SEQUENCE LISTING

<110> Thompson, Peter A.
Baum, Peter R.
Tan, Phillip
Blankenship, John W.
Natarajan, Sateesh

<120> CD86 ANTAGONIST MULTI-TARGET BINDING PROTEINS

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<140> PCT
<141> 2009-10-02

<160> 422

<170> FastSEQ for Windows Version 4.0

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<211> 161
<212> PRT
<213> Homo sapiens

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

<210> 2
<211> 152
<212> PRT
<213> Homo sapiens

<400> 2
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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr

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                85                  90                  95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110
Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    130                 135                 140
Leu Phe Pro Gly Pro Ser Lys Pro
145                 150
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<210> 3
<211> 115
<212> PRT
<213> Homo sapiens

<400> 3

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Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
 1               5                  10                  15
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
            20                  25                  30
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
        35                  40                  45
Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp
    50                  55                  60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65                  70                  75                  80
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
                85                  90                  95
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Ala Gln
            100                 105                 110
Ile Tyr Val
        115
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<210> 4
<211> 7
<212> PRT
<213> Homo sapiens

<400> 4

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Ser Pro Gly Lys Ala Thr Glu
 1               5
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<210> 5
<211> 9
<212> PRT
<213> Homo sapiens

<400> 5

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 1               5
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<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6

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Leu Met Tyr Pro Pro Pro Tyr Tyr Leu
 1               5
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<210> 7
<211> 178
<212> PRT

<213> Homo sapiens

<400> 7

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

<210> 8
<211> 1700
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide coding fusion protein having a CTLA4 ectodomain and an IL10 domain

<400> 8

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aagcttgccg ccatggaagc accagcgcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccatcga gaaaaccatc tccaaagcca agggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1080
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1140
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1200
tctagcccag gccagggcac ccagtctgag aacagctgca cccacttccc aggcaacctg 1260
cctaacatgc ttcgagatct ccgagatgcc ttcagcagag tgaagacttt ctttcaaatg 1320
aaggatcagc tggacaactt gttgttaaag gagtccttgc tggaggactt taagggttac 1380
ctgggttgcc aagccttgtc tgagatgatc cagttttacc tggaggaggt gatgccccaa 1440
gctgagaacc aagacccaga catcaaggcg catgtgaact ccctggggga gaacctgaag 1500
accctcaggc tgaggctacg gcgctgtcat cgatttcttc cctgtgaaaa caagagcaag 1560
gccgtggagc aggtgaagaa tgcctttaat aagctccaag agaaaggcat ctacaaagcc 1620
atgagtgagt ttgacatctt catcaactac atagaagcct acatgacaat gaagatacga 1680
aactaatcta gagcggccgc                                             1700
```

<210> 9
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an IL10 domain

<400> 9

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

450 455 460
Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu
465 470 475 480
Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys
485 490 495
Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly
500 505 510
Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu
515 520 525
Ala Tyr Met Thr Met Lys Ile Arg Asn
530 535

<210> 10
<211> 1158
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide coding CTLA4-Ig construct

<400> 10
aagcttgccg ccatggaagc accagcgcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagccgg tggcagcagg ggaacgtctt ctcatgctcc 1080
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taatctagag cggccgcc 1158

<210> 11
<211> 356
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4-Ig construct

<400> 11
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
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Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125

```
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130                 135                 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145                 150                 155                 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly
        355
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<210> 12
<211> 1880
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein
having a CTLA4 ectodomain and a PDL1 domain

<400> 12

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gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1080
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1140
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1200
tcttttactg tcacggttcc caaggaccta tatgtggtag agtatggtag caatatgaca 1260
attgaatgca aattcccagt agaaaaacaa ttagacctgg ctgcactaat tgtctattgg 1320
gaaatggagg ataagaacat tattcaattt gtgcatggag aggaagacct gaaggttcag 1380
catagtagct acagacagag ggcccggctg ttgaaggacc agctctccct gggaaatgct 1440
gcacttcaga tcacagatgt gaaattgcag gatgcagggg tgtaccgctg catgatcagc 1500
tatggtggtg ccgactacaa gcgaattact gtgaaagtca atgccccata caacaaaatc 1560
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aaccaaagaa ttttggttgt ggatccagtc acctctgaac atgaactgac atgtcaggct 1620
gagggctacc ccaaggccga agtcatctgg acaagcagtg accatcaagt cctgagtggt 1680
aagaccacca ccaccaattc caagagagag gagaagcttt tcaatgtgac cagcacactg 1740
agaatcaaca caacaactaa tgagattttc tactgcactt ttaggagatt agatcctgag 1800
gaaaaccata cagctgaatt ggtcatccca gaactacctc tggcacatcc tccaaatgaa 1860
aggtaatcta gagcggccgc 1880

<210> 13
<211> 597
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and a PDL1 domain

<400> 13

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

405 410 415
Glu Met Glu Asp Lys Asn Ile Ile Gln Phe Val His Gly Glu Glu Asp
420 425 430
Leu Lys Val Gln His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys
435 440 445
Asp Gln Leu Ser Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys
450 455 460
Leu Gln Asp Ala Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Ala
465 470 475 480
Asp Tyr Lys Arg Ile Thr Val Lys Val Asn Ala Pro Tyr Asn Lys Ile
485 490 495
Asn Gln Arg Ile Leu Val Val Asp Pro Val Thr Ser Glu His Glu Leu
500 505 510
Thr Cys Gln Ala Glu Gly Tyr Pro Lys Ala Glu Val Ile Trp Thr Ser
515 520 525
Ser Asp His Gln Val Leu Ser Gly Lys Thr Thr Thr Thr Asn Ser Lys
530 535 540
Arg Glu Glu Lys Leu Phe Asn Val Thr Ser Thr Leu Arg Ile Asn Thr
545 550 555 560
Thr Thr Asn Glu Ile Phe Tyr Cys Thr Phe Arg Arg Leu Asp Pro Glu
565 570 575
Glu Asn His Thr Ala Glu Leu Val Ile Pro Glu Leu Pro Leu Ala His
580 585 590
Pro Pro Asn Glu Arg
595

<210> 14
<211> 338
<212> PRT
<213> Homo sapiens

<400> 14
Met Val Val Met Ala Pro Arg Thr Leu Phe Leu Leu Leu Ser Gly Ala
1 5 10 15
Leu Thr Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
20 25 30
Ser Ala Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
35 40 45
Met Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ser
50 55 60
Ala Cys Pro Arg Met Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly
65 70 75 80
Pro Glu Tyr Trp Glu Glu Glu Thr Arg Asn Thr Lys Ala His Ala Gln
85 90 95
Thr Asp Arg Met Asn Leu Gln Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
100 105 110
Glu Ala Ser Ser His Thr Leu Gln Trp Met Ile Gly Cys Asp Leu Gly
115 120 125
Ser Asp Gly Arg Leu Leu Arg Gly Tyr Glu Gln Tyr Ala Tyr Asp Gly
130 135 140
Lys Asp Tyr Leu Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
145 150 155 160
Asp Thr Ala Ala Gln Ile Ser Lys Arg Lys Cys Glu Ala Ala Asn Val
165 170 175
Ala Glu Gln Arg Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu
180 185 190
His Arg Tyr Leu Glu Asn Gly Lys Glu Met Leu Gln Arg Ala Asp Pro
195 200 205
Pro Lys Thr His Val Thr His His Pro Val Phe Asp Tyr Glu Ala Thr
210 215 220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Ile Leu Thr
225 230 235 240
Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Val Glu Leu Val Glu
245 250 255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
260 265 270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu

275 280 285
Gly Leu Pro Glu Pro Leu Met Leu Arg Trp Lys Gln Ser Ser Leu Pro
290 295 300
Thr Ile Pro Ile Met Gly Ile Val Ala Gly Leu Val Val Leu Ala Ala
305 310 315 320
Val Val Thr Gly Ala Ala Val Ala Ala Val Leu Trp Arg Lys Lys Ser
325 330 335
Ser Asp

<210> 15
<211> 318
<212> PRT
<213> Homo sapiens

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

<210> 16
<211> 2105
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein
having a CTLA4 ectodomain and an HLA-G5 domain

<400> 16
aagcttgccg ccatggaagc accagcgcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1080
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1140
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1200
tctggctccc actccatgag gtatttcagc gccgccgtgt cccggcccgg ccgcggggag 1260
ccccgcttca tcgccatggg ctacgtggac gacacgcagt tcgtgcggtt cgacagcgac 1320
tcggcgtgtc cgaggatgga gccgcgggcg ccgtgggtgg agcaggaggg gccggagtat 1380
tgggaagagg agacacggaa caccaaggcc cacgcacaga ctgacagaat gaacctgcag 1440
accctgcgcg gctactacaa ccagagcgag gccagttctc acaccctcca gtggatgatt 1500
ggctgcgacc tggggtccga cggacgcctc ctccgcgggt atgaacagta tgcctacgat 1560
ggcaaggatt acctcaccct gaacgaggac ctgcgctcct ggaccgcagc ggacactgcg 1620
gctcagatct ccaagcgcaa gtgtgaggcg gccaatgtgg ctgaacaaag gagagcctac 1680
ctggagggca cgtgcgtgga gtggctccac agatacctgg agaacgggaa ggagatgctg 1740
cagcgcgcgg acccccccaa gacacacgtg acccaccacc ctgtctttga ctatgaggcc 1800
accctgaggt gctgggccct gggcttctac cctgcggaga tcatactgac ctggcagcgg 1860
gatggggagg accagaccca ggacgtggag ctcgtggaga ccaggcctgc aggggatgga 1920
accttccaga agtgggcagc tgtggtggtg ccttctggag aggagcagag atacacgtgc 1980
catgtgcagc atgaggggct gccggagccc ctcatgctga gatggagtaa ggagggagat 2040
ggaggcatca tgtctgttag ggaaagcagg agcctctctg aagaccttta atctagagcg 2100
gccgc 2105

<210> 17
<211> 672
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an
HLA-G5 domain

<400> 17
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
        355                 360                 365
Gln Lys Ala Arg His Ser Pro Asn Ser Gly Ser His Ser Met Arg Tyr
    370                 375                 380
Phe Ser Ala Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile
385                 390                 395                 400
Ala Met Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp
                405                 410                 415
Ser Ala Cys Pro Arg Met Glu Pro Arg Ala Pro Trp Val Glu Gln Glu
            420                 425                 430
Gly Pro Glu Tyr Trp Glu Glu Glu Thr Arg Asn Thr Lys Ala His Ala
        435                 440                 445
Gln Thr Asp Arg Met Asn Leu Gln Thr Leu Arg Gly Tyr Tyr Asn Gln
    450                 455                 460
Ser Glu Ala Ser Ser His Thr Leu Gln Trp Met Ile Gly Cys Asp Leu
465                 470                 475                 480
Gly Ser Asp Gly Arg Leu Leu Arg Gly Tyr Glu Gln Tyr Ala Tyr Asp
                485                 490                 495
Gly Lys Asp Tyr Leu Thr Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala
            500                 505                 510
Ala Asp Thr Ala Ala Gln Ile Ser Lys Arg Lys Cys Glu Ala Ala Asn
        515                 520                 525
Val Ala Glu Gln Arg Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp
    530                 535                 540
Leu His Arg Tyr Leu Glu Asn Gly Lys Glu Met Leu Gln Arg Ala Asp
545                 550                 555                 560
Pro Pro Lys Thr His Val Thr His His Pro Val Phe Asp Tyr Glu Ala
                565                 570                 575
Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Ile Leu
            580                 585                 590
Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Val Glu Leu Val
        595                 600                 605
Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
    610                 615                 620
Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His
625                 630                 635                 640
Glu Gly Leu Pro Glu Pro Leu Met Leu Arg Trp Ser Lys Glu Gly Asp
                645                 650                 655
Gly Gly Ile Met Ser Val Arg Glu Ser Arg Ser Leu Ser Glu Asp Leu
            660                 665                 670
```

<210> 18
<211> 728

<212> PRT
<213> Homo sapiens

<400> 18

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

```
Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp
        515                 520                 525
Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
    530                 535                 540
Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys
545                 550                 555                 560
Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly
                565                 570                 575
Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
            580                 585                 590
Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
        595                 600                 605
Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
    610                 615                 620
Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu
625                 630                 635                 640
Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
                645                 650                 655
Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
            660                 665                 670
Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu
        675                 680                 685
Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly
    690                 695                 700
Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
705                 710                 715                 720
Leu Thr Tyr Lys Val Pro Gln Ser
                725
```

<210> 19
<211> 290
<212> PRT
<213> Homo sapiens

<400> 19

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

```
Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
            260                 265                 270
Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
        275                 280                 285
Glu Thr
    290
```

<210> 20
<211> 723
<212> PRT
<213> Homo sapiens

<400> 20

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

Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys Tyr
435 440 445
Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys
450 455 460
Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile
465 470 475 480
Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr
485 490 495
Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His
500 505 510
Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg
515 520 525
Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly
530 535 540
Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu
545 550 555 560
Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu
565 570 575
Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile
580 585 590
Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser
595 600 605
Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu
610 615 620
Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His
625 630 635 640
His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala
645 650 655
Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu
660 665 670
Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro
675 680 685
Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val
690 695 700
Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val
705 710 715 720
Pro Gln Ser

<210> 21
<211> 285
<212> PRT
<213> Homo sapiens

<400> 21
Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
1 5 10 15
Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
20 25 30
Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
35 40 45
Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
50 55 60
Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
65 70 75 80
Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
85 90 95
Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
100 105 110
Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
115 120 125
Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
130 135 140
Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
145 150 155 160
Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg
165 170 175

```
Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg
            180                 185                 190
Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr
        195                 200                 205
Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly
    210                 215                 220
Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe
225                 230                 235                 240
Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg
                245                 250                 255
Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His
            260                 265                 270
Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Glu Thr
        275                 280                 285


<210> 22
<211> 210
<212> PRT
<213> Hoomo sapiens

<400> 22
Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
 1                5                  10                  15
Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
            20                  25                  30
Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
        35                  40                  45
Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
    50                  55                  60
Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
65                  70                  75                  80
Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
                85                  90                  95
Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
            100                 105                 110
Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
        115                 120                 125
Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
    130                 135                 140
Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
145                 150                 155                 160
Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
                165                 170                 175
Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser
            180                 185                 190
Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
        195                 200                 205
Gly Lys
    210


<210> 23
<211> 3794
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein
      having a CTLA4 ectodomain and an HGF domain

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<210> 24
<211> 1074
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an
HGF domain

<400> 24

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Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
355 360 365
Gln Lys Ala Arg His Ser Pro Asn Ser Gln Arg Lys Arg Arg Asn Thr
370 375 380
Ile His Glu Phe Lys Lys Ser Ala Lys Thr Thr Leu Ile Lys Ile Asp
385 390 395 400
Pro Ala Leu Lys Ile Lys Thr Lys Lys Val Asn Thr Ala Asp Gln Cys
405 410 415
Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu Pro Phe Thr Cys Lys Ala
420 425 430
Phe Val Phe Asp Lys Ala Arg Lys Gln Cys Leu Trp Phe Pro Phe Asn
435 440 445
Ser Met Ser Ser Gly Val Lys Lys Glu Phe Gly His Glu Phe Asp Leu
450 455 460
Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys Ile Ile Gly Lys Gly Arg
465 470 475 480
Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys Ser Gly Ile Lys Cys Gln
485 490 495
Pro Trp Ser Ser Met Ile Pro His Glu His Ser Phe Leu Pro Ser Ser
500 505 510
Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg Gly
515 520 525
Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg Tyr

530 535 540
Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr Cys
545 550 555 560
Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly Lys
565 570 575
Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe Leu
580 585 590
Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg Asn
595 600 605
Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His Thr
610 615 620
Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met Asn
625 630 635 640
Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln Gly
645 650 655
Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro Cys
660 665 670
Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro Glu
675 680 685
Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro Asp
690 695 700
Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg Val
705 710 715 720
Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln Asp
725 730 735
Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln Thr
740 745 750
Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp Leu
755 760 765
His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu Asn
770 775 780
Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys Tyr Thr
785 790 795 800
Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys Glu
805 810 815
Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile Ser
820 825 830
Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr Arg
835 840 845
Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His Ile
850 855 860
Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg Gln
865 870 875 880
Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly Ile
885 890 895
His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu Asn
900 905 910
Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu Met
915 920 925
Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile Asp
930 935 940
Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser Val
945 950 955 960
Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu Arg
965 970 975
Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His His
980 985 990
Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala Glu
995 1000 1005
Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu Val
1010 1015 1020
Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro Gly
1025 1030 1035 1040
Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val Ala
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Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val Pro
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Gln Ser

<210> 25
<211> 229
<212> PRT
<213> Homo sapiens

<400> 25
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Val Gln Cys Arg Ala Ser Arg Tyr Pro Ile Ala Val Asp Cys Ser Trp
        35   40   45
Thr Leu Pro Pro Ala Pro Asn Ser Thr Ser Pro Val Ser Phe Ile Ala
    50   55   60
Thr Tyr Arg Leu Gly Met Ala Ala Arg Gly His Ser Trp Pro Cys Leu
65   70   75   80
Gln Gln Thr Pro Thr Ser Thr Ser Cys Thr Ile Thr Asp Val Gln Leu
                85   90   95
Phe Ser Met Ala Pro Tyr Val Leu Asn Val Thr Ala Val His Pro Trp
            100   105   110
Gly Ser Ser Ser Ser Phe Val Pro Phe Ile Thr Glu His Ile Ile Lys
        115   120   125
Pro Asp Pro Pro Glu Gly Val Arg Leu Ser Pro Leu Ala Glu Arg Gln
    130   135   140
Leu Gln Val Gln Trp Glu Pro Pro Gly Ser Trp Pro Phe Pro Glu Ile
145   150   155   160
Phe Ser Leu Lys Tyr Trp Ile Arg Tyr Lys Arg Gln Gly Ala Ala Arg
                165   170   175
Phe His Arg Val Gly Pro Ile Glu Ala Thr Ser Phe Ile Leu Arg Ala
            180   185   190
Val Arg Pro Arg Ala Arg Tyr Tyr Val Gln Val Ala Ala Gln Asp Leu
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Thr Asp Tyr Gly Glu Leu Ser Asp Trp Ser Leu Pro Ala Thr Ala Thr
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Met Ser Leu Gly Lys
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<210> 26
<211> 253
<212> PRT
<213> Homo sapiens

<400> 26
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            20   25   30
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        35   40   45
Leu Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro
    50   55   60
Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg
65   70   75   80
Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr
                85   90   95
Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys
            100   105   110
Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu
        115   120   125
Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys
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Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser
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Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn

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                165                 170                 175
Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn
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Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser
        195                 200                 205
Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys
    210                 215                 220
Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala
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Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
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<210> 27
<211> 2486
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein having a CTLA4 ectodomain and an IL35 domain

<400> 27

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<210> 28
<211> 799

<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an IL35 domain

<400> 28

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Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35                  40                  45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50                  55                  60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65                  70                  75                  80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85                  90                  95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100                 105                 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115                 120                 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130                 135                 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145                 150                 155                 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
        355                 360                 365
Gln Lys Ala Arg His Ser Pro Asn Ser Arg Lys Gly Pro Pro Ala Ala
    370                 375                 380
Leu Thr Leu Pro Arg Val Gln Cys Arg Ala Ser Arg Tyr Pro Ile Ala
385                 390                 395                 400
Val Asp Cys Ser Trp Thr Leu Pro Pro Ala Pro Asn Ser Thr Ser Pro
                405                 410                 415
Val Ser Phe Ile Ala Thr Tyr Arg Leu Gly Met Ala Ala Arg Gly His
            420                 425                 430
Ser Trp Pro Cys Leu Gln Gln Thr Pro Thr Ser Thr Ser Cys Thr Ile
        435                 440                 445
Thr Asp Val Gln Leu Phe Ser Met Ala Pro Tyr Val Leu Asn Val Thr
    450                 455                 460
Ala Val His Pro Trp Gly Ser Ser Ser Ser Phe Val Pro Phe Ile Thr
465                 470                 475                 480
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Glu His Ile Ile Lys Pro Asp Pro Pro Glu Gly Val Arg Leu Ser Pro
                485                 490                 495
Leu Ala Glu Arg Gln Leu Gln Val Gln Trp Glu Pro Pro Gly Ser Trp
            500                 505                 510
Pro Phe Pro Glu Ile Phe Ser Leu Lys Tyr Trp Ile Arg Tyr Lys Arg
        515                 520                 525
Gln Gly Ala Ala Arg Phe His Arg Val Gly Pro Ile Glu Ala Thr Ser
    530                 535                 540
Phe Ile Leu Arg Ala Val Arg Pro Arg Ala Arg Tyr Tyr Val Gln Val
545                 550                 555                 560
Ala Ala Gln Asp Leu Thr Asp Tyr Gly Glu Leu Ser Asp Trp Ser Leu
                565                 570                 575
Pro Ala Thr Ala Thr Met Ser Leu Gly Lys Gly Gly Gly Ser Gly Gly
            580                 585                 590
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Arg Asn Leu Pro Val Ala
        595                 600                 605
Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu
    610                 615                 620
Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu
625                 630                 635                 640
Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
                645                 650                 655
Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys
            660                 665                 670
Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly
        675                 680                 685
Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu
    690                 695                 700
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr
705                 710                 715                 720
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
                725                 730                 735
Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe
            740                 745                 750
Asn Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe
        755                 760                 765
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
    770                 775                 780
Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
785                 790                 795


<210> 29
<211> 200
<212> PRT
<213> Homo sapiens

<400> 29
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1                5                  10                  15
Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
            20                  25                  30
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
        35                  40                  45
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
    50                  55                  60
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65                  70                  75                  80
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
                85                  90                  95
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
            100                 105                 110
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
        115                 120                 125
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
    130                 135                 140
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
145                 150                 155                 160
```

Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
165 170 175
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
180 185 190
Gly Ala Gly Thr Ser Ser Ser His
195 200

<210> 30
<211> 1707
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein having a CTLA4 ectodomain and an HVEM ectodomain

<400> 30
aagcttgccg ccatggaagc accagcgcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1080
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1140
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1200
tctctgccgt cctgcaagga ggacgagtac ccagtgggct ccgagtgctg ccccaagtgc 1260
agtccaggtt atcgtgtgaa ggaggcctgc ggggagctga cgggcacagt gtgtgaaccc 1320
tgccctccag gcacctacat tgcccacctc aatggcctaa gcaagtgtct gcagtgccaa 1380
atgtgtgacc cagccatggg cctgcgcgcg agccggaact gctccaggac agagaacgcc 1440
gtgtgtggct gcagcccagg ccacttctgc atcgtccagg acggggacca ctgcgccgcg 1500
tgccgcgctt acgccacctc cagcccgggc cagagggtgc agaagggagg caccgagagt 1560
caggacaccc tgtgtcagaa ctgccccccg gggaccttct ctcccaatgg gaccctggag 1620
gaatgtcagc accagaccaa gtgcagctgg ctggtgacga aggccggagc tgggaccagc 1680
agctcccact aaatctagag cggccgc 1707

<210> 31
<211> 539
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an HVEM ectodomain

<400> 31
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80

Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
355 360 365
Gln Lys Ala Arg His Ser Pro Asn Ser Leu Pro Ser Cys Lys Glu Asp
370 375 380
Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr
385 390 395 400
Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro
405 410 415
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
420 425 430
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
435 440 445
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His
450 455 460
Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr
465 470 475 480
Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser
485 490 495
Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn
500 505 510
Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val
515 520 525
Thr Lys Ala Gly Ala Gly Thr Ser Ser Ser His
530 535

<210> 32
<211> 238
<212> PRT
<213> Homo sapiens

<400> 32
Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1 5 10 15

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

<210> 33
<211> 230
<212> PRT
<213> Homo sapiens

<400> 33

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

<210> 34
<211> 1823
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein having a CTLA4 ectodomain and an PDL2 domain

<400> 34
aagcttgccg ccatggaagc accagcgcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1080
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1140
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1200
tctttattca cagtgacagt ccctaaggaa ctgtacataa tagagcatgg cagcaatgtg 1260
accctggaat gcaactttga cactggaagt catgtgaacc ttggagcaat aacagccagt 1320
ttgcaaaagg tggaaaatga tacatcccca caccgtgaaa gagccacttt gctggaggag 1380
cagctgcccc tagggaaggc ctcgttccac atacctcaag tccaagtgag ggacgaagga 1440
cagtaccaat gcataatcat ctatggggtc gcctgggact acaagtacct gaccctgaaa 1500
gtcaaagctt cctacaggaa aataaacact cacatcctaa aggttccaga aacagatgag 1560
gtagagctca cctgccaggc tacaggttat cctctggcag aagtatcctg gccaaacgtc 1620
agcgttcctg ccaacaccag ccactccagg acccctgaag gcctctacca ggtcaccagt 1680
gttctgcgcc taaagccacc ccctggcaga aacttcagct gtgtgttctg gaatactcac 1740
gtgagggaac ttactttggc cagcattgac cttcaaagtc agatggaacc caggacccat 1800
ccaacttaat ctagagcggc cgc 1823

<210> 35
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an PDL2 domain

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

```
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130                 135                 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145                 150                 155                 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
        355                 360                 365
Gln Lys Ala Arg His Ser Pro Asn Ser Leu Phe Thr Val Thr Val Pro
    370                 375                 380
Lys Glu Leu Tyr Ile Ile Glu His Gly Ser Asn Val Thr Leu Glu Cys
385                 390                 395                 400
Asn Phe Asp Thr Gly Ser His Val Asn Leu Gly Ala Ile Thr Ala Ser
                405                 410                 415
Leu Gln Lys Val Glu Asn Asp Thr Ser Pro His Arg Glu Arg Ala Thr
            420                 425                 430
Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys Ala Ser Phe His Ile Pro
        435                 440                 445
Gln Val Gln Val Arg Asp Glu Gly Gln Tyr Gln Cys Ile Ile Ile Tyr
    450                 455                 460
Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr Leu Lys Val Lys Ala Ser
465                 470                 475                 480
Tyr Arg Lys Ile Asn Thr His Ile Leu Lys Val Pro Glu Thr Asp Glu
                485                 490                 495
Val Glu Leu Thr Cys Gln Ala Thr Gly Tyr Pro Leu Ala Glu Val Ser
            500                 505                 510
Trp Pro Asn Val Ser Val Pro Ala Asn Thr Ser His Ser Arg Thr Pro
        515                 520                 525
Glu Gly Leu Tyr Gln Val Thr Ser Val Leu Arg Leu Lys Pro Pro Pro
    530                 535                 540
Gly Arg Asn Phe Ser Cys Val Phe Trp Asn Thr His Val Arg Glu Leu
545                 550                 555                 560
Thr Leu Ala Ser Ile Asp Leu Gln Ser Gln Met Glu Pro Arg Thr His
                565                 570                 575
Pro Thr
```

<210> 36

<400> 36
000

<210> 37

<220>

<223> Nucleotide expression cassette of a fusion protein having a CTLA4 ectodomain and an HVEM ectodomain

<400> 37
000

<210> 38

<220>
<223> Fusion protein having a CTLA4 ectodomain and an HVEM ectodomain

<400> 38
000

<210> 39
<211> 164
<212> PRT
<213> Homo sapiens

<400> 39
Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30
Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45
Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60
Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80
Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95
Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110
Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
115 120 125
Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140
Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145 150 155 160
Glu Pro Leu Gly

<210> 40
<211> 255
<212> PRT
<213> Homo sapiens

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

130 135 140
Pro Glu Ala Ala Ser Ser Pro Arg Lys Ser Gly Ala Ser Asp Arg Gln
145 150 155 160
Arg Arg Arg Gly Gly Trp Glu Thr Cys Gly Cys Glu Pro Gly Arg Pro
165 170 175
Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser Pro Gly Ala Pro Gln Ala
180 185 190
Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg Ala Leu Leu Pro Trp Gln
195 200 205
Gln Lys Trp Val Gln Glu Gly Gly Ser Asp Gln Arg Pro Gly Pro Cys
210 215 220
Ser Ser Ala Ala Ala Ala Gly Pro Cys Arg Arg Glu Arg Glu Thr Gln
225 230 235 240
Ser Trp Pro Pro Ser Ser Leu Ala Gly Pro Asp Gly Val Gly Ser
245 250 255

<210> 41
<211> 1631
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide expression cassette of a fusion protein having a CTLA4 ectodomain and an GITR domain

<400> 41
aagcttgccg ccatggaagc accagcgcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gtatgcacgt ggcccagcct gctgtggtac tggccagcag ccgaggcatc 120
gccagctttg tgtgtgagta tgcatctcca ggcaaagcca ctgaggtccg ggtgacagtg 180
cttcggcagg ctgacagcca ggtgactgaa gtctgtgcgg caacctacat gatggggaat 240
gagttgacct tcctagatga ttccatctgc acgggcacct ccagtggaaa tcaagtgaac 300
ctcactatcc aaggactgag ggccatggac acgggactct acatctgcaa ggtggagctc 360
atgtacccac cgccatacta cctgggcata ggcaacggaa cccagattta tgtaattgat 420
ccagaaccgt gcccagattc tgacctcgag cccaaatctt ctgacaaaac tcacacatgc 480
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 780
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 960
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1020
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1080
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1140
cagaggcaca acaattcttc cctgaataca agaactcaga aagcacgtca ttctccgaat 1200
tctcagcgcc ccaccggggg tcccgggtgc ggccctgggc gcctcctgct tgggacggga 1260
acggacgcgc gctgctgccg ggttcacacg acgcgctgct gccgcgatta cccgggcgag 1320
gagtgctgtt ccgagtggga ctgcatgtgt gtccagcctg aattccactg cggagaccct 1380
tgctgcacga cctgccggca ccacccttgt cccccaggcc aggggtaca gtcccagggg 1440
aaattcagtt ttggcttcca gtgtatcgac tgtgcctcgg ggaccttctc cgggggccac 1500
gaaggccact gcaaaccttg gacagactgc acccagttcg ggtttctcac tgtgttccct 1560
gggaacaaga cccacaacgc tgtgtgcgtc ccagggtccc ccccggcaga gccgcttggg 1620
taagcggccg c 1631

<210> 42
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein having a CTLA4 ectodomain and an GITR domain

<400> 42
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15

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

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 1   5   10   15
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 1   5   10   15
Pro Asn Ser

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Cys Pro Asn Ser
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Cys Pro Asn Ser
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Cys Pro Asn Ser

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Cys Pro Asn Ser
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Pro Cys Pro Asn Ser
            20

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Pro Cys Pro Asn Ser
            20

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Pro Cys Pro Asn Ser
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<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 146
Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
 1   5   10   15
Asp Cys Pro Asn Ser
            20

<210> 147
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 147
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Cys Pro Asn Ser
            20

<210> 148
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 148
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 149
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 149
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            20   25   30
Gly Ser Asn Ser
        35

<210> 150
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

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

<210> 151
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 151
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 152
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 152

Asn Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15
Gly Ser Gly Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
20 25 30
Gly Gly Gly Ser Gly Asn Ser
35

<210> 153
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 153
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15
Ser Gly Asn Ser
20

<210> 154
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 154
Ser Pro Pro Ser Pro Asn Ser
1 5

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 155
Glu Pro Thr Ser Thr Asp Lys Thr His Thr Ser Pro Pro Ser Pro Asn
1 5 10 15
Ser

<210> 156
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 156
Glu Pro Thr Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
1 5 10 15
Ser

<210> 157
<211> 19

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 157
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Pro Pro Cys
 1   5   10   15
Pro Asn Ser

<210> 158
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 158
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Asn Ser
 1   5   10

<210> 159
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 159
Arg Thr Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys
 1   5   10   15
Ala Arg His Ser Gly His
            20

<210> 160
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

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

<210> 161
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 161
Arg Thr Gln Ser Glu Glu Gln Gln Arg Arg Ala Leu Glu Gln Lys Leu
 1   5   10   15
Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys Gly Ser Ala
            20   25   30
Asp Thr Cys
        35

<210> 162
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 162
Arg Thr Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe
 1   5   10   15
Phe Thr Cys Gly Ser Ala Asp Thr Cys
            20   25

<210> 163
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 163
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 164
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 164
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser
 1   5   10   15

<210> 165
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 165
Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 166
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 166
Gly Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
 1   5   10   15
Cys Pro

<210> 167
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterologous leader sequence

<400> 167
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly
            20

<210> 168
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterologous leader sequence

<400> 168
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1   5   10   15
Asp Thr Thr Gly
            20

<210> 169
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide coding a heterologous leader
      sequence

<400> 169
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

<210> 170
<211> 1611
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding a CTLA4::IL10 fusion protein with H68 linker

<400> 170
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cttgaccgaa agttacagcc cgaattctag cccaggccag 1140
ggcacccagt ctgagaacag ctgcacccac ttcccaggca acctgcctaa catgcttcga 1200
gatctccgag atgccttcag cagagtgaag actttctttc aaatgaagga tcagctggac 1260
aacttgttgt taaaggagtc cttgctggag gactttaagg gttacctggg ttgccaagcc 1320
ttgtctgaga tgatccagtt ttacctggag gaggtgatgc cccaagctga gaaccaagac 1380
ccagacatca aggcgcatgt gaactccctg ggggagaacc tgaagaccct caggctgagg 1440
ctacggcgct gtcatcgatt tcttccctgt gaaaacaaga gcaaggccgt ggagcaggtg 1500
aagaatgcct ttaataagct ccaagagaaa ggcatctaca aagccatgag tgagtttgac 1560
atcttcatca actacataga agcctacatg acaatgaaga tacgaaacta a 1611

<210> 171
<211> 536
<212> PRT
<213> Artificial Sequence

<220>
<223> A CTLA4::IL10 fusion protein with H68 linker

<400> 171
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1   5   10   15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20   25   30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35   40   45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50   55   60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65   70   75   80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85   90   95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100   105   110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115   120   125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130   135   140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145   150   155   160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165   170   175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180   185   190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195   200   205

```
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
        355                 360                 365
Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser
    370                 375                 380
Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg
385                 390                 395                 400
Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys
                405                 410                 415
Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe
            420                 425                 430
Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr
        435                 440                 445
Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys
    450                 455                 460
Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg
465                 470                 475                 480
Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala
                485                 490                 495
Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile
            500                 505                 510
Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala
        515                 520                 525
Tyr Met Thr Met Lys Ile Arg Asn
    530                 535
```

<210> 172
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding a CTLA4::IL10 fusion protein with H75 linker

<400> 172
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacagg aactcagatg gcaggtcatt ctccgaattc tagcccaggc 1140
cagggcaccc agtctgagaa cagctgcacc cacttcccag gcaacctgcc taacatgctt 1200
cgagatctcc gagatgcctt cagcagagtg aagactttct ttcaaatgaa ggatcagctg 1260
gacaacttgt tgttaaagga gtccttgctg gaggacttta agggttacct gggttgccaa 1320
gccttgtctg agatgatcca gttttacctg gaggaggtga tgccccaagc tgagaaccaa 1380
gacccagaca tcaaggcgca tgtgaactcc ctgggggaga acctgaagac cctcaggctg 1440
aggctacggc gctgtcatcg atttcttccc tgtgaaaaca agagcaaggc cgtggagcag 1500
gtgaagaatg cctttaataa gctccaagag aaaggcatct acaaagccat gagtgagttt 1560
gacatcttca tcaactacat agaagcctac atgacaatga agatacgaaa ctaa 1614

<210> 173
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> A CTLA4::IL10 fusion protein with H75 linker

<400> 173
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1   5   10   15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20   25   30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35   40   45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50   55   60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65   70   75   80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85   90   95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100   105   110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115   120   125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130   135   140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145   150   155   160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165   170   175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180   185   190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195   200   205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210   215   220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225   230   235   240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245   250   255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260   265   270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275   280   285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290   295   300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305   310   315   320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325   330   335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340   345   350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr

```
        355                 360                 365
Gln Met Ala Gly His Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln
    370                 375                 380
Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu
385                 390                 395                 400
Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met
                405                 410                 415
Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp
            420                 425                 430
Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe
        435                 440                 445
Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile
    450                 455                 460
Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu
465                 470                 475                 480
Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys
                485                 490                 495
Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly
            500                 505                 510
Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu
        515                 520                 525
Ala Tyr Met Thr Met Lys Ile Arg Asn
    530                 535
```

<210> 174
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding a CTLA4::IL10 fusion protein with H77 linker

<400> 174

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atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cttgaccgaa ccgaattcta gcccaggcca gggcacccag 1140
tctgagaaca gctgcaccca cttcccaggc aacctgccta acatgcttcg agatctccga 1200
gatgccttca gcagagtgaa gactttcttt caaatgaagg atcagctgga caacttgttg 1260
ttaaaggagt ccttgctgga ggactttaag ggttacctgg gttgccaagc cttgtctgag 1320
atgatccagt tttacctgga ggaggtgatg ccccaagctg agaaccaaga cccagacatc 1380
aaggcgcatg tgaactccct gggggagaac ctgaagaccc tcaggctgag gctacggcgc 1440
tgtcatcgat ttcttccctg tgaaaacaag agcaaggccg tggagcaggt gaagaatgcc 1500
tttaataagc tccaagagaa aggcatctac aaagccatga gtgagtttga catcttcatc 1560
aactacatag aagcctacat gacaatgaag atacgaaact aa                    1602
```

<210> 175
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> A CTLA4::IL10 fusion protein with H77 linker

<400> 175

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Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1               5                  10                  15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20                  25                  30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35                  40                  45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50                  55                  60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65                  70                  75                  80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85                  90                  95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100                 105                 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115                 120                 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130                 135                 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145                 150                 155                 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
        355                 360                 365
Thr Glu Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
    370                 375                 380
Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
385                 390                 395                 400
Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
                405                 410                 415
Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
            420                 425                 430
Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
        435                 440                 445
Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
    450                 455                 460
Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
465                 470                 475                 480
Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
                485                 490                 495
Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
            500                 505                 510
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Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
515 520 525
Met Lys Ile Arg Asn
530

<210> 176
<211> 1593
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding a CTLA4::IL10 fusion protein with H78 linker

<400> 176
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cccgaattct agcccaggcc agggcaccca gtctgagaac 1140
agctgcaccc acttcccagg caacctgcct aacatgcttc gagatctccg agatgccttc 1200
agcagagtga agactttctt tcaaatgaag gatcagctgg acaacttgtt gttaaaggag 1260
tccttgctgg aggactttaa gggttacctg ggttgccaag ccttgtctga gatgatccag 1320
ttttacctgg aggaggtgat gccccaagct gagaaccaag acccagacat caaggcgcat 1380
gtgaactccc tgggggagaa cctgaagacc ctcaggctga ggctacggcg ctgtcatcga 1440
tttcttccct gtgaaaacaa gagcaaggcc gtggagcagg tgaagaatgc ctttaataag 1500
ctccaagaga aaggcatcta caaagccatg agtgagtttg acatcttcat caactacata 1560
gaagcctaca tgacaatgaa gatacgaaac taa 1593

<210> 177
<211> 530
<212> PRT
<213> Artificial Sequence

<220>
<223> A CTLA4::IL10 fusion protein with H78 linker

<400> 177
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys

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

<210> 178
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding a CTLA4::IL10 fusion
protein with H79 linker

<400> 178
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180

```
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttccgaattc tagcccaggc cagggcaccc agtctgagaa cagctgcacc 1140
cacttcccag gcaacctgcc taacatgctt cgagatctcc gagatgcctt cagcagagtg 1200
aagactttct ttcaaatgaa ggatcagctg gacaacttgt tgttaaagga gtccttgctg 1260
gaggacttta agggttacct gggttgccaa gccttgtctg agatgatcca gttttacctg 1320
gaggaggtga tgccccaagc tgagaaccaa gacccagaca tcaaggcgca tgtgaactcc 1380
ctgggggaga acctgaagac cctcaggctg aggctacggc gctgtcatcg atttcttccc 1440
tgtgaaaaca agagcaaggc cgtggagcag gtgaagaatg cctttaataa gctccaagag 1500
aaaggcatct acaaagccat gagtgagttt gacatcttca tcaactacat agaagcctac 1560
atgacaatga agatacgaaa ctaa                                        1584
```

<210> 179
<211> 527
<212> PRT
<213> Artificial Sequence

<220>
<223> A CTLA4::IL10 fusion protein with H79 linker

<400> 179

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

```
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Pro Asn Ser Ser
        355                 360                 365
Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly
    370                 375                 380
Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val
385                 390                 395                 400
Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys
                405                 410                 415
Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu
            420                 425                 430
Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu
        435                 440                 445
Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn
    450                 455                 460
Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro
465                 470                 475                 480
Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn
                485                 490                 495
Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile
            500                 505                 510
Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
        515                 520                 525
```

<210> 180
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding a CTLA4::monoIL10
fusion protein

<400> 180

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atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cttgaccgaa agttacagcc cgaattctag cccaggccag 1140
ggcacccagt ctgagaacag ctgcacccac ttcccaggca acctgcctaa catgcttcga 1200
gatctccgag atgccttcag cagagtgaag actttctttc aaatgaagga tcagctggac 1260
aacttgttgt taaaggagtc cttgctggag gactttaagg gttacctggg ttgccaagcc 1320
ttgtctgaga tgatccagtt ttacctggag gaggtgatgc cccaagctga gaaccaagac 1380
ccagacatca aggcgcatgt gaactccctg ggggagaacc tgaagaccct caggctgagg 1440
```

ctacggcgct gtcatcgatt tcttccctgt gaaaacggtg gtggatccgg cggtaagagc 1500
aaggccgtgg agcaggtgaa gaatgccttt aataagctcc aagagaaagg catctacaaa 1560
gccatgagtg agtttgacat cttcatcaac tacatagaag cctacatgac aatgaagata 1620
cgaaactaa 1629

<210> 181
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> A CTLA4::monoIL10 fusion protein

<400> 181
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
355 360 365
Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser
370 375 380
Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg
385 390 395 400
Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys
405 410 415
Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe
420 425 430

```
Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr
        435                 440                 445
Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys
    450                 455                 460
Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg
465                 470                 475                 480
Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Gly Gly Gly Ser
                485                 490                 495
Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys
            500                 505                 510
Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe
        515                 520                 525
Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
    530                 535                 540
```

<210> 182
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10::FUN1 fusion protein

<400> 182

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agcccaggcc agggcaccca gtctgagaac agctgcaccc acttcccagg caacctgcct 60
aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggtaact cattattcaa ccaagaagtt 1200
caaattccct tgaccgaaag ttacagcccg aattctgagg tccaactgca gcagtctgga 1260
cctgagctgg agaagcctgg cgcttcagtg aagatatcct gcaaggcttc tggttactca 1320
ttcactgact acaacatgaa ctgggtgaag cagagcaatg gaaagagcct tgagtggatt 1380
ggaaatattg atccttacta tggtggtact agttacaatc agaagttcaa gggcaaggcc 1440
acattgactg tagacaaatc ctccagcaca gcctacatgc agctcaacag cctgacatct 1500
gaagactctg cagtctattt ctgtgcaaga tgggactata ggtacgacga cgggagggct 1560
tactatgtta tggacttctg gggtcaagga acctcagtca ccgtctcctc agggggtgga 1620
ggctctggtg gcggtggctc tggcggaggt ggatccggtg gcggcggatc tgagctccag 1680
atgacccagt ctccatcatc tctggctgcg tctgcaggag aaaaggtcac tatgagctgt 1740
aagtccagtc aaagtgtttt atacagttca aatcagaaga actacttggc ctggtaccag 1800
cagaaaccag ggcagtctcc taaactgctg atctactggg catccactag ggaatctggt 1860
gtccctgatc gcttcacagg cagtggatct gggacacatt ttactctgac cgtcagcagt 1920
gtgcaagctg aagacctggc agtttattac tgtcatcaat acctctactc gtggacgttc 1980
ggtggaggca ccaacctgga aatcaaacgg taa                                2013
```

<210> 183
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10::FUN1 fusion protein

<400> 183
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145 150 155 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
165 170 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
180 185 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
195 200 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
210 215 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225 230 235 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
245 250 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
260 265 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
275 280 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
290 295 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305 310 315 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
325 330 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
340 345 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
355 360 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
370 375 380
Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val
385 390 395 400
Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Glu Val Gln Leu
405 410 415
Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser Val Lys Ile
420 425 430
Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Asn Met Asn Trp
435 440 445
Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asp
450 455 460
Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala
465 470 475 480
Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Asn
485 490 495
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Trp Asp
500 505 510
Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe Trp Gly
515 520 525

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Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
    530                 535                 540
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln
545                 550                 555                 560
Met Thr Gln Ser Pro Ser Ser Leu Ala Ala Ser Ala Gly Glu Lys Val
                565                 570                 575
Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln
            580                 585                 590
Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
        595                 600                 605
Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
    610                 615                 620
Phe Thr Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr Val Ser Ser
625                 630                 635                 640
Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr
                645                 650                 655
Ser Trp Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg
            660                 665                 670
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<210> 184
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10::3D1 fusion protein

<400> 184

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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
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gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggtaact cattattcaa ccaagaagtt 1200
caaattccct tgaccgaaag ttacagcccg aattctcagg tccagctgca gcagtctggg 1260
cctgagctgg tgaggcctgg ggaatcagtg aagatttcct gcaagggttc cggctacaca 1320
ttcactgatt atgctataca gtgggtgaag cagagtcatg caaagagtct agagtggatt 1380
ggagttatta atatttacta tgataataca aactacaacc agaagtttaa gggcaaggcc 1440
acaatgactg tagacaaatc ctccagcaca gcctatatgg aacttgccag attgacatct 1500
gaggattctg ccatctatta ctgtgcaaga gcggcctggt atatggacta ctggggtcaa 1560
ggaacctcag tcaccgtctc ctcagggggt ggaggctctg gtggcggtgg ctctggcgga 1620
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gtgtcagcag gagagaaggt cactatgagc tgcaaatcca gtcagagtct gctcaacagt 1740
agaacccgag agaactactt ggcttggtac cagcagaaac cagggcagtc tcctaaactg 1800
ctgatctact gggcatccac tagggaatct ggggtccctg atcgcttcac aggcagtgga 1860
tctgggacag atttcactct caccatcagc agtgtgcagg ctgaagacct ggcagtttat 1920
tactgcacgc aatcttataa tctttacacg ttcggagggg ggaccaagct ggaaataaaa 1980
taa                                                                 1983
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<210> 185
<211> 660
<212> PRT

<213> Artificial Sequence

<220>
<223> IL10::3D1 fusion protein

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

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Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala Arg Ala Ala
            500                 505                 510
Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        515                 520                 525
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala
545                 550                 555                 560
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
                565                 570                 575
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
            580                 585                 590
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
        595                 600                 605
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
    610                 615                 620
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
625                 630                 635                 640
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
                645                 650                 655
Leu Glu Ile Lys
            660
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<210> 186
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding FUN1::IL10 fusion protein

<400> 186

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aatggaaaga gccttgagtg gattggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240
atgcagctca acagcctgac atctgaagac tctgcagtct atttctgtgc aagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggtca aggaacctca 360
gtcaccgtct cctcaggggg tggaggctct ggtggcggtg gctctggcgg aggtggatcc 420
ggtggcggcg gatctgagct ccagatgacc cagtctccat catctctggc tgcgtctgca 480
ggagaaaagg tcactatgag ctgtaagtcc agtcaaagtg ttttatacag ttcaaatcag 540
aagaactact tggcctggta ccagcagaaa ccagggcagt ctcctaaact gctgatctac 600
tgggcatcca ctagggaatc tggtgtccct gatcgcttca caggcagtgg atctgggaca 660
cattttactc tgaccgtcag cagtgtgcaa gctgaagacc tggcagttta ttactgtcat 720
caatacctct actcgtggac gttcggtgga ggcaccaacc tggaaatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
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cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
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tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt aactcattat tcaaccaaga agttcaaatt 1500
cccttgaccg aaagttacag cccgaattct agcccaggcc agggcaccca gtctgagaac 1560
agctgcaccc acttcccagg caacctgcct aacatgcttc gagatctccg agatgccttc 1620
agcagagtga agactttctt tcaaatgaag gatcagctgg acaacttgtt gttaaaggag 1680
tccttgctgg aggactttaa gggttacctg ggttgccaag ccttgtctga gatgatccag 1740
ttttacctgg aggaggtgat gccccaagct gagaaccaag acccagacat caaggcgcat 1800
gtgaactccc tgggggagaa cctgaagacc ctcaggctga ggctacggcg ctgtcatcga 1860
tttcttccct gtgaaaacaa gagcaaggcc gtggagcagg tgaagaatgc ctttaataag 1920
ctccaagaga aaggcatcta caaagccatg agtgagtttg acatcttcat caactacata 1980
gaagcctaca tgacaatgaa gatacgaaac taa                              2013
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<210> 187
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1::IL10 fusion protein

<400> 187
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
            20   25   30
Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
        35   40   45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
            100   105   110
Asp Phe Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
        115   120   125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130   135   140
Ser Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ala Ala Ser Ala
145   150   155   160
Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr
                165   170   175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            180   185   190
Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
        195   200   205
Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr His Phe Thr Leu
    210   215   220
Thr Val Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His
225   230   235   240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile
                245   250   255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260   265   270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275   280   285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290   295   300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305   310   315   320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325   330   335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340   345   350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355   360   365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370   375   380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385   390   395   400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405   410   415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420   425   430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435   440   445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450   455   460

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Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
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Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln
                485                 490                 495
Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro
            500                 505                 510
Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn
        515                 520                 525
Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys
    530                 535                 540
Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu
545                 550                 555                 560
Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser
                565                 570                 575
Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn
            580                 585                 590
Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu
        595                 600                 605
Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys
    610                 615                 620
Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys
625                 630                 635                 640
Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe
                645                 650                 655
Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
            660                 665                 670
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<210> 188
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding 3D1::IL10 fusion protein

<400> 188

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catgcaaaga gtctagagtg gattggagtt attaatattt actatgataa tacaaactac 180
aaccagaagt ttaagggcaa ggccacaatg actgtagaca aatcctccag cacagcctat 240
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tcacagtctc catcctccct ggctgtgtca gcaggagaga aggtcactat gagctgcaaa 480
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caggctgaag acctggcagt ttattactgc acgcaatctt ataatcttta cacgttcgga 720
gggggggacca agctggaaat aaaactcgag cccaaatctt ctgacaaaac tcacacatgc 780
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa 840
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1020
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1080
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1200
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1260
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380
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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 1680
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 1740
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 1800
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ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 1860
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 1920
agtgagtttg acatcttcat caactacata gaagcctaca tgacaatgaa gatacgaaac 1980
taa 1983

<210> 189
<211> 660
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1::IL10 fusion protein

<400> 189

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

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Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        435                 440                 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450                 455                 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465                 470                 475                 480
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
                485                 490                 495
Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
            500                 505                 510
Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
        515                 520                 525
Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
    530                 535                 540
Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
545                 550                 555                 560
Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
                565                 570                 575
Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn
            580                 585                 590
Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
        595                 600                 605
His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
    610                 615                 620
Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
625                 630                 635                 640
Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
                645                 650                 655
Lys Ile Arg Asn
            660
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<210> 190
<211> 1611
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::IL10 I87A
fusion protein

<400> 190

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atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cttgaccgaa agttacagcc cgaattctag cccaggccag 1140
ggcacccagt ctgagaacag ctgcacccac ttcccaggca acctgcctaa catgcttcga 1200
gatctccgag atgccttcag cagagtgaag actttctttc aaatgaagga tcagctggac 1260
aacttgttgt taaaggagtc cttgctggag gactttaagg gttacctggg ttgccaagcc 1320
ttgtctgaga tgatccagtt ttacctggag gaggtgatgc cccaagctga gaaccaagac 1380
ccagacgcca aggcgcatgt gaactccctg ggggagaacc tgaagaccct caggctgagg 1440
ctacggcgct gtcatcgatt tcttccctgt gaaaacaaga gcaaggccgt ggagcaggtg 1500
aagaatgcct ttaataagct ccaagagaaa ggcatctaca aagccatgag tgagtttgac 1560
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atcttcatca actacataga agcctacatg acaatgaaga tacgaaacta a 1611

<210> 191
<211> 536
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::IL10 I87A fusion protein

<400> 191
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
355 360 365
Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser
370 375 380
Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg
385 390 395 400
Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys
405 410 415
Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe
420 425 430
Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr
435 440 445
Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ala Lys

450 455 460
Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg
465 470 475 480
Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala
485 490 495
Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile
500 505 510
Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala
515 520 525
Tyr Met Thr Met Lys Ile Arg Asn
530 535

<210> 192
<211> 1611
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::IL10 I87S
fusion protein

<400> 192
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cttgaccgaa agttacagcc cgaattctag cccaggccag 1140
ggcacccagt ctgagaacag ctgcacccac ttcccaggca acctgcctaa catgcttcga 1200
gatctccgag atgccttcag cagagtgaag actttctttc aaatgaagga tcagctggac 1260
aacttgttgt taaaggagtc cttgctggag gactttaagg gttacctggg ttgccaagcc 1320
ttgtctgaga tgatccagtt ttacctggag gaggtgatgc cccaagctga gaaccaagac 1380
ccagacagca aggcgcatgt gaactccctg ggggagaacc tgaagaccct caggctgagg 1440
ctacggcgct gtcatcgatt tcttccctgt gaaaacaaga gcaaggccgt ggagcaggtg 1500
aagaatgcct ttaataagct ccaagagaaa ggcatctaca aagccatgag tgagtttgac 1560
atcttcatca actacataga agcctacatg acaatgaaga tacgaaacta a 1611

<210> 193
<211> 536
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::IL10 I87S fusion protein

<400> 193
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60

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Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65                  70                  75                  80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85                  90                  95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100                 105                 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115                 120                 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130                 135                 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145                 150                 155                 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165                 170                 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180                 185                 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195                 200                 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210                 215                 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
        355                 360                 365
Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser
    370                 375                 380
Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg
385                 390                 395                 400
Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys
                405                 410                 415
Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe
            420                 425                 430
Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr
        435                 440                 445
Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ser Lys
    450                 455                 460
Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg
465                 470                 475                 480
Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala
                485                 490                 495
Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile
            500                 505                 510
Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala
        515                 520                 525
Tyr Met Thr Met Lys Ile Arg Asn
    530                 535
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<210> 194
<211> 1635
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding mouse CTLA4::mouse
IL10 fusion protein with H68 linker

<400> 194
gccatacagg tgacccaacc ttcagtggtg ttggctagca gccatggtgt cgccagcttt 60
ccatgtgaat attcaccatc acacaacact gatgaggtcc gggtgactgt gctgcggcag 120
acaaatgacc aaatgactga ggtctgtgcc acgacattca cagagaagaa tacagtgggc 180
ttcctagatt acccccttctg cagtggtacc tttaatgaaa gcagagtgaa cctcaccatc 240
caaggactga gagctgttga cacgggactg tacctctgca aggtggaact catgtaccca 300
ccgccatact ttgtgggcat gggcaacggg acgcagattt atgtcattga tccagaacca 360
tgcccggatt ctgacctcga gcccagagtg cccataacac agaacccctg tcctccactc 420
aaagagtgtc ccccatgcgc agctccagac gcagcgggtg cgccatccgt cttcatcttc 480
cctccaaaga tcaaggatgt actcatgatc tccctgagcc ccatggtcac atgtgtggtg 540
gtggatgtga gcgaggatga cccagacgtc cagatcagct ggtttgtgaa caacgtggaa 600
gtacacacag ctcagacaca aacccataga gaggattaca acagtactct ccgggtggtc 660
agtgccctcc ccatccagca ccaggactgg atgagtggca aggcgttcgc atgcgcggtc 720
aacaacagag ccctcccatc ccccatcgag aaaaccatct caaaacccag agggccagta 780
agagctccac aggtatatgt cttgcctcca ccagcagaag agatgactaa gaaagagttc 840
agtctgacct gcatgatcgc aggcttctta cctgccgaaa ttgctgtgga ctggaccagc 900
aatgggcgta cagagcaaaa ctacaagaac accgcaacag tcctggactc tgatggttct 960
tacttcatgt acagcaagct cagagtacaa aagagcactt gggaaagagg aagtctttc 1020
gcctgctcag tggtccacga gggtctgcac aatcacctta cgactaagac catctcccgg 1080
tctctgggta aaaactcatt attcaaccaa gaagttcaaa ttcccttgac cgaaagttac 1140
agcccgaatt ctagcagggg ccagtacagc cgggaagaca ataactgcac ccacttccca 1200
gtcggccaga gccacatgct cctagagctg cggactgcct tcagccaggt gaagactttc 1260
tttcaaacaa aggaccagct ggacaacata ctgctaaccg actccttaat gcaggacttt 1320
aagggttact tgggttgcca agccttatcg gaaatgatcc agttttacct ggtagaagtg 1380
atgccccagg cagagaagca tggcccagaa atcaaggagc atttgaactc cctgggtgag 1440
aagctgaaga ccctcaggat gcggctgagg cgctgtcatc gatttctccc ctgtgaaaat 1500
aagagcaagg cagtggagca ggtgaagagt gattttaata agctccaaga ccaaggtgtc 1560
tacaaggcca tgaatgaatt tgacatcttc atcaactgca tagaagcata catgatgatc 1620
aaaatgaaaa gctaa 1635

<210> 195
<211> 544
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse CTLA4::mouse IL10 fusion protein with H68
linker

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

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        195                 200                 205
His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
    210                 215                 220
Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val
225                 230                 235                 240
Asn Asn Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
                245                 250                 255
Arg Gly Pro Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala
            260                 265                 270
Glu Glu Met Thr Lys Lys Glu Phe Ser Leu Thr Cys Met Ile Ala Gly
        275                 280                 285
Phe Leu Pro Ala Glu Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr
    290                 295                 300
Glu Gln Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser
305                 310                 315                 320
Tyr Phe Met Tyr Ser Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg
                325                 330                 335
Gly Ser Leu Phe Ala Cys Ser Val Val His Glu Gly Leu His Asn His
            340                 345                 350
Leu Thr Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys Asn Ser Leu Phe
        355                 360                 365
Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
    370                 375                 380
Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe Pro
385                 390                 395                 400
Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln
                405                 410                 415
Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu
            420                 425                 430
Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
        435                 440                 445
Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln Ala
    450                 455                 460
Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly Glu
465                 470                 475                 480
Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe Leu
                485                 490                 495
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp Phe
            500                 505                 510
Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe Asp
        515                 520                 525
Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys Ser
    530                 535                 540
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<210> 196
<211> 1638
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding mouse CTLA4::mouse IL10 fusion protein with H75 linker

<400> 196

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gccatacagg tgacccaacc ttcagtggtg ttggctagca gccatggtgt cgccagcttt 60
ccatgtgaat attcaccatc acacaacact gatgaggtcc gggtgactgt gctgcggcag 120
acaaatgacc aaatgactga ggtctgtgcc acgacattca cagagaagaa tacagtgggc 180
ttcctagatt acccccttctg cagtggtacc tttaatgaaa gcagagtgaa cctcaccatc 240
caaggactga gagctgttga cacgggactg tacctctgca aggtggaact catgtaccca 300
ccgccatact ttgtgggcat gggcaacggg acgcagattt atgtcattga tccagaacca 360
tgcccggatt ctgacctcga gcccagagtg cccataacac agaaccctg tcctccactc 420
aaagagtgtc ccccatgcgc agctccagac gcagcgggtg cgccatccgt cttcatcttc 480
cctccaaaga tcaaggatgt actcatgatc tccctgagcc ccatggtcac atgtgtggtg 540
gtggatgtga gcgaggatga cccagacgtc cagatcagct ggtttgtgaa caacgtggaa 600
gtacacacag ctcagacaca aacccataga gaggattaca acagtactct ccgggtggtc 660
agtgccctcc ccatccagca ccaggactgg atgagtggca aggcgttcgc atgcgcggtc 720
aacaacagag ccctcccatc ccccatcgag aaaaccatct caaaacccag agggccagta 780
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agagctccac aggtatatgt cttgcctcca ccagcagaag agatgactaa gaaagagttc 840
agtctgacct gcatgatcac aggcttctta cctgccgaaa ttgctgtgga ctggaccagc 900
aatgggcgta cagagcaaaa ctacaagaac accgcaacag tcctggactc tgatggttct 960
tacttcatgt acagcaagct cagagtacaa aagagcactt gggaaagagg aagtcttttc 1020
gcctgctcag tggtccacga gggtctgcac aatcacctta cgactaagac catctcccgg 1080
tctctgggta aacagaggca caacaattct tccctgaata caggaactca gatggcaggt 1140
cattctccga attctagcag gggccagtac agccgggaag acaataactg cacccacttc 1200
ccagtcggcc agagccacat gctcctagag ctgcggactg ccttcagcca ggtgaagact 1260
ttctttcaaa caaaggacca gctggacaac atactgctaa ccgactcctt aatgcaggac 1320
tttaagggtt acttgggttg ccaagcctta tcggaaatga tccagtttta cctggtagaa 1380
gtgatgcccc aggcagagaa gcatggccca gaaatcaagg agcatttgaa ctccctgggt 1440
gagaagctga agaccctcag gatgcggctg aggcgctgtc atcgatttct cccctgtgaa 1500
aataagagca aggcagtgga gcaggtgaag agtgatttta ataagctcca agaccaaggt 1560
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atcaaaatga aaagctaa 1638

<210> 197
<211> 545
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse CTLA4::mouse IL10 fusion protein with H75
linker

<400> 197
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Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln Met Thr Glu Val
35 40 45
Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly Phe Leu Asp Tyr
50 55 60
Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val Asn Leu Thr Ile
65 70 75 80
Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Leu Cys Lys Val Glu
85 90 95
Leu Met Tyr Pro Pro Pro Tyr Phe Val Gly Met Gly Asn Gly Thr Gln
100 105 110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro
115 120 125
Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu Lys Glu Cys Pro
130 135 140
Pro Cys Ala Ala Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe
145 150 155 160
Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val
165 170 175
Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile
180 185 190
Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr
195 200 205
His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
210 215 220
Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val
225 230 235 240
Asn Asn Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
245 250 255
Arg Gly Pro Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala
260 265 270
Glu Glu Met Thr Lys Lys Glu Phe Ser Leu Thr Cys Met Ile Thr Gly
275 280 285
Phe Leu Pro Ala Glu Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr
290 295 300
Glu Gln Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser
305 310 315 320
Tyr Phe Met Tyr Ser Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg
325 330 335

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Gly Ser Leu Phe Ala Cys Ser Val Val His Glu Gly Leu His Asn His
            340                 345                 350
Leu Thr Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys Gln Arg His Asn
        355                 360                 365
Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn
    370                 375                 380
Ser Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe
385                 390                 395                 400
Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser
                405                 410                 415
Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu
            420                 425                 430
Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln
        435                 440                 445
Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln
    450                 455                 460
Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly
465                 470                 475                 480
Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe
                485                 490                 495
Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp
            500                 505                 510
Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe
        515                 520                 525
Asp Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys
    530                 535                 540
Ser
545
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<210> 198
<211> 1920
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding GITR::3D1 fusion protein

<400> 198

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tgctgttccg agtgggactg catgtgtgtc cagcctgaat tccactgcgg agacccttgc 180
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aacaagaccc acaacgctgt gtgcgtccca gggtccccgc cggcagagcc gcttgggctc 420
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 480
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 540
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 600
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 660
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 720
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 780
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 840
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 900
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 960
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gagctggtga ggcctgggga atcagtgaag atttcctgca agggttccgg ctacacattc 1260
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gattctgcca tctattactg tgcaagagcg gcctggtata tggactactg gggtcaagga 1500
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ggatccggtg gcggcggatc tgacattgtg ctgtcacagt ctccatcctc cctggctgtg 1620
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acccgagaga actacttggc ttggtaccag cagaaaccag ggcagtctcc taaactgctg 1740
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gggacagatt tcactctcac catcagcagt gtgcaggctg aagacctggc agtttattac 1860
tgcacgcaat cttataatct ttacacgttc ggaggggggga ccaagctgga aataaaataa 1920

<210> 199
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> GITR::3D1 fusion protein

<400> 199
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Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr Thr Arg Cys
20 25 30
Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp Asp Cys Met
35 40 45
Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys Thr Thr Cys
50 55 60
Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser Gln Gly Lys
65 70 75 80
Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly Thr Phe Ser
85 90 95
Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys Thr Gln Phe
100 105 110
Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys
115 120 125
Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Leu Glu Pro Lys Ser
130 135 140
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
145 150 155 160
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
165 170 175
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
180 185 190
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
195 200 205
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
210 215 220
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
225 230 235 240
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
245 250 255
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
260 265 270
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
275 280 285
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
290 295 300
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
305 310 315 320
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
325 330 335
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
340 345 350
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
355 360 365
Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
370 375 380
Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Gln Gln Ser Gly Pro
385 390 395 400
Glu Leu Val Arg Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser
405 410 415
Gly Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His

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            420                 425                 430
Ala Lys Ser Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn
        435                 440                 445
Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp
    450                 455                 460
Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu
465                 470                 475                 480
Asp Ser Ala Ile Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr
                485                 490                 495
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
            500                 505                 510
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
        515                 520                 525
Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu
    530                 535                 540
Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg
545                 550                 555                 560
Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
                565                 570                 575
Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro
            580                 585                 590
Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        595                 600                 605
Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln Ser
    610                 615                 620
Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
625                 630                 635
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<210> 200
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding HVEM::3D1 fusion protein

<400> 200

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tgtgacccag ccatgggcct gcgcgcgagc cggaactgct ccaggacaga gaacgccgtg 240
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cgcgcttacg ccacctccag cccgggccag agggtgcaga agggaggcac cgagagtcag 360
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tgtcagcacc agaccaagtg cagctggctg gtgacgaagg ccggagctgg gaccagcagc 480
tcccacctcg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 540
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccccaa aacccaagga caccctcatg 600
atctcccgga ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 660
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ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 960
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1140
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gaagttcaaa ttcccttgac cgaaagttac agcccgaatt ctcaggtcca gctgcagcag 1260
tctgggcctg agctggtgag gcctggggaa tcagtgaaga tttcctgcaa gggttccggc 1320
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acatctgagg attctgccat ctattactgt gcaagagcgg cctggtatat ggactactgg 1560
ggtcaaggaa cctcagtcac cgtctcctca gggggtggag gctctggtgg cggtggctct 1620
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ctggctgtgt cagcaggaga gaaggtcact atgagctgca aatccagtca gagtctgctc 1740
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aaactgctga tctactgggc atccactagg gaatctgggg tccctgatcg cttcacaggc 1860
agtggatctg ggacagattt cactctcacc atcagcagtg tgcaggctga agacctggca 1920
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<210> 201
<211> 662
<212> PRT
<213> Artificial Sequence

<220>
<223> HVEM::3D1 fusion protein

<400> 201
Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys
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Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
35 40 45
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
50 55 60
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
65 70 75 80
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
85 90 95
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
100 105 110
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
115 120 125
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
130 135 140
Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr Ser Ser
145 150 155 160
Ser His Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
165 170 175
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
180 185 190
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
210 215 220
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225 230 235 240
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
260 265 270
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
275 280 285
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
290 295 300
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
355 360 365
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln
385 390 395 400
Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val
405 410 415
Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu Ser Val

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            420                 425                 430
Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr Ala Ile
        435                 440                 445
Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly Val
    450                 455                 460
Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys Gly
465                 470                 475                 480
Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
                485                 490                 495
Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala Arg
            500                 505                 510
Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
        515                 520                 525
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    530                 535                 540
Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser Pro Ser Ser
545                 550                 555                 560
Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser
                565                 570                 575
Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr
            580                 585                 590
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser
        595                 600                 605
Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
    610                 615                 620
Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
625                 630                 635                 640
Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly
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<210> 202
<211> 2163
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding PDL1::3D1 fusion protein

<400> 202

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agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240
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atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa 600
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ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 720
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780
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caaattccct tgaccgaaag ttacagcccg aattctcagg tccagctgca gcagtctggg 1440
cctgagctgg tgaggcctgg ggaatcagtg aagatttcct gcaagggttc cggctacaca 1500
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<210> 203
<211> 720
<212> PRT
<213> Artificial Sequence

<220>
<223> PDL1::3D1 fusion protein

<400> 203

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        35                  40                  45
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Leu Glu Pro Lys
    210                 215                 220
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365
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Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
    450                 455                 460
Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Gln Gln Ser Gly
465                 470                 475                 480
Pro Glu Leu Val Arg Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly
                485                 490                 495
Ser Gly Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser
            500                 505                 510
His Ala Lys Ser Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp
        515                 520                 525
Asn Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val
    530                 535                 540
Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser
545                 550                 555                 560
Glu Asp Ser Ala Ile Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp
                565                 570                 575
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly
            580                 585                 590
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        595                 600                 605
Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
    610                 615                 620
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
625                 630                 635                 640
Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
                645                 650                 655
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
            660                 665                 670
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        675                 680                 685
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln
    690                 695                 700
Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
705                 710                 715                 720
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<210> 204
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding PDL2::3D1 fusion protein

<400> 204

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caaaaggtgg aaaatgatac atccccacac cgtgaaagag ccactttgct ggaggagcag 180
ctgcccttag ggaaggcctc gttccacata cctcaagtcc aagtgaggga cgaaggacag 240
taccaatgca taatcatcta tggggtcgcc tgggactaca agtacctgac tctgaaagtc 300
aaagcttcct acaggaaaat aaacactcac atcctaaagg ttccagaaac agatgaggta 360
gagctcacct gccaggctac aggttatcct ctggcagaag tatcctggcc aaacgtcagc 420
gttcctgcca acaccagcca ctccaggacc cctgaaggcc tctaccaggt caccagtgtt 480
ctgcgcctaa agccaccccc tggcagaaac ttcagctgtg tgttctggaa tactcacgtg 540
agggaactta ctttggccag cattgacctt caaagtcaga tggaacccag gacccatcca 600
actctcgagc ccaaatcttc tgacaaaact cacacatgcc caccgtgccc agcacctgaa 660
gccgcgggtg caccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 720
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tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 780
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 840
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 900
ctgaatggca aggcgtacgc gtgcgcggtc tccaacaaag ccctcccagc ccccatcgag 960
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tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1080
ccaagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1140
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1200
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1260
aaccactaca cgcagaagag cctctccctg tctccgggta actcattatt caaccaagaa 1320
gttcaaattc ccttgaccga aagttacagc ccgaattctc aggtccagct gcagcagtct 1380
gggcctgagc tggtgaggcc tggggaatca gtgaagattt cctgcaaggg ttccggctac 1440
acattcactg attatgctat acagtgggtg aagcagagtc atgcaaagag tctagagtgg 1500
attggagtta ttaatattta ctatgataat acaaactaca accagaagtt taagggcaag 1560
gccacaatga ctgtagacaa atcctccagc acagcctata tggaacttgc cagattgaca 1620
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caaggaacct cagtcaccgt ctcctcaggg ggtggaggct ctggtggcgg tggctctggc 1740
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gctgtgtcag caggagagaa ggtcactatg agctgcaaat ccagtcagag tctgctcaac 1860
agtagaaccc gagagaacta cttggcttgg taccagcaga aaccagggca gtctcctaaa 1920
ctgctgatct actgggcatc cactagggaa tctggggtcc ctgatcgctt cacaggcagt 1980
ggatctggga cagatttcac tctcaccatc agcagtgtgc aggctgaaga cctggcagtt 2040
tattactgca cgcaatctta taatctttac acgttcggag gggggaccaa gctggaaata 2100
aaataa 2106

<210> 205
<211> 701
<212> PRT
<213> Artificial Sequence

<220>
<223> PDL2::3D1 fusion protein

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
275 280 285
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
290 295 300
Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
305 310 315 320
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
325 330 335
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
340 345 350
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
355 360 365
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
370 375 380
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
385 390 395 400
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
405 410 415
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
420 425 430
Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser
435 440 445
Tyr Ser Pro Asn Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
450 455 460
Val Arg Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr
465 470 475 480
Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys
485 490 495
Ser Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn
500 505 510
Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser
515 520 525
Ser Ser Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser
530 535 540
Ala Ile Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly
545 550 555 560
Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
565 570 575
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
580 585 590
Leu Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val
595 600 605
Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg
610 615 620
Glu Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
625 630 635 640
Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
645 650 655
Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
660 665 670
Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn
675 680 685
Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
690 695 700

<210> 206
<211> 1806
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding TGFBetaR1::3D1 fusion protein

<400> 206
gcggcgctgc tcccgggggc gacggcgtta cagtgtttct gccacctctg tacaaaagac 60
aattttactt gtgtgacaga tgggctctgc tttgtctctg tcacagagac cacagacaaa 120

gttatacaca acagcatgtg tatagctgaa attgacttaa ttccgcgaga taggccgttt 180
gtatgtgcac cctcttcaaa aactgggtct gtgactacaa catattgctg caatcaggac 240
cattgcaata aaatagaact tccaactact gtaaagtcat cacctggcct tggtcctgtg 300
gaactcgagc ccaaatcttc tgacaaaact cacacatgcc caccgtgccc agcacctgaa 360
gccgcgggtg caccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 420
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 480
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 540
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 600
ctgaatggca aggcgtacgc gtgcgcggtc tccaacaaag ccctcccagc ccccatcgag 660
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 720
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 780
ccaagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 840
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 900
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 960
aaccactaca cgcagaagag cctctccctg tctccgggta actcattatt caaccaagaa 1020
gttcaaattc ccttgaccga aagttacagc ccgaattctc aggtccagct gcagcagtct 1080
gggcctgagc tggtgaggcc tggggaatca gtgaagattt cctgcaaggg ttccggctac 1140
acattcactg attatgctat acagtgggtg aagcagagtc atgcaaagag tctagagtgg 1200
attggagtta ttaatattta ctatgataat acaaactaca accagaagtt taagggcaag 1260
gccacaatga ctgtagacaa atcctccagc acagcctata tggaacttgc cagattgaca 1320
tctgaggatt ctgccatcta ttactgtgca agagcggcct ggtatatgga ctactggggt 1380
caaggaacct cagtcaccgt ctcctcaggg ggtggaggct ctggtggcgg tggctctggc 1440
ggaggtggat ccggtggcgg cggatctgac attgtgctgt cacagtctcc atcctccctg 1500
gctgtgtcag caggagagaa ggtcactatg agctgcaaat ccagtcagag tctgctcaac 1560
agtagaaccc gagagaacta cttggcttgg taccagcaga aaccagggca gtctcctaaa 1620
ctgctgatct actgggcatc cactagggaa tctggggtcc ctgatcgctt cacaggcagt 1680
ggatctggga cagatttcac tctcaccatc agcagtgtgc aggctgaaga cctggcagtt 1740
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aaataa 1806

<210> 207
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> TGFBetaR1::3D1 fusion protein

<400> 207
Ala Ala Leu Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu
 1   5   10   15
Cys Thr Lys Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val
            20   25   30
Ser Val Thr Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile
        35   40   45
Ala Glu Ile Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro
    50   55   60
Ser Ser Lys Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp
65   70   75   80
His Cys Asn Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly
                85   90   95
Leu Gly Pro Val Glu Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr
            100   105   110
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe
        115   120   125
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    130   135   140
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
145   150   155   160
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                165   170   175
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            180   185   190
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
        195   200   205
Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    210   215   220
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

225 230 235 240
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
245 250 255
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
260 265 270
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
275 280 285
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
290 295 300
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
305 310 315 320
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu
325 330 335
Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn
340 345 350
Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly
355 360 365
Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp
370 375 380
Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp
385 390 395 400
Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys
405 410 415
Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala
420 425 430
Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr
435 440 445
Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser
450 455 460
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
465 470 475 480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser
485 490 495
Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys
500 505 510
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu
515 520 525
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
530 535 540
Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser
545 550 555 560
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu
565 570 575
Asp Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe
580 585 590
Gly Gly Gly Thr Lys Leu Glu Ile Lys
595 600

<210> 208
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::monoIL10 I87A
fusion protein

<400> 208
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tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
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tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttcaaattcc cttgaccgaa agttacagcc cgaattctag cccaggccag 1140
ggcacccagt ctgagaacag ctgcacccac ttcccaggca acctgcctaa catgcttcga 1200
gatctccgag atgccttcag cagagtgaag actttctttc aaatgaagga tcagctggac 1260
aacttgttgt taaaggagtc cttgctggag gactttaagg gttacctggg ttgccaagcc 1320
ttgtctgaga tgatccagtt ttacctggag gaggtgatgc cccaagctga gaaccaagac 1380
ccagacgcca aggcgcatgt gaactccctg ggggagaacc tgaagaccct caggctgagg 1440
ctacggcgct gtcatcgatt tcttccctgt gaaaacggtg gtggatccgg cggtaagagc 1500
aaggccgtgg agcaggtgaa gaatgccttt aataagctcc aagagaaagg catctacaaa 1560
gccatgagtg agtttgacat cttcatcaac tacatagaag cctacatgac aatgaagata 1620
cgaaactaa 1629

<210> 209
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::monoIL10 I87A fusion protein

<400> 209
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
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Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20   25   30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35   40   45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50   55   60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65   70   75   80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85   90   95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100   105   110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115   120   125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130   135   140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145   150   155   160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165   170   175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180   185   190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195   200   205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210   215   220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225   230   235   240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245   250   255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260   265   270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275   280   285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290   295   300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
355 360 365
Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser
370 375 380
Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg
385 390 395 400
Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys
405 410 415
Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe
420 425 430
Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr
435 440 445
Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ala Lys
450 455 460
Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg
465 470 475 480
Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Gly Gly Gly Ser
485 490 495
Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys
500 505 510
Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe
515 520 525
Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
530 535 540

<210> 210
<211> 2001
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding monoIL10::3D1 fusion protein

<400> 210
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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaacct cgagcccaaa tcttctgaca aaactcacac atgcccaccg 540
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 600
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 660
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 720
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 780
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tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 960
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aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1140
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ttattcaacc aagaagttca aattcccttg accgaaagtt acagcccgaa ttctcaggtc 1260
cagctgcagc agtctgggcc tgagctggtg aggcctgggg aatcagtgaa gatttcctgc 1320
aagggttccg gctacacatt cactgattat gctatacagt gggtgaagca gagtcatgca 1380
aagagtctag agtggattgg agttattaat atttactatg ataatacaaa ctacaaccag 1440
aagtttaagg gcaaggccac aatgactgta gacaaatcct ccagcacagc ctatatggaa 1500
cttgccagat tgacatctga ggattctgcc atctattact gtgcaagagc ggcctggtat 1560
atggactact ggggtcaagg aacctcagtc accgtctcct caggggtgg aggctctggt 1620

ggcggtggct ctggcggagg tggatccggt ggcggcggat ctgacattgt gctgtcacag 1680
tctccatcct ccctggctgt gtcagcagga gagaaggtca ctatgagctg caaatccagt 1740
cagagtctgc tcaacagtag aacccgagag aactacttgg cttggtacca gcagaaacca 1800
gggcagtctc ctaaactgct gatctactgg gcatccacta gggaatctgg ggtccctgat 1860
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcagcag tgtgcaggct 1920
gaagacctgg cagtttatta ctgcacgcaa tcttataatc tttacacgtt cggaggggg 1980
accaagctgg aaataaaata a 2001

<210> 211
<211> 666
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10::3D1 fusion protein

<400> 211
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
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Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
115 120 125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
130 135 140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile
145 150 155 160
Thr Met Lys Ile Arg Asn Leu Glu Pro Lys Ser Ser Asp Lys Thr His
165 170 175
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
180 185 190
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
195 200 205
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
210 215 220
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
225 230 235 240
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
245 250 255
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
260 265 270
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
275 280 285
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
290 295 300
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
305 310 315 320
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
325 330 335
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
340 345 350
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
355 360 365
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
370 375 380
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser
385 390 395 400
Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro

405 410 415
Asn Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro
420 425 430
Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr
435 440 445
Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu
450 455 460
Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln
465 470 475 480
Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr
485 490 495
Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr
500 505 510
Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr
515 520 525
Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
530 535 540
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln
545 550 555 560
Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser
565 570 575
Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr
580 585 590
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
595 600 605
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly
610 615 620
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
625 630 635 640
Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr
645 650 655
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
660 665

<210> 212
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10 I87A::3D1 fusion protein

<400> 212
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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggtaact cattattcaa ccaagaagtt 1200
caaattccct tgaccgaaag ttacagcccg aattctcagg tccagctgca gcagtctggg 1260
cctgagctgg tgaggcctgg ggaatcagtg aagatttcct gcaagggttc cggctacaca 1320
ttcactgatt atgctataca gtgggtgaag cagagtcatg caaagagtct agagtggatt 1380

ggagttatta atatttacta tgataataca aactacaacc agaagtttaa gggcaaggcc 1440
acaatgactg tagacaaatc ctccagcaca gcctatatgg aacttgccag attgacatct 1500
gaggattctg ccatctatta ctgtgcaaga gcggcctggt atatggacta ctggggtcaa 1560
ggaacctcag tcaccgtctc ctcaggggt ggaggctctg gtggcggtgg ctctggcgga 1620
ggtggatccg gtggcggcgg atctgacatt gtgctgtcac agtctccatc ctccctggct 1680
gtgtcagcag gagagaaggt cactatgagc tgcaaatcca gtcagagtct gctcaacagt 1740
agaacccgag agaactactt ggcttggtac cagcagaaac cagggcagtc tcctaaactg 1800
ctgatctact gggcatccac tagggaatct ggggtccctg atcgcttcac aggcagtgga 1860
tctgggacag atttcactct caccatcagc agtgtgcagg ctgaagacct ggcagtttat 1920
tactgcacgc aatcttataa tctttacacg ttcggagggg ggaccaagct ggaaataaaa 1980
taa 1983

<210> 213
<211> 660
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A::3D1 fusion protein

<400> 213
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145 150 155 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
165 170 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
180 185 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
195 200 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
210 215 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225 230 235 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
245 250 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
260 265 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
275 280 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
290 295 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305 310 315 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
325 330 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
340 345 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
355 360 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

370 375 380
Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val
385 390 395 400
Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu
405 410 415
Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu Ser Val Lys Ile
420 425 430
Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp
435 440 445
Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly Val Ile Asn
450 455 460
Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala
465 470 475 480
Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Ala
485 490 495
Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala Arg Ala Ala
500 505 510
Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
515 520 525
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
530 535 540
Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala
545 550 555 560
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
565 570 575
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
580 585 590
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
595 600 605
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
610 615 620
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
625 630 635 640
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
645 650 655
Leu Glu Ile Lys
660

<210> 214
<211> 2001
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding monoIL10 I87A::3D1
fusion protein

<400> 214
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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
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ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaacct cgagcccaaa tcttctgaca aaactcacac atgcccaccg 540
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 600
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 660
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 720
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ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 840
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aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1080
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1140

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cagctgcagc agtctgggcc tgagctggtg aggcctgggg aatcagtgaa gatttcctgc 1320
aagggttccg gctacacatt cactgattat gctatacagt gggtgaagca gagtcatgca 1380
aagagtctag agtggattgg agttattaat atttactatg ataatacaaa ctacaaccag 1440
aagtttaagg gcaaggccac aatgactgta gacaaatcct ccagcacagc ctatatggaa 1500
cttgccagat tgacatctga ggattctgcc atctattact gtgcaagagc ggcctggtat 1560
atggactact ggggtcaagg aacctcagtc accgtctcct caggggtgg aggctctggt 1620
ggcggtggct ctggcggagg tggatccggt ggcggcggat ctgacattgt gctgtcacag 1680
tctccatcct ccctggctgt gtcagcagga gagaaggtca ctatgagctg caaatccagt 1740
cagagtctgc tcaacagtag aacccgagag aactacttgg cttggtacca gcagaaacca 1800
gggcagtctc ctaaactgct gatctactgg gcatccacta gggaatctgg ggtccctgat 1860
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcagcag tgtgcaggct 1920
gaagacctgg cagtttatta ctgcacgcaa tcttataatc tttacacgtt cggaggggg 1980
accaagctgg aaataaaata a 2001

<210> 215
<211> 666
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10 I87A::3D1 fusion protein

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

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            340                 345                 350
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        355                 360                 365
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    370                 375                 380
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser
385                 390                 395                 400
Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro
                405                 410                 415
Asn Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro
            420                 425                 430
Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr
        435                 440                 445
Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu
    450                 455                 460
Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln
465                 470                 475                 480
Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr
                485                 490                 495
Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr
            500                 505                 510
Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr
        515                 520                 525
Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    530                 535                 540
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln
545                 550                 555                 560
Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser
                565                 570                 575
Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr
            580                 585                 590
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        595                 600                 605
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly
    610                 615                 620
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
625                 630                 635                 640
Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr
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Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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<210> 216
<211> 1071
<212> DNA
<213> Artificial Sequence

<220>
<223> LEA29-Fc - a CTLA4 variant

<400> 216

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gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacg agggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
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accgtggaca agagccggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtta a 1071

<210> 217
<211> 356
<212> PRT
<213> Artificial Sequence

<220>
<223> LEA29-Fc - a CTLA4 variant

<400> 217
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1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly
355

<210> 218
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding LEA29Y::IL10 fusion
protein with H75 linker

<400> 218
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaatacact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacg agggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacagg aactcagatg gcaggtcatt ctccgaattc tagcccaggc 1140
cagggcaccc agtctgagaa cagctgcacc cacttcccag gcaacctgcc taacatgctt 1200
cgagatctcc gagatgcctt cagcagagtg aagactttct ttcaaatgaa ggatcagctg 1260
gacaacttgt tgttaaagga gtccttgctg gaggacttta agggttacct gggttgccaa 1320
gccttgtctg agatgatcca gttttacctg gaggaggtga tgccccaagc tgagaaccaa 1380
gacccagacg ccaaggcgca tgtgaactcc ctgggggaga acctgaagac cctcaggctg 1440
aggctacggc gctgtcatcg atttcttccc tgtgaaaaca agagcaaggc cgtggagcag 1500
gtgaagaatg cctttaataa gctccaagag aaaggcatct acaaagccat gagtgagttt 1560
gacatcttca tcaactacat agaagcctac atgacaatga agatacgaaa ctaa 1614

<210> 219
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> LEA29Y::IL10 fusion protein with H75 linker

<400> 219
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1   5   10   15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val
            20   25   30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35   40   45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50   55   60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65   70   75   80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85   90   95
Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile
            100   105   110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115   120   125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130   135   140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145   150   155   160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165   170   175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180   185   190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195   200   205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210   215   220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala

```
225                 230                 235                 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245                 250                 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260                 265                 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275                 280                 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr
        355                 360                 365
Gln Met Ala Gly His Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln
    370                 375                 380
Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu
385                 390                 395                 400
Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met
                405                 410                 415
Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp
            420                 425                 430
Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe
        435                 440                 445
Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ala
    450                 455                 460
Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu
465                 470                 475                 480
Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys
                485                 490                 495
Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly
            500                 505                 510
Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu
        515                 520                 525
Ala Tyr Met Thr Met Lys Ile Arg Asn
    530                 535
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<210> 220
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::monoIL10
fusion protein with H79 linker

<400> 220

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atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
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gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa ctcattattc 1080
aaccaagaag ttccgaattc tagcccaggc cagggcaccc agtctgagaa cagctgcacc 1140
cacttcccag gcaacctgcc taacatgctt cgagatctcc gagatgcctt cagcagagtg 1200
aagactttct ttcaaatgaa ggatcagctg gacaacttgt tgttaaagga gtccttgctg 1260
gaggacttta agggttacct gggttgccaa gccttgtctg agatgatcca gttttacctg 1320
gaggaggtga tgccccaagc tgagaaccaa gacccagaca tcaaggcgca tgtgaactcc 1380
ctgggggaga acctgaagac cctcaggctg aggctacggc gctgtcatcg atttcttccc 1440
tgtgaaaacg gtggtggatc cggcggtaag agcaaggccg tggagcaggt gaagaatgcc 1500
tttaataagc tccaagagaa aggcatctac aaagccatga gtgagtttga catcttcatc 1560
aactacatag aagcctacat gacaatgaag atacgaaact aa 1602

<210> 221
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::monoIL10 fusion protein with H79 linker

<400> 221
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1   5   10   15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20   25   30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35   40   45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50   55   60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65   70   75   80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85   90   95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100   105   110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115   120   125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130   135   140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145   150   155   160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165   170   175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180   185   190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195   200   205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210   215   220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225   230   235   240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245   250   255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260   265   270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275   280   285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290   295   300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305   310   315   320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325   330   335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340   345   350
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Pro Asn Ser Ser
        355   360   365
Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly
    370   375   380

Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val
385 390 395 400
Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys
405 410 415
Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu
420 425 430
Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu
435 440 445
Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn
450 455 460
Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro
465 470 475 480
Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln
485 490 495
Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
500 505 510
Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
515 520 525
Met Lys Ile Arg Asn
530

<210> 222
<211> 1608
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::monoIL10
fusion protein with H80 linker

<400> 222
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacacc gaattctagc ccaggccagg gcacccagtc tgagaacagc 1140
tgcacccact tcccaggcaa cctgcctaac atgcttcgag atctccgaga tgccttcagc 1200
agagtgaaga ctttctttca aatgaaggat cagctggaca acttgttgtt aaaggagtcc 1260
ttgctggagg actttaaggg ttacctgggt tgccaagcct tgtctgagat gatccagttt 1320
tacctggagg aggtgatgcc ccaagctgag aaccaagacc cagacatcaa ggcgcatgtg 1380
aactccctgg gggagaacct gaagacgctc aggctgaggc tacggcgctg tcatcgattt 1440
cttccctgtg aaaacggtgg tggatccggc ggtaagagca aggccgtgga gcaggtgaag 1500
aatgccttta ataagctcca agagaaaggc atctacaaag ccatgagtga gtttgacatc 1560
ttcatcaact acatagaagc ctacatgaca atgaagatac gaaactaa 1608

<210> 223
<211> 535
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::monoIL10 fusion protein with H80 linker

<400> 223

Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Pro Asn
355 360 365
Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
370 375 380
Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
385 390 395 400
Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu
405 410 415
Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
420 425 430
Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
435 440 445
Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
450 455 460
Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
465 470 475 480
Leu Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val
485 490 495
Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr
500 505 510
Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr
515 520 525
Met Thr Met Lys Ile Arg Asn

530 535

<210> 224
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0114 - a generated variant of humanized FUN1

<400> 224
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggata caccttcacc gactacaaca tgaactgggt gcaacaggcc 120
cctggaaaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcag agtcaccata accgcggaca cgtctacaga cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aacatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 480
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 600
tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 660
gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa 1473

<210> 225
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0114 - a generated variant of humanized FUN1

<400> 225
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Asn Met Asn Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
100 105 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu

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145                 150                 155                 160
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
                165                 170                 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            180                 185                 190
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
        195                 200                 205
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    210                 215                 220
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His
225                 230                 235                 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                245                 250                 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
```

<210> 226
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0115 - a generated variant of humanized FUN1

<400> 226

```
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc gactacaaca tgaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 480
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 600
tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 660
gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
```

```
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa                               1473

<210> 227
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0115 - a generated variant of
      humanized FUN1

<400> 227
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30
Asn Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
            100                 105                 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
145                 150                 155                 160
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
                165                 170                 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            180                 185                 190
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
        195                 200                 205
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    210                 215                 220
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His
225                 230                 235                 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                245                 250                 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
```

```
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
```

<210> 228
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0116 - a generated variant of humanized FUN1

<400> 228

```
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactacaaca tgaactggat acgccaggct 120
ccagggaagg ggctggagtg ggtttcaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 480
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 600
tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 660
gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa                               1473
```

<210> 229
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0116 - a generated variant of humanized FUN1

<400> 229

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
```

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

<210> 230
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0117 - a generated variant of

humanized FUN1

<400> 230
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggata caccttcacc gactacaaca tgaactgggt gcaacaggcc 120
cctggaaaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcag agtcaccata accgcggaca cgtctacaga cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aacatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat ccagatgacc cagtctccat cctccctgtc tgcatctgta 480
ggagacagag tcaccatcac ttgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta tcagcagaaa ccagggaaag ttcctaagct cctgatctat 600
tgggcatcca ctagggaatc tggggtccca tctcggttca gtggcagtgg atctgggaca 660
gatttcactc tcaccatcag cagcctgcag cctgaagatg ttgcaactta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa 1473

<210> 231
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0117 - a generated variant of
humanized FUN1

<400> 231
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Asn Met Asn Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
100 105 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
145 150 155 160
Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr
165 170 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
180 185 190
Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
195 200 205
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
210 215 220
Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys His

```
225                 230                 235                 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                245                 250                 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
```

<210> 232
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0118 - a generated variant of humanized FUN1

<400> 232

```
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc gactacaaca tgaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat ccagatgacc cagtctccat cctccctgtc tgcatctgta 480
ggagacagag tcaccatcac ttgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta tcagcagaaa ccagggaaag ttcctaagct cctgatctat 600
tgggcatcca ctagggaatc tggggtccca tctcggttca gtggcagtgg atctgggaca 660
gatttcactc tcaccatcag cagcctgcag cctgaagatg ttgcaactta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
```

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa 1473

<210> 233
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0118 - a generated variant of humanized FUN1

<400> 233
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Asn Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
100 105 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
145 150 155 160
Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr
165 170 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
180 185 190
Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
195 200 205
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
210 215 220
Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys His
225 230 235 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
245 250 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
260 265 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
275 280 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305 310 315 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
355 360 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
370 375 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385 390 395 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
405 410 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
420 425 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

```
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
```

<210> 234
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0119 - a generated variant of humanized FUN1

<400> 234

```
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactacaaca tgaactggat acgccaggct 120
ccagggaagg ggctggagtg ggtttcaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat ccagatgacc cagtctccat cctccctgtc tgcatctgta 480
ggagacagag tcaccatcac ttgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta tcagcagaaa ccagggaaag ttcctaagct cctgatctat 600
tgggcatcca ctagggaatc tggggtccca tctcggttca gtggcagtgg atctgggaca 660
gatttcactc tcaccatcag cagcctgcag cctgaagatg ttgcaactta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa                              1473
```

<210> 235
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized FUN1 SMIP M0119 - a generated variant of humanized FUN1

<400> 235

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

```
            100                 105                 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
145                 150                 155                 160
Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr
                165                 170                 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            180                 185                 190
Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
        195                 200                 205
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    210                 215                 220
Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys His
225                 230                 235                 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                245                 250                 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
```

<210> 236
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding humanized FUN1
M0115::IL10 fusion protein

<400> 236
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc gactacaaca tgaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420

ggtggcggcg gatctgacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 480
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 600
tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 660
gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt aactcattat tcaaccaaga agttcaaatt 1500
cccttgaccg aaagttacag cccgaattct agcccaggcc agggcaccca gtctgagaac 1560
agctgcaccc acttcccagg caacctgcct aacatgcttc gagatctccg agatgccttc 1620
agcagagtga agactttctt tcaaatgaag gatcagctgg acaacttgtt gttaaaggag 1680
tccttgctgg aggactttaa gggttacctg ggttgccaag ccttgtctga gatgatccag 1740
ttttacctgg aggaggtgat gccccaagct gagaaccaag acccagacat caaggcgcat 1800
gtgaactccc tgggggagaa cctgaagacc ctcaggctga ggctacggcg ctgtcatcga 1860
tttcttccct gtgaaaacaa gagcaaggcc gtggagcagg tgaagaatgc ctttaataag 1920
ctccaagaga aaggcatcta caaagccatg agtgagtttg acatcttcat caactacata 1980
gaagcctaca tgacaatgaa gatacgaaac taa 2013

<210> 237
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized FUN1 M0115::IL10 fusion protein

<400> 237
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
Asn Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
100 105 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
145 150 155 160
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
165 170 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
180 185 190
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
195 200 205
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
210 215 220
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His
225 230 235 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile

245 250 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
260 265 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
275 280 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305 310 315 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
355 360 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
370 375 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385 390 395 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
405 410 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
420 425 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
435 440 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
450 455 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465 470 475 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln
485 490 495
Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro
500 505 510
Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn
515 520 525
Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys
530 535 540
Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu
545 550 555 560
Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser
565 570 575
Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn
580 585 590
Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu
595 600 605
Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys
610 615 620
Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys
625 630 635 640
Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe
645 650 655
Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
660 665 670

<210> 238
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-mouse CD86 (GL1) SMIP

<400> 238
gaggtgcagc tggtggagtc tgctggaggt ttagtgcagc ctggaaggtc cctaaaactc 60
tcctgtgcag cctcaggatt cactttcagt gactattaca tggcctgggt ccgccaggct 120
ccaacgaagg ggctggagtg ggtcgcaacc attagtcatg acggtagtag tacttactat 180
cgagactccg tgaagggccg attcacaatc tccagagata atgcaaaaac catcctatac 240

```
ctgcaaatgg acagtctgag gtctgaggac acggccactt atttctgtgc aagacagaat 300
attatggatt attggggcca aggagtcatg gtcacagtct cctcaggggg tggaggctct 360
ggtggcggtg gctctggcgg aggtggatcc ggtggcggcg gatctgacat tgtgatgacc 420
cagactccat cctcccaggc tgtgtcagca ggggagaagg tcactatgag ctgcaagtcc 480
agtcagagtc ttttgtacag tagagaccag agtaactact tggcctggta ccagcagaaa 540
cctgggcagt ctcctaaact acttatctac ttggcatcca ctagggaatc aggggtccct 600
gatcgcttca taggcagtgg ctctgggaca gacttcactc tgaccatcag cagtgtgcag 660
gctgaagatc tggcagatta ttactgtcag cagcattaca actatccgct cacgttcggt 720
tctgggacca agctagaaat caaactcgag cccaaatctt ctgacaaaac tcacacatgc 780
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa 840
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1020
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1080
gccctcccag ccccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1200
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1260
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320
tacagcaagc tcaccgtgga caagagccgg tggcagcagg ggaacgtctt ctcatgctcc 1380
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440
taa                                                               1443
```

<210> 239
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-mouse CD86 (GL1) SMIP

<400> 239

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

290 295 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
325 330 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala
340 345 350
Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
370 375 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

<210> 240
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding anti-mouse CD86 (GL1)
heavy chain

<400> 240
gaggtgcagc tggtggagtc tgctggaggt ttagtgcagc ctggaaggtc cctaaaactc 60
tcctgtgcag cctcaggatt cactttcagt gactattaca tggcctgggt ccgccaggct 120
ccaacgaagg ggctggagtg ggtcgcaacc attagtcatg acggtagtag tacttactat 180
cgagactccg tgaagggccg attcacaatc tccagagata atgcaaaaac catcctatac 240
ctgcaaatgg acagtctgag gtctgaggac acggccactt atttctgtgc aagacagaat 300
attatggatt attggggcca aggagtcatg gtcacagtct cctca 345

<210> 241
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) heavy chain

<400> 241
Glu Val Gln Leu Val Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser His Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Ile Leu Tyr
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95
Ala Arg Gln Asn Ile Met Asp Tyr Trp Gly Gln Gly Val Met Val Thr
100 105 110
Val Ser Ser
115

<210> 242
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding Anti-mouse CD86 (GL1)
light chain

<400> 242
gacattgtga tgacccagac tccatcctcc caggctgtgt cagcagggga gaaggtcact 60
atgagctgca agtccagtca gagtcttttg tacagtagag accagagtaa ctacttggcc 120
tggtaccagc agaaacctgg gcagtctcct aaactactta tctacttggc atccactagg 180
gaatcagggg tccctgatcg cttcataggc agtggctctg ggacagactt cactctgacc 240
atcagcagtg tgcaggctga agatctggca gattattact gtcagcagca ttacaactat 300
ccgctcacgt tcggttctgg gaccaagcta gaaatcaaa 339

<210> 243
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) light chain

<400> 243
Asp Ile Val Met Thr Gln Thr Pro Ser Ser Gln Ala Val Ser Ala Gly
1 5 10 15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30
Arg Asp Gln Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Ser Pro Lys Leu Leu Ile Tyr Leu Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr Tyr Cys Gln Gln
85 90 95
His Tyr Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
100 105 110
Lys

<210> 244
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) scFv linker

<400> 244
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser
20

<210> 245
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) HCDR1

<400> 245
Asp Tyr Tyr Met Ala
 1   5

<210> 246
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) HCDR2

<400> 246
Thr Ile Ser His Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val Lys
 1   5   10   15
Gly

<210> 247
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) HCDR3

<400> 247
Gln Asn Ile Met Asp Tyr
 1   5

<210> 248
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) LCDR1

<400> 248
Lys Ser Ser Gln Ser Leu Leu Tyr Ser Arg Asp Gln Ser Asn Tyr Leu
 1   5   10   15
Ala

<210> 249
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) LCDR2

<400> 249
Leu Ala Ser Thr Arg Glu Ser
 1   5

<210> 250
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-mouse CD86 (GL1) LCDR3

<400> 250
Gln Gln His Tyr Asn Tyr Pro Leu Thr
 1   5

<210> 251
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding mouse anti-CD86::IL10
      fusion protein

<400> 251
gaggtgcagc tggtggagtc tgctggaggt ttagtgcagc ctggaaggtc cctaaaactc 60
tcctgtgcag cctcaggatt cactttcagt gactattaca tggcctgggt ccgccaggct 120
ccaacgaagg ggctggagtg ggtcgcaacc attagtcatg acggtagtag tacttactat 180
cgagactccg tgaagggccg attcacaatc tccagagata atgcaaaaac catcctatac 240
ctgcaaatgg acagtctgag gtctgaggac acggccactt atttctgtgc aagacagaat 300
attatggatt attggggcca aggagtcatg gtcacagtct cctcaggggg tggaggctct 360
ggtggcggtg gctctggcgg aggtggatcc ggtggcggcg gatctgacat tgtgatgacc 420
cagactccat cctcccaggc tgtgtcagca ggggagaagg tcactatgag ctgcaagtcc 480
agtcagagtc ttttgtacag tagagaccag agtaactact tggcctggta ccagcagaaa 540
cctgggcagt ctcctaaact acttatctac ttggcatcca ctagggaatc aggggtccct 600
gatcgcttca taggcagtgg ctctgggaca gacttcactc tgaccatcag cagtgtgcag 660
gctgaagatc tggcagatta ttactgtcag cagcattaca actatccgct cacgttcggt 720
tctgggacca agctagaaat caaactcgag cccaaatctt ctgacaaaac tcacacatgc 780
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa 840
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1020
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1080
gccctcccag ccccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1200
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1260
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380
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ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 1860
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 1920
agtgagtttg acatcttcat caactacata gaagcctaca tgacaatgaa gatacgaaac 1980
taa   1983

<210> 252
<211> 660
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse anti-CD86::IL10 fusion protein

<400> 252
Glu Val Gln Leu Val Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30
Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu Glu Trp Val
        35   40   45
Ala Thr Ile Ser His Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val
    50   55   60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Ile Leu Tyr
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95
Ala Arg Gln Asn Ile Met Asp Tyr Trp Gly Gln Gly Val Met Val Thr
            100                 105                 110
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125
Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ser
    130                 135                 140
Ser Gln Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145                 150                 155                 160
Ser Gln Ser Leu Leu Tyr Ser Arg Asp Gln Ser Asn Tyr Leu Ala Trp
                165                 170                 175
Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Leu Ala
            180                 185                 190
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser
        195                 200                 205
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
    210                 215                 220
Ala Asp Tyr Tyr Cys Gln Gln His Tyr Asn Tyr Pro Leu Thr Phe Gly
225                 230                 235                 240
Ser Gly Thr Lys Leu Glu Ile Lys Leu Glu Pro Lys Ser Ser Asp Lys
                245                 250                 255
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro
            260                 265                 270
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        275                 280                 285
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    290                 295                 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305                 310                 315                 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                325                 330                 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala
            340                 345                 350
Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        355                 360                 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    370                 375                 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385                 390                 395                 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                405                 410                 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            420                 425                 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        435                 440                 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450                 455                 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465                 470                 475                 480
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
                485                 490                 495
Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
            500                 505                 510
Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
        515                 520                 525
Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
    530                 535                 540
Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
545                 550                 555                 560
Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
                565                 570                 575
Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn
            580                 585                 590
Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
        595                 600                 605
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His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
    610                 615                 620
Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
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Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
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Lys Ile Arg Asn
            660
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<210> 253
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10::humanized Fun1 M0115 fusion protein

<400> 253

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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
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agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
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gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
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<210> 254
<211> 670
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10::humanized Fun1 M0115 fusion protein

<400> 254

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Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20                  25                  30
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Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35                  40                  45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145                 150                 155                 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                165                 170                 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
            180                 185                 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        195                 200                 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    210                 215                 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225                 230                 235                 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                245                 250                 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
            260                 265                 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        275                 280                 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    290                 295                 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305                 310                 315                 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                325                 330                 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            340                 345                 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        355                 360                 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    370                 375                 380
Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val
385                 390                 395                 400
Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu
                405                 410                 415
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            420                 425                 430
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asn Trp
        435                 440                 445
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Asn Ile Asp
    450                 455                 460
Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val
465                 470                 475                 480
Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                485                 490                 495
Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp
            500                 505                 510
Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe Trp Gly
        515                 520                 525
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
    530                 535                 540
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
545                 550                 555                 560
Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala
                565                 570                 575
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Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln
580 585 590
Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
595 600 605
Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
610 615 620
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
625 630 635 640
Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr
645 650 655
Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
660 665 670

<210> 255
<211> 1983
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10::anti-mouse CD86
fusion protein

<400> 255
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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
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gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
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gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
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cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
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tgtcagcagc attacaacta tccgctcacg ttcggttctg ggaccaagct agaaatcaaa 1980
taa 1983

<210> 256
<211> 660
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10::anti-mouse CD86 fusion protein

<400> 256

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            20                  25                  30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35                  40                  45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145                 150                 155                 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                165                 170                 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
            180                 185                 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        195                 200                 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    210                 215                 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225                 230                 235                 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                245                 250                 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
            260                 265                 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        275                 280                 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    290                 295                 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305                 310                 315                 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                325                 330                 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            340                 345                 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        355                 360                 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    370                 375                 380
Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val
385                 390                 395                 400
Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Glu Val Gln Leu
                405                 410                 415
Val Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu
            420                 425                 430
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp
        435                 440                 445
Val Arg Gln Ala Pro Thr Lys Gly Leu Glu Trp Val Ala Thr Ile Ser
    450                 455                 460
His Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val Lys Gly Arg Phe
465                 470                 475                 480
Thr Ile Ser Arg Asp Asn Ala Lys Thr Ile Leu Tyr Leu Gln Met Asp
                485                 490                 495
Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gln Asn
            500                 505                 510
Ile Met Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser Ser Gly
        515                 520                 525
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    530                 535                 540
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Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ser Ser Gln Ala Val
545                 550                 555                 560
Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
                565                 570                 575
Leu Tyr Ser Arg Asp Gln Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
            580                 585                 590
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Leu Ala Ser Thr Arg Glu
        595                 600                 605
Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp Phe
    610                 615                 620
Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr Tyr
625                 630                 635                 640
Cys Gln Gln His Tyr Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys
                645                 650                 655
Leu Glu Ile Lys
            660
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<210> 257
<211> 2016
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10 I87A::humanized
Fun1 M0115 fusion protein with H75 linker

<400> 257

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ggggtccctg accgattcag tggcagcggg tctgggacag atttcactct caccatcagc 1920
agcctgcagg ctgaagatgt ggcagtttat tactgtcatc aatacctcta ctcgtggacg 1980
tttggccagg ggaccaagct ggagatcaaa cggtaa                           2016
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<210> 258
<211> 671
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A::humanized Fun1 M0115 fusion protein
with H75 linker

<400> 258

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

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                500                 505                 510
Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe Trp
        515                 520                 525
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
545                 550                 555                 560
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
                565                 570                 575
Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
            580                 585                 590
Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        595                 600                 605
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
    610                 615                 620
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
625                 630                 635                 640
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln Tyr Leu
                645                 650                 655
Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            660                 665                 670
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<210> 259
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10 I87A::anti-mouse CD86 fusion protein with H75 linker

<400> 259

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agcccaggcc agggcaccca gtctgagaac agctgcaccc acttcccagg caacctgcct 60
aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggtcaga ggcacaacaa ttcttccctg 1200
aatacaggaa ctcagatggc aggtcattct ccgaattctg aggtgcagct ggtggagtct 1260
gctggaggtt tagtgcagcc tggaaggtcc ctaaaactct cctgtgcagc ctcaggattc 1320
actttcagtg actattacat ggcctgggtc cgccaggctc caacgaaggg gctggagtgg 1380
gtcgcaacca ttagtcatga cggtagtagt acttactatc gagactccgt gaagggccga 1440
ttcacaatct ccagagataa tgcaaaaacc atcctatacc tgcaaatgga cagtctgagg 1500
tctgaggaca cggccactta tttctgtgca agacagaata ttatggatta ttggggccaa 1560
ggagtcatgg tcacagtctc ctcaggggt ggaggctctg gtggcggtgg ctctggcgga 1620
ggtggatccg gtggcggcgg atctgacatt gtgatgaccc agactccatc ctcccaggct 1680
gtgtcagcag gggagaaggt cactatgagc tgcaagtcca gtcagagtct tttgtacagt 1740
agagaccaga gtaactactt ggcctggtac cagcagaaac ctgggcagtc tcctaaacta 1800
cttatctact tggcatccac tagggaatca ggggtccctg atcgcttcat aggcagtggc 1860
tctgggacag acttcactct gaccatcagc agtgtgcagg ctgaagatct ggcagattat 1920
tactgtcagc agcattacaa ctatccgctc acgttcggtt ctgggaccaa gctagaaatc 1980
aaataa                                                          1986
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<210> 260
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A::anti-mouse CD86 fusion protein with H75 linker

<400> 260

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

Ser His Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val Lys Gly Arg
465 470 475 480
Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Ile Leu Tyr Leu Gln Met
485 490 495
Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gln
500 505 510
Asn Ile Met Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser Ser
515 520 525
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
530 535 540
Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ser Ser Gln Ala
545 550 555 560
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
565 570 575
Leu Leu Tyr Ser Arg Asp Gln Ser Asn Tyr Leu Ala Trp Tyr Gln Gln
580 585 590
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Leu Ala Ser Thr Arg
595 600 605
Glu Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
610 615 620
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
625 630 635 640
Tyr Cys Gln Gln His Tyr Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr
645 650 655
Lys Leu Glu Ile Lys
660

<210> 261
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::IL10 I87A
fusion protein with H75 linker

<400> 261
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tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacagg aactcagatg gcaggtcatt ctccgaattc tagcccaggc 1140
cagggcaccc agtctgagaa cagctgcacc cacttcccag gcaacctgcc taacatgctt 1200
cgagatctcc gagatgcctt cagcagagtg aagactttct ttcaaatgaa ggatcagctg 1260
gacaacttgt tgttaaagga gtccttgctg gaggacttta agggttacct gggttgccaa 1320
gccttgtctg agatgatcca gttttacctg gaggaggtga tgccccaagc tgagaaccaa 1380
gacccagacg ccaaggcgca tgtgaactcc ctgggggaga acctgaagac cctcaggctg 1440
aggctacggc gctgtcatcg atttcttccc tgtgaaaaca agagcaaggc cgtggagcag 1500
gtgaagaatg cctttaataa gctccaagag aaaggcatct acaaagccat gagtgagttt 1560
gacatcttca tcaactacat agaagcctac atgacaatga agatacgaaa ctaa 1614

<210> 262
<211> 537

<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::IL10 I87A fusion protein with H75 linker

<400> 262
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1   5   10   15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20   25   30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35   40   45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50   55   60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65   70   75   80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85   90   95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100   105   110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
        115   120   125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    130   135   140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145   150   155   160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                165   170   175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            180   185   190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        195   200   205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    210   215   220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225   230   235   240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                245   250   255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            260   265   270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        275   280   285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290   295   300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305   310   315   320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325   330   335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340   345   350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr
        355   360   365
Gln Met Ala Gly His Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln
    370   375   380
Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu
385   390   395   400
Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met
                405   410   415
Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp
            420   425   430
Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe
        435   440   445
Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ala
    450   455   460
Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu
465   470   475   480
Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys

485 490 495
Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly
500 505 510
Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu
515 520 525
Ala Tyr Met Thr Met Lys Ile Arg Asn
530 535

<210> 263
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> Lymphotoxin beta receptor (LTBetaR) - Ig
synthesized molecule

<400> 263
atgctcctgc cttgggccac ctctgccccc ggcctggcct gggggcctct ggtgctgggc 60
ctcttcgggc tcctggcagc atcgcagccc caggcggtgc ctccatatgc gtcggagaac 120
cagacctgca gggaccagga aaaggaatac tatgagcccc agcaccgcat ctgctgctcc 180
cgctgcccgc caggcaccta tgtctcagct aaatgtagcc gcatccggga cacagtttgt 240
gccacatgtg ccgagaactc ctacaacgag cactggaact acctgaccat ctgccagctg 300
tgccgccccc gtgacccagt gatgggccta gaggagattg ccccctgcac aagcaaacgg 360
aagacccagt gccgctgcca gccgggaatg ttctgtgctg cctgggccct agagtgcaca 420
cactgcgagc tactttctga ctgcccgcct ggcactgaag ccgagctcaa agatgaagtt 480
gggaagggta acaaccactg cgtcccctgc aaggcagggc acttccagaa tacctcctcc 540
cccagcgccc gctgccagcc ccacaccagg tgtgagaacc aaggtctggt ggaggcagct 600
ccaggcactg cccagtccga cacaacctgc aaaaatccat tagagccact gcccccagag 660
atgtcaggaa ccatgctgat gctcgagccc aaatcttctg acaaaactca cacatgccca 720
ccgtgcccag cacctgaagc cgcgggtgca ccgtcagtct tcctcttccc cccaaaaccc 780
aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 840
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 900
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 960
gtcctgcacc aggactggct gaatggcaag gcgtacgcgt gcgcggtctc caacaaagcc 1020
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1080
gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1140
ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1200
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1260
agcaagctca ccgtggacaa gagccggtgg cagcagggga acgtcttctc atgctccgtg 1320
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggttaa 1380

<210> 264
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> Lymphotoxin beta receptor (LTBetaR) - Ig
synthesized molecule

<400> 264
Met Leu Leu Pro Trp Ala Thr Ser Ala Pro Gly Leu Ala Trp Gly Pro
1 5 10 15
Leu Val Leu Gly Leu Phe Gly Leu Leu Ala Ala Ser Gln Pro Gln Ala
20 25 30
Val Pro Pro Tyr Ala Ser Glu Asn Gln Thr Cys Arg Asp Gln Glu Lys
35 40 45
Glu Tyr Tyr Glu Pro Gln His Arg Ile Cys Cys Ser Arg Cys Pro Pro
50 55 60
Gly Thr Tyr Val Ser Ala Lys Cys Ser Arg Ile Arg Asp Thr Val Cys
65 70 75 80
Ala Thr Cys Ala Glu Asn Ser Tyr Asn Glu His Trp Asn Tyr Leu Thr
85 90 95
Ile Cys Gln Leu Cys Arg Pro Cys Asp Pro Val Met Gly Leu Glu Glu
100 105 110

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Ile Ala Pro Cys Thr Ser Lys Arg Lys Thr Gln Cys Arg Cys Gln Pro
        115                 120                 125
Gly Met Phe Cys Ala Ala Trp Ala Leu Glu Cys Thr His Cys Glu Leu
    130                 135                 140
Leu Ser Asp Cys Pro Pro Gly Thr Glu Ala Glu Leu Lys Asp Glu Val
145                 150                 155                 160
Gly Lys Gly Asn Asn His Cys Val Pro Cys Lys Ala Gly His Phe Gln
                165                 170                 175
Asn Thr Ser Ser Pro Ser Ala Arg Cys Gln Pro His Thr Arg Cys Glu
            180                 185                 190
Asn Gln Gly Leu Val Glu Ala Ala Pro Gly Thr Ala Gln Ser Asp Thr
        195                 200                 205
Thr Cys Lys Asn Pro Leu Glu Pro Leu Pro Pro Glu Met Ser Gly Thr
    210                 215                 220
Met Leu Met Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
225                 230                 235                 240
Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe
                245                 250                 255
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        275                 280                 285
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    290                 295                 300
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305                 310                 315                 320
Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val
                325                 330                 335
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
        355                 360                 365
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    370                 375                 380
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385                 390                 395                 400
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                405                 410                 415
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            420                 425                 430
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455
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<210> 265
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding LTBetaR::M0115 fusion protein

<400> 265
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atgctcctgc cttgggccac ctctgccccc ggcctggcct gggggcctct ggtgctgggc 60
ctcttcgggc tcctggcagc atcgcagccc caggcggtgc ctccatatgc gtcggagaac 120
cagacctgca gggaccagga aaaggaatac tatgagcccc agcaccgcat ctgctgctcc 180
cgctgcccgc caggcaccta tgtctcagct aaatgtagcc gcatccggga cacagtttgt 240
gccacatgtg ccgagaactc ctacaacgag cactggaact acctgaccat ctgccagctg 300
tgccgccccc gtgacccagt gatgggccta gaggagattg ccccctgcac aagcaaacgg 360
aagacccagt gccgctgcca gccgggaatg ttctgtgctg cctgggcccc agagtgcaca 420
cactgcgagc tactttctga ctgcccgcct ggcactgaag ccgagctcaa agatgaagtt 480
gggaagggta acaaccactg cgtcccctgc aaggcagggc acttccagaa tacctcctcc 540
cccagcgccc gctgccagcc ccacaccagg tgtgagaacc aaggtctggt ggaggcagct 600
ccaggcactg cccagtccga cacaacctgc aaaaatccat tagagccact gccccagag 660
atgtcaggaa ccatgctgat gctcgagccc aaatcttctg acaaaactca cacatgccca 720
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ccgtgcccag cacctgaagc cgcgggtgca ccgtcagtct tcctcttccc cccaaaaccc 780
aaggacaccc tcatgatctc ccggaccccc gaggtcacat gcgtggtggt ggacgtgagc 840
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 900
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 960
gtcctgcacc aggactggct gaatggcaag gcgtacgcgt gcgcggtctc caacaaagcc 1020
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1080
gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1140
ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1200
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1260
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1320
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtcag 1380
aggcacaaca attcttccct gaatacagga actcagatgg caggtcattc tccgaattct 1440
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 1500
tcctgcaagg cttctggata caccttcacc gactacaaca tgaactgggt gcgacaggcc 1560
cctggacaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 1620
aatcagaagt tcaagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 1680
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatgggac 1740
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 1800
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 1860
ggtggcggcg gatctgacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 1920
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaaccag 1980
aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 2040
tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 2100
gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcat 2160
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<210> 266
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> LTBetaR::M0115 fusion protein

<400> 266
Met Leu Leu Pro Trp Ala Thr Ser Ala Pro Gly Leu Ala Trp Gly Pro
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Leu Val Leu Gly Leu Phe Gly Leu Leu Ala Ala Ser Gln Pro Gln Ala
            20   25   30
Val Pro Pro Tyr Ala Ser Glu Asn Gln Thr Cys Arg Asp Gln Glu Lys
        35   40   45
Glu Tyr Tyr Glu Pro Gln His Arg Ile Cys Cys Ser Arg Cys Pro Pro
    50   55   60
Gly Thr Tyr Val Ser Ala Lys Cys Ser Arg Ile Arg Asp Thr Val Cys
65   70   75   80
Ala Thr Cys Ala Glu Asn Ser Tyr Asn Glu His Trp Asn Tyr Leu Thr
                85   90   95
Ile Cys Gln Leu Cys Arg Pro Cys Asp Pro Val Met Gly Leu Glu Glu
            100   105   110
Ile Ala Pro Cys Thr Ser Lys Arg Lys Thr Gln Cys Arg Cys Gln Pro
        115   120   125
Gly Met Phe Cys Ala Ala Trp Ala Leu Glu Cys Thr His Cys Glu Leu
    130   135   140
Leu Ser Asp Cys Pro Pro Gly Thr Glu Ala Glu Leu Lys Asp Glu Val
145   150   155   160
Gly Lys Gly Asn Asn His Cys Val Pro Cys Lys Ala Gly His Phe Gln
                165   170   175
Asn Thr Ser Ser Pro Ser Ala Arg Cys Gln Pro His Thr Arg Cys Glu
            180   185   190
Asn Gln Gly Leu Val Glu Ala Ala Pro Gly Thr Ala Gln Ser Asp Thr
        195   200   205
Thr Cys Lys Asn Pro Leu Glu Pro Leu Pro Pro Glu Met Ser Gly Thr
    210   215   220
Met Leu Met Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
225   230   235   240
Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe
                245   250   255
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

260 265 270
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
275 280 285
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
290 295 300
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305 310 315 320
Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val
325 330 335
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
340 345 350
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
355 360 365
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
370 375 380
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385 390 395 400
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
405 410 415
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
420 425 430
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
435 440 445
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn
450 455 460
Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
465 470 475 480
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
485 490 495
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
500 505 510
Asn Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
515 520 525
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
530 535 540
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
545 550 555 560
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
565 570 575
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
580 585 590
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
595 600 605
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
610 615 620
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
625 630 635 640
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
645 650 655
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
660 665 670
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
675 680 685
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
690 695 700
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His
705 710 715 720
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
725 730 735
Lys Arg

<210> 267
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> PDL1 Ig synthesized molecule

<400> 267
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gaatgcaaat tcccagtaga aaaacaatta gacctggctg cactaattgt ctattgggaa 120
atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat 180
agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240
cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300
ggtggtgccg actacaagcg aattactgtg aaagtcaatg ccccatacaa caaaatcaac 360
caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420
ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag 480
accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga 540
atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa 600
aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 720
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780
cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1260
agccggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320
cactacacgc agaagagcct ctccctgtct ccgggttaa 1359

<210> 268
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> PDL1 Ig synthesized molecule

<400> 268
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
 1   5   10   15
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115   120   125
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130   135   140
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145   150   155   160
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165   170   175
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180   185   190
Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195   200   205
Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Leu Glu Pro Lys
    210   215   220
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225   230   235   240
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

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                245                 250                 255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
Leu Ser Pro Gly
    450
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<210> 269
<211> 1302
<212> DNA
<213> Artificial Sequence

<220>
<223> PDL2 Ig synthesized molecule

<400> 269
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caaaaggtgg aaaatgatac atccccacac cgtgaaagag ccactttgct ggaggagcag 180
ctgcccttag ggaaggcctc gttccacata cctcaagtcc aagtgaggga cgaaggacag 240
taccaatgca taatcatcta tggggtcgcc tgggactaca agtacctgac tctgaaagtc 300
aaagcttcct acaggaaaat aaacactcac atcctaaagg ttccagaaac agatgaggta 360
gagctcacct gccaggctac aggttatcct ctggcagaag tatcctggcc aaacgtcagc 420
gttcctgcca acaccagcca ctccaggacc cctgaaggcc tctaccaggt caccagtgtt 480
ctgcgcctaa agccaccccc tggcagaaac ttcagctgtg tgttctggaa tactcacgtg 540
agggaactta ctttggccag cattgacctt caaagtcaga tggaacccag gacccatcca 600
actctcgagc ccaaatcttc tgacaaaact cacacatgcc caccgtgccc agcacctgaa 660
gccgcgggtg caccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 720
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aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 840
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 900
ctgaatggca aggcgtacgc gtgcgcggtc tccaacaaag ccctcccagc ccccatcgag 960
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1020
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1080
ccaagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1140
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1200
aagagccggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1260
aaccactaca cgcagaagag cctctccctg tctccgggtt aa                    1302
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<210> 270
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> PDL2 Ig synthesized molecule

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

<210> 271
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> (GITR-L)-AFH synthesized molecule

<400> 271
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tggcacgaag attacaagga tgacgacgat aaggattaca aggatgacga cgataaggat 120
tacaaggatg acgacgataa gctcgagcaa ttagagactg ctaaggagcc ctgtatggct 180
aagtttggac cattaccctc aaaatggcaa atggcatctt ctgaacctcc ttgcgtgaat 240
aaggtgtctg actggaagct ggagatactt cagaatggct tatatttaat ttatggccaa 300
gtggctccca atgcaaacta caatgatgta gctccttttg aggtgcggct gtataaaaac 360
aaagacatga tacaaactct aacaaacaaa tctaaaatcc aaaatgtagg agggacttat 420
gaattgcatg ttggggacac catagacttg atattcaact ctgagcatca ggttctaaaa 480
aataatacat actggggtat cattttacta gcaaatcccc aattcatctc ctaa 534

<210> 272
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> (GITR-L)-AFH synthesized molecule

<400> 272
Ser Gly Ser His His His His His His Leu Asn Asp Ile Phe Glu Ala
 1   5   10   15
Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp Asp Asp Lys Asp
            20   25   30
Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Leu
        35   40   45
Glu Gln Leu Glu Thr Ala Lys Glu Pro Cys Met Ala Lys Phe Gly Pro
    50   55   60
Leu Pro Ser Lys Trp Gln Met Ala Ser Ser Glu Pro Pro Cys Val Asn
65   70   75   80
Lys Val Ser Asp Trp Lys Leu Glu Ile Leu Gln Asn Gly Leu Tyr Leu
                85   90   95
Ile Tyr Gly Gln Val Ala Pro Asn Ala Asn Tyr Asn Asp Val Ala Pro
            100   105   110
Phe Glu Val Arg Leu Tyr Lys Asn Lys Asp Met Ile Gln Thr Leu Thr
        115   120   125
Asn Lys Ser Lys Ile Gln Asn Val Gly Gly Thr Tyr Glu Leu His Val
    130   135   140
Gly Asp Thr Ile Asp Leu Ile Phe Asn Ser Glu His Gln Val Leu Lys
145   150   155   160
Asn Asn Thr Tyr Trp Gly Ile Ile Leu Leu Ala Asn Pro Gln Phe Ile
                165   170   175
Ser

<210> 273
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<223> mIg LIGHT synthesized molecule

<400> 273
agctccccca gagtgcccat aacacagaac ccctgtcctc cactcaaaga gtgtccccca 60
tgcgcagctc cagacgcagc gggtgcgcca tccgtcttca tcttccctcc aaagatcaag 120
gatgtactca tgatctccct gagccccatg gtcacatgtg tggtggtgga tgtgagcgag 180
gatgacccag acgtccagat cagctggttt gtgaacaacg tggaagtaca cacagctcag 240
acacaaaccc atagagagga ttacaacagt actctccggg tggtcagtgc cctccccatc 300
cagcaccagg actggatgag tggcaaggcg ttcgcatgcg cggtcaacaa cagagccctc 360
ccatccccca tcgagaaaac catctcaaaa cccagagggc cagtaagagc tccacaggta 420
tatgtcttgc ctccaccagc agaagagatg actaagaaag agttcagtct gacctgcatg 480
atcacaggct tcttacctgc cgaaattgct gtggactgga ccagcaatgg gcgtacagag 540
caaaactaca agaacaccgc aacagtcctg gactctgatg gttcttactt catgtacagc 600
aagctcagag tacaaaagag cacttgggaa agaggaagtc ttttcgcctg ctcagtggtc 660
cacgagggtc tgcacaatca ccttacgact aagaccatct cccggtctct gggtaaaaac 720
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttacagccc gaattctgac 780

ggacctgcag gctcctggga gcagctgata caagagcgaa ggtctcacga ggtcaaccca 840
gcagcgcatc tcacaggggc caactccagc ttgaccggca gcgggggcc gctgttatgg 900
gagactcagc tgggcctggc cttcctgagg ggcctcagct accacgatgg ggcccttgtg 960
gtcaccaaag ctggctacta ctacatctac tccaaggtgc agctgggcgg tgtgggctgc 1020
ccgctgggcc tggccagcac catcacccac ggcctctaca agcgcacacc ccgctacccc 1080
gaggagctgg agctgttggt cagccagcag tcaccctgcg gacgggccac cagcagctcc 1140
cgggtctggt gggacagcag cttcctgggt ggtgtggtac acctggaggc tggggagaag 1200
gtggtcgtcc gtgtgctgga tgaacgcctg gttcgactgc gtgatggtac ccggtcttac 1260
ttcggggctt tcatggtgta g 1281

<210> 274
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> mIg LIGHT synthesized molecule

<400> 274

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

385 390 395 400
Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu Arg Asp Gly
405 410 415
Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
420 425

<210> 275
<211> 2022
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding monoIL10-A2
hinge::M0115 fusion protein with H75 linker

<400> 275
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aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaacct cgagccccca cctcccccat gcccaccgtg cccagcacct 540
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccccaa aacccaagga caccctcatg 600
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 660
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 720
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 780
tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 840
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 900
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 960
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1020
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1080
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1140
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1200
tccctgaata caggaactca gatggcaggt cattctccga attctcaggt gcagctggtg 1260
cagtctgggg ctgaggtgaa gaagcctggg gcctcagtga aggtctcctg caaggcttct 1320
ggatacacct tcaccgacta caacatgaac tgggtgcgac aggcccctgg acaagggctt 1380
gagtggatgg gaaatattga tccttactat ggtggtacta gttacaatca gaagttcaag 1440
ggcagggtca ccatgaccag ggacacgtcc atcagcacag cctacatgga gctgagcagg 1500
ctgagatctg acgacacggc cgtgtattac tgtgcgagat gggactatag gtacgacgac 1560
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gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 1740
atcaactgca agtccagcca gagtgtttta tacagctcca accagaagaa ctacttagct 1800
tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 1860
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 1920
atcagcagcc tgcaggctga agatgtggca gtttattact gtcatcaata cctctactcg 1980
tggacgtttg gccaggggac caagctggag atcaaacggt aa 2022

<210> 276
<211> 673
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10-A2 hinge::M0115 fusion protein with H75
linker

<400> 276
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Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
115 120 125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
130 135 140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile
145 150 155 160
Thr Met Lys Ile Arg Asn Leu Glu Pro Pro Pro Pro Pro Cys Pro Pro
165 170 175
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
180 185 190
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
210 215 220
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225 230 235 240
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
245 250 255
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
260 265 270
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
275 280 285
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
290 295 300
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305 310 315 320
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
325 330 335
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
340 345 350
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
355 360 365
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
385 390 395 400
Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
405 410 415
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
420 425 430
Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn
435 440 445
Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
450 455 460
Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys
465 470 475 480
Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met
485 490 495
Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
500 505 510
Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp
515 520 525
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
530 535 540
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
545 550 555 560
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
565 570 575
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
580 585 590

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Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        595                 600                 605
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    610                 615                 620
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
625                 630                 635                 640
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln
                645                 650                 655
Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            660                 665                 670
Arg
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<210> 277
<211> 1185
<212> DNA
<213> Artificial Sequence

<220>
<223> HVEM Ig synthesized molecule

<400> 277
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ccaggttatc gtgtgaagga ggcctgcggg gagctgacgg gcacagtgtg tgaaccctgc 120
cctccaggca cctacattgc ccacctcaat ggcctaagca agtgtctgca gtgccaaatg 180
tgtgacccag ccatgggcct gcgcgcgagc cggaactgct ccaggacaga gaacgccgtg 240
tgtggctgca gcccaggcca cttctgcatc gtccaggacg gggaccactg cgccgcgtgc 300
cgcgcttacg ccacctccag cccgggccag agggtgcaga agggaggcac cgagagtcag 360
gacaccctgt gtcagaactg ccccccgggg accttctctc ccaatgggac cctggaggaa 420
tgtcagcacc agaccaagtg cagctggctg gtgacgaagg ccggagctgg gaccagcagc 480
tcccacctcg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 540
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 600
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 660
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 720
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 780
tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 840
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 900
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 960
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1020
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1080
gacaagagcc ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1140
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttaa   1185

<210> 278
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> HVEM Ig synthesized molecule

<400> 278
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Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
            20                  25                  30
Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
        35                  40                  45
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
    50                  55                  60
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
65                  70                  75                  80
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
                85                  90                  95
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
            100                 105                 110
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
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        115                 120                 125
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
    130                 135                 140
Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr Ser Ser
145                 150                 155                 160
Ser His Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                165                 170                 175
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            180                 185                 190
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        195                 200                 205
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    210                 215                 220
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225                 230                 235                 240
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                245                 250                 255
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            260                 265                 270
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        275                 280                 285
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    290                 295                 300
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
305                 310                 315                 320
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                325                 330                 335
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            340                 345                 350
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        355                 360                 365
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    370                 375                 380
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
385                 390
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<210> 279
<211> 1179
<212> DNA
<213> Artificial Sequence

<220>
<223> IL10-Fc synthesized molecule

<400> 279

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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agccggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggttaa                          1179
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<210> 280

<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10-Fc synthesized molecule

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

<210> 281
<211> 1179
<212> DNA
<213> Artificial Sequence

<220>
<223> IL10 I87A-Fc synthesized molecule

<400> 281
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aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agccggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggttaa 1179

<210> 282
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A-Fc synthesized molecule

<400> 282
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Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145 150 155 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
165 170 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
180 185 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
195 200 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
210 215 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225 230 235 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
245 250 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
260 265 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
275 280 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu

290 295 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305 310 315 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
325 330 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
340 345 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
355 360 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
370 375 380
Lys Ser Leu Ser Leu Ser Pro Gly
385 390

<210> 283
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> monoIL10-Fc synthesized molecule

<400> 283
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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatg 480
acaatgaaga tacgaaacct cgagcccaaa tcttctgaca aaactcacac atgcccaccg 540
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 600
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 660
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 720
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 780
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 840
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 900
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 960
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1020
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1080
aagctcaccg tggacaagag ccggtggcag caggggaacg tcttctcatg ctccgtgatg 1140
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggttaa 1197

<210> 284
<211> 398
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10-Fc synthesized molecule

<400> 284
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

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Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
        115                 120                 125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
    130                 135                 140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met
145                 150                 155                 160
Thr Met Lys Ile Arg Asn Leu Glu Pro Lys Ser Ser Asp Lys Thr His
                165                 170                 175
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            180                 185                 190
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        195                 200                 205
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    210                 215                 220
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
225                 230                 235                 240
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                245                 250                 255
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            260                 265                 270
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        275                 280                 285
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    290                 295                 300
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
305                 310                 315                 320
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                325                 330                 335
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            340                 345                 350
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        355                 360                 365
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    370                 375                 380
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
385                 390                 395
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<210> 285
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> monoIL10 I87A-Fc synthesized molecule

<400> 285

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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaacct cgagcccaaa tcttctgaca aaactcacac atgcccaccg 540
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 600
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 660
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 720
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 780
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 840
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 900
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 960
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1020
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1080
aagctcaccg tggacaagag ccggtggcag caggggaacg tcttctcatg ctccgtgatg 1140
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<210> 286
<211> 398
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10 I87A-Fc synthesized molecule

<400> 286
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
115 120 125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
130 135 140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile
145 150 155 160
Thr Met Lys Ile Arg Asn Leu Glu Pro Lys Ser Ser Asp Lys Thr His
165 170 175
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
180 185 190
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
195 200 205
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
210 215 220
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
225 230 235 240
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
245 250 255
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
260 265 270
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
275 280 285
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
290 295 300
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
305 310 315 320
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
325 330 335
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
340 345 350
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
355 360 365
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
370 375 380
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
385 390 395

<210> 287
<211> 1239
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-IL10 synthesized molecule

<400> 287
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ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 720
acaagaactc agaaagcacg tcattctccg aattctagcc caggccaggg cacccagtct 780
gagaacagct gcacccactt cccaggcaac ctgcctaaca tgcttcgaga tctccgagat 840
gccttcagca gagtgaagac tttctttcaa atgaaggatc agctggacaa cttgttgtta 900
aaggagtcct tgctggagga ctttaagggt tacctgggtt gccaagcctt gtctgagatg 960
atccagtttt acctggagga ggtgatgccc caagctgaga accaagaccc agacatcaag 1020
gcgcatgtga actccctggg ggagaacctg aagaccctca ggctgaggct acggcgctgt 1080
catcgatttc ttccctgtga aaacaagagc aaggccgtgg agcaggtgaa gaatgccttt 1140
aataagctcc aagagaaagg catctacaaa gccatgagtg agtttgacat cttcatcaac 1200
tacatagaag cctacatgac aatgaagata cgaaactaa 1239

<210> 288
<211> 412
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc-IL10 synthesized molecule

<400> 288
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1   5   10   15
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100   105   110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115   120   125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130   135   140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145   150   155   160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165   170   175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180   185   190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195   200   205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210   215   220
Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225   230   235   240
Thr Arg Thr Gln Lys Ala Arg His Ser Pro Asn Ser Ser Pro Gly Gln
                245   250   255
Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro
            260   265   270
Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe

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        275                 280                 285
Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu
    290                 295                 300
Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
305                 310                 315                 320
Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
                325                 330                 335
Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
            340                 345                 350
Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
        355                 360                 365
Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
    370                 375                 380
Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
385                 390                 395                 400
Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
                405                 410
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<210> 289
<211> 1236
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-IL10 I87A synthesized molecule

<400> 289

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ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccgat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctagcccag gccagggcac ccagtctgag 780
aacagctgca cccacttccc aggcaacctg cctaacatgc ttcgagatct ccgagatgcc 840
ttcagcagag tgaagacttt ctttcaaatg aaggatcagc tggacaactt gttgttaaag 900
gagtccttgc tggaggactt taagggttac ctgggttgcc aagccttgtc tgagatgatc 960
cagttttacc tggaggaggt gatgccccaa gctgagaacc aagacccaga cgccaaggcg 1020
catgtgaact ccctggggga gaacctgaag accctcaggc tgaggctacg gcgctgtcat 1080
cgatttcttc cctgtgaaaa caagagcaag gccgtggagc aggtgaagaa tgcctttaat 1140
aagctccaag agaaaggcat ctacaaagcc atgagtgagt ttgacatctt catcaactac 1200
atagaagcct acatgacaat gaagatacga aactaa                          1236
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<210> 290
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc-IL10 I87A synthesized molecule

<400> 290

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1               5                  10                  15
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
```

65 70 75 80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220
Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln
225 230 235 240
Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly
245 250 255
Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn
260 265 270
Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
275 280 285
Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
290 295 300
Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile
305 310 315 320
Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro
325 330 335
Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu
340 345 350
Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys
355 360 365
Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu
370 375 380
Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
385 390 395 400
Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
405 410

<210> 291
<211> 1254
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-monoIL10 synthesized molecule

<400> 291
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acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctagcccag gccagggcac ccagtctgag 780
aacagctgca cccacttccc aggcaacctg cctaacatgc ttcgagatct ccgagatgcc 840

ttcagcagag tgaagacttt ctttcaaatg aaggatcagc tggacaactt gttgttaaag 900
gagtccttgc tggaggactt taagggttac ctgggttgcc aagccttgtc tgagatgatc 960
cagttttacc tggaggaggt gatgccccaa gctgagaacc aagacccaga catcaaggcg 1020
catgtgaact ccctggggga gaacctgaag accctcaggc tgaggctacg gcgctgtcat 1080
cgatttcttc cctgtgaaaa cggtggtgga tccggcggta agagcaaggc cgtggagcag 1140
gtgaagaatg cctttaataa gctccaagag aaaggcatct acaaagccat gagtgagttt 1200
gacatcttca tcaactacat agaagcctac atgacaatga agatacgaaa ctaa 1254

<210> 292
<211> 417
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc-monoIL10 synthesized molecule

<400> 292

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

405 410 415
Asn

<210> 293
<211> 1254
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-monoIL10 I87A synthesized molecule

<400> 293
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 60
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctagcccag gccagggcac ccagtctgag 780
aacagctgca cccacttccc aggcaacctg cctaacatgc ttcgagatct ccgagatgcc 840
ttcagcagag tgaagacttt ctttcaaatg aaggatcagc tggacaactt gttgttaaag 900
gagtccttgc tggaggactt taagggttac ctgggttgcc aagccttgtc tgagatgatc 960
cagttttacc tggaggaggt gatgccccaa gctgagaacc aagacccaga cgccaaggcg 1020
catgtgaact ccctgggggа gaacctgaag accctcaggc tgaggctacg gcgctgtcat 1080
cgatttcttc cctgtgaaaa cggtggtgga tccggcggta agagcaaggc cgtggagcag 1140
gtgaagaatg cctttaataa gctccaagag aaaggcatct acaaagccat gagtgagttt 1200
gacatcttca tcaactacat agaagcctac atgacaatga agatacgaaa ctaa 1254

<210> 294
<211> 417
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc-monoIL10 I87A synthesized molecule

<400> 294
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

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            180                 185                 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220
Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln
225                 230                 235                 240
Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Ser Pro Gly Gln Gly
                245                 250                 255
Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn
            260                 265                 270
Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
        275                 280                 285
Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
    290                 295                 300
Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile
305                 310                 315                 320
Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro
                325                 330                 335
Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu
            340                 345                 350
Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Gly
        355                 360                 365
Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala
    370                 375                 380
Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe
385                 390                 395                 400
Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg
                405                 410                 415
Asn
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<210> 295
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse IL10-mouse null Fc synthesized molecule

<400> 295

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cacatgctcc tagagctgcg gactgccttc agccaggtga agactttctt tcaaacaaag 120
gaccagctgg acaacatact gctaaccgac tccttaatgc aggactttaa gggttacttg 180
ggttgccaag ccttatcgga aatgatccag ttttacctgg tagaagtgat gccccaggca 240
gagaagcatg gcccagaaat caaggagcat ttgaattccc tgggtgagaa gctgaagacc 300
ctcaggatgc ggctgaggcg ctgtcatcga tttctcccct gtgaaaataa gagcaaggca 360
gtggagcagg tgaagagtga ttttaataag ctccaagacc aaggtgtcta caaggccatg 420
aatgaatttg acatcttcat caactgcata gaagcataca tgatgatcaa aatgaaaagc 480
ctcgagccca gagtgcccat aacacagaac ccctgtcctc cactcaaaga gtgtccccca 540
tgcgcagctc cagacgcagc gggtgcgcca tccgtcttca tcttccctcc aaagatcaag 600
gatgtactca tgatctccct gagccccatg gtcacatgtg tggtggtgga tgtgagcgag 660
gatgacccag acgtccagat cagctggttt gtgaacaacg tggaagtaca cacagctcag 720
acacaaaccc atagagagga ttacaacagt actctccggg tggtcagtgc cctccccatc 780
cagcaccagg actggatgag tggcaaggcg ttcgcatgcg cggtcaacaa cagagccctc 840
ccatccccca tcgagaaaac catctcaaaa cccagagggc cagtaagagc tccacaggta 900
tatgtcttgc ctccaccagc agaagagatg actaagaaag agttcagtct gacctgcatg 960
atcgcaggct tcttacctgc cgaaattgct gtggactgga ccagcaatgg gcgtacagag 1020
caaaactaca agaacaccgc aacagtcctg gactctgatg gttcttactt catgtacagc 1080
aagctcagag tacaaaagag cacttgggaa agaggaagtc ttttcgcctg ctcagtggtc 1140
cacgagggtc tgcacaatca ccttacgact aagaccatct cccggtctct gggtaaataa 1200
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<210> 296
<211> 399
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse IL10-mouse null Fc synthesized molecule

<400> 296
Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His Phe Pro
1 5 10 15
Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe Ser Gln
20 25 30
Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile Leu Leu
35 40 45
Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro Gln Ala
65 70 75 80
Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu Gly Glu
85 90 95
Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser Asp Phe
115 120 125
Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu Phe Asp
130 135 140
Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met Lys Ser
145 150 155 160
Leu Glu Pro Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu Lys
165 170 175
Glu Cys Pro Pro Cys Ala Ala Pro Asp Ala Ala Gly Ala Pro Ser Val
180 185 190
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
195 200 205
Pro Met Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
210 215 220
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
225 230 235 240
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
245 250 255
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala
260 265 270
Cys Ala Val Asn Asn Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile
275 280 285
Ser Lys Pro Arg Gly Pro Val Arg Ala Pro Gln Val Tyr Val Leu Pro
290 295 300
Pro Pro Ala Glu Glu Met Thr Lys Lys Glu Phe Ser Leu Thr Cys Met
305 310 315 320
Ile Ala Gly Phe Leu Pro Ala Glu Ile Ala Val Asp Trp Thr Ser Asn
325 330 335
Gly Arg Thr Glu Gln Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp Ser
340 345 350
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Gln Lys Ser Thr
355 360 365
Trp Glu Arg Gly Ser Leu Phe Ala Cys Ser Val Val His Glu Gly Leu
370 375 380
His Asn His Leu Thr Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys
385 390 395

<210> 297
<211> 1095
<212> DNA
<213> Artificial Sequence

<220>
<223> mouse CTLA4-mouse null2 Fc synthesized molecule

<400> 297
gccatacagg tgacccaacc ttcagtggtg ttggctagca gccatggtgt cgccagcttt 60
ccatgtgaat attcaccatc acacaacact gatgaggtcc gggtgactgt gctgcggcag 120

acaaatgacc aaatgactga ggtctgtgcc acgacattca cagagaagaa tacagtgggc 180
ttcctagatt acccccttctg cagtggtacc tttaatgaaa gcagagtgaa cctcaccatc 240
caaggactga gagctgttga cacgggactg tacctctgca aggtggaact catgtaccca 300
ccgccatact ttgtgggcat gggcaacggg acgcagattt atgtcattga tccagaacca 360
tgcccggatt ctgacctcga gcccagagtg cccataacac agaacccctg tcctccactc 420
aaagagtgtc ccccatgcgc agctccagac gcagcgggtg cgccatccgt cttcatcttc 480
cctccaaaga tcaaggatgt actcatgatc tccctgagcc ccatggtcac atgtgtggtg 540
gtggatgtga gcgaggatga cccagacgtc cagatcagct ggtttgtgaa caacgtggaa 600
gtacacacag ctcagacaca aacccataga gaggattaca acagtactct ccgggtggtc 660
agtgccctcc ccatccagca ccaggactgg atgagtggca aggcgttcgc atgcgcggtc 720
aacaacagag ccctcccatc ccccatcgag aaaaccatct caaaacccag agggccagta 780
agagctccac aggtatatgt cttgcctcca ccagcagaag agatgactaa gaaagagttc 840
agtctgacct gcatgatcgc aggcttctta cctgccgaaa ttgctgtgga ctggaccagc 900
aatgggcgta cagagcaaaa ctacaagaac accgcaacag tcctggactc tgatggttct 960
tacttcatgt acagcaagct cagagtacaa aagagcactt gggaaagagg aagtcttttc 1020
gcctgctcag tggtccacga gggtctgcac aatcacctta cgactaagac catctcccgg 1080
tctctgggta aataa 1095

<210> 298
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse CTLA4-mouse null2 Fc synthesized molecule

<400> 298
Ala Ile Gln Val Thr Gln Pro Ser Val Val Leu Ala Ser Ser His Gly
 1   5   10   15
Val Ala Ser Phe Pro Cys Glu Tyr Ser Pro Ser His Asn Thr Asp Glu
            20   25   30
Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln Met Thr Glu Val
        35   40   45
Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly Phe Leu Asp Tyr
    50   55   60
Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val Asn Leu Thr Ile
65   70   75   80
Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Leu Cys Lys Val Glu
                85   90   95
Leu Met Tyr Pro Pro Pro Tyr Phe Val Gly Met Gly Asn Gly Thr Gln
            100   105   110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro
        115   120   125
Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu Lys Glu Cys Pro
    130   135   140
Pro Cys Ala Ala Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe
145   150   155   160
Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val
                165   170   175
Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile
            180   185   190
Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr
        195   200   205
His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
    210   215   220
Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val
225   230   235   240
Asn Asn Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
                245   250   255
Arg Gly Pro Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala
            260   265   270
Glu Glu Met Thr Lys Lys Glu Phe Ser Leu Thr Cys Met Ile Ala Gly
        275   280   285
Phe Leu Pro Ala Glu Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr
    290   295   300
Glu Gln Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser
305   310   315   320
Tyr Phe Met Tyr Ser Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg

325 330 335
Gly Ser Leu Phe Ala Cys Ser Val Val His Glu Gly Leu His Asn His
340 345 350
Leu Thr Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys
355 360

<210> 299
<211> 858
<212> DNA
<213> Artificial Sequence

<220>
<223> NHP CD86-AFH synthesized molecule

<400> 299
atgggactga gtaacattct ctttgtgatg gccttcctgc tctctggtgc tgctcccctg 60
aagattcagg cttatttcaa tgagactgca gacctgccat gccagtttgc aaactctcaa 120
aaccgaagcc tgagtgagct agtagtattt tggcagaacc aggaaaactt ggttctgaat 180
gaggtatact taggcaaaga gaaatttgac agcgttcatt ccaagtatat gggccgcaca 240
agttttgatc cggagagttg gaccctgagg cttcacaacc ttcagatcaa ggacaagggc 300
ttgtatcaat gtatcatcca ccacaaaagg cccacaggaa tgatccgcat ccaccagatg 360
aactctgaac tgtcagtgct tgctaacttc agtcaacctg aaatagtccc aatttctaat 420
ataacagaaa atatgtacat aaatttgacc tgctcatcta tacacggtta cccagaacct 480
gagaagatga gtgttttgct aagaaccaag aactcaacta tcgagtatga tggtgttatg 540
cagaaatctc aagataatgt cacagaactg tacgacgttt ccatcagctt gtctgtttca 600
ttccctgatg ttacgagcaa catgaccatc ttctgtgttc tggaaactga caagacacag 660
cttttatcct caccttttctc tatagagctt gaggaccctc agcctccccc agactcctcg 720
agcctgaacg acatcttcga ggctcagaaa atcgaatggc acgaagatta caaggatgac 780
gacgataagg attacaagga tgacgacgat aaggattaca aggatgacga cgataagcat 840
catcatcatc atcactga 858

<210> 300
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> NHP CD86-AFH synthesized molecule

<400> 300
Asn Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15
Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
20 25 30
Pro Cys Gln Phe Ala Asn Ser Gln Asn Arg Ser Leu Ser Glu Leu Val
35 40 45
Val Phe Trp Gln Asn Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50 55 60
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65 70 75 80
Ser Phe Asp Pro Glu Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
85 90 95
Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Arg Pro Thr
100 105 110
Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
115 120 125
Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
130 135 140
Met Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
145 150 155 160
Glu Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
165 170 175
Asp Gly Val Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
180 185 190
Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
195 200 205
Thr Ile Phe Cys Val Leu Glu Thr Asp Lys Thr Gln Leu Leu Ser Ser

210 215 220
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp Ser Ser
225 230 235 240
Ser Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp
245 250 255
Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp
260 265 270
Tyr Lys Asp Asp Asp Asp Lys His His His His His His
275 280 285

<210> 301
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::IL10 fusion protein with H69 linker

<400> 301
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtga gcagaagctg 1080
agcaacatgg agaacagact gaagcccttc ttcacaagcg gctcagcaga cacctccccg 1140
aattctagcc caggccaggg cacccagtct gagaacagct gcacccactt cccaggcaac 1200
ctgcctaaca tgcttcgaga tctccgagat gccttcagca gagtgaagac tttctttcaa 1260
atgaaggatc agctggacaa cttgttgtta aaggagtcct tgctggagga ctttaagggt 1320
tacctgggtt gccaagcctt gtctgagatg atccagtttt acctggagga ggtgatgccc 1380
caagctgaga accaagaccc agacatcaag gcgcatgtga actccctggg ggagaacctg 1440
aagaccctca ggctgaggct acggcgctgt catcgatttc ttccctgtga aaacaagagc 1500
aaggccgtgg agcaggtgaa gaatgccttt aataagctcc aagagaaagg catctacaaa 1560
gccatgagtg agtttgacat cttcatcaac tacatagaag cctacatgac aatgaagata 1620
cgaaactaa 1629

<210> 302
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::IL10 fusion protein with H69 linker

<400> 302
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln

65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys
355 360 365
Pro Phe Phe Thr Ser Gly Ser Ala Asp Thr Ser Pro Asn Ser Ser Pro
370 375 380
Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn
385 390 395 400
Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys
405 410 415
Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu
420 425 430
Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser
435 440 445
Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn
450 455 460
Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu
465 470 475 480
Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys
485 490 495
Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys
500 505 510
Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe
515 520 525
Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
530 535 540

<210> 303
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> FUN1 SMIP synthesized molecule

<400> 303
gaggtccaac tgcagcagtc tggacctgag ctggagaagc ctggcgcttc agtgaagata 60
tcctgcaagg cttctggtta ctcattcact gactacaaca tgaactgggt gaagcagagc 120
aatggaaaga gccttgagtg gattggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240
atgcagctca acagcctgac atctgaagac tctgcagtct atttctgtgc aagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggtca aggaacctca 360
gtcaccgtct cctcaggggg tggaggctct ggtggcggtg gctctggcgg aggtggatcc 420
ggtggcggcg gatctgagct ccagatgacc cagtctccat catctctggc tgcgtctgca 480
ggagaaaagg tcactatgag ctgtaagtcc agtcaaagtg ttttatacag ttcaaatcag 540
aagaactact tggcctggta ccagcagaaa ccagggcagt ctcctaaact gctgatctac 600
tgggcatcca ctagggaatc tggtgtccct gatcgcttca caggcagtgg atctgggaca 660
cattttactc tgaccgtcag cagtgtgcaa gctgaagacc tggcagttta ttactgtcat 720
caatacctct actcgtggac gttcggtgga ggcaccaacc tggaaatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagccgg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt taa 1473

<210> 304
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 SMIP synthesized molecule

<400> 304
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
            20   25   30
Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
        35   40   45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
            100   105   110
Asp Phe Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
        115   120   125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130   135   140
Ser Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ala Ala Ser Ala
145   150   155   160
Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr
                165   170   175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            180   185   190
Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
        195   200   205
Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr His Phe Thr Leu
    210   215   220
Thr Val Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His
225   230   235   240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile

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


<210> 305
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 heavy chain

<400> 305
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
 1                5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
            20                  25                  30
Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
            100                 105                 110
Asp Phe Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120                 125


<210> 306
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 light chain
```

<400> 306
Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ala Ala Ser Ala Gly
 1   5   10   15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20   25   30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr
65   70   75   80
Val Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
                85   90   95
Tyr Leu Tyr Ser Trp Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys
            100   105   110
Arg

<210> 307
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 scFV linker

<400> 307
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser
            20

<210> 308
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 HCDR1

<400> 308
Asp Tyr Asn Met Asn
 1   5

<210> 309
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 HCDR2

<400> 309
Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly
 1   5   10   15

<210> 310
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 HCDR3

<400> 310
Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe
 1   5   10   15

<210> 311
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 LCDR1

<400> 311
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
 1   5   10   15
Ala

<210> 312
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 LCDR2

<400> 312
Trp Ala Ser Thr Arg Glu Ser
 1   5

<210> 313
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 LCDR3

<400> 313
His Gln Tyr Leu Tyr Ser Trp Thr
 1   5

<210> 314
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> FUN1 PIMS synthesized molecule

<400> 314
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 60
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctgaggtcc aactgcagca gtctggacct 780

gagctggaga agcctggcgc ttcagtgaag atatcctgca aggcttctgg ttactcattc 840
actgactaca acatgaactg ggtgaagcag agcaatggaa agagccttga gtggattgga 900
aatattgatc cttactatgg tggtactagt tacaatcaga agttcaaggg caaggccaca 960
ttgactgtag acaaatcctc cagcacagcc tacatgcagc tcaacagcct gacatctgaa 1020
gactctgcag tctatttctg tgcaagatgg gactataggt acgacgacgg gagggcttac 1080
tatgttatgg acttctgggg tcaaggaacc tcagtcaccg tctcctcagg gggtggaggc 1140
tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctga gctccagatg 1200
acccagtctc catcatctct ggctgcgtct gcaggagaaa aggtcactat gagctgtaag 1260
tccagtcaaa gtgttttata cagttcaaat cagaagaact acttggcctg gtaccagcag 1320
aaaccagggc agtctcctaa actgctgatc tactgggcat ccactaggga atctggtgtc 1380
cctgatcgct tcacaggcag tggatctggg acacatttta ctctgaccgt cagcagtgtg 1440
caagctgaag acctggcagt ttattactgt catcaatacc tctactcgtg gacgttcggt 1500
ggaggcacca acctggaaat caaacggtaa 1530

<210> 315
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> FUN1 PIMS synthesized molecule

<400> 315

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

```
        355                 360                 365
Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    370                 375                 380
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Met
385                 390                 395                 400
Thr Gln Ser Pro Ser Ser Leu Ala Ala Ser Ala Gly Glu Lys Val Thr
                405                 410                 415
Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            420                 425                 430
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu
        435                 440                 445
Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
    450                 455                 460
Thr Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr Val Ser Ser Val
465                 470                 475                 480
Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr Ser
                485                 490                 495
Trp Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg
            500                 505
```

<210> 316
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D1 SMIP synthesized molecule

<400> 316

```
caggtccagc tgcagcagtc tgggcctgag ctggtgaggc ctggggaatc agtgaagatt 60
tcctgcaagg gttccggcta cacattcact gattatgcta tacagtgggt gaagcagagt 120
catgcaaaga gtctagagtg gattggagtt attaatattt actatgataa tacaaactac 180
aaccagaagt ttaagggcaa ggccacaatg actgtagaca aatcctccag cacagcctat 240
atggaacttg ccagattgac atctgaggat tctgccatct attactgtgc aagagcggcc 300
tggtatatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagg gggtggaggc 360
tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctga cattgtgctg 420
tcacagtctc catcctccct ggctgtgtca gcaggagaga aggtcactat gagctgcaaa 480
tccagtcaga gtctgctcaa cagtagaacc cgagagaact acttggcttg gtaccagcag 540
aaaccagggc agtctcctaa actgctgatc tactgggcat ccactaggga atctggggtc 600
cctgatcgct tcacaggcag tggatctggg acagatttca ctctcaccat cagcagtgtg 660
caggctgaag acctggcagt ttattactgc acgcaatctt ataatcttta cacgttcgga 720
gggggacca agctggaaat aaaactcgag cccaaatctt ctgacaaaac tcacacatgc 780
ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa 840
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 960
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1020
accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1080
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1200
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1260
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320
tacagcaagc tcaccgtgga caagagccgg tggcagcagg ggaacgtctt ctcatgctcc 1380
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440
taa                                                                 1443
```

<210> 317
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 SMIP synthesized molecule

<400> 317

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
```

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

<210> 318
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 heavy chain

<400> 318

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

<210> 319
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 light chain

<400> 319

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

<210> 320
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1scFv linker

<400> 320

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1               5                  10                  15
Gly Gly Gly Ser
            20
```

<210> 321
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 HCDR1

<400> 321

```
Asp Tyr Ala Ile Gln
```

1 5

<210> 322
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 HCDR2

<400> 322
Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15
Gly

<210> 323
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 HCDR3

<400> 323
Ala Ala Trp Tyr Met Asp Tyr
1 5

<210> 324
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 LCDR1

<400> 324
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu
1 5 10 15
Ala

<210> 325
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 LCDR2

<400> 325
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 326
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 LCDR3

<400> 326

Thr Gln Ser Tyr Asn Leu Tyr Thr
1 5

<210> 327
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D1 PIMS synthesized molecule

<400> 327
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 60
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctcaggtcc agctgcagca gtctgggcct 780
gagctggtga ggcctgggga atcagtgaag atttcctgca agggttccgg ctacacattc 840
actgattatg ctatacagtg ggtgaagcag agtcatgcaa agagtctaga gtggattgga 900
gttattaata tttactatga taatacaaac tacaaccaga agtttaaggg caaggccaca 960
atgactgtag acaaatcctc cagcacagcc tatatggaac ttgccagatt gacatctgag 1020
gattctgcca tctattactg tgcaagagcg gcctggtata tggactactg gggtcaagga 1080
acctcagtca ccgtctcctc agggggtgga ggctctggtg gcggtggctc tggcggaggt 1140
ggatccggtg gcggcggatc tgacattgtg ctgtcacagt ctccatcctc cctggctgtg 1200
tcagcaggag agaaggtcac tatgagctgc aaatccagtc agagtctgct caacagtaga 1260
acccgagaga actacttggc ttggtaccag cagaaaccag ggcagtctcc taaactgctg 1320
atctactggg catccactag ggaatctggg gtccctgatc gcttcacagg cagtggatct 1380
gggacagatt tcactctcac catcagcagt gtgcaggctg aagacctggc agtttattac 1440
tgcacgcaat cttataatct ttacacgttc ggaggggggga ccaagctgga aataaaataa 1500

<210> 328
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 PIMS synthesized molecule

<400> 328
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

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

<210> 329
<211> 2016
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding M0115::IL10 I87A
fusion protein with H75 linker

<400> 329
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tcctgcaagg cttctggata caccttcacc gactacaaca tgaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaaat attgatcctt actatggtgg tactagttac 180
aatcagaagt tcaagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagatgggac 300
tataggtacg acgacgggag ggcttactat gttatggact tctggggcca agggaccacg 360
gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 420
ggtggcggcg gatctgacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 480
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaaccag 540
aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 600
tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 660

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gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcat 720
caatacctct actcgtggac gtttggccag gggaccaagc tggagatcaa acggctcgag 780
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgcgggt 840
gcaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 900
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 960
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 1020
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1080
aaggcgtacg cgtgcgcggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1140
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1200
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tccaagcgac 1260
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1320
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1380
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1440
acgcagaaga gcctctccct gtctccgggt cagaggcaca acaattcttc cctgaataca 1500
ggaactcaga tggcaggtca ttctccgaat tctagcccag gccagggcac ccagtctgag 1560
aacagctgca cccacttccc aggcaacctg cctaacatgc ttcgagatct ccgagatgcc 1620
ttcagcagag tgaagacttt ctttcaaatg aaggatcagc tggacaactt gttgttaaag 1680
gagtccttgc tggaggactt taagggttac ctgggttgcc aagccttgtc tgagatgatc 1740
cagttttacc tggaggaggt gatgccccaa gctgagaacc aagacccaga cgccaaggcg 1800
catgtgaact ccctgggggа gaacctgaag accctcaggc tgaggctacg gcgctgtcat 1860
cgatttcttc cctgtgaaaa caagagcaag gccgtggagc aggtgaagaa tgcctttaat 1920
aagctccaag agaaaggcat ctacaaagcc atgagtgagt ttgacatctt catcaactac 1980
atagaagcct acatgacaat gaagatacga aactaa                           2016

<210> 330
<211> 671
<212> PRT
<213> Artificial Sequence

<220>
<223> M0115::IL10 I87A fusion protein with H75 linker

<400> 330
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30
Asn Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met
            100                 105                 110
Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140
Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
145                 150                 155                 160
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr
                165                 170                 175
Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            180                 185                 190
Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly
        195                 200                 205
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    210                 215                 220
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His
225                 230                 235                 240
Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                245                 250                 255
Lys Arg Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
            260                 265                 270
Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
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        275                 280                 285
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
305                 310                 315                 320
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350
Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
        355                 360                 365
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    370                 375                 380
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
385                 390                 395                 400
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                405                 410                 415
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            420                 425                 430
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        435                 440                 445
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    450                 455                 460
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465                 470                 475                 480
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
                485                 490                 495
Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Ser
            500                 505                 510
Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly
        515                 520                 525
Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val
    530                 535                 540
Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys
545                 550                 555                 560
Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu
                565                 570                 575
Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu
            580                 585                 590
Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu Asn
        595                 600                 605
Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro
    610                 615                 620
Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn
625                 630                 635                 640
Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile
                645                 650                 655
Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
            660                 665                 670
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<210> 331
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> GL1 PIMS synthesized molecule

<400> 331
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ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctgaggtgc agctggtgga gtctgctgga 780
ggtttagtgc agcctggaag gtccctaaaa ctctcctgtg cagcctcagg attcactttc 840
agtgactatt acatggcctg ggtccgccag gctccaacga aggggctgga gtgggtcgca 900
accattagtc atgacggtag tagtacttac tatcgagact ccgtgaaggg ccgattcaca 960
atctccagag ataatgcaaa aaccatccta tacctgcaaa tggacagtct gaggtctgag 1020
gacacggcca cttatttctg tgcaagacag aatattatgg attattgggg ccaaggagtc 1080
atggtcacag tctcctcagg gggtggaggc tctggtggcg gtggctctgg cggaggtgga 1140
tccggtggcg gcggatctga cattgtgatg acccagactc catcctccca ggctgtgtca 1200
gcaggggaga aggtcactat gagctgcaag tccagtcaga gtcttttgta cagtagagac 1260
cagagtaact acttggcctg gtaccagcag aaacctgggc agtctcctaa actacttatc 1320
tacttggcat ccactaggga atcaggggtc cctgatcgct tcataggcag tggctctggg 1380
acagacttca ctctgaccat cagcagtgtg caggctgaag atctggcaga ttattactgt 1440
cagcagcatt acaactatcc gctcacgttc ggttctggga ccaagctaga aatcaaataa 1500

<210> 332
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> GL1 PIMS synthesized molecule

<400> 332
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100   105   110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115   120   125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130   135   140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145   150   155   160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165   170   175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180   185   190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195   200   205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210   215   220
Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln
225   230   235   240
Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Glu Val Gln Leu Val
                245   250   255
Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser
            260   265   270
Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val
        275   280   285
Arg Gln Ala Pro Thr Lys Gly Leu Glu Trp Val Ala Thr Ile Ser His
    290   295   300
Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr
305   310   315   320

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Ile Ser Arg Asp Asn Ala Lys Thr Ile Leu Tyr Leu Gln Met Asp Ser
                325                 330                 335
Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Gln Asn Ile
            340                 345                 350
Met Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser Ser Gly Gly
        355                 360                 365
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    370                 375                 380
Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ser Ser Gln Ala Val Ser
385                 390                 395                 400
Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu
                405                 410                 415
Tyr Ser Arg Asp Gln Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
            420                 425                 430
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Leu Ala Ser Thr Arg Glu Ser
        435                 440                 445
Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr Tyr Cys
465                 470                 475                 480
Gln Gln His Tyr Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
                485                 490                 495
Glu Ile Lys
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<210> 333
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding GL1::IL10 I87A fusion
protein with H75 linker

<400> 333

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tcctgtgcag cctcaggatt cactttcagt gactattaca tggcctgggt ccgccaggct 120
ccaacgaagg ggctggagtg ggtcgcaacc attagtcatg acggtagtag tacttactat 180
cgagactccg tgaagggccg attcacaatc tccagagata atgcaaaaac catcctatac 240
ctgcaaatgg acagtctgag gtctgaggac acggccactt atttctgtgc aagacagaat 300
attatggatt attggggcca aggagtcatg gtcacagtct cctcaggggg tggaggctct 360
ggtggcggtg gctctggcgg aggtggatcc ggtggcggcg gatctgacat tgtgatgacc 420
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agtcagagtc ttttgtacag tagagaccag agtaactact tggcctggta ccagcagaaa 540
cctgggcagt ctcctaaact acttatctac ttggcatcca ctagggaatc aggggtccct 600
gatcgcttca taggcagtgg ctctgggaca gacttcactc tgaccatcag cagtgtgcag 660
gctgaagatc tggcagatta ttactgtcag cagcattaca actatccgct cacgttcggt 720
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ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccaaaa 840
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 900
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accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1080
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1140
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1200
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1260
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1380
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1440
cagaggcaca acaattcttc cctgaataca ggaactcaga tggcaggtca ttctccgaat 1500
tctagcccag gccagggcac ccagtctgag aacagctgca cccacttccc aggcaacctg 1560
cctaacatgc ttcgagatct ccgagatgcc ttcagcagag tgaagacttt ctttcaaatg 1620
aaggatcagc tggacaactt gttgttaaag gagtccttgc tggaggactt taagggttac 1680
ctgggttgcc aagccttgtc tgagatgatc cagttttacc tggaggaggt gatgccccaa 1740
gctgagaacc aagacccaga cgccaaggcg catgtgaact ccctggggga gaacctgaag 1800
accctcaggc tgaggctacg gcgctgtcat cgatttcttc cctgtgaaaa caagagcaag 1860
gccgtggagc aggtgaagaa tgcctttaat aagctccaag agaaaggcat ctacaaagcc 1920
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atgagtgagt ttgacatctt catcaactac atagaagcct acatgacaat gaagatacga 1980
aactaa 1986

<210> 334
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> GL1::IL10 I87A fusion protein with H75 linker

<400> 334
Glu Val Gln Leu Val Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser His Asp Gly Ser Ser Thr Tyr Tyr Arg Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Ile Leu Tyr
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95
Ala Arg Gln Asn Ile Met Asp Tyr Trp Gly Gln Gly Val Met Val Thr
100 105 110
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Ser
130 135 140
Ser Gln Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160
Ser Gln Ser Leu Leu Tyr Ser Arg Asp Gln Ser Asn Tyr Leu Ala Trp
165 170 175
Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Leu Ala
180 185 190
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser
195 200 205
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220
Ala Asp Tyr Tyr Cys Gln Gln His Tyr Asn Tyr Pro Leu Thr Phe Gly
225 230 235 240
Ser Gly Thr Lys Leu Glu Ile Lys Leu Glu Pro Lys Ser Ser Asp Lys
245 250 255
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro
260 265 270
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
325 330 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala
340 345 350
Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
370 375 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445

```
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450                 455                 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465                 470                 475                 480
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
                485                 490                 495
His Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
            500                 505                 510
Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
        515                 520                 525
Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
    530                 535                 540
Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
545                 550                 555                 560
Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
                565                 570                 575
Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val
            580                 585                 590
Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        595                 600                 605
Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
    610                 615                 620
Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
625                 630                 635                 640
Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                645                 650                 655
Met Lys Ile Arg Asn
            660
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<210> 335
<211> 1737
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::PDL2 fusion
protein with H65 linker

<400> 335
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atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccgat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacaag aactcagaaa gcacgtcatt ctccgaattc tttattcaca 1140
gtgacagtcc ctaaggaact gtacataata gagcatggca gcaatgtgac cctggaatgc 1200
aactttgaca ctggaagtca tgtgaacctt ggagcaataa cagccagttt gcaaaaggtg 1260
gaaaatgata catccccaca ccgtgaaaga gccactttgc tggaggagca gctgccccta 1320
gggaaggcct cgttccacat acctcaagtc caagtgaggg acgaaggaca gtaccaatgc 1380
ataatcatct atggggtcgc ctgggactac aagtacctga ccctgaaagt caaagcttcc 1440
tacaggaaaa taaacactca catcctaaag gttccagaaa cagatgaggt agagctcacc 1500
tgccaggcta caggttatcc tctggcagaa gtatcctggc caaacgtcag cgttcctgcc 1560
aacaccagcc actccaggac ccctgaaggc ctctaccagg tcaccagtgt tctgcgccta 1620
aagccacccc ctggcagaaa cttcagctgt gtgttctgga atactcacgt gagggaactt 1680
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actttggcca gcattgacct tcaaagtcag atggaaccca ggacccatcc aacttaa 1737

<210> 336
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::PDL2 fusion protein with H65 linker

<400> 336
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
355 360 365
Gln Lys Ala Arg His Ser Pro Asn Ser Leu Phe Thr Val Thr Val Pro
370 375 380
Lys Glu Leu Tyr Ile Ile Glu His Gly Ser Asn Val Thr Leu Glu Cys
385 390 395 400
Asn Phe Asp Thr Gly Ser His Val Asn Leu Gly Ala Ile Thr Ala Ser
405 410 415
Leu Gln Lys Val Glu Asn Asp Thr Ser Pro His Arg Glu Arg Ala Thr
420 425 430
Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys Ala Ser Phe His Ile Pro
435 440 445
Gln Val Gln Val Arg Asp Glu Gly Gln Tyr Gln Cys Ile Ile Ile Tyr

```
    450                 455                 460
Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr Leu Lys Val Lys Ala Ser
465                 470                 475                 480
Tyr Arg Lys Ile Asn Thr His Ile Leu Lys Val Pro Glu Thr Asp Glu
                485                 490                 495
Val Glu Leu Thr Cys Gln Ala Thr Gly Tyr Pro Leu Ala Glu Val Ser
            500                 505                 510
Trp Pro Asn Val Ser Val Pro Ala Asn Thr Ser His Ser Arg Thr Pro
        515                 520                 525
Glu Gly Leu Tyr Gln Val Thr Ser Val Leu Arg Leu Lys Pro Pro Pro
    530                 535                 540
Gly Arg Asn Phe Ser Cys Val Phe Trp Asn Thr His Val Arg Glu Leu
545                 550                 555                 560
Thr Leu Ala Ser Ile Asp Leu Gln Ser Gln Met Glu Pro Arg Thr His
                565                 570                 575
Pro Thr
```

<210> 337
<211> 1551
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::GITR fusion protein with H65 linker

<400> 337

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atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacaag aactcagaaa gcacgtcatt ctccgaattc tcagcgcccc 1140
accgggggtc ccgggtgcgg ccctgggcgc ctcctgcttg ggacgggaac ggacgcgcgc 1200
tgctgccggg ttcacacgac gcgctgctgc cgcgattacc cgggcgagga gtgctgttcc 1260
gagtgggact gcatgtgtgt ccagcctgaa ttccactgcg gagacccttg ctgcacgacc 1320
tgccggcacc acccttgtcc cccaggccag ggggtacagt cccaggggaa attcagtttt 1380
ggcttccagt gtatcgactg tgcctcgggg accttctccg ggggccacga aggccactgc 1440
aaaccttgga cagactgcac ccagttcggg tttctcactg tgttccctgg gaacaagacc 1500
cacaacgctg tgtgcgtccc agggtccccc ccggcagagc cgcttgggta a           1551
```

<210> 338
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::GITR fusion protein with H65 linker

<400> 338

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Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1               5                  10                  15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
```

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

<210> 339
<211> 1437
<212> DNA

<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4::TGFBetaR1
fusion protein with H65 linker

<400> 339
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300
ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1080
aattcttccc tgaatacaag aactcagaaa gcacgtcatt ctccgaattc tgcggcgctg 1140
ctcccggggg cgacggcgtt acagtgtttc tgccacctct gtacaaaaga caatttact 1200
tgtgtgacag atgggctctg ctttgtctct gtcacagaga ccacagacaa agttatacac 1260
aacagcatgt gtatagctga aattgactta attcctcgag ataggccgtt tgtatgtgca 1320
ccctcttcaa aaactgggtc tgtgactaca acatattgct gcaatcagga ccattgcaat 1380
aaaatagaac ttccaactac tgtaaagtca tcacctggcc ttggtcctgt ggaataa 1437

<210> 340
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4::TGFBetaR1 fusion protein with H65 linker

<400> 340
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
1 5 10 15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
20 25 30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
35 40 45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
50 55 60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65 70 75 80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
85 90 95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
100 105 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Leu Glu Pro Lys
115 120 125
Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
130 135 140
Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
145 150 155 160
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
165 170 175
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
180 185 190
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
195 200 205
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

210 215 220
Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala
225 230 235 240
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
245 250 255
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
260 265 270
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
275 280 285
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
290 295 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305 310 315 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
325 330 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
340 345 350
Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr
355 360 365
Gln Lys Ala Arg His Ser Pro Asn Ser Ala Ala Leu Leu Pro Gly Ala
370 375 380
Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr
385 390 395 400
Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp
405 410 415
Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro
420 425 430
Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val
435 440 445
Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu
450 455 460
Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu
465 470 475

<210> 341
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> Human CD86-AFH synthesized molecule

<400> 341
ctgaagattc aagcttattt caataagact gcagacctgc catgccaatt tgcaaactct 60
caaaaccaaa gcctgagtga gctagtagta ttttggcagg accaggaaaa cttggttctg 120
aatgaggtat acttaggcaa agagaaattt gacagcgttc attccaagta tatgggccgc 180
acaagttttg attcagacag ttggaccctg agacttcaca atcttcagat caaggacaag 240
ggcttgtatc aatgtatcat ccatcacaaa aagcccacag gaatgattcg catccaccag 300
atgaattctg aactgtcagt gcttgctaac ttcagtcaac ctgaaatagt accaatttct 360
aatataacag aaaatgtgta cataaatttg acctgctcat ctatacacgg ttacccagaa 420
cctaagaaga tgagtgtttt gctaagaacc aagaattcaa ctatcgagta tgatggtatt 480
atgcagaaat ctcaagataa tgtcacagaa ctgtacgacg tttccatcag cttgtctgtt 540
tcattccctg atgttacgag caatatgacc atcttctgta ttctggaaac tgacaagacg 600
cggcttttat cttcaccttt ctctatagag cttgaggacc ctcagcctcc cccagactct 660
agactgaacg acatcttcga ggctcagaaa atcgaatggc acgaagatta caaggatgac 720
gacgataagg attacaagga tgacgacgat aaggattaca aggatgacga cgataagcat 780
catcatcatc atcactga 798

<210> 342
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD86-AFH synthesized molecule

<400> 342

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

<210> 343
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse CD86-AFH synthesized molecule

<400> 343

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gtggagacgc aagcttattt caatgggact gcatatctgc cgtgcccatt tacaaaggct 60
caaaacataa gcctgagtga gctggtagta ttttggcagg accagcaaaa gttggttctg 120
tacgagcact atttgggcac agagaaactt gatagtgtga atgccaagta cctgggccgc 180
acgagctttg acaggaacaa ctggactcta cgacttcaca atgttcagat caaggacatg 240
ggctcgtatg attgttttat acaaaaaaag ccacccacag gatcaattat cctccaacag 300
acattaacag aactgtcagt gatcgccaac ttcagtgaac ctgaaataaa actggctcag 360
aatgtaacag gaaattctgg cataaatttg acctgcacgt ctaagcaagg tcacccgaaa 420
cctaagaaga tgtattttct gataactaat tcaactaatg agtatggtga taacatgcag 480
atatcacaag ataatgtcac agaactgttc agtatctcca acagcctctc tctttcattc 540
ccggatggtg tgtggcatat gaccgttgtg tgtgttctgg aaacggagtc aatgaagatt 600
tcctccaaac ctctcaattt cactcaagag tttccatctc ctcaaacgta ttggaaggag 660
tctagactga acgacatctt cgaggctcag aaaatcgaat ggcacgaaga ttacaaggat 720
gacgacgata aggattacaa ggatgacgac gataaggatt acaaggatga cgacgataag 780
catcatcatc atcatcactg a                                           801
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<210> 344
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse CD86-AFH synthesized molecule

<400> 344
Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro
 1   5   10   15
Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val Phe Trp
            20   25   30
Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly Thr Glu
        35   40   45
Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser Phe Asp
    50   55   60
Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys Asp Met
65   70   75   80
Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly Ser Ile
                85   90   95
Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn Phe Ser
            100   105   110
Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser Gly Ile
        115   120   125
Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys Lys Met
    130   135   140
Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn Met Gln
145   150   155   160
Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn Ser Leu
                165   170   175
Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val Cys Val
            180   185   190
Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn Phe Thr
        195   200   205
Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ser Arg Leu Asn
    210   215   220
Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp
225   230   235   240
Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp
                245   250   255
Asp Asp Asp Lys His His His His His His
            260   265

<210> 345
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> GITR Ig synthesized molecule

<400> 345
cagcgcccca ccgggggtcc cgggtgcggc cctgggcgcc tcctgcttgg gacgggaacg 60
gacgcgcgct gctgccgggt tcacacgacg cgctgctgcc gcgattaccc gggcgaggag 120
tgctgttccg agtgggactg catgtgtgtc cagcctgaat tccactgcgg agacccttgc 180
tgcacgacct gccggcacca cccttgtccc ccaggccagg gggtacagtc ccaggggaaa 240
ttcagttttg gcttccagtg tatcgactgt gcctcgggga ccttctccgg gggccacgaa 300
ggccactgca aaccttggac agactgcacc cagttcgggt ttctcactgt gttccctggg 360
aacaagaccc acaacgctgt gtgcgtccca gggtccccgc cggcagagcc gcttgggctc 420
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 480
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 540
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 600
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 660
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 720
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 780
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 840
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 900
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 960
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1020
cggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1080
tacacgcaga agagcctctc cctgtctccg ggttaa 1116

<210> 346
<211> 371

<212> PRT
<213> Artificial Sequence

<220>
<223> GITR Ig synthesized molecule

<400> 346
Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg Leu Leu Leu
 1   5   10   15
Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr Thr Arg Cys
            20   25   30
Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp Asp Cys Met
        35   40   45
Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys Thr Thr Cys
    50   55   60
Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser Gln Gly Lys
65   70   75   80
Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly Thr Phe Ser
                85   90   95
Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys Thr Gln Phe
            100   105   110
Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys
        115   120   125
Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Leu Glu Pro Lys Ser
    130   135   140
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
145   150   155   160
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                165   170   175
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            180   185   190
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        195   200   205
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    210   215   220
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
225   230   235   240
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
                245   250   255
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            260   265   270
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        275   280   285
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    290   295   300
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
305   310   315   320
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                325   330   335
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            340   345   350
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        355   360   365
Ser Pro Gly
    370

<210> 347
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> PD1 Ig synthesized molecule

<400> 347
ttagactccc cagacaggcc ctggaacccc cccaccttct ccccagccct gctcgtggtg 60
accgaagggg acaacgccac cttcacctgc agcttctcca acacatcgga gagcttcgtg 120

ctaaactggt accgcatgag ccccagcaac cagacggaca agctggccgc cttccccgag 180
gaccgcagcc agcccggcca ggactgccgc ttccgtgtca cacaactgcc caacgggcgt 240
gacttccaca tgagcgtggt cagggcccgg cgcaatgaca gcggcaccta cctctgtggg 300
gccatctccc tggcccccaa ggcgcagatc aaagagagcc tgcgggcaga gctcagggtg 360
acagagagaa gggcagaagt gcccacagcc caccccagcc cctcacccag gccagccggc 420
cagttccaac tcgagcagcc cagagggccc acaatcaagc cctgtcctcc atgcaaatgc 480
ccggctccaa atcttcttgg tggttcatcc gtcttcatct tccctccaaa gatcaaggat 540
gtactcatga tctccctgag ccccatagtc acatgtgtgg tggtggatgt gagcgaggac 600
gacccagatg tccagatcag ctggtttgtg aacaacgtgg aagtacacac agctcagaca 660
caaacccata gagaggatta caacagtact ctccgggtgg tcagtgccct ccccatccag 720
caccaggact ggatgagtgg caaggagttc aaatgcaagg tcaacaacaa agacctccca 780
gcgcccatcg agagaaccat ctcaaaaccc aaagggtcag taagagctcc acaggtatat 840
gtcttgcctc caccagaaga agagatgact aagaaacagg tcactctgac ctgcatggtc 900
acagacttca tgcctgaaga catttacgtg gagtggacta acaacgggaa aacagagcta 960
aactacaaga acactgaacc agtcctggac tctgatggtt cttacttcat gtacagcaag 1020
ctgagagtgg aaaagaagaa ctgggtggaa agaaatagct actcctgttc agtggtccac 1080
gagggtctgc acaatcacca cacgactaag agcttctccc ggactccggg taaataa 1137

<210> 348
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> PD1 Ig synthesized molecule

<400> 348
Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1   5   10   15
Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20   25   30
Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35   40   45
Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50   55   60
Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65   70   75   80
Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
                85   90   95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
            100   105   110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
        115   120   125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Leu
    130   135   140
Glu Gln Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
145   150   155   160
Pro Ala Pro Asn Leu Leu Gly Gly Ser Ser Val Phe Ile Phe Pro Pro
                165   170   175
Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
            180   185   190
Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
        195   200   205
Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
    210   215   220
Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
225   230   235   240
His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
                245   250   255
Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
            260   265   270
Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
        275   280   285
Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
    290   295   300
Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
305   310   315   320
Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe

325 330 335
Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
340 345 350
Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
355 360 365
Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
370 375

<210> 349
<211> 1995
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10 I87A::M0115
fusion protein with H81 linker

<400> 349
agcccaggcc agggcaccca gtctgagaac agctgcaccc acttcccagg caacctgcct 60
aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggtgaag ttcaaattcc cttgaccgaa 1200
agttacagcc cgaattctca ggtgcagctg gtgcagtctg gggctgaggt gaagaagcct 1260
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aactgggtgc gacaggcccc tggacaaggg cttgagtgga tgggaaatat tgatccttac 1380
tatggtggta ctagttacaa tcagaagttc aagggcaggg tcaccatgac cagggacacg 1440
tccatcagca cagcctacat ggagctgagc aggctgagat ctgacgacac ggccgtgtat 1500
tactgtgcga gatgggacta taggtacgac gacgggaggg cttactatgt tatggacttc 1560
tggggccaag ggaccacggt caccgtctcc tcaggtggag gcggttcagg cggaggtgga 1620
tccggcggtg gcggatcggg tggcggcgga tctgacatcg tgatgaccca gtctccagac 1680
tccctggctg tgtctctggg cgagagggcc accatcaact gcaagtccag ccagagtgtt 1740
ttatacagct ccaaccagaa gaactactta gcttggtacc agcagaaacc aggacagcct 1800
cctaagctgc tcatttactg ggcatctacc cgggaatccg gggtccctga ccgattcagt 1860
ggcagcgggt ctgggacaga tttcactctc accatcagca gcctgcaggc tgaagatgtg 1920
gcagtttatt actgtcatca atacctctac tcgtggacgt ttggccaggg gaccaagctg 1980
gagatcaaac ggtaa 1995

<210> 350
<211> 664
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A::M0115 fusion protein with H81 linker

<400> 350
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu

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        35                  40                  45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145                 150                 155                 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                165                 170                 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
            180                 185                 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        195                 200                 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    210                 215                 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225                 230                 235                 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                245                 250                 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
            260                 265                 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        275                 280                 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    290                 295                 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305                 310                 315                 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                325                 330                 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            340                 345                 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        355                 360                 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    370                 375                 380
Lys Ser Leu Ser Leu Ser Pro Gly Glu Val Gln Ile Pro Leu Thr Glu
385                 390                 395                 400
Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
                405                 410                 415
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
            420                 425                 430
Tyr Thr Phe Thr Asp Tyr Asn Met Asn Trp Val Arg Gln Ala Pro Gly
        435                 440                 445
Gln Gly Leu Glu Trp Met Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr
    450                 455                 460
Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr
465                 470                 475                 480
Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
                485                 490                 495
Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly
            500                 505                 510
Arg Ala Tyr Tyr Val Met Asp Phe Trp Gly Gln Gly Thr Thr Val Thr
        515                 520                 525
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    530                 535                 540
Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp
545                 550                 555                 560
Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser
                565                 570                 575
Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
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580 585 590
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
595 600 605
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
610 615 620
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val
625 630 635 640
Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln
645 650 655
Gly Thr Lys Leu Glu Ile Lys Arg
660

<210> 351
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10 I87A::M0115
fusion protein with H82 linker

<400> 351
agcccaggcc agggcaccca gtctgagaac agctgcaccc acttcccagg caacctgcct 60
aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
cactacacgc agaagagcct ctccctgtct ccgggtcacg acggctcttc cctgaataca 1200
ccgaattctc aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc tggggcctca 1260
gtgaaggtct cctgcaaggc ttctggatac accttcaccg actacaacat gaactgggtg 1320
cgacaggccc ctggacaagg gcttgagtgg atgggaaata ttgatcctta ctatggtggt 1380
actagttaca atcagaagtt caagggcagg gtcaccatga ccagggacac gtccatcagc 1440
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agatgggact ataggtacga cgacgggagg gcttactatg ttatggactt ctggggccaa 1560
gggaccacgg tcaccgtctc ctcaggtgga ggcggttcag gcggaggtgg atccggcggt 1620
ggcggatcgg gtggcggcgg atctgacatc gtgatgaccc agtctccaga ctccctggct 1680
gtgtctctgg gcgagagggc caccatcaac tgcaagtcca gccagagtgt tttatacagc 1740
tccaaccaga agaactactt agcttggtac cagcagaaac caggacagcc tcctaagctg 1800
ctcatttact gggcatctac ccgggaatcc ggggtccctg accgattcag tggcagcggg 1860
tctgggacag atttcactct caccatcagc agcctgcagg ctgaagatgt ggcagtttat 1920
tactgtcatc aatacctcta ctcgtggacg tttggccagg ggaccaagct ggagatcaaa 1980
cggtaa 1986

<210> 352
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A::M0115 fusion protein with H82 linker

<400> 352
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro

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 1               5                  10                  15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20                  25                  30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35                  40                  45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145                 150                 155                 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                165                 170                 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
            180                 185                 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        195                 200                 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    210                 215                 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225                 230                 235                 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                245                 250                 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
            260                 265                 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        275                 280                 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    290                 295                 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305                 310                 315                 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                325                 330                 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            340                 345                 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        355                 360                 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    370                 375                 380
Lys Ser Leu Ser Leu Ser Pro Gly His Asp Gly Ser Ser Leu Asn Thr
385                 390                 395                 400
Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
                405                 410                 415
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
            420                 425                 430
Thr Asp Tyr Asn Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        435                 440                 445
Glu Trp Met Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn
    450                 455                 460
Gln Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
465                 470                 475                 480
Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
                485                 490                 495
Tyr Tyr Cys Ala Arg Trp Asp Tyr Arg Tyr Asp Asp Gly Arg Ala Tyr
            500                 505                 510
Tyr Val Met Asp Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        515                 520                 525
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
```

```
545                 550                 555                 560
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
                565                 570                 575
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
            580                 585                 590
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
        595                 600                 605
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    610                 615                 620
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
625                 630                 635                 640
Tyr Cys His Gln Tyr Leu Tyr Ser Trp Thr Phe Gly Gln Gly Thr Lys
                645                 650                 655
Leu Glu Ile Lys Arg
            660
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<210> 353
<211> 2001
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding IL10 I87A::MO115
fusion protein with H83 linker

<400> 353

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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacgc caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacaa gagcaaggcc 360
gtggagcagg tgaagaatgc ctttaataag ctccaagaga aaggcatcta caaagccatg 420
agtgagtttg acatcttcat caactacata gaagcctaca ttacaatgaa gatacgaaac 480
ctcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaagcc 540
gcgggtgcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 600
cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 660
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 720
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780
aatggcaagg cgtacgcgtg cgcggtctcc aacaaagccc tcccagcccc catcgagaaa 840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 900
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1140
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aagcctgggg cctcagtgaa ggtctcctgc aaggcttctg gatacacctt caccgactac 1320
aacatgaact gggtgcgaca ggcccctgga caagggcttg agtggatggg aaatattgat 1380
ccttactatg gtggtactag ttacaatcag aagttcaagg gcagggtcac catgaccagg 1440
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ccagactccc tggctgtgtc tctgggcgag agggccacca tcaactgcaa gtccagccag 1740
agtgttttat acagctccaa ccagaagaac tacttagctt ggtaccagca gaaaccagga 1800
cagcctccta agctgctcat ttactgggca tctacccggg aatccggggt ccctgaccga 1860
ttcagtggca gcgggtctgg gacagatttc actctcacca tcagcagcct gcaggctgaa 1920
gatgtggcag tttattactg tcatcaatac ctctactcgt ggacgtttgg ccaggggacc 1980
aagctggaga tcaaacggta a                                          2001
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<210> 354
<211> 666
<212> PRT
<213> Artificial Sequence

<220>

<223> IL10 I87A::M0115 fusion protein with H83 linker

<400> 354
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile Thr Met Lys Ile Arg Asn
145 150 155 160
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
165 170 175
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
180 185 190
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
195 200 205
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
210 215 220
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225 230 235 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
245 250 255
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
260 265 270
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
275 280 285
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
290 295 300
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305 310 315 320
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
325 330 335
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
340 345 350
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
355 360 365
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
370 375 380
Lys Ser Leu Ser Leu Ser Pro Gly Ser Ser Leu Asn Thr Gly Thr Gln
385 390 395 400
Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly
405 410 415
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
420 425 430
Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asn Trp Val Arg Gln Ala
435 440 445
Pro Gly Gln Gly Leu Glu Trp Met Gly Asn Ile Asp Pro Tyr Tyr Gly
450 455 460
Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Met Thr Arg
465 470 475 480
Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser
485 490 495
Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Tyr Arg Tyr Asp
500 505 510
Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe Trp Gly Gln Gly Thr Thr

515 520 525
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
530 535 540
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser
545 550 555 560
Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys
565 570 575
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
580 585 590
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
595 600 605
Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
610 615 620
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu
625 630 635 640
Asp Val Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr Ser Trp Thr Phe
645 650 655
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
660 665

<210> 355
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H68 Linker

<400> 355
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Ser Pro Asn Ser
20

<210> 356
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> H69 Linker

<400> 356
Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr
1 5 10 15
Ser Gly Ser Ala Asp Thr Ser Pro Asn Ser
20 25

<210> 357
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> H77 Linker

<400> 357
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Pro Asn
1 5 10 15
Ser

<210> 358
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> H78 Linker

<400> 358
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Pro Asn Ser
 1   5   10

<210> 359
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> H79 Linker

<400> 359
Asn Ser Leu Phe Asn Gln Glu Val Pro Asn Ser
 1   5   10

<210> 360
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H80 Linker

<400> 360
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Pro Asn Ser
 1   5   10

<210> 361
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> H81 Linker

<400> 361
Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
 1   5   10

<210> 362
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> H82 Linker

<400> 362
His Asp Gly Ser Ser Leu Asn Thr Pro Asn Ser
 1   5   10

<210> 363
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> H83 Linker

<400> 363
Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
 1   5   10   15

<210> 364
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A2 Hinge

<400> 364
Pro Pro Pro Pro Pro Cys Pro Pro Cys
 1   5

<210> 365
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75 Linker

<400> 365
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 366
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75aLinker

<400> 366
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Lys Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 367
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75b Linker

<400> 367
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 368
<211> 21

<212> PRT
<213> Artificial Sequence

<220>
<223> H75c Linker

<400> 368
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 369
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75d Linker

<400> 369
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 370
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75e Linker

<400> 370
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 371
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75f Linker

<400> 371
Gln Arg His Ala Asn Ser Ala Leu Asn Thr Gly Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 372
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75g Linker

<400> 372
Gln Arg His Asn Ala Ala Ser Leu Asn Thr Gly Thr Gln Met Ala Gly

1 5 10 15
His Ser Pro Asn Ser
20

<210> 373
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75h Linker

<400> 373
Gln Arg His Ala Ala Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1 5 10 15
His Ser Pro Asn Ser
20

<210> 374
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H68a Linker

<400> 374
Asn Ser Leu Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Ser Pro Asn Ser
20

<210> 375
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H68b Linker

<400> 375
Asn Ser Gly Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Ser Pro Asn Ser
20

<210> 376
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H68c Linker

<400> 376
Asn Ser Gly Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Ser Pro Asn Ser
20

<210> 377
<211> 16
<212> PRT

<213> Artificial Sequence

<220>
<223> H68s Linker

<400> 377
Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
 1   5   10   15

<210> 378
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Region Linker Subunit

<400> 378
Gly Gly Gly Gly Ser
 1   5

<210> 379
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10 Linker

<400> 379
Gly Gly Gly Ser Gly Gly
 1   5

<210> 380
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10 synthesized molecule

<400> 380
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
 1   5   10   15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20   25   30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35   40   45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50   55   60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65   70   75   80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85   90   95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100   105   110
Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
        115   120   125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
    130   135   140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met
145   150   155   160
Thr Met Lys Ile Arg Asn
                165

<210> 381
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87A synthesized molecule

<400> 381
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ala Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145 150 155 160

<210> 382
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> IL10 I87S synthesized molecule

<400> 382
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ser Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145 150 155 160

<210> 383
<211> 10
<212> PRT
<213> Homo sapiens

<400> 383
Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 1   5   10

<210> 384
<211> 7
<212> PRT
<213> Homo sapiens

<400> 384
Glu Arg Lys Cys Cys Val Glu
 1   5

<210> 385
<211> 12
<212> PRT
<213> Homo sapiens

<400> 385
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr
 1   5   10

<210> 386
<211> 10
<212> PRT
<213> Homo sapiens

<400> 386
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 1   5   10

<210> 387
<211> 7
<212> PRT
<213> Homo sapiens

<400> 387
Glu Ser Lys Tyr Gly Pro Pro
 1   5

<210> 388
<211> 5
<212> PRT
<213> Homo sapiens

<400> 388
Cys Pro Arg Cys Pro
 1   5

<210> 389
<211> 5
<212> PRT
<213> Homo sapiens

<400> 389
Cys Pro Ser Cys Pro
 1   5

<210> 390
<211> 17
<212> PRT

<213> Homo sapiens

<400> 390
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
 1   5   10   15
Pro

<210> 391
<211> 15
<212> PRT
<213> Homo sapiens

<400> 391
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 1   5   10   15

<210> 392
<211> 34
<212> PRT
<213> Homo sapiens

<400> 392
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
 1   5   10   15
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20   25   30
Asn Thr

<210> 393
<211> 24
<212> PRT
<213> Homo sapiens

<400> 393
Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu Glu Gln
 1   5   10   15
Glu Glu Arg Glu Thr Lys Thr Pro
            20

<210> 394
<211> 19
<212> PRT
<213> Homo sapiens

<400> 394
Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
 1   5   10   15
Ser Pro Ser

<210> 395
<211> 6
<212> PRT
<213> Homo sapiens

<400> 395
Val Pro Pro Pro Pro Pro
 1   5

<210> 396

<211> 107
<212> PRT
<213> Homo sapiens

<400> 396
Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
 1   5   10   15
Ser Ser Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
            20   25   30
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
        35   40   45
Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
    50   55   60
Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65   70   75   80
His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
                85   90   95
His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala
            100   105

<210> 397
<211> 112
<212> PRT
<213> Homo sapiens

<400> 397
Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg
 1   5   10   15
Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala
            20   25   30
Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly
        35   40   45
Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala
    50   55   60
Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile
65   70   75   80
Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp
                85   90   95
His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro
            100   105   110

<210> 398
<211> 5
<212> PRT
<213> Homo sapiens

<400> 398
Cys Pro Pro Cys Pro
 1   5

<210> 399
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CTLA4 x IL10 IgA
      fusion protein

<400> 399
atgcacgtgg cccagcctgc tgtggtactg gccagcagcc gaggcatcgc cagctttgtg 60
tgtgagtatg catctccagg caaagccact gaggtccggg tgacagtgct tcggcaggct 120
gacagccagg tgactgaagt ctgtgcggca acctacatga tggggaatga gttgaccttc 180
ctagatgatt ccatctgcac gggcacctcc agtggaaatc aagtgaacct cactatccaa 240
ggactgaggg ccatggacac gggactctac atctgcaagg tggagctcat gtacccaccg 300

ccatactacc tgggcatagg caacggaacc cagatttatg taattgatcc agaaccgtgc 360
ccagattctg acctcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 420
gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 540
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 600
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 660
caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 720
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 780
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 840
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 900
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 960
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1020
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtcc ctcaactcca 1080
cctaccccat ctccctcaac tccacctacc ccatctccct caccgaattc tagcccaggc 1140
cagggcaccc agtctgagaa cagctgcacc cacttcccag gcaacctgcc taacatgctt 1200
cgagatctcc gagatgcctt cagcagagtg aagactttct ttcaaatgaa ggatcagctg 1260
gacaacttgt tgttaaagga gtccttgctg gaggacttta agggttacct gggttgccaa 1320
gccttgtctg agatgatcca gttttacctg gaggaggtga tgccccaagc tgagaaccaa 1380
gacccagaca tcaaggcgca tgtgaactcc ctgggggaga acctgaagac cctcaggctg 1440
aggctacggc gctgtcatcg atttcttccc tgtgaaaaca agagcaaggc cgtggagcag 1500
gtgaagaatg cctttaataa gctccaagag aaaggcatct acaaagccat gagtgagttt 1560
gacatcttca tcaactacat agaagcctac atgacaatga agatacgaaa ctaa 1614

<210> 400
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4 x IL10 IgA fusion protein

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

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    290                 295                 300
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
305                 310                 315                 320
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                325                 330                 335
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            340                 345                 350
Leu Ser Pro Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
        355                 360                 365
Pro Thr Pro Ser Pro Ser Pro Asn Ser Ser Pro Gly Gln Gly Thr Gln
    370                 375                 380
Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu
385                 390                 395                 400
Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met
                405                 410                 415
Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp
            420                 425                 430
Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe
        435                 440                 445
Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile
    450                 455                 460
Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu
465                 470                 475                 480
Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys
                485                 490                 495
Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly
            500                 505                 510
Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu
        515                 520                 525
Ala Tyr Met Thr Met Lys Ile Arg Asn
    530                 535
```

<210> 401
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> M0115 PIMS synthesized molecule

<400> 401

```
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 60
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctcaggtgc agctggtgca gtctggggct 780
gaggtgaaga agcctggggc ctcagtgaag gtctcctgca aggcttctgg atacaccttc 840
accgactaca acatgaactg ggtgcgacag gcccctggac aagggcttga gtggatggga 900
aatattgatc cttactatgg tggtactagt tacaatcaga agttcaaggg cagggtcacc 960
atgaccaggg acacgtccat cagcacagcc tacatggagc tgagcaggct gagatctgac 1020
gacacggccg tgtattactg tgcgagatgg gactataggt acgacgacgg gagggcttac 1080
tatgttatgg acttctgggg ccaagggacc acggtcaccg tctcctcagg tggaggcggt 1140
tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catcgtgatg 1200
acccagtctc cagactccct ggctgtgtct ctgggcgaga gggccaccat caactgcaag 1260
tccagccaga gtgttttata cagctccaac cagaagaact acttagcttg gtaccagcag 1320
aaaccaggac agcctcctaa gctgctcatt tactgggcat ctacccggga atccggggtc 1380
cctgaccgat tcagtggcag cgggtctggg acagatttca ctctcaccat cagcagcctg 1440
caggctgaag atgtggcagt ttattactgt catcaatacc tctactcgtg gacgtttggc 1500
```

caggggacca agctggagat caaacggtaa 1530

<210> 402
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> M0115 PIMS synthesized molecule

<400> 402
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220
Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln
225 230 235 240
Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Val
245 250 255
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
260 265 270
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asn Trp Val
275 280 285
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
290 295 300
Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr
305 310 315 320
Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg
325 330 335
Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Tyr
340 345 350
Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe Trp Gly Gln
355 360 365
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
370 375 380
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
385 390 395 400
Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr
405 410 415
Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
420 425 430
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
435 440 445
Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe

```
    450                 455                 460
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
465                 470                 475                 480
Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr Ser
                485                 490                 495
Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            500                 505
```

<210> 403
<211> 1095
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding murine CTLA4 fusion
to human Fc domains

<400> 403

```
gccatacagg tgacccaacc ttcagtggtg ttggctagca gccatggtgt cgccagcttt 60
ccatgtgaat attcaccatc acacaacact gatgaggtcc gggtgactgt gctgcggcag 120
acaaatgacc aaatgactga ggtctgtgcc acgacattca cagagaagaa tacagtgggc 180
ttcctagatt acccccttctg cagtggtacc tttaatgaaa gcagagtgaa cctcaccatc 240
caaggactga gagctgttga cacgggactg tacctctgca aggtggaact catgtaccca 300
ccgccatact ttgtgggcat gggcaacggg acgcagattt atgtcattga tccagaacca 360
tgcccggatt ctgacctcga gcccagagtg cccataacac agaaccctg tcctccactc 420
aaagagtgtc ccccatgcgc agctccagac gcagcgggtg cgccatccgt cttcatcttc 480
cctccaaaga tcaaggatgt actcatgatc tccctgagcc ccatggtcac atgtgtggtg 540
gtggatgtga gcgaggatga cccagacgtc cagatcagct ggtttgtgaa caacgtggaa 600
gtacacacag ctcagacaca aacccataga gaggattaca acagtactct ccgggtggtc 660
agtgccctcc ccatccagca ccaggactgg atgagtggca aggcgttcgc atgcgcggtc 720
aacaacagag ccctcccatc ccccatcgag aaaaccatct caaaacccag agggccagta 780
agagctccac aggtatatgt cttgcctcca ccagcagaag agatgactaa gaaagagttc 840
agtctgacct gcatgatcgc aggcttctta cctgccgaaa ttgctgtgga ctggaccagc 900
aatgggcgta cagagcaaaa ctacaagaac accgcaacag tcctggactc tgatggttct 960
tacttcatgt acagcaagct cagagtacaa aagagcactt gggaaagagg aagtcttttc 1020
gcctgctcag tggtccacga gggtctgcac aatcacctta cgactaagac catctcccgg 1080
tctctgggta aataa                                                  1095
```

<210> 404
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine CTLA4 fusion to human Fc domains

<400> 404

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

```
Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val
                165                 170                 175
Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile
            180                 185                 190
Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr
        195                 200                 205
His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
    210                 215                 220
Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val
225                 230                 235                 240
Asn Asn Arg Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
                245                 250                 255
Arg Gly Pro Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala
            260                 265                 270
Glu Glu Met Thr Lys Lys Glu Phe Ser Leu Thr Cys Met Ile Ala Gly
        275                 280                 285
Phe Leu Pro Ala Glu Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr
    290                 295                 300
Glu Gln Asn Tyr Lys Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser
305                 310                 315                 320
Tyr Phe Met Tyr Ser Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg
                325                 330                 335
Gly Ser Leu Phe Ala Cys Ser Val Val His Glu Gly Leu His Asn His
            340                 345                 350
Leu Thr Thr Lys Thr Ile Ser Arg Ser Leu Gly Lys
        355                 360
```

<210> 405
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding PD1 ectodomain fused to a C-terminal AviTag

<400> 405
ttagactccc cagacaggcc ctggaacccc cccaccttct ccccagccct gctcgtggtg 60
accgaagggg acaacgccac cttcacctgc agcttctcca acacatcgga gagcttcgtg 120
ctaaactggt accgcatgag ccccagcaac cagacggaca agctggccgc cttccccgag 180
gaccgcagcc agcccggcca ggactgccgc ttccgtgtca cacaactgcc caacgggcgt 240
gacttccaca tgagcgtggt cagggcccgg cgcaatgaca gcggcaccta cctctgtggg 300
gccatctccc tggcccccaa ggcgcagatc aaagagagcc tgcgggcaga gctcagggtg 360
acagagagaa gggcagaagt gcccacagcc caccccagcc cctcacccag gccagccggc 420
cagttccaat ctagactgaa cgacatcttc gaggctcaga aaatcgaatg gcacgaagat 480
tacaaggatg acgacgataa ggattacaag gatgacgacg ataaggatta caaggatgac 540
gacgataagc atcatcatca tcatcactga   570

<210> 406
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> PD1 ectodomain fused to a C-terminal AviTag

<400> 406
```
Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1                5                  10                  15
Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20                  25                  30
Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35                  40                  45
Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50                  55                  60
Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65                  70                  75                  80
```

Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
85 90 95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
100 105 110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
115 120 125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Ser
130 135 140
Arg Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp
145 150 155 160
Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp
165 170 175
Tyr Lys Asp Asp Asp Asp Lys His His His His His His
180 185

<210> 407
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> H75i Linker

<400> 407
Gln Arg His Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser
1 5 10 15
Pro Asn Ser

<210> 408
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75j Linker

<400> 408
Gln Arg His Gly Gly Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1 5 10 15
His Ser Pro Asn Ser
20

<210> 409
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 CH2 and CH3 regions

<400> 409
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

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


<210> 410
<211> 124
<212> PRT
<213> Homo sapiens

<400> 410
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1               5                  10                  15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20                  25                  30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35                  40                  45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50                  55                  60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65                  70                  75                  80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85                  90                  95
Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
            100                 105                 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120


<210> 411
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4 with  A29Y L104E mutatations

<400> 411
Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile
 1               5                  10                  15
Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val
            20                  25                  30
Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35                  40                  45
Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50                  55                  60
Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65                  70                  75                  80
Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85                  90                  95
Met Tyr Pro Pro Pro Tyr Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile
            100                 105                 110
Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
        115                 120
```

<210> 412
<211> 134
<212> PRT
<213> Homo sapiens

<400> 412

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

<210> 413
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> FUN1 PIMS M0115 synthesized molecule

<400> 413

```
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 60
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggcgt acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaactcat tattcaacca agaagttcaa 720
attcccttga ccgaaagtta cagcccgaat tctcaggtgc agctggtgca gtctggggct 780
gaggtgaaga agcctggggc ctcagtgaag gtctcctgca aggcttctgg atacaccttc 840
accgactaca acatgaactg ggtgcgacag gcccctggac aagggcttga gtggatggga 900
aatattgatc cttactatgg tggtactagt tacaatcaga agttcaaggg cagggtcacc 960
atgaccaggg acacgtccat cagcacagcc tacatggagc tgagcaggct gagatctgac 1020
gacacggccg tgtattactg tgcgagatgg gactataggt acgacgacgg gagggcttac 1080
tatgttatgg acttctgggg ccaagggacc acggtcaccg tctcctcagg tggaggcggt 1140
tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catcgtgatg 1200
acccagtctc cagactccct ggctgtgtct ctgggcgaga gggccaccat caactgcaag 1260
tccagccaga gtgttttata cagctccaac cagaagaact acttagcttg gtaccagcag 1320
aaaccaggac agcctcctaa gctgctcatt tactgggcat ctacccggga atccggggtc 1380
cctgaccgat tcagtggcag cgggtctggg acagatttca ctctcaccat cagcagcctg 1440
caggctgaag atgtggcagt ttattactgt catcaatacc tctactcgtg gacgtttggc 1500
caggggacca agctggagat caaacggtaa                                  1530
```

<210> 414
<211> 509
<212> PRT
<213> Artificial Sequence

<220>

<223> FUN1 PIMS M0115 synthesized molecule

<400> 414

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1               5                  10                  15
Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220
Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln
225                 230                 235                 240
Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Val
                245                 250                 255
Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
            260                 265                 270
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asn Trp Val
        275                 280                 285
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Asn Ile Asp Pro
    290                 295                 300
Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr
305                 310                 315                 320
Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg
                325                 330                 335
Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Tyr
            340                 345                 350
Arg Tyr Asp Asp Gly Arg Ala Tyr Tyr Val Met Asp Phe Trp Gly Gln
        355                 360                 365
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    370                 375                 380
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
385                 390                 395                 400
Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr
                405                 410                 415
Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys
            420                 425                 430
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        435                 440                 445
Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
    450                 455                 460
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
465                 470                 475                 480
Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln Tyr Leu Tyr Ser
                485                 490                 495
Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            500                 505
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<210> 415
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2CH3 desLys

<400> 415
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205
Lys Ser Leu Ser Leu Ser Pro Gly
210 215

<210> 416
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2CH3 Null2

<400> 416
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

145 150 155 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 417
<211> 216
<212> PRT
<213> Human IgG1 CH2CH3 Null2 desLysArtificial Sequence

<220>
<223> Human IgG1 CH2CH3 Null2 desLys

<400> 417
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205
Lys Ser Leu Ser Leu Ser Pro Gly
210 215

<210> 418
<211> 160
<212> PRT
<213> Homo sapiens

<400> 418
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140
Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145 150 155 160

<210> 419
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterologous leader sequence

<220>
<221> VARIANT
<222> 23
<223> Xaa = Any Amino Acid

<400> 419
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Xaa
20

<210> 420
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterologous leader sequence

<220>
<221> VARIANT
<222> 23, 24
<223> Xaa = Any Amino Acid

<400> 420
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Xaa Xaa
20

<210> 421
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterologous leader sequence

<220>
<221> VARIANT
<222> 23, 24, 25
<223> Xaa = Any Amino Acid

<400> 421
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Xaa Xaa Xaa
20 25

<210> 422
<211> 4
<212> PRT
<213> Unknown

<220>
<223> A naturally occurring or added motif that confers the capacity to form a disulfide bond

<400> 422
Cys Pro Pro Cys
 1