtgctg   240
gccaacggca gcctgaagat caagaaaccc atgatgagaa acgacagcgg cacctacaac   300
gtgatggtgt acggcaccaa cggcatgacc agactggaaa aggacctgga cgtgcggatc   360
ctggaaaggg tgtccaagcc catgatccac tgggagtgcc ccaacaccac cctgacctgt   420
gctgtgctgc agggcaccga cttcgagctg aagctgtacc agggcgagac actgctgaac   480
tccctgcccc agaaaaacat gagctaccag tggaccaacc tgaacgcccc cttcaagtgc   540
gaggccatca accccgtgtc caaagaaagc aagatggaag tcgtgaactg ccccgagaag   600
ggcctgagct gccacaccca gagcagcccc aagctgttct gggccctggt ggtggtggcc   660
ggcgtgctgt tttgttacgg cctgctcgtg accgtggccc tgtgcgtgat ctggaccagc   720

gtgctgaagt ggatcagaaa gaagttcccc cacatcttca agcagccctt caagaaaacc 780
accggcgctg cccaggaaga ggacgcctgc agctgtagat gccctcagga agaagaaggc 840
ggcggaggcg gctacgagct g 861

<210> 112
<211> 287
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD2-CD28Cys-41BBic

<400> 112
Met Lys Cys Lys Phe Leu Gly Ser Phe Phe Leu Leu Phe Ser Leu Ser
 1   5   10   15
Gly Lys Gly Ala Asp Cys Arg Asp Asn Glu Thr Ile Trp Gly Val Leu
            20   25   30
Gly His Gly Ile Thr Leu Asn Ile Pro Asn Phe Gln Met Thr Asp Asp
        35   40   45
Ile Asp Glu Val Arg Trp Val Arg Arg Gly Thr Leu Val Ala Glu Phe
    50   55   60
Lys Arg Lys Lys Pro Pro Phe Leu Ile Ser Glu Thr Tyr Glu Val Leu
65   70   75   80
Ala Asn Gly Ser Leu Lys Ile Lys Lys Pro Met Met Arg Asn Asp Ser
                85   90   95
Gly Thr Tyr Asn Val Met Val Tyr Gly Thr Asn Gly Met Thr Arg Leu
            100   105   110
Glu Lys Asp Leu Asp Val Arg Ile Leu Glu Arg Val Ser Lys Pro Met
        115   120   125
Ile His Trp Glu Cys Pro Asn Thr Thr Leu Thr Cys Ala Val Leu Gln
    130   135   140
Gly Thr Asp Phe Glu Leu Lys Leu Tyr Gln Gly Glu Thr Leu Leu Asn
145   150   155   160
Ser Leu Pro Gln Lys Asn Met Ser Tyr Gln Trp Thr Asn Leu Asn Ala
                165   170   175
Pro Phe Lys Cys Glu Ala Ile Asn Pro Val Ser Lys Glu Ser Lys Met
            180   185   190
Glu Val Val Asn Cys Pro Glu Lys Gly Leu Ser Cys His Thr Gln Ser
        195   200   205
Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe
    210   215   220
Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Ser
225   230   235   240
Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln Pro
                245   250   255
Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser Cys
            260   265   270
Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu
        275   280   285

<210> 113
<211> 1080
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-3aas-CD28Cys tm ic-41BB

<400> 113
atgttctgct tctggcggac aagcgccctg gccgtgctgc tgatctgggg agtgtttgtg 60
gccggcagca gctgcaccga caagaaccag accacccaga acaacagcag cagccccctg 120
acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc 180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc 240
agctgcacaa tcgcctacaa ggtggacacc aagaccaacg agacaagctg cctgggcaga 300
aacatcacct gggccagcac cccagaccac agccctgagc tgcagatcag cgccgtgaca 360
ctgcagcacg agggcaccta cacatgcgag acagtgaccc ccgagggcaa cttcgagaag 420
aactacgatc tgcaggtgct ggtgcccccc gaagtgacct acttccccga gaagaataga 480
agcgccgtgt gcgaggccat ggctggcaaa cctgccgccc agatctcttg gagccctgac 540

ggcgactgtg tgaccaccag cgagagccac agcaacggca cagtgaccgt gcggagcacc 600
tgtcactggg agcagaacaa cgtgtccgac gtgtcctgca tcgtgtccca cctgaccggc 660
aaccagagcc tgagcatcga gctgagcaga ggcggaaacc agtcctgcca cacccagagc 720
agccccaagc tgttctgggc cctggtggtg gtggccggcg tgctgttttg ttacggcctg 780
ctcgtgaccg tggccctgtg cgtgatctgg accaacagca gaagaaacag aggcggccag 840
agcgactaca tgaacatgac ccccagaagg cctggcctga ccagaaagcc ctaccagcct 900
tacgcccctg ccagagactt cgccgcctac agacctagcg tgctgaagtg gatcagaaag 960
aagttccccc acatcttcaa gcagcccttc aagaaaacca ccggcgctgc ccaggaagag 1020
gacgcctgca gctgtagatg ccctcaggaa gaagaaggcg gcggaggcgg ctacgagctg 1080

<210> 114
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD200R-3aas-CD28Cys tm ic-41BB

<400> 114
Met Phe Cys Phe Trp Arg Thr Ser Ala Leu Ala Val Leu Leu Ile Trp
 1   5   10   15
Gly Val Phe Val Ala Gly Ser Ser Cys Thr Asp Lys Asn Gln Thr Thr
            20   25   30
Gln Asn Asn Ser Ser Ser Pro Leu Thr Gln Val Asn Thr Thr Val Ser
        35   40   45
Val Gln Ile Gly Thr Lys Ala Leu Leu Cys Cys Phe Ser Ile Pro Leu
    50   55   60
Thr Lys Ala Val Leu Ile Thr Trp Ile Ile Lys Leu Arg Gly Leu Pro
65   70   75   80
Ser Cys Thr Ile Ala Tyr Lys Val Asp Thr Lys Thr Asn Glu Thr Ser
                85   90   95
Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro Asp His Ser Pro
            100   105   110
Glu Leu Gln Ile Ser Ala Val Thr Leu Gln His Glu Gly Thr Tyr Thr
        115   120   125
Cys Glu Thr Val Thr Pro Glu Gly Asn Phe Glu Lys Asn Tyr Asp Leu
    130   135   140
Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Pro Glu Lys Asn Arg
145   150   155   160
Ser Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala Ala Gln Ile Ser
                165   170   175
Trp Ser Pro Asp Gly Asp Cys Val Thr Thr Ser Glu Ser His Ser Asn
            180   185   190
Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Asn Asn Val
        195   200   205
Ser Asp Val Ser Cys Ile Val Ser His Leu Thr Gly Asn Gln Ser Leu
    210   215   220
Ser Ile Glu Leu Ser Arg Gly Gly Asn Gln Ser Cys His Thr Gln Ser
225   230   235   240
Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe
                245   250   255
Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn
            260   265   270
Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro
        275   280   285
Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala
    290   295   300
Arg Asp Phe Ala Ala Tyr Arg Pro Ser Val Leu Lys Trp Ile Arg Lys
305   310   315   320
Lys Phe Pro His Ile Phe Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala
                325   330   335
Ala Gln Glu Glu Asp Ala Cys Ser Cys Arg Cys Pro Gln Glu Glu Glu
            340   345   350
Gly Gly Gly Gly Gly Tyr Glu Leu
        355   360

<210> 115
<211> 966

<212> DNA
<213> Artificial Sequence

<220>
<223> muCD200R-CD28Cys tm ic-41BB

<400> 115
atgttctgct tctggcggac aagcgccctg gccgtgctgc tgatctgggg agtgtttgtg 60
gccggcagca gctgcaccga caagaaccag accacccaga acaacagcag cagccccctg 120
acccaagtga acaccaccgt gtccgtgcag atcggcacca aggccctgct gtgctgtttc 180
agcatccctc tgaccaaggc tgtgctgatc acctggatca tcaagctgag aggcctgccc 240
agctgcacaa tcgcctacaa ggtggacacc aagaccaacg agacaagctg cctgggcaga 300
aacatcacct gggccagcac cccagaccac agccctgagc tgcagatcag cgccgtgaca 360
ctgcagcacg agggcaccta cacatgcgag acagtgaccc ccgagggcaa cttcgagaag 420
aactacgatc tgcaggtgct ggtgcccccc gaagtgacct acttccccga gaagaataga 480
agcgccgtgt gcgaggccat ggctggcaaa cctgccgccc agatctcttg gagccctgac 540
ggcgactgtg tgaccaccag cgagagccac agcaacggca cagtgaccgt gcggagcacc 600
tgtcactggg agcagaacaa cgtgtccgac gtgtcctgca tcgtgtccca cctgaccggc 660
aaccagagcc tgagcatcga gctgagcaga ggcggaaacc agtccctgag gccctgccac 720
acccagagca gccccaagct gttctgggcc ctggtggtgg tggccggcgt gctgttttgt 780
tacggcctgc tcgtgaccgt ggccctgtgc gtgatctgga ccagcgtgct gaagtggatc 840
agaaagaagt tcccccacat cttcaagcag cccttcaaga aaaccaccgg cgctgcccag 900
gaagaggacg cctgcagctg tagatgccct caggaagaag aaggcggcgg aggcggctac 960
gagctg 966

<210> 116
<211> 322
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD200R-CD28Cys tm ic-41BB

<400> 116
Met Phe Cys Phe Trp Arg Thr Ser Ala Leu Ala Val Leu Leu Ile Trp
1 5 10 15
Gly Val Phe Val Ala Gly Ser Ser Cys Thr Asp Lys Asn Gln Thr Thr
20 25 30
Gln Asn Asn Ser Ser Ser Pro Leu Thr Gln Val Asn Thr Thr Val Ser
35 40 45
Val Gln Ile Gly Thr Lys Ala Leu Leu Cys Cys Phe Ser Ile Pro Leu
50 55 60
Thr Lys Ala Val Leu Ile Thr Trp Ile Ile Lys Leu Arg Gly Leu Pro
65 70 75 80
Ser Cys Thr Ile Ala Tyr Lys Val Asp Thr Lys Thr Asn Glu Thr Ser
85 90 95
Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro Asp His Ser Pro
100 105 110
Glu Leu Gln Ile Ser Ala Val Thr Leu Gln His Glu Gly Thr Tyr Thr
115 120 125
Cys Glu Thr Val Thr Pro Glu Gly Asn Phe Glu Lys Asn Tyr Asp Leu
130 135 140
Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Pro Glu Lys Asn Arg
145 150 155 160
Ser Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala Ala Gln Ile Ser
165 170 175
Trp Ser Pro Asp Gly Asp Cys Val Thr Thr Ser Glu Ser His Ser Asn
180 185 190
Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Asn Asn Val
195 200 205
Ser Asp Val Ser Cys Ile Val Ser His Leu Thr Gly Asn Gln Ser Leu
210 215 220
Ser Ile Glu Leu Ser Arg Gly Gly Asn Gln Ser Leu Arg Pro Cys His
225 230 235 240
Thr Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly
245 250 255
Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile
260 265 270

```
Trp Thr Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe
        275                 280                 285
Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala
    290                 295                 300
Cys Ser Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr
305                 310                 315                 320
Glu Leu
```

<210> 117
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> muFas tm-CD28

<400> 117

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atgctgtgga tctgggccgt gctgcctctg gtgctggctg gatcacagct gagagtgcac      60
acccagggca ccaacagcat cagcgagagc ctgaagctga gaagaagagt gcgcgagaca     120
gacaagaact gcagcgaggg cctgtaccag ggcggaccct tctgctgtca gccttgccag     180
cccggcaaga aaaaggtgga agattgcaag atgaacggcg gcacccctac ctgcgccccc     240
tgtacagagg gcaaagagta catggacaag aaccactacg ccgacaagtg cagacggtgc     300
accctgtgcg acgaggaaca cggcctggaa gtggaaacaa actgcaccct gacccagaac     360
accaagtgca agtgcaaacc cgacttctac tgcgacagcc ccggctgcga gcactgcgtc     420
agatgtgcct cttgcgagca cggcaccctg gaaccttgta ccgccaccag caacaccaac     480
tgccggaagc agagccccag aaacagactg tggctgctga ccatcctggt gctgctgatc     540
cccctggtgt tcatctacaa cagcagaaga aacagaggcg gccagagcga ctacatgaac     600
atgaccccca gaaggcctgg cctgaccaga aagccctacc agccttacgc ccctgccaga     660
gacttcgccg cctacagacc t                                               681
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<210> 118
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> muFas tm-CD28

<400> 118

```
Met Leu Trp Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln
 1               5                  10                  15
Leu Arg Val His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys
            20                  25                  30
Leu Arg Arg Arg Val Arg Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu
        35                  40                  45
Tyr Gln Gly Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys
    50                  55                  60
Lys Val Glu Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro
65                  70                  75                  80
Cys Thr Glu Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys
                85                  90                  95
Cys Arg Arg Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu
            100                 105                 110
Thr Asn Cys Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp
        115                 120                 125
Phe Tyr Cys Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser
    130                 135                 140
Cys Glu His Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn
145                 150                 155                 160
Cys Arg Lys Gln Ser Pro Arg Asn Arg Leu Trp Leu Leu Thr Ile Leu
                165                 170                 175
Val Leu Leu Ile Pro Leu Val Phe Ile Tyr Asn Ser Arg Arg Asn Arg
            180                 185                 190
Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu
        195                 200                 205
Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala
    210                 215                 220
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Tyr Arg Pro
225

<210> 119
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> muFas-CD28tm

<400> 119
atgctgtgga tctgggccgt gctgcctctg gtgctggctg gatcacagct gagagtgcac 60
acccagggca ccaacagcat cagcgagagc ctgaagctga gaagaagagt gcgcgagaca 120
gacaagaact gcagcgaggg cctgtaccag ggcggaccct tctgctgtca gccttgccag 180
cccggcaaga aaaaggtgga agattgcaag atgaacggcg gcacccctac ctgcgccct 240
tgtacagagg gcaaagagta catggacaag aaccactacg ccgacaagtg cagacggtgc 300
accctgtgcg acgaggaaca cggcctggaa gtggaaacaa actgcaccct gacccagaac 360
accaagtgca agtgcaaacc cgacttctac tgcgacagcc ccggctgcga gcactgcgtc 420
agatgtgcct cttgcgagca cggcaccctg gaaccttgta ccgccaccag caacaccaac 480
tgccggaagc agagccccag aaacagattc tgggccctgg tggtggtggc cggcgtgctg 540
ttttgttacg gcctgctcgt gaccgtggcc ctgtgcgtga tctggaccaa cagcagaaga 600
aacagaggcg gccagagcga ctacatgaac atgaccccca gaaggcctgg cctgaccaga 660
aagccctacc agccttacgc ccctgccaga gacttcgccg cctacagacc t 711

<210> 120
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> muFas-CD28tm

<400> 120
Met Leu Trp Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln
1 5 10 15
Leu Arg Val His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys
20 25 30
Leu Arg Arg Arg Val Arg Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu
35 40 45
Tyr Gln Gly Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys
50 55 60
Lys Val Glu Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro
65 70 75 80
Cys Thr Glu Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys
85 90 95
Cys Arg Arg Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu
100 105 110
Thr Asn Cys Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp
115 120 125
Phe Tyr Cys Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser
130 135 140
Cys Glu His Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn
145 150 155 160
Cys Arg Lys Gln Ser Pro Arg Asn Arg Phe Trp Ala Leu Val Val Val
165 170 175
Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys
180 185 190
Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr
195 200 205
Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln
210 215 220
Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
225 230 235

<210> 121
<211> 738
<212> DNA

<213> Artificial Sequence

<220>
<223> muFas-CD28Cys

<400> 121
atgctgtgga tctgggccgt gctgcctctg gtgctggctg gatcacagct gagagtgcac 60
acccagggca ccaacagcat cagcgagagc ctgaagctga gaagaagagt gcgcgagaca 120
gacaagaact gcagcgaggg cctgtaccag ggcggaccct tctgctgtca gccttgccag 180
cccggcaaga aaaaggtgga agattgcaag atgaacggcg gcacccctac ctgcgccct 240
tgtacagagg gcaaagagta catggacaag aaccactacg ccgacaagtg cagacggtgc 300
accctgtgcg acgaggaaca cggcctggaa gtggaaacaa actgcaccct gacccagaac 360
accaagtgca agtgcaaacc cgacttctac tgcgacagcc ccggctgcga gcactgcgtc 420
agatgtgcct cttgcgagca cggcaccctg gaaccttgta ccgccaccag caacaccaac 480
tgccggaagc agagccccag aaacagatgc cacacccaga gcagccccaa gctgttctgg 540
gccctggtgg tggtggccgg cgtgctgttt tgttacggcc tgctcgtgac cgtggccctg 600
tgcgtgatct ggaccaacag cagaagaaac agaggcggcc agagcgacta catgaacatg 660
acccccagaa ggcctggcct gaccagaaag ccctaccagc cttacgcccc tgccagagac 720
ttcgccgcct acagacct 738

<210> 122
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> muFas-CD28Cys

<400> 122
Met Leu Trp Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln
1 5 10 15
Leu Arg Val His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys
20 25 30
Leu Arg Arg Arg Val Arg Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu
35 40 45
Tyr Gln Gly Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys
50 55 60
Lys Val Glu Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro
65 70 75 80
Cys Thr Glu Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys
85 90 95
Cys Arg Arg Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu
100 105 110
Thr Asn Cys Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp
115 120 125
Phe Tyr Cys Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser
130 135 140
Cys Glu His Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn
145 150 155 160
Cys Arg Lys Gln Ser Pro Arg Asn Arg Cys His Thr Gln Ser Ser Pro
165 170 175
Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe Cys Tyr
180 185 190
Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn Ser Arg
195 200 205
Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
210 215 220
Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp
225 230 235 240
Phe Ala Ala Tyr Arg Pro
245

<210> 123
<211> 711
<212> DNA
<213> Artificial Sequence

<220>

<223> muFas-9aas-CD28Cys

<400> 123
atgctgtgga tctgggccgt gctgcctctg gtgctggctg gatcacagct gagagtgcac 60
acccagggca ccaacagcat cagcgagagc ctgaagctga gaagaagagt gcgcgagaca 120
gacaagaact gcagcgaggg cctgtaccag ggcggaccct tctgctgtca gccttgccag 180
cccggcaaga aaaaggtgga agattgcaag atgaacggcg gcacccctac ctgcgccct 240
tgtacagagg gcaaagagta catggacaag aaccactacg ccgacaagtg cagacggtgc 300
accctgtgcg acgaggaaca cggcctggaa gtggaaacaa actgcaccct gacccagaac 360
accaagtgca agtgcaaacc cgacttctac tgcgacagcc ccggctgcga gcactgcgtc 420
agatgtgcct cttgcgagca cggcaccctg gaaccttgta ccgccaccag caacaccaac 480
tgccacaccc agagcagccc caagctgttc tgggccctgg tggtggtggc cggcgtgctg 540
ttttgttacg gcctgctcgt gaccgtggcc ctgtgcgtga tctggaccaa cagcagaaga 600
aacagaggcg gccagagcga ctacatgaac atgaccccca gaaggcctgg cctgaccaga 660
aagccctacc agccttacgc ccctgccaga gacttcgccg cctacagacc t 711

<210> 124
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> muFas-9aas-CD28Cys

<400> 124
Met Leu Trp Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln
1 5 10 15
Leu Arg Val His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys
20 25 30
Leu Arg Arg Arg Val Arg Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu
35 40 45
Tyr Gln Gly Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys
50 55 60
Lys Val Glu Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro
65 70 75 80
Cys Thr Glu Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys
85 90 95
Cys Arg Arg Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu
100 105 110
Thr Asn Cys Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp
115 120 125
Phe Tyr Cys Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser
130 135 140
Cys Glu His Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn
145 150 155 160
Cys His Thr Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val
165 170 175
Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys
180 185 190
Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr
195 200 205
Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln
210 215 220
Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
225 230 235

<210> 125
<211> 693
<212> DNA
<213> Artificial Sequence

<220>
<223> muPD1tm-CD28

<400> 125
atgtgggtgc gacaggtgcc ctggtctttc acctgggctg tgctgcagct gagctggcag 60
tctggctggc tgctggaagt gcctaacggc ccttggagaa gcctgacctt ctaccccgct 120
tggctgaccg tgtctgaggg cgccaacgcc accttcacct gtagcctgag caattggagc 180

gaggacctga tgctgaactg gaacagactg agccccagca accagaccga gaagcaggcc 240
gccttctgca acggcctgtc tcagcctgtg caggacgcca gattccagat catccagctg 300
cccaacagac acgacttcca catgaacatc ctggacacca gaagaaacga cagcggcatc 360
tacctgtgcg gcgccatcag cctgcacccc aaggccaaga tcgaggaatc tcctggcgcc 420
gagctggtcg tgaccgagag aatcctggaa acctccacca gataccccag ccccagccct 480
aagcccgagg gcagatttca gggcatggtc atcggcatca tgagcgccct cgtgggcatc 540
ccagtgttgc tgctgctggc ctgggccctg aacagcagaa gaaacagagg cggccagagc 600
gactacatga acatgacccc cagaaggcct ggcctgacca gaaagcccta ccagccttac 660
gcccctgcca gagacttcgc cgcctacaga cct 693

<210> 126
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> muPD1tm-CD28

<400> 126
Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
 1   5   10   15
Leu Ser Trp Gln Ser Gly Trp Leu Leu Glu Val Pro Asn Gly Pro Trp
            20   25   30
Arg Ser Leu Thr Phe Tyr Pro Ala Trp Leu Thr Val Ser Glu Gly Ala
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Leu Ser Asn Trp Ser Glu Asp Leu Met
    50   55   60
Leu Asn Trp Asn Arg Leu Ser Pro Ser Asn Gln Thr Glu Lys Gln Ala
65   70   75   80
Ala Phe Cys Asn Gly Leu Ser Gln Pro Val Gln Asp Ala Arg Phe Gln
                85   90   95
Ile Ile Gln Leu Pro Asn Arg His Asp Phe His Met Asn Ile Leu Asp
            100   105   110
Thr Arg Arg Asn Asp Ser Gly Ile Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
His Pro Lys Ala Lys Ile Glu Glu Ser Pro Gly Ala Glu Leu Val Val
    130   135   140
Thr Glu Arg Ile Leu Glu Thr Ser Thr Arg Tyr Pro Ser Pro Ser Pro
145   150   155   160
Lys Pro Glu Gly Arg Phe Gln Gly Met Val Ile Gly Ile Met Ser Ala
                165   170   175
Leu Val Gly Ile Pro Val Leu Leu Leu Leu Ala Trp Ala Leu Asn Ser
            180   185   190
Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg
        195   200   205
Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg
    210   215   220
Asp Phe Ala Ala Tyr Arg Pro
225   230

<210> 127
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> muPD1-CD28tm

<400> 127
atgtgggtgc gacaggtgcc ctggtctttc acctgggctg tgctgcagct gagctggcag 60
tctggctggc tgctggaagt gcctaacggc ccttggagaa gcctgacctt ctaccccgct 120
tggctgaccg tgtctgaggg cgccaacgcc accttcacct gtagcctgag caattggagc 180
gaggacctga tgctgaactg gaacagactg agccccagca accagaccga gaagcaggcc 240
gccttctgca acggcctgtc tcagcctgtg caggacgcca gattccagat catccagctg 300
cccaacagac acgacttcca catgaacatc ctggacacca gaagaaacga cagcggcatc 360
tacctgtgcg gcgccatcag cctgcacccc aaggccaaga tcgaggaatc tcctggcgcc 420
gagctggtcg tgaccgagag aatcctggaa acctccacca gataccccag ccccagccct 480
aagcccgagg gcagatttca gggcatgttc tgggccctgg tggtggtggc cggcgtgctg 540

ttttgttacg gcctgctcgt gaccgtggcc ctgtgcgtga tctggaccaa cagcagaaga 600
aacagaggcg gccagagcga ctacatgaac atgaccccca gaaggcctgg cctgaccaga 660
aagccctacc agccttacgc ccctgccaga gacttcgccg cctacagacc t 711

<210> 128
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> muPD1-CD28tm

<400> 128
Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
 1   5   10   15
Leu Ser Trp Gln Ser Gly Trp Leu Leu Glu Val Pro Asn Gly Pro Trp
            20   25   30
Arg Ser Leu Thr Phe Tyr Pro Ala Trp Leu Thr Val Ser Glu Gly Ala
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Leu Ser Asn Trp Ser Glu Asp Leu Met
    50   55   60
Leu Asn Trp Asn Arg Leu Ser Pro Ser Asn Gln Thr Glu Lys Gln Ala
65   70   75   80
Ala Phe Cys Asn Gly Leu Ser Gln Pro Val Gln Asp Ala Arg Phe Gln
                85   90   95
Ile Ile Gln Leu Pro Asn Arg His Asp Phe His Met Asn Ile Leu Asp
            100   105   110
Thr Arg Arg Asn Asp Ser Gly Ile Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
His Pro Lys Ala Lys Ile Glu Glu Ser Pro Gly Ala Glu Leu Val Val
    130   135   140
Thr Glu Arg Ile Leu Glu Thr Ser Thr Arg Tyr Pro Ser Pro Ser Pro
145   150   155   160
Lys Pro Glu Gly Arg Phe Gln Gly Met Phe Trp Ala Leu Val Val Val
                165   170   175
Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys
            180   185   190
Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr
        195   200   205
Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln
    210   215   220
Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
225   230   235

<210> 129
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> muPD1-CD28Cys

<400> 129
atgtgggtgc gacaggtgcc ctggtctttc acctgggctg tgctgcagct gagctggcag 60
tctggctggc tgctggaagt gcctaacggc ccttggagaa gcctgacctt ctaccccgct 120
tggctgaccg tgtctgaggg cgccaacgcc accttcacct gtagcctgag caattggagc 180
gaggacctga tgctgaactg gaacagactg agccccagca accagaccga gaagcaggcc 240
gccttctgca acggcctgtc tcagcctgtg caggacgcca gattccagat catccagctg 300
cccaacagac acgacttcca catgaacatc ctggacacca gaagaaacga cagcggcatc 360
tacctgtgcg gcgccatcag cctgcacccc aaggccaaga tcgaggaatc tcctggcgcc 420
gagctggtcg tgaccgagag aatcctggaa acctccacca gataccccag ccccagccct 480
aagcccgagg gcagatttca gggcatgtgc cacacccaga gcagccccaa gctgttctgg 540
gctctggtgg tggtggccgg cgtgctgttt tgttacggcc tgctcgtgac cgtggccctg 600
tgcgtgatct ggaccaacag cagacggaac agaggcggcc agagcgacta catgaatatg 660
acccccagaa ggcctggcct gaccagaaag ccctaccagc cttacgcccc tgccagagac 720
ttcgccgcct acagacct 738

<210> 130

<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> muPD1-CD28Cys

<400> 130
Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
 1   5   10   15
Leu Ser Trp Gln Ser Gly Trp Leu Leu Glu Val Pro Asn Gly Pro Trp
            20   25   30
Arg Ser Leu Thr Phe Tyr Pro Ala Trp Leu Thr Val Ser Glu Gly Ala
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Leu Ser Asn Trp Ser Glu Asp Leu Met
    50   55   60
Leu Asn Trp Asn Arg Leu Ser Pro Ser Asn Gln Thr Glu Lys Gln Ala
65   70   75   80
Ala Phe Cys Asn Gly Leu Ser Gln Pro Val Gln Asp Ala Arg Phe Gln
                85   90   95
Ile Ile Gln Leu Pro Asn Arg His Asp Phe His Met Asn Ile Leu Asp
            100   105   110
Thr Arg Arg Asn Asp Ser Gly Ile Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
His Pro Lys Ala Lys Ile Glu Glu Ser Pro Gly Ala Glu Leu Val Val
    130   135   140
Thr Glu Arg Ile Leu Glu Thr Ser Thr Arg Tyr Pro Ser Pro Ser Pro
145   150   155   160
Lys Pro Glu Gly Arg Phe Gln Gly Met Cys His Thr Gln Ser Ser Pro
                165   170   175
Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe Cys Tyr
            180   185   190
Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn Ser Arg
        195   200   205
Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
    210   215   220
Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp
225   230   235   240
Phe Ala Ala Tyr Arg Pro
                245

<210> 131
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> muPD1-9aas-CD28Cys

<400> 131
atgtgggtgc gacaggtgcc ctggtctttc acctgggctg tgctgcagct gagctggcag   60
tctggctggc tgctggaagt gcctaacggc ccttggagaa gcctgacctt ctaccccgct   120
tggctgaccg tgtctgaggg cgccaacgcc accttcacct gtagcctgag caattggagc   180
gaggacctga tgctgaactg gaacagactg agccccagca accagaccga gaagcaggcc   240
gccttctgca acggcctgtc tcagcctgtg caggacgcca gattccagat catccagctg   300
cccaacagac acgacttcca catgaacatc ctggacacca gaagaaacga cagcggcatc   360
tacctgtgcg gcgccatcag cctgcacccc aaggccaaga tcgaggaatc tcctggcgcc   420
gagctggtcg tgaccgagag aatcctggaa acctccacca gataccccag ccccagccct   480
tgccacaccc agagcagccc caagctgttc tgggctctgg tggtggtggc cggcgtgctg   540
ttttgttacg gcctgctcgt gaccgtggcc ctgtgcgtga tctggaccaa cagcagacgg   600
aacagaggcg gccagagcga ctacatgaat atgaccccca gaaggcctgg cctgaccaga   660
aagccctacc agccttacgc ccctgccaga gacttcgccg cctacagacc t   711

<210> 132
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> muPD1-9aas-CD28Cys

<400> 132
Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
 1   5   10   15
Leu Ser Trp Gln Ser Gly Trp Leu Leu Glu Val Pro Asn Gly Pro Trp
            20   25   30
Arg Ser Leu Thr Phe Tyr Pro Ala Trp Leu Thr Val Ser Glu Gly Ala
        35   40   45
Asn Ala Thr Phe Thr Cys Ser Leu Ser Asn Trp Ser Glu Asp Leu Met
    50   55   60
Leu Asn Trp Asn Arg Leu Ser Pro Ser Asn Gln Thr Glu Lys Gln Ala
65   70   75   80
Ala Phe Cys Asn Gly Leu Ser Gln Pro Val Gln Asp Ala Arg Phe Gln
                85   90   95
Ile Ile Gln Leu Pro Asn Arg His Asp Phe His Met Asn Ile Leu Asp
            100   105   110
Thr Arg Arg Asn Asp Ser Gly Ile Tyr Leu Cys Gly Ala Ile Ser Leu
        115   120   125
His Pro Lys Ala Lys Ile Glu Glu Ser Pro Gly Ala Glu Leu Val Val
    130   135   140
Thr Glu Arg Ile Leu Glu Thr Ser Thr Arg Tyr Pro Ser Pro Ser Pro
145   150   155   160
Cys His Thr Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val
                165   170   175
Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys
            180   185   190
Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr
        195   200   205
Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln
    210   215   220
Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
225   230   235

<210> 133
<211> 675
<212> DNA
<213> Artificial Sequence

<220>
<223> muPD1-21aas-CD28Cys

<400> 133
atgtgggtgc gacaggtgcc ctggtctttc acctgggctg tgctgcagct gagctggcag 60
tctggctggc tgctggaagt gcctaacggc ccttggagaa gcctgacctt ctaccccgct 120
tggctgaccg tgtctgaggg cgccaacgcc accttcacct gtagcctgag caattggagc 180
gaggacctga tgctgaactg gaacagactg agccccagca accagaccga gaagcaggcc 240
gccttctgca acggcctgtc tcagcctgtg caggacgcca gattccagat catccagctg 300
cccaacagac acgacttcca catgaacatc ctggacacca gaagaaacga cagcggcatc 360
tacctgtgcg gcgccatcag cctgcacccc aaggccaaga tcgaggaatc tcctggcgcc 420
gagctggtcg tgaccgagag aatctgccac acccagagca gccccaagct gttctgggct 480
ctggtggtgg tggccggcgt gctgttttgt tacggcctgc tcgtgaccgt ggccctgtgc 540
gtgatctgga ccaacagcag acggaacaga ggcggccaga gcgactacat gaatatgacc 600
cccagaaggc ctggcctgac cagaaagccc taccagcctt acgcccctgc cagagacttc 660
gccgcctaca gacct   675

<210> 134
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> muPD1-21aas-CD28Cys

<400> 134
Met Trp Val Arg Gln Val Pro Trp Ser Phe Thr Trp Ala Val Leu Gln
 1   5   10   15

Leu Ser Trp Gln Ser Gly Trp Leu Leu Glu Val Pro Asn Gly Pro Trp
20 25 30
Arg Ser Leu Thr Phe Tyr Pro Ala Trp Leu Thr Val Ser Glu Gly Ala
35 40 45
Asn Ala Thr Phe Thr Cys Ser Leu Ser Asn Trp Ser Glu Asp Leu Met
50 55 60
Leu Asn Trp Asn Arg Leu Ser Pro Ser Asn Gln Thr Glu Lys Gln Ala
65 70 75 80
Ala Phe Cys Asn Gly Leu Ser Gln Pro Val Gln Asp Ala Arg Phe Gln
85 90 95
Ile Ile Gln Leu Pro Asn Arg His Asp Phe His Met Asn Ile Leu Asp
100 105 110
Thr Arg Arg Asn Asp Ser Gly Ile Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125
His Pro Lys Ala Lys Ile Glu Glu Ser Pro Gly Ala Glu Leu Val Val
130 135 140
Thr Glu Arg Ile Cys His Thr Gln Ser Ser Pro Lys Leu Phe Trp Ala
145 150 155 160
Leu Val Val Val Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr
165 170 175
Val Ala Leu Cys Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly
180 185 190
Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg
195 200 205
Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg
210 215 220
Pro
225

<210> 135
<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> muLag3tm-CD28

<400> 135
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gtgtcatctg gccctggcaa agaactgccc gtcgtgtggg ctcaggaagg cgctcctgtg 120
catctgccct gcagcctgaa gtcccccaac ctggacccca acttcctgag aagaggcggc 180
gtgatctggc agcaccagcc tgattctggc cagcccacac ctatccctgc cctggatctg 240
caccagggca tgcctagccc tagacagcct gcccctggca gatacaccgt gctgtctgtg 300
gctcctggcg gcctgagaag tggcagacag cctctgcacc ctcacgtgca gctggaagag 360
aggggactgc agaggggcga cttcagcctg tggctgaggc ctgccctgag aacagatgcc 420
ggcgagtacc acgctaccgt gcggctgcct aacagagccc tgagctgctc cctgagactg 480
agagtgggcc aggccagcat gatcgcctct ccatctggcg tgctgaagct gagcgactgg 540
gtgctgctga actgcagctt ctccagaccc gacagacccg tgtccgtgca ctggttccag 600
ggacagaaca gagtgcccgt gtacaacagc cccagacact tcctggccga gacattcctg 660
ctgctgcccc aggtgtcccc tctggactct ggcacatggg gctgcgtgct gacatacagg 720
gacggcttca acgtgtccat cacctacaac ctgaaggtgc tgggcctgga acccgtggct 780
cctctgacag tgtacgccgc cgagggcagc agagtggaac tgccttgtca tctgccaccc 840
ggcgtgggca caccttctct gctgatcgcc aagtggaccc ctccaggcgg aggacctgaa 900
ctgccagtgg ctggcaagag cggcaacttc accctgcacc tggaagcagt gggcctggct 960
caggccggca cctacacctg tagcatccat ctgcagggcc agcagctgaa cgccaccgtg 1020
acactggccg tgatcaccgt gacccccaag agctttggcc tgcctggctc cagaggcaag 1080
ctgctgtgtg aagtgacccc cgccagcggc aaagaaagat tcgtgtggcg gcctctgaac 1140
aacctgagca gatcctgccc aggccccgtg ctggaaatcc aggaagccag actgctggcc 1200
gagcggtggc agtgccagct gtatgaggga cagcgactgc tgggcgccac tgtgtacgct 1260
gctgagtcta gctctggcgc ccacagcgcc agaagaatca gcggcgatct gaagggcggc 1320
cacctggtgc tggtgctgat cctgggcgct ctgagcctgt tcctgctggt ggctggcgct 1380
ttcggcttta acagcagaag aaacagaggc ggccagagcg actacatgaa catgaccccc 1440
agaaggcctg gcctgaccag aaagccctac cagccttacg cccctgccag agacttcgcc 1500
gcctacagac ct 1512

<210> 136
<211> 504
<212> PRT

<213> Artificial Sequence

<220>
<223> muLag3tm-CD28

<400> 136
Met Arg Glu Asp Leu Leu Leu Gly Phe Leu Leu Leu Gly Leu Leu Trp
 1   5   10   15
Glu Ala Pro Val Val Ser Ser Gly Pro Gly Lys Glu Leu Pro Val Val
            20   25   30
Trp Ala Gln Glu Gly Ala Pro Val His Leu Pro Cys Ser Leu Lys Ser
        35   40   45
Pro Asn Leu Asp Pro Asn Phe Leu Arg Arg Gly Gly Val Ile Trp Gln
    50   55   60
His Gln Pro Asp Ser Gly Gln Pro Thr Pro Ile Pro Ala Leu Asp Leu
65   70   75   80
His Gln Gly Met Pro Ser Pro Arg Gln Pro Ala Pro Gly Arg Tyr Thr
                85   90   95
Val Leu Ser Val Ala Pro Gly Gly Leu Arg Ser Gly Arg Gln Pro Leu
            100   105   110
His Pro His Val Gln Leu Glu Glu Arg Gly Leu Gln Arg Gly Asp Phe
        115   120   125
Ser Leu Trp Leu Arg Pro Ala Leu Arg Thr Asp Ala Gly Glu Tyr His
    130   135   140
Ala Thr Val Arg Leu Pro Asn Arg Ala Leu Ser Cys Ser Leu Arg Leu
145   150   155   160
Arg Val Gly Gln Ala Ser Met Ile Ala Ser Pro Ser Gly Val Leu Lys
                165   170   175
Leu Ser Asp Trp Val Leu Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg
            180   185   190
Pro Val Ser Val His Trp Phe Gln Gly Gln Asn Arg Val Pro Val Tyr
        195   200   205
Asn Ser Pro Arg His Phe Leu Ala Glu Thr Phe Leu Leu Leu Pro Gln
    210   215   220
Val Ser Pro Leu Asp Ser Gly Thr Trp Gly Cys Val Leu Thr Tyr Arg
225   230   235   240
Asp Gly Phe Asn Val Ser Ile Thr Tyr Asn Leu Lys Val Leu Gly Leu
                245   250   255
Glu Pro Val Ala Pro Leu Thr Val Tyr Ala Ala Glu Gly Ser Arg Val
            260   265   270
Glu Leu Pro Cys His Leu Pro Pro Gly Val Gly Thr Pro Ser Leu Leu
        275   280   285
Ile Ala Lys Trp Thr Pro Pro Gly Gly Gly Pro Glu Leu Pro Val Ala
    290   295   300
Gly Lys Ser Gly Asn Phe Thr Leu His Leu Glu Ala Val Gly Leu Ala
305   310   315   320
Gln Ala Gly Thr Tyr Thr Cys Ser Ile His Leu Gln Gly Gln Gln Leu
                325   330   335
Asn Ala Thr Val Thr Leu Ala Val Ile Thr Val Thr Pro Lys Ser Phe
            340   345   350
Gly Leu Pro Gly Ser Arg Gly Lys Leu Leu Cys Glu Val Thr Pro Ala
        355   360   365
Ser Gly Lys Glu Arg Phe Val Trp Arg Pro Leu Asn Asn Leu Ser Arg
    370   375   380
Ser Cys Pro Gly Pro Val Leu Glu Ile Gln Glu Ala Arg Leu Leu Ala
385   390   395   400
Glu Arg Trp Gln Cys Gln Leu Tyr Glu Gly Gln Arg Leu Leu Gly Ala
                405   410   415
Thr Val Tyr Ala Ala Glu Ser Ser Ser Gly Ala His Ser Ala Arg Arg
            420   425   430
Ile Ser Gly Asp Leu Lys Gly Gly His Leu Val Leu Val Leu Ile Leu
        435   440   445
Gly Ala Leu Ser Leu Phe Leu Leu Val Ala Gly Ala Phe Gly Phe Asn
    450   455   460
Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro
465   470   475   480
Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala
                485   490   495

Arg Asp Phe Ala Ala Tyr Arg Pro
500

<210> 137
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> muLag3-CD28tm

<400> 137
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catctgccct gcagcctgaa gtcccccaac ctggacccca acttcctgag aagaggcggc 180
gtgatctggc agcaccagcc tgattctggc cagcccacac ctatccctgc cctggatctg 240
caccagggca tgcctagccc tagacagcct gcccctggca gatacaccgt gctgtctgtg 300
gctcctggcg gcctgagaag tggcagacag cctctgcacc ctcacgtgca gctggaagag 360
aggggactgc agaggggcga cttcagcctg tggctgaggc ctgccctgag aacagatgcc 420
ggcgagtacc acgctaccgt gcggctgcct aacagagccc tgagctgctc cctgagactg 480
agagtgggcc aggccagcat gatcgcctct ccatctggcg tgctgaagct gagcgactgg 540
gtgctgctga actgcagctt ctccagaccc gacagacccg tgtccgtgca ctggttccag 600
ggacagaaca gagtgcccgt gtacaacagc cccagacact tcctggccga gacattcctg 660
ctgctgcccc aggtgtcccc tctggactct ggcacatggg gctgcgtgct gacatacagg 720
gacggcttca acgtgtccat cacctacaac ctgaaggtgc tgggcctgga acccgtggct 780
cctctgacag tgtacgccgc cgagggcagc agagtggaac tgccttgtca tctgccaccc 840
ggcgtgggca caccttctct gctgatcgcc aagtggaccc ctccaggcgg aggacctgaa 900
ctgccagtgg ctggcaagag cggcaacttc accctgcacc tggaagcagt gggcctggct 960
caggccggca cctacacctg tagcatccat ctgcagggcc agcagctgaa cgccaccgtg 1020
acactggccg tgatcaccgt gacccccaag agctttggcc tgcctggctc cagaggcaag 1080
ctgctgtgtg aagtgacccc cgccagcggc aaagaaagat tcgtgtggcg gcctctgaac 1140
aacctgagca gatcctgccc aggccccgtg ctggaaatcc aggaagccag actgctggcc 1200
gagcggtggc agtgccagct gtatgaggga cagcgactgc tgggcgccac tgtgtacgct 1260
gctgagtcta gctctggcgc ccacagcgcc agaagaatca gcggcgatct gaagggcggc 1320
cacctgttct gggccctggt ggtggtggcc ggcgtgctgt tttgttacgg cctgctcgtg 1380
accgtggccc tgtgcgtgat ctggaccaac agcagaagaa acagaggcgg ccagagcgac 1440
tacatgaaca tgacccccag aaggcctggc ctgaccagaa agccctacca gccttacgcc 1500
cctgccagag acttcgccgc ctacagacct 1530

<210> 138
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> muLag3-CD28tm

<400> 138
Met Arg Glu Asp Leu Leu Leu Gly Phe Leu Leu Leu Gly Leu Leu Trp
1 5 10 15
Glu Ala Pro Val Val Ser Ser Gly Pro Gly Lys Glu Leu Pro Val Val
20 25 30
Trp Ala Gln Glu Gly Ala Pro Val His Leu Pro Cys Ser Leu Lys Ser
35 40 45
Pro Asn Leu Asp Pro Asn Phe Leu Arg Arg Gly Gly Val Ile Trp Gln
50 55 60
His Gln Pro Asp Ser Gly Gln Pro Thr Pro Ile Pro Ala Leu Asp Leu
65 70 75 80
His Gln Gly Met Pro Ser Pro Arg Gln Pro Ala Pro Gly Arg Tyr Thr
85 90 95
Val Leu Ser Val Ala Pro Gly Gly Leu Arg Ser Gly Arg Gln Pro Leu
100 105 110
His Pro His Val Gln Leu Glu Glu Arg Gly Leu Gln Arg Gly Asp Phe
115 120 125
Ser Leu Trp Leu Arg Pro Ala Leu Arg Thr Asp Ala Gly Glu Tyr His
130 135 140
Ala Thr Val Arg Leu Pro Asn Arg Ala Leu Ser Cys Ser Leu Arg Leu
145 150 155 160

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Arg Val Gly Gln Ala Ser Met Ile Ala Ser Pro Ser Gly Val Leu Lys
                165                 170                 175
Leu Ser Asp Trp Val Leu Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg
            180                 185                 190
Pro Val Ser Val His Trp Phe Gln Gly Gln Asn Arg Val Pro Val Tyr
        195                 200                 205
Asn Ser Pro Arg His Phe Leu Ala Glu Thr Phe Leu Leu Leu Pro Gln
    210                 215                 220
Val Ser Pro Leu Asp Ser Gly Thr Trp Gly Cys Val Leu Thr Tyr Arg
225                 230                 235                 240
Asp Gly Phe Asn Val Ser Ile Thr Tyr Asn Leu Lys Val Leu Gly Leu
                245                 250                 255
Glu Pro Val Ala Pro Leu Thr Val Tyr Ala Ala Glu Gly Ser Arg Val
            260                 265                 270
Glu Leu Pro Cys His Leu Pro Pro Gly Val Gly Thr Pro Ser Leu Leu
        275                 280                 285
Ile Ala Lys Trp Thr Pro Pro Gly Gly Gly Pro Glu Leu Pro Val Ala
    290                 295                 300
Gly Lys Ser Gly Asn Phe Thr Leu His Leu Glu Ala Val Gly Leu Ala
305                 310                 315                 320
Gln Ala Gly Thr Tyr Thr Cys Ser Ile His Leu Gln Gly Gln Gln Leu
                325                 330                 335
Asn Ala Thr Val Thr Leu Ala Val Ile Thr Val Thr Pro Lys Ser Phe
            340                 345                 350
Gly Leu Pro Gly Ser Arg Gly Lys Leu Leu Cys Glu Val Thr Pro Ala
        355                 360                 365
Ser Gly Lys Glu Arg Phe Val Trp Arg Pro Leu Asn Asn Leu Ser Arg
    370                 375                 380
Ser Cys Pro Gly Pro Val Leu Glu Ile Gln Glu Ala Arg Leu Leu Ala
385                 390                 395                 400
Glu Arg Trp Gln Cys Gln Leu Tyr Glu Gly Gln Arg Leu Leu Gly Ala
                405                 410                 415
Thr Val Tyr Ala Ala Glu Ser Ser Ser Gly Ala His Ser Ala Arg Arg
            420                 425                 430
Ile Ser Gly Asp Leu Lys Gly Gly His Leu Phe Trp Ala Leu Val Val
        435                 440                 445
Val Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu
    450                 455                 460
Cys Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp
465                 470                 475                 480
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr
                485                 490                 495
Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
            500                 505                 510
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<210> 139
<211> 1557
<212> DNA
<213> Artificial Sequence

<220>
<223> muLag3-CD28Cys

<400> 139

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gtgtcatctg gccctggcaa agaactgccc gtcgtgtggg ctcaggaagg cgctcctgtg     120
catctgccct gcagcctgaa gtcccccaac ctggacccca acttcctgag aagaggcggc     180
gtgatctggc agcaccagcc tgattctggc cagcccacac ctatccctgc cctggatctg     240
caccagggca tgcctagccc tagacagcct gcccctggca gatacaccgt gctgtctgtg     300
gctcctggcg gcctgagaag tggcagacag cctctgcacc ctcacgtgca gctggaagag     360
aggggactgc agaggggcga cttcagcctg tggctgaggc ctgccctgag aacagatgcc     420
ggcgagtacc acgctaccgt gcggctgcct aacagagccc tgagctgctc cctgagactg     480
agagtgggcc aggccagcat gatcgcctct ccatctggcg tgctgaagct gagcgactgg     540
gtgctgctga actgcagctt ctccagaccc gacagacccg tgtccgtgca ctggttccag     600
ggacagaaca gagtgcccgt gtacaacagc cccagacact tcctggccga gacattcctg     660
ctgctgcccc aggtgtcccc tctggactct ggcacatggg gctgcgtgct gacatacagg     720
gacggcttca acgtgtccat cacctacaac ctgaaggtgc tgggcctgga acccgtggct     780
cctctgacag tgtacgccgc cgagggcagc agagtggaac tgccttgtca tctgccaccc     840
```

```
ggcgtgggca caccttctct gctgatcgcc aagtggaccc ctccaggcgg aggacctgaa      900
ctgccagtgg ctggcaagag cggcaacttc accctgcacc tggaagcagt gggcctggct      960
caggccggca cctacacctg tagcatccat ctgcagggcc agcagctgaa cgccaccgtg     1020
acactggccg tgatcaccgt gacccccaag agctttggcc tgcctggctc cagaggcaag     1080
ctgctgtgtg aagtgacccc cgccagcggc aaagaaagat tcgtgtggcg gcctctgaac     1140
aacctgagca gatcctgccc aggccccgtg ctggaaatcc aggaagccag actgctggcc     1200
gagcggtggc agtgccagct gtatgaggga cagcgactgc tgggcgccac tgtgtacgct     1260
gctgagtcta gctctggcgc ccacagcgcc agaagaatca gcggcgatct gaagggcggc     1320
cacctgtgcc acacccagag cagccccaag ctgttctggg ccctggtggt ggtggccggc     1380
gtgctgtttt gttacggcct gctcgtgacc gtggccctgt gcgtgatctg gaccaacagc     1440
agaagaaaca gaggcggcca gagcgactac atgaacatga cccccagaag gcctggcctg     1500
accagaaagc cctaccagcc ttacgccccc gccagagact tcgccgccta cagacct        1557

<210> 140
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> muLag3-CD28Cys

<400> 140
Met Arg Glu Asp Leu Leu Leu Gly Phe Leu Leu Leu Gly Leu Leu Trp
 1               5                  10                  15
Glu Ala Pro Val Val Ser Ser Gly Pro Gly Lys Glu Leu Pro Val Val
            20                  25                  30
Trp Ala Gln Glu Gly Ala Pro Val His Leu Pro Cys Ser Leu Lys Ser
        35                  40                  45
Pro Asn Leu Asp Pro Asn Phe Leu Arg Arg Gly Gly Val Ile Trp Gln
    50                  55                  60
His Gln Pro Asp Ser Gly Gln Pro Thr Pro Ile Pro Ala Leu Asp Leu
65                  70                  75                  80
His Gln Gly Met Pro Ser Pro Arg Gln Pro Ala Pro Gly Arg Tyr Thr
                85                  90                  95
Val Leu Ser Val Ala Pro Gly Gly Leu Arg Ser Gly Arg Gln Pro Leu
            100                 105                 110
His Pro His Val Gln Leu Glu Glu Arg Gly Leu Gln Arg Gly Asp Phe
        115                 120                 125
Ser Leu Trp Leu Arg Pro Ala Leu Arg Thr Asp Ala Gly Glu Tyr His
    130                 135                 140
Ala Thr Val Arg Leu Pro Asn Arg Ala Leu Ser Cys Ser Leu Arg Leu
145                 150                 155                 160
Arg Val Gly Gln Ala Ser Met Ile Ala Ser Pro Ser Gly Val Leu Lys
                165                 170                 175
Leu Ser Asp Trp Val Leu Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg
            180                 185                 190
Pro Val Ser Val His Trp Phe Gln Gly Gln Asn Arg Val Pro Val Tyr
        195                 200                 205
Asn Ser Pro Arg His Phe Leu Ala Glu Thr Phe Leu Leu Leu Pro Gln
    210                 215                 220
Val Ser Pro Leu Asp Ser Gly Thr Trp Gly Cys Val Leu Thr Tyr Arg
225                 230                 235                 240
Asp Gly Phe Asn Val Ser Ile Thr Tyr Asn Leu Lys Val Leu Gly Leu
                245                 250                 255
Glu Pro Val Ala Pro Leu Thr Val Tyr Ala Ala Glu Gly Ser Arg Val
            260                 265                 270
Glu Leu Pro Cys His Leu Pro Pro Gly Val Gly Thr Pro Ser Leu Leu
        275                 280                 285
Ile Ala Lys Trp Thr Pro Pro Gly Gly Gly Pro Glu Leu Pro Val Ala
    290                 295                 300
Gly Lys Ser Gly Asn Phe Thr Leu His Leu Glu Ala Val Gly Leu Ala
305                 310                 315                 320
Gln Ala Gly Thr Tyr Thr Cys Ser Ile His Leu Gln Gly Gln Gln Leu
                325                 330                 335
Asn Ala Thr Val Thr Leu Ala Val Ile Thr Val Thr Pro Lys Ser Phe
            340                 345                 350
Gly Leu Pro Gly Ser Arg Gly Lys Leu Leu Cys Glu Val Thr Pro Ala
        355                 360                 365
```

```
Ser Gly Lys Glu Arg Phe Val Trp Arg Pro Leu Asn Asn Leu Ser Arg
    370                 375                 380
Ser Cys Pro Gly Pro Val Leu Glu Ile Gln Glu Ala Arg Leu Leu Ala
385                 390                 395                 400
Glu Arg Trp Gln Cys Gln Leu Tyr Glu Gly Gln Arg Leu Leu Gly Ala
                405                 410                 415
Thr Val Tyr Ala Ala Glu Ser Ser Ser Gly Ala His Ser Ala Arg Arg
            420                 425                 430
Ile Ser Gly Asp Leu Lys Gly Gly His Leu Cys His Thr Gln Ser Ser
        435                 440                 445
Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe Cys
    450                 455                 460
Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn Ser
465                 470                 475                 480
Arg Arg Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg
                485                 490                 495
Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg
            500                 505                 510
Asp Phe Ala Ala Tyr Arg Pro
        515
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<210> 141
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> muLag3-9aas-CD28Cys

<400> 141

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atgagagagg acctgctgct gggctttctg ctgctgggac tgctgtggga ggcccctgtg      60
gtgtcatctg gccctggcaa agaactgccc gtcgtgtggg ctcaggaagg cgctcctgtg     120
catctgccct gcagcctgaa gtcccccaac ctggacccca acttcctgag aagaggcggc     180
gtgatctggc agcaccagcc tgattctggc cagcccacac ctatccctgc cctggatctg     240
caccagggca tgcctagccc tagacagcct gcccctggca gatacaccgt gctgtctgtg     300
gctcctggcg gcctgagaag tggcagacag cctctgcacc ctcacgtgca gctggaagag     360
aggggactgc agaggggcga cttcagcctg tggctgaggc ctgccctgag aacagatgcc     420
ggcgagtacc acgctaccgt gcggctgcct aacagagccc tgagctgctc cctgagactg     480
agagtgggcc aggccagcat gatcgcctct ccatctggcg tgctgaagct gagcgactgg     540
gtgctgctga actgcagctt ctccagaccc gacagacccg tgtccgtgca ctggttccag     600
ggacagaaca gagtgcccgt gtacaacagc cccagacact tcctggccga gacattcctg     660
ctgctgcccc aggtgtcccc tctggactct ggcacatggg gctgcgtgct gacatacagg     720
gacggcttca acgtgtccat cacctacaac ctgaaggtgc tgggcctgga acccgtggct     780
cctctgacag tgtacgccgc cgagggcagc agagtggaac tgccttgtca tctgccaccc     840
ggcgtgggca caccttctct gctgatcgcc aagtggaccc ctccaggcgg aggacctgaa     900
ctgccagtgg ctggcaagag cggcaacttc accctgcacc tggaagcagt gggcctggct     960
caggccggca cctacacctg tagcatccat ctgcagggcc agcagctgaa cgccaccgtg    1020
acactggccg tgatcaccgt gaccccaag agctttggcc tgcctggctc cagaggcaag    1080
ctgctgtgtg aagtgacccc cgccagcggc aaagaaagat tcgtgtggcg gcctctgaac    1140
aacctgagca gatcctgccc aggccccgtg ctggaaatcc aggaagccag actgctggcc    1200
gagcggtggc agtgccagct gtatgaggga cagcgactgc tgggcgccac tgtgtacgct    1260
gctgagtcta gctctggcgc ccacagcgcc agaagaatct gccacaccca gagcagcccc    1320
aagctgttct gggccctggt ggtggtggcc ggcgtgctgt tttgttacgg cctgctcgtg    1380
accgtggccc tgtgcgtgat ctggaccaac agcagaagaa acagaggcgg ccagagcgac    1440
tacatgaaca tgacccccag aaggcctggc ctgaccagaa agccctacca gccttacgcc    1500
cctgccagag acttcgccgc ctacagacct                                     1530
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<210> 142
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> muLag3-9aas-CD28Cys

<400> 142

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Met Arg Glu Asp Leu Leu Leu Gly Phe Leu Leu Leu Gly Leu Leu Trp
 1               5                  10                  15
```

```
Glu Ala Pro Val Val Ser Ser Gly Pro Gly Lys Glu Leu Pro Val Val
            20                  25                  30
Trp Ala Gln Glu Gly Ala Pro Val His Leu Pro Cys Ser Leu Lys Ser
        35                  40                  45
Pro Asn Leu Asp Pro Asn Phe Leu Arg Arg Gly Gly Val Ile Trp Gln
    50                  55                  60
His Gln Pro Asp Ser Gly Gln Pro Thr Pro Ile Pro Ala Leu Asp Leu
65                  70                  75                  80
His Gln Gly Met Pro Ser Pro Arg Gln Pro Ala Pro Gly Arg Tyr Thr
                85                  90                  95
Val Leu Ser Val Ala Pro Gly Gly Leu Arg Ser Gly Arg Gln Pro Leu
            100                 105                 110
His Pro His Val Gln Leu Glu Glu Arg Gly Leu Gln Arg Gly Asp Phe
        115                 120                 125
Ser Leu Trp Leu Arg Pro Ala Leu Arg Thr Asp Ala Gly Glu Tyr His
    130                 135                 140
Ala Thr Val Arg Leu Pro Asn Arg Ala Leu Ser Cys Ser Leu Arg Leu
145                 150                 155                 160
Arg Val Gly Gln Ala Ser Met Ile Ala Ser Pro Ser Gly Val Leu Lys
                165                 170                 175
Leu Ser Asp Trp Val Leu Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg
            180                 185                 190
Pro Val Ser Val His Trp Phe Gln Gly Gln Asn Arg Val Pro Val Tyr
        195                 200                 205
Asn Ser Pro Arg His Phe Leu Ala Glu Thr Phe Leu Leu Leu Pro Gln
    210                 215                 220
Val Ser Pro Leu Asp Ser Gly Thr Trp Gly Cys Val Leu Thr Tyr Arg
225                 230                 235                 240
Asp Gly Phe Asn Val Ser Ile Thr Tyr Asn Leu Lys Val Leu Gly Leu
                245                 250                 255
Glu Pro Val Ala Pro Leu Thr Val Tyr Ala Ala Glu Gly Ser Arg Val
            260                 265                 270
Glu Leu Pro Cys His Leu Pro Pro Gly Val Gly Thr Pro Ser Leu Leu
        275                 280                 285
Ile Ala Lys Trp Thr Pro Pro Gly Gly Gly Pro Glu Leu Pro Val Ala
    290                 295                 300
Gly Lys Ser Gly Asn Phe Thr Leu His Leu Glu Ala Val Gly Leu Ala
305                 310                 315                 320
Gln Ala Gly Thr Tyr Thr Cys Ser Ile His Leu Gln Gly Gln Gln Leu
                325                 330                 335
Asn Ala Thr Val Thr Leu Ala Val Ile Thr Val Thr Pro Lys Ser Phe
            340                 345                 350
Gly Leu Pro Gly Ser Arg Gly Lys Leu Leu Cys Glu Val Thr Pro Ala
        355                 360                 365
Ser Gly Lys Glu Arg Phe Val Trp Arg Pro Leu Asn Asn Leu Ser Arg
    370                 375                 380
Ser Cys Pro Gly Pro Val Leu Glu Ile Gln Glu Ala Arg Leu Leu Ala
385                 390                 395                 400
Glu Arg Trp Gln Cys Gln Leu Tyr Glu Gly Gln Arg Leu Leu Gly Ala
                405                 410                 415
Thr Val Tyr Ala Ala Glu Ser Ser Ser Gly Ala His Ser Ala Arg Arg
            420                 425                 430
Ile Cys His Thr Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val
        435                 440                 445
Val Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu
    450                 455                 460
Cys Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp
465                 470                 475                 480
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr
                485                 490                 495
Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
            500                 505                 510
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<210> 143
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> muTim3tm-CD28

<400> 143
atgttcagcg gcctgaccct gaactgcgtg ctcctgctgc tgcagctgct gctggccaga 60
agcctggaaa acgcctacgt gttcgaagtg ggcaagaacg cctacctgcc ctgcagctac 120
accctgtcta cacctggcgc cctggtgcct atgtgttggg gcaagggctt ctgcccttgg 180
agccagtgca ccaacgagct gctgagaacc gacgagagaa acgtgaccta ccagaagtcc 240
agcagatacc agctgaaggg cgacctgaac aagggcgacg tgtccctgat catcaagaac 300
gtgaccctgg acgaccacgg cacctactgc tgcagaatcc agttccccgg cctgatgaac 360
gacaagaagc tggaactgaa gctggacatc aaggccgcca aagtgacccc tgcccagaca 420
gcccacggcg actctacaac agccagcccc agaaccctga ccaccgagag gaacggcagc 480
gagacacaga ccctcgtgac actgcacaac aacaacggca ccaagatcag cacctgggcc 540
gacgagatca aggacagcgg cgagacaatc agaaccgcca tccacatcgg cgtgggcgtg 600
tccgctggac tgacactggc tctgatcatc ggagtgctga tcaacagcag aagaaacaga 660
ggcggccaga gcgactacat gaacatgacc cccagaaggc ctggcctgac cagaaagccc 720
taccagcctt acgcccctgc cagagacttc gccgcctaca gacct 765

<210> 144
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> muTim3tm-CD28

<400> 144
Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Leu Gln Leu
1 5 10 15
Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
20 25 30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
35 40 45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
50 55 60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65 70 75 80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
85 90 95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
100 105 110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
115 120 125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
130 135 140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145 150 155 160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
165 170 175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
180 185 190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
195 200 205
Ile Ile Gly Val Leu Ile Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser
210 215 220
Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro
225 230 235 240
Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
245 250 255

<210> 145
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> muTim3-CD28tm

<400> 145
atgttcagcg gcctgaccct gaactgcgtg ctcctgctgc tgcagctgct gctggccaga 60
agcctggaaa acgcctacgt gttcgaagtg ggcaagaacg cctacctgcc ctgcagctac 120
accctgtcta cacctggcgc cctggtgcct atgtgttggg gcaagggctt ctgcccttgg 180
agccagtgca ccaacgagct gctgagaacc gacgagagaa acgtgaccta ccagaagtcc 240
agcagatacc agctgaaggg cgacctgaac aagggcgacg tgtccctgat catcaagaac 300
gtgaccctgg acgaccacgg cacctactgc tgcagaatcc agttccccgg cctgatgaac 360
gacaagaagc tggaactgaa gctggacatc aaggccgcca aagtgacccc tgcccagaca 420
gcccacggcg actctacaac agccagcccc agaaccctga ccaccgagag gaacggcagc 480
gagacacaga ccctcgtgac actgcacaac aacaacggca ccaagatcag cacctgggcc 540
gacgagatca aggacagcgg cgagacaatc agaaccgcct tctgggccct ggtggtggtg 600
gccggcgtgc tgttttgtta cggcctgctc gtgaccgtgg ccctgtgcgt gatctggacc 660
aacagcagaa gaaacagagg cggccagagc gactacatga acatgacccc cagaaggcct 720
ggcctgacca gaaagcccta ccagccttac gcccctgcca gagacttcgc cgcctacaga 780
cct 783

<210> 146
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> muTim3-CD28tm

<400> 146
Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Leu Gln Leu
 1   5   10   15
Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
            20   25   30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
        35   40   45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
    50   55   60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65   70   75   80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
                85   90   95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
            100   105   110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
        115   120   125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
    130   135   140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145   150   155   160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
                165   170   175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
            180   185   190
Ala Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe Cys Tyr Gly
        195   200   205
Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn Ser Arg Arg
    210   215   220
Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
225   230   235   240
Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe
                245   250   255
Ala Ala Tyr Arg Pro
            260

<210> 147
<211> 810
<212> DNA
<213> Artificial Sequence

<220>
<223> muTim3-CD28Cys

<400> 147
atgttcagcg gcctgaccct gaactgcgtg ctcctgctgc tgcagctgct gctggccaga 60
agcctggaaa acgcctacgt gttcgaagtg ggcaagaacg cctacctgcc ctgcagctac 120
accctgtcta cacctggcgc cctggtgcct atgtgttggg gcaagggctt ctgcccttgg 180
agccagtgca ccaacgagct gctgagaacc gacgagagaa acgtgaccta ccagaagtcc 240
agcagatacc agctgaaggg cgacctgaac aagggcgacg tgtccctgat catcaagaac 300
gtgaccctgg acgaccacgg cacctactgc tgcagaatcc agttccccgg cctgatgaac 360
gacaagaagc tggaactgaa gctggacatc aaggccgcca aagtgacccc tgcccagaca 420
gcccacggcg actctacaac agccagcccc agaaccctga ccaccgagag gaacggcagc 480
gagacacaga ccctcgtgac actgcacaac aacaacggca ccaagatcag cacctgggcc 540
gacgagatca aggacagcgg cgagacaatc agaaccgcct gccacaccca gagcagcccc 600
aagctgttct gggccctggt ggtggtggcc ggcgtgctgt tttgttacgg cctgctcgtg 660
accgtggccc tgtgcgtgat ctggaccaac agcagaagaa acagaggcgg ccagagcgac 720
tacatgaaca tgacccccag aaggcctggc ctgaccagaa agccctacca gccttacgcc 780
cctgccagag acttcgccgc ctacagacct 810

<210> 148
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> muTim3-CD28Cys

<400> 148
Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Leu Gln Leu
 1   5   10   15
Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
            20   25   30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
        35   40   45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
    50   55   60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65   70   75   80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
                85   90   95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
            100   105   110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
        115   120   125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
    130   135   140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145   150   155   160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
                165   170   175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
            180   185   190
Ala Cys His Thr Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val
        195   200   205
Val Ala Gly Val Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu
    210   215   220
Cys Val Ile Trp Thr Asn Ser Arg Arg Asn Arg Gly Gly Gln Ser Asp
225   230   235   240
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr
                245   250   255
Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
            260   265   270

<210> 149
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> muTim3-9aas-CD28Cys

<400> 149
atgttcagcg gcctgaccct gaactgcgtg ctcctgctgc tgcagctgct gctggccaga 60
agcctggaaa acgcctacgt gttcgaagtg ggcaagaacg cctacctgcc ctgcagctac 120
accctgtcta cacctggcgc cctggtgcct atgtgttggg gcaagggctt ctgcccttgg 180
agccagtgca ccaacgagct gctgagaacc gacgagagaa acgtgaccta ccagaagtcc 240
agcagatacc agctgaaggg cgacctgaac aagggcgacg tgtccctgat catcaagaac 300
gtgaccctgg acgaccacgg cacctactgc tgcagaatcc agttccccgg cctgatgaac 360
gacaagaagc tggaactgaa gctggacatc aaggccgcca aagtgacccc tgcccagaca 420
gcccacggcg actctacaac agccagcccc agaaccctga ccaccgagag gaacggcagc 480
gagacacaga ccctcgtgac actgcacaac aacaacggca ccaagatcag cacctgggcc 540
gacgagatca agtgccacac ccagagcagc cccaagctgt tctgggccct ggtggtggtg 600
gccggcgtgc tgttttgtta cggcctgctc gtgaccgtgg ccctgtgcgt gatctggacc 660
aacagcagaa gaaacagagg cggccagagc gactacatga acatgacccc cagaaggcct 720
ggcctgacca gaaagcccta ccagccttac gcccctgcca gagacttcgc cgcctacaga 780
cct 783

<210> 150
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> muTim3-9aas-CD28Cys

<400> 150
Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Leu Gln Leu
 1   5   10   15
Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
            20   25   30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
        35   40   45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
    50   55   60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65   70   75   80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
                85   90   95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
            100   105   110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
        115   120   125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
    130   135   140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145   150   155   160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
                165   170   175
Ser Thr Trp Ala Asp Glu Ile Lys Cys His Thr Gln Ser Ser Pro Lys
            180   185   190
Leu Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe Cys Tyr Gly
        195   200   205
Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn Ser Arg Arg
    210   215   220
Asn Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
225   230   235   240
Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe
                245   250   255
Ala Ala Tyr Arg Pro
            260

<210> 151
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3tm-CD28

<400> 151
atgtgggaag cgcagtttct tggacttctt tttctccagc cgctgtgggt tgcgccagta 60
aagccgctcc aacccggtgc agaggttccg gtagtgtggg cgcaagaggg tgcaccagcg 120
cagctcccct gcagtccgac gattccgctg caagatttgt cactgcttag aagggcgggc 180
gtaacgtggc agcaccaacc ggatagtggc cctccggctg cagcaccagg gcacccactc 240
gcccccggcc ctcatcccgc agcaccgagc agctggggtc ctagaccacg cagatataca 300
gtactctcag taggtcccgg cggcctgcgg tccggtcgct tgccccttca acctagagta 360
cagctggatg aaagaggtcg acaacggggt gatttctccc tctggttgag gcctgcacga 420
cgagcagatg ctggggagta tagggctgcc gtacacctgc gagaccgcgc acttagttgt 480
agactccggc tccggctggg acaggcctct atgacagcgt ccccccctgg gtccctgcga 540
gcctctgatt gggtaatact caactgctca ttttctcggc cagatcgccc cgctagtgtt 600
cattggttcc gaaatcgcgg ccaaggtcgc gtgcctgttc gagaatctcc acaccaccat 660
ttggcggagt cttttctttt tctgcctcag gtctccccta tggactctgg accgtggggc 720
tgtattttga catatcggga tgggtttaac gtgagtataa tgtataatct cactgtcttg 780
ggtcttgagc cacctacgcc gctgacggtg tacgcgggag ccggcagccg ggttggtctg 840
ccctgcaggc tgcctgcagg agtcgggaca aggtcattcc ttacagcaaa gtggaccccg 900
ccaggtgggg ggcccgacct ccttgtaacg ggagataatg gagatttcac tctgagactt 960
gaggatgtct ctcaagctca ggctgggact tatacatgtc acattcactt gcaagaacag 1020
cagttgaatg cgacggttac cctggctatc ataacagtaa cacctaaatc tttcggtagt 1080
ccgggtagcc tgggcaaact gttgtgtgag gtaacccccg tgtcaggtca agagcggttc 1140
gtctggagct cattggacac tccctcacag cgatccttta gcggaccctg gctcgaagcc 1200
caagaagccc agctgctttc ccaaccatgg cagtgtcaac tctatcaggg tgagcgcctt 1260
ctcggtgcgg ctgtctactt caccgaattg tcctctccgg gagcgcaaag aagtggacgc 1320
gccccagggg ccctcccggc aggacacctt ctgctgtttt tgattttggg ggtacttagt 1380
ttgctgctgc ttgtcacagg cgctttcggt ttccgcagca agcggagcag aggcggccac 1440
agcgactaca tgaacatgac ccctagacgg cctggcccca ccagaaagca ctaccagccc 1500
tacgcccctc cccgggactt tgccgcctac agaagc 1536

<210> 152
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3tm-CD28

<400> 152
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
 1   5   10   15
Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
            20   25   30
Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
        35   40   45
Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
    50   55   60
His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65   70   75   80
Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
                85   90   95
Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
            100   105   110
Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
        115   120   125
Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130   135   140
Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145   150   155   160
Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165   170   175
Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180   185   190
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195   200   205
Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210   215   220
Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225   230   235   240
Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn

```
                245                 250                 255
Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260                 265                 270
Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275                 280                 285
Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290                 295                 300
Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305                 310                 315                 320
Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325                 330                 335
Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340                 345                 350
Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355                 360                 365
Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370                 375                 380
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385                 390                 395                 400
Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405                 410                 415
Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420                 425                 430
Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
        435                 440                 445
His Leu Leu Leu Phe Leu Ile Leu Gly Val Leu Ser Leu Leu Leu Leu
    450                 455                 460
Val Thr Gly Ala Phe Gly Phe Arg Ser Lys Arg Ser Arg Gly Gly His
465                 470                 475                 480
Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
                485                 490                 495
His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
            500                 505                 510
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<210> 153
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3 ectodomain

<400> 153

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atgtgggaag cgcagtttct tggacttctt tttctccagc cgctgtgggt tgcgccagta      60
aagccgctcc aacccggtgc agaggttccg gtagtgtggg cgcaagaggg tgcaccagcg     120
cagctcccct gcagtccgac gattccgctg caagatttgt cactgcttag aagggcgggc     180
gtaacgtggc agcaccaacc ggatagtggc cctccggctg cagcaccagg gcacccactc     240
gcccccggcc ctcatcccgc agcaccgagc agctggggtc ctagaccacg cagatataca     300
gtactctcag taggtcccgg cggcctgcgg tccggtcgct tgccccttca acctagagta     360
cagctggatg aaagaggtcg acaacggggt gatttctccc tctggttgag gcctgcacga     420
cgagcagatg ctggggagta tagggctgcc gtacacctgc gagaccgcgc acttagttgt     480
agactccggc tccggctggg acaggcctct atgacagcgt ccccccctgg gtccctgcga     540
gcctctgatt gggtaatact caactgctca ttttctcggc cagatcgccc cgctagtgtt     600
cattggttcc gaaatcgcgg ccaaggtcgc gtgcctgttc gagaatctcc acaccaccat     660
ttggcggagt cttttctttt tctgcctcag gtctccccta tggactctgg accgtggggc     720
tgtattttga catatcggga tgggtttaac gtgagtataa tgtataatct cactgtcttg     780
ggtcttgagc cacctacgcc gctgacggtg tacgcgggag ccggcagccg ggttggtctg     840
ccctgcaggc tgcctgcagg agtcgggaca aggtcattcc ttacagcaaa gtggaccccg     900
ccaggtgggg ggcccgacct ccttgtaacg ggagataatg gagatttcac tctgagactt     960
gaggatgtct ctcaagctca ggctgggact tatacatgtc acattcactt gcaagaacag    1020
cagttgaatg cgacggttac cctggctatc ataacagtaa cacctaaatc tttcggtagt    1080
ccgggtagcc tgggcaaact gttgtgtgag gtaacccccg tgtcaggtca agagcggttc    1140
gtctggagct cattggacac tccctcacag cgatccttta gcggaccctg gctcgaagcc    1200
caagaagccc agctgctttc ccaaccatgg cagtgtcaac tctatcaggg tgagcgcctt    1260
ctcggtgcgg ctgtctactt caccgaattg tcctctccgg gagcgcaaag aagtggacgc    1320
gccccagggg ccctcccggc aggacacctt                                     1350
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<210> 154

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3 ectodomain

<400> 154
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
 1   5   10   15
Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
            20   25   30
Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
        35   40   45
Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
    50   55   60
His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65   70   75   80
Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
                85   90   95
Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
            100   105   110
Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
        115   120   125
Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130   135   140
Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145   150   155   160
Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165   170   175
Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180   185   190
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195   200   205
Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210   215   220
Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225   230   235   240
Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245   250   255
Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260   265   270
Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275   280   285
Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290   295   300
Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305   310   315   320
Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325   330   335
Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340   345   350
Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355   360   365
Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370   375   380
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385   390   395   400
Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405   410   415
Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420   425   430
Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
        435   440   445
His Leu
    450

<210> 155

<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3 transmembrane domain

<400> 155
ctgctgtttt tgattttggg ggtacttagt ttgctgctgc ttgtcacagg cgctttcggt 60
ttc 63

<210> 156
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3 transmembrane domain

<400> 156
Leu Leu Phe Leu Ile Leu Gly Val Leu Ser Leu Leu Leu Leu Val Thr
1 5 10 15
Gly Ala Phe Gly Phe
20

<210> 157
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3-CD28tm

<400> 157
atgtgggaag cgcagtttct tggacttctt tttctccagc cgctgtgggt tgcgccagta 60
aagccgctcc aacccggtgc agaggttccg gtagtgtggg cgcaagaggg tgcaccagcg 120
cagctcccct gcagtccgac gattccgctg caagatttgt cactgcttag aagggcgggc 180
gtaacgtggc agcaccaacc ggatagtggc cctccggctg cagcaccagg gcacccactc 240
gcccccggcc ctcatcccgc agcaccgagc agctggggtc ctagaccacg cagatataca 300
gtactctcag taggtcccgg cggcctgcgg tccggtcgct tgccccttca acctagagta 360
cagctggatg aaagaggtcg acaacggggt gatttctccc tctggttgag gcctgcacga 420
cgagcagatg ctggggagta tagggctgcc gtacacctgc gagaccgcgc acttagttgt 480
agactccggc tccggctggg acaggcctct atgacagcgt ccccccctgg gtccctgcga 540
gcctctgatt gggtaatact caactgctca ttttctcggc cagatcgccc cgctagtgtt 600
cattggttcc gaaatcgcgg ccaaggtcgc gtgcctgttc gagaatctcc acaccaccat 660
ttggcggagt cttttctttt tctgcctcag gtctccccta tggactctgg accgtggggc 720
tgtattttga catatcggga tgggtttaac gtgagtataa tgtataatct cactgtcttg 780
ggtcttgagc cacctacgcc gctgacggtg tacgcgggag ccggcagccg ggttggtctg 840
ccctgcaggc tgcctgcagg agtcgggaca aggtcattcc ttacagcaaa gtggaccccg 900
ccaggtgggg ggcccgacct ccttgtaacg ggagataatg gagatttcac tctgagactt 960
gaggatgtct ctcaagctca ggctgggact tatacatgtc acattcactt gcaagaacag 1020
cagttgaatg cgacggttac cctggctatc ataacagtaa cacctaaatc tttcggtagt 1080
ccgggtagcc tgggcaaact gttgtgtgag gtaacccccg tgtcaggtca agagcggttc 1140
gtctggagct cattggacac tccctcacag cgatccttta gcggaccctg gctcgaagcc 1200
caagaagccc agctgctttc ccaaccatgg cagtgtcaac tctatcaggg tgagcgcctt 1260
ctcggtgcgg ctgtctactt caccgaattg tcctctccgg gagcgcaaag aagtggacgc 1320
gccccagggg ccctcccggc aggacacctt ttctgggtgc tggtggtggt cggaggcgtg 1380
ctggcctgct acagcctgct ggtcaccgtg gccttcatca tcttttgggt ccgcagcaag 1440
cggagcagag gcggccacag cgactacatg aacatgaccc ctagacggcc tggccccacc 1500
agaaagcact accagcccta cgcccctccc cgggactttg ccgcctacag aagc 1554

<210> 158
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3-CD28tm

<400> 158
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
 1   5   10   15
Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
            20   25   30
Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
        35   40   45
Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
    50   55   60
His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65   70   75   80
Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
                85   90   95
Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
            100   105   110
Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
        115   120   125
Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130   135   140
Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145   150   155   160
Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165   170   175
Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180   185   190
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195   200   205
Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210   215   220
Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225   230   235   240
Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245   250   255
Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260   265   270
Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275   280   285
Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290   295   300
Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305   310   315   320
Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325   330   335
Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340   345   350
Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355   360   365
Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370   375   380
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385   390   395   400
Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405   410   415
Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420   425   430
Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
        435   440   445
His Leu Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    450   455   460
Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
465   470   475   480
Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                485   490   495
Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            500   505   510
Phe Ala Ala Tyr Arg Ser
        515

<210> 159
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3-12aas-CD28Cys

<400> 159
atgtgggaag cgcagtttct tggacttctt tttctccagc cgctgtgggt tgcgccagta 60
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cagctcccct gcagtccgac gattccgctg caagatttgt cactgcttag aagggcgggc 180
gtaacgtggc agcaccaacc ggatagtggc cctccggctg cagcaccagg gcacccactc 240
gcccccggcc ctcatcccgc agcaccgagc agctggggtc ctagaccacg cagatataca 300
gtactctcag taggtcccgg cggcctgcgg tccggtcgct tgccccttca acctagagta 360
cagctggatg aaagaggtcg acaacggggt gatttctccc tctggttgag gcctgcacga 420
cgagcagatg ctggggagta tagggctgcc gtacacctgc gagaccgcgc acttagttgt 480
agactccggc tccggctggg acaggcctct atgacagcgt ccccccctgg gtccctgcga 540
gcctctgatt gggtaatact caactgctca ttttctcggc cagatcgccc cgctagtgtt 600
cattggttcc gaaatcgcgg ccaaggtcgc gtgcctgttc gagaatctcc acaccaccat 660
ttggcggagt cttttctttt tctgcctcag gtctccccta tggactctgg accgtggggc 720
tgtattttga catatcggga tgggtttaac gtgagtataa tgtataatct cactgtcttg 780
ggtcttgagc cacctacgcc gctgacggtg tacgcgggag ccggcagccg ggttggtctg 840
ccctgcaggc tgcctgcagg agtcgggaca aggtcattcc ttacagcaaa gtggaccccg 900
ccaggtgggg ggcccgacct ccttgtaacg ggagataatg gagatttcac tctgagactt 960
gaggatgtct ctcaagctca ggctgggact tatacatgtc acattcactt gcaagaacag 1020
cagttgaatg cgacggttac cctggctatc ataacagtaa cacctaaatc tttcggtagt 1080
ccgggtagcc tgggcaaact gttgtgtgag gtaacccccg tgtcaggtca agagcggttc 1140
gtctggagct cattggacac tccctcacag cgatccttta gcggaccctg gctcgaagcc 1200
caagaagccc agctgctttc ccaaccatgg cagtgtcaac tctatcaggg tgagcgcctt 1260
ctcggtgcgg ctgtctactt caccgaattg tcctctccgg gagcgcaaag aagttgtccc 1320
agccctctgt ttcccggccc tagcaagcct ttctgggtgc tggtggtggt cggaggcgtg 1380
ctggcctgct acagcctgct ggtcaccgtg gccttcatca tcttttgggt ccgcagcaag 1440
cggagcagag gcggccacag cgactacatg aacatgaccc ctagacggcc tggccccacc 1500
agaaagcact accagcccta cgcccctccc cgggactttg ccgcctacag aagc 1554

<210> 160
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3-12aas-CD28Cys

<400> 160
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
1 5 10 15
Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
20 25 30
Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
35 40 45
Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
50 55 60
His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65 70 75 80
Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
85 90 95
Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
100 105 110
Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
115 120 125
Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
130 135 140
Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145 150 155 160
Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
165 170 175

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Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180                 185                 190
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195                 200                 205
Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210                 215                 220
Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225                 230                 235                 240
Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245                 250                 255
Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260                 265                 270
Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275                 280                 285
Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290                 295                 300
Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305                 310                 315                 320
Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325                 330                 335
Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340                 345                 350
Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355                 360                 365
Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370                 375                 380
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385                 390                 395                 400
Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405                 410                 415
Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420                 425                 430
Pro Gly Ala Gln Arg Ser Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser
        435                 440                 445
Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    450                 455                 460
Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
465                 470                 475                 480
Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                485                 490                 495
Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            500                 505                 510
Phe Ala Ala Tyr Arg Ser
        515
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<210> 161
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3-12aas

<400> 161

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atgtgggaag cgcagtttct tggacttctt tttctccagc cgctgtgggt tgcgccagta      60
aagccgctcc aacccggtgc agaggttccg gtagtgtggg cgcaagaggg tgcaccagcg     120
cagctcccct gcagtccgac gattccgctg caagatttgt cactgcttag aagggcgggc     180
gtaacgtggc agcaccaacc ggatagtggc cctccggctg cagcaccagg gcacccactc     240
gcccccggcc ctcatcccgc agcaccgagc agctggggtc ctagaccacg cagatataca     300
gtactctcag taggtcccgg cggcctgcgg tccggtcgct tgccccttca acctagagta     360
cagctggatg aaagaggtcg acaacggggt gatttctccc tctggttgag gcctgcacga     420
cgagcagatg ctggggagta tagggctgcc gtacacctgc gagaccgcgc acttagttgt     480
agactccggc tccggctggg acaggcctct atgacagcgt ccccccctgg gtccctgcga     540
gcctctgatt gggtaatact caactgctca ttttctcggc cagatcgccc cgctagtgtt     600
cattggttcc gaaatcgcgg ccaaggtcgc gtgcctgttc gagaatctcc acaccaccat     660
ttggcggagt cttttctttt tctgcctcag gtctccccta tggactctgg accgtggggc     720
tgtattttga catatcggga tgggtttaac gtgagtataa tgtataatct cactgtcttg     780
ggtcttgagc cacctacgcc gctgacggtg tacgcgggag ccggcagccg ggttggtctg     840
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ccctgcaggc tgcctgcagg agtcgggaca aggtcattcc ttacagcaaa gtggaccccg 900
ccaggtgggg ggcccgacct ccttgtaacg ggagataatg gagatttcac tctgagactt 960
gaggatgtct ctcaagctca ggctgggact tatacatgtc acattcactt gcaagaacag 1020
cagttgaatg cgacggttac cctggctatc ataacagtaa cacctaaatc tttcggtagt 1080
ccgggtagcc tgggcaaact gttgtgtgag gtaacccccg tgtcaggtca agagcggttc 1140
gtctggagct cattggacac tccctcacag cgatccttta gcggaccctg gctcgaagcc 1200
caagaagccc agctgctttc ccaaccatgg cagtgtcaac tctatcaggg tgagcgcctt 1260
ctcggtgcgg ctgtctactt caccgaattg tcctctccgg gagcgcaaag aagt 1314

<210> 162
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3-12aas

<400> 162
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
 1   5   10   15
Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
            20   25   30
Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
        35   40   45
Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
    50   55   60
His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65   70   75   80
Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
                85   90   95
Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
            100   105   110
Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
        115   120   125
Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130   135   140
Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145   150   155   160
Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165   170   175
Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180   185   190
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195   200   205
Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210   215   220
Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225   230   235   240
Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245   250   255
Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260   265   270
Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275   280   285
Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290   295   300
Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305   310   315   320
Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325   330   335
Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340   345   350
Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355   360   365
Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370   375   380
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385   390   395   400

Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
405 410 415
Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
420 425 430
Pro Gly Ala Gln Arg Ser
435

<210> 163
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> huLag3-CD28Cys

<400> 163
atgtgggaag cgcagtttct tggacttctt tttctccagc cgctgtgggt tgcgccagta 60
aagccgctcc aacccggtgc agaggttccg gtagtgtggg cgcaagaggg tgcaccagcg 120
cagctccccc gcagtccgac gattccgctg caagatttgt cactgcttag aagggcgggc 180
gtaacgtggc agcaccaacc ggatagtggc cctccggctg cagcaccagg gcacccactc 240
gcccccggcc ctcatcccgc agcaccgagc agctggggtc ctagaccacg cagatataca 300
gtactctcag taggtcccgg cggcctgcgg tccggtcgct tgccccttca acctagagta 360
cagctggatg aaagaggtcg acaacggggt gatttctccc tctggttgag gcctgcacga 420
cgagcagatg ctggggagta tagggctgcc gtacacctgc gagaccgcgc acttagttgt 480
agactccggc tccggctggg acaggcctct atgacagcgt ccccccctgg gtccctgcga 540
gcctctgatt gggtaatact caactgctca ttttctcggc cagatcgccc cgctagtgtt 600
cattggttcc gaaatcgcgg ccaaggtcgc gtgcctgttc gagaatctcc acaccaccat 660
ttggcggagt cttttctttt tctgcctcag gtctccccta tggactctgg accgtggggc 720
tgtattttga catatcggga tgggtttaac gtgagtataa tgtataatct cactgtcttg 780
ggtcttgagc cacctacgcc gctgacggtg tacgcgggag ccggcagccg ggttggtctg 840
ccctgcaggc tgcctgcagg agtcgggaca aggtcattcc ttacagcaaa gtggaccccg 900
ccaggtgggg ggcccgacct ccttgtaacg ggagataatg gagatttcac tctgagactt 960
gaggatgtct ctcaagctca ggctgggact tatacatgtc acattcactt gcaagaacag 1020
cagttgaatg cgacggttac cctggctatc ataacagtaa cacctaaatc tttcggtagt 1080
ccgggtagcc tgggcaaact gttgtgtgag gtaacccccg tgtcaggtca agagcggttc 1140
gtctggagct cattggacac tccctcacag cgatccttta gcggaccctg gctcgaagcc 1200
caagaagccc agctgctttc ccaaccatgg cagtgtcaac tctatcaggg tgagcgcctt 1260
ctcggtgcgg ctgtctactt caccgaattg tcctctccgg gagcgcaaag aagtggacgc 1320
gccccagggg ccctcccggc aggacacctt tgtcccagcc ctctgtttcc cggccctagc 1380
aagcctttct gggtgctggt ggtggtcgga ggcgtgctgg cctgctacag cctgctggtc 1440
accgtggcct tcatcatctt ttgggtccgc agcaagcgga gcagaggcgg ccacagcgac 1500
tacatgaaca tgacccctag acggcctggc cccaccagaa agcactacca gccctacgcc 1560
cctccccggg actttgccgc ctacagaagc 1590

<210> 164
<211> 530
<212> PRT
<213> Artificial Sequence

<220>
<223> huLag3-CD28Cys

<400> 164
Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
1 5 10 15
Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
20 25 30
Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
35 40 45
Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
50 55 60
His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65 70 75 80
Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
85 90 95
Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
100 105 110
Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln

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        115                 120                 125
Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130                 135                 140
Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145                 150                 155                 160
Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165                 170                 175
Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180                 185                 190
Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195                 200                 205
Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210                 215                 220
Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225                 230                 235                 240
Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245                 250                 255
Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260                 265                 270
Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275                 280                 285
Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290                 295                 300
Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305                 310                 315                 320
Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325                 330                 335
Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340                 345                 350
Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355                 360                 365
Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370                 375                 380
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385                 390                 395                 400
Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405                 410                 415
Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420                 425                 430
Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
        435                 440                 445
His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
    450                 455                 460
Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
465                 470                 475                 480
Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly
                485                 490                 495
Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
            500                 505                 510
Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
        515                 520                 525
Arg Ser
    530
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<210> 165
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3tm-CD28

<400> 165
atgttctccc atcttccctt cgactgtgtg ttgctccttc tcctcctgct tctcacccgg 60
tcaagcgaag tagagtaccg ggcggaagta ggtcagaacg catatctccc ctgtttttac 120
acacccgctg cgccgggaaa cctggttccc gtgtgttggg gaaaggggc atgccctgtt 180
ttcgagtgtg gcaacgtggt cctccggacg gatgagcgag acgtgaatta ttggacgagc 240
agatattggt tgaatggcga ttttagaaag ggtgatgtga gcttgaccat tgagaatgta 300

acgcttgctg atagcgggat atattgctgt agaattcaaa tccctggtat aatgaacgac 360
gaaaaattca atctgaagct ggtaattaag ccggccaagg tgacacccgc cccgacacga 420
cagcgcgact tcacggctgc ctttccacgc atgttgacca caaggggaca tggtccagcg 480
gagacccaga cacttggtag cctcccggac ataaacctca cacaaatatc cacgttggcg 540
aacgagctcc gagattccag gcttgcgaat gacctgaggg attctggagc taccatcaga 600
atcggtatct acataggtgc cgggatatgc gccggtctcg cacttgcctt gattttcggg 660
gcactgattc gcagcaagcg gagcagaggc ggccacagcg actacatgaa catgacccct 720
agacggcctg gccccaccag aaagcactac cagccctacg cccctccccg ggactttgcc 780
gcctacagaa gc 792

<210> 166
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3tm-CD28

<400> 166
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1   5   10   15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
            20   25   30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
        35   40   45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
    50   55   60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65   70   75   80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
                85   90   95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
            100   105   110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
        115   120   125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
    130   135   140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145   150   155   160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
                165   170   175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
            180   185   190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
        195   200   205
Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Arg
    210   215   220
Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro
225   230   235   240
Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
                245   250   255
Arg Asp Phe Ala Ala Tyr Arg Ser
            260

<210> 167
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3 ectodomain

<400> 167
atgttctccc atcttccctt cgactgtgtg ttgctccttc tcctcctgct tctcacccgg 60
tcaagcgaag tagagtaccg ggcggaagta ggtcagaacg catatctccc ctgtttttac 120
acacccgctg cgccgggaaa cctggttccc gtgtgttggg gaaaggggc atgccctgtt 180
ttcgagtgtg gcaacgtggt cctccggacg gatgagcgag acgtgaatta ttggacgagc 240
agatattggt tgaatggcga ttttagaaag ggtgatgtga gcttgaccat tgagaatgta 300

acgcttgctg atagcgggat atattgctgt agaattcaaa tccctggtat aatgaacgac 360
gaaaaattca atctgaagct ggtaattaag ccggccaagg tgacacccgc cccgacacga 420
cagcgcgact tcacggctgc ctttccacgc atgttgacca caaggggaca tggtccagcg 480
gagacccaga cacttggtag cctcccggac ataaacctca cacaaatatc cacgttggcg 540
aacgagctcc gagattccag gcttgcgaat gacctgaggg attctggagc taccatcaga 600
atcggt 606

<210> 168
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3 ectodomain

<400> 168
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1   5   10   15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
            20   25   30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
        35   40   45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
    50   55   60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65   70   75   80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
                85   90   95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
            100   105   110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
        115   120   125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
    130   135   140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145   150   155   160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
                165   170   175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
            180   185   190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly
        195   200

<210> 169
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3 transmembrane

<400> 169
atctacatag gtgccgggat atgcgccggt ctcgcacttg ccttgatttt cggggcactg 60
att 63

<210> 170
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3 transmembrane

<400> 170
Ile Tyr Ile Gly Ala Gly Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile
 1   5   10   15
Phe Gly Ala Leu Ile
            20

<210> 171
<211> 810
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3-CD28tm

<400> 171
atgttctccc atcttccctt cgactgtgtg ttgctccttc tcctcctgct tctcacccgg 60
tcaagcgaag tagagtaccg ggcggaagta ggtcagaacg catatctccc ctgtttttac 120
acacccgctg cgccgggaaa cctggttccc gtgtgttggg gaaaggggc atgccctgtt 180
ttcgagtgtg gcaacgtggt cctccggacg gatgagcgag acgtgaatta ttggacgagc 240
agatattggt tgaatggcga ttttagaaag ggtgatgtga gcttgaccat tgagaatgta 300
acgcttgctg atagcgggat atattgctgt agaattcaaa tccctggtat aatgaacgac 360
gaaaaattca atctgaagct ggtaattaag ccggccaagg tgacacccgc cccgacacga 420
cagcgcgact tcacggctgc ctttccacgc atgttgacca caaggggaca tggtccagcg 480
gagacccaga cacttggtag cctcccggac ataaacctca cacaaatatc cacgttggcg 540
aacgagctcc gagattccag gcttgcgaat gacctgaggg attctggagc taccatcaga 600
atcggtttct gggtgctggt ggtggtcgga ggcgtgctgg cctgctacag cctgctggtc 660
accgtggcct tcatcatctt ttgggtccgc agcaagcgga gcagaggcgg ccacagcgac 720
tacatgaaca tgacccctag acggcctggc cccaccagaa agcactacca gccctacgcc 780
cctccccggg actttgccgc ctacagaagc 810

<210> 172
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3-CD28tm

<400> 172
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1   5   10   15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
            20   25   30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
        35   40   45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
    50   55   60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65   70   75   80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
                85   90   95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
            100   105   110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
        115   120   125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
    130   135   140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145   150   155   160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
                165   170   175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
            180   185   190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Phe Trp Val Leu Val Val
        195   200   205
Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
    210   215   220
Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp
225   230   235   240
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
                245   250   255
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
            260   265   270

<210> 173
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3-CD28Cys

<400> 173
atgttctccc atcttccctt cgactgtgtg ttgctccttc tcctcctgct tctcacccgg 60
tcaagcgaag tagagtaccg ggcggaagta ggtcagaacg catatctccc ctgtttttac 120
acacccgctg cgccgggaaa cctggttccc gtgtgttggg gaaaggggc atgccctgtt 180
ttcgagtgtg gcaacgtggt cctccggacg gatgagcgag acgtgaatta ttggacgagc 240
agatattggt tgaatggcga ttttagaaag ggtgatgtga gcttgaccat tgagaatgta 300
acgcttgctg atagcgggat atattgctgt agaattcaaa tccctggtat aatgaacgac 360
gaaaaattca atctgaagct ggtaattaag ccggccaagg tgacacccgc cccgacacga 420
cagcgcgact tcacggctgc ctttccacgc atgttgacca caaggggaca tggtccagcg 480
gagacccaga cacttggtag cctcccggac ataaacctca cacaaatatc cacgttggcg 540
aacgagctcc gagattccag gcttgcgaat gacctgaggg attctggagc taccatcaga 600
atcggttgtc ccagccctct gtttcccggc cctagcaagc ctttctgggt gctggtggtg 660
gtcggaggcg tgctggcctg ctacagcctg ctggtcaccg tggccttcat catcttttgg 720
gtccgcagca agcggagcag aggcggccac agcgactaca tgaacatgac ccctagacgg 780
cctggcccca ccagaaagca ctaccagccc tacgcccctc cccgggactt tgccgcctac 840
agaagc 846

<210> 174
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3-CD28Cys

<400> 174
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1   5   10   15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
            20   25   30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
        35   40   45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
    50   55   60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65   70   75   80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
                85   90   95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
            100   105   110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
        115   120   125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
    130   135   140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145   150   155   160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
                165   170   175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
            180   185   190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Cys Pro Ser Pro Leu Phe
        195   200   205
Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
    210   215   220
Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
225   230   235   240
Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met
                245   250   255
Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala

260 265 270
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
275 280

<210> 175
<211> 810
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3-12aas-CD28Cys

<400> 175
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acacccgctg cgccgggaaa cctggttccc gtgtgttggg gaaaggggc atgccctgtt 180
ttcgagtgtg gcaacgtggt cctccggacg gatgagcgag acgtgaatta ttggacgagc 240
agatattggt tgaatggcga ttttagaaag ggtgatgtga gcttgaccat tgagaatgta 300
acgcttgctg atagcgggat atattgctgt agaattcaaa tccctggtat aatgaacgac 360
gaaaaattca atctgaagct ggtaattaag ccggccaagg tgacacccgc cccgacacga 420
cagcgcgact tcacggctgc ctttccacgc atgttgacca caaggggaca tggtccagcg 480
gagacccaga cacttggtag cctcccggac ataaacctca cacaaatatc cacgttggcg 540
aacgagctcc gagattccag gcttgcgaat tgtcccagcc ctctgtttcc cggccctagc 600
aagcctttct gggtgctggt ggtggtcgga ggcgtgctgg cctgctacag cctgctggtc 660
accgtggcct tcatcatctt ttgggtccgc agcaagcgga gcagaggcgg ccacagcgac 720
tacatgaaca tgacccctag acggcctggc cccaccagaa agcactacca gccctacgcc 780
cctccccggg actttgccgc ctacagaagc 810

<210> 176
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3-12aas-CD28Cys

<400> 176
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Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
130 135 140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Cys Pro
180 185 190
Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
195 200 205
Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
210 215 220
Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp
225 230 235 240
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr

245 250 255
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
260 265 270

<210> 177
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> huTim3-12aas

<400> 177
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acacccgctg cgccgggaaa cctggttccc gtgtgttggg gaaaggggc atgccctgtt 180
ttcgagtgtg gcaacgtggt cctccggacg gatgagcgag acgtgaatta ttggacgagc 240
agatattggt tgaatggcga ttttagaaag ggtgatgtga gcttgaccat tgagaatgta 300
acgcttgctg atagcgggat atattgctgt agaattcaaa tccctggtat aatgaacgac 360
gaaaaattca atctgaagct ggtaattaag ccggccaagg tgacacccgc cccgacacga 420
cagcgcgact tcacggctgc ctttccacgc atgttgacca caaggggaca tggtccagcg 480
gagacccaga cacttggtag cctcccggac ataaacctca cacaaatatc cacgttggcg 540
aacgagctcc gagattccag gcttgcgaat 570

<210> 178
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> huTim3-12aas

<400> 178
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
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Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
130 135 140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn
180 185 190