SEQUENCE LISTING

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<120> COMBINATION OF BLyS AND/OR APRIL INHIBITION AND IMMUNNOSUPPRESSANTS FOR TREATMENT OF AUTOIMMUNE DISEASE

<130> 07-04PC

<150> 60/908,365
<151> 2007-03-27

<160> 41

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1377
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (14)...(892)

<400> 1

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agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg    49
               Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
                1               5                  10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg   97
Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
         15                  20                  25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg   145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
     30                  35                  40

ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc   193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
 45                  50                  55                  60

acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc   241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
                 65                  70                  75

aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc   289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
             80                  85                  90

tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc   337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
         95                  100                 105

agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga   385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
    110                 115                 120

gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag   433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu
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```
125                 130                 135                 140

cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt   481
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
                145                 150                 155

gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt   529
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
            160                 165                 170

gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag   577
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
        175                 180                 185

agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt   625
Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
    190                 195                 200

ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg   673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
205                 210                 215                 220

agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag   721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
                225                 230                 235

tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac   769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
            240                 245                 250

ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg   817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
        255                 260                 265

cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg   865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
    270                 275                 280

cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg         912
Pro Ala Gln Glu Gly Gly Pro Gly Ala
285                 290

aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972
gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032
gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092
ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152
gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggaggtc 1212
ggggcactct gagtcccagt tcccagtgca gctgtaggtc gtcatcacct aaccacacgt 1272
gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctcctc ctggagaata 1332
aaacctttgg cagctgccct tcctcaaaaa aaaaaaaaaa aaaaa                 1377

<210> 2
<211> 293
<212> PRT
<213> homo sapiens

<400> 2
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1               5                  10                  15
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
            20                  25                  30
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
        35                  40                  45
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
    50                  55                  60
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65                  70                  75                  80
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
```

```
                  85                  90                  95
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
             100                 105                 110
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
         115                 120                 125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
     130                 135                 140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145                 150                 155                 160
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
                 165                 170                 175
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
             180                 185                 190
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
         195                 200                 205
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
     210                 215                 220
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
225                 230                 235                 240
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
                 245                 250                 255
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
             260                 265                 270
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
         275                 280                 285
Gly Gly Pro Gly Ala
     290
```

<210> 3
<211> 586
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (27)...(578)

<400> 3

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gcagcttgtg cggcggcgtc ggcacc atg agg cga ggg ccc cgg agc ctg cgg  53
                              Met Arg Arg Gly Pro Arg Ser Leu Arg
                                1               5

ggc agg gac gcg cca gcc ccc acg ccc tgc gtc ccg gcc gag tgc ttc  101
Gly Arg Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe
 10                  15                  20                  25

gac ctg ctg gtc cgc cac tgc gtg gcc tgc ggg ctc ctg cgc acg ccg  149
Asp Leu Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro
                 30                  35                  40

cgg ccg aaa ccg gcc ggg gcc agc agc cct gcg ccc agg acg gcg ctg  197
Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu
             45                  50                  55

cag ccg cag gag tcg gtg ggc gcg ggg gcc ggc gag gcg gcg ctg ccc  245
Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Leu Pro
         60                  65                  70

ctg ccc ggg ctg ctc ttt ggc gcc ccc gcg ctg ctg ggc ctg gca ctg  293
Leu Pro Gly Leu Leu Phe Gly Ala Pro Ala Leu Leu Gly Leu Ala Leu
     75                  80                  85

gtc ctg gcg ctg gtc ctg gtg ggt ctg gtg agc tgg agg cgg cga cag  341
Val Leu Ala Leu Val Leu Val Gly Leu Val Ser Trp Arg Arg Arg Gln
 90                  95                  100                 105

cgg cgg ctt cgc ggc gcg tcc tcc gca gag gcc ccc gac gga gac aag  389
```

```
Arg Arg Leu Arg Gly Ala Ser Ser Ala Glu Ala Pro Asp Gly Asp Lys
                110                 115                 120

gac gcc cca gag ccc ctg gac aag gtc atc att ctg tct ccg gga atc   437
Asp Ala Pro Glu Pro Leu Asp Lys Val Ile Ile Leu Ser Pro Gly Ile
            125                 130                 135

tct gat gcc aca gct cct gcc tgg cct cct cct ggg gaa gac cca gga   485
Ser Asp Ala Thr Ala Pro Ala Trp Pro Pro Pro Gly Glu Asp Pro Gly
        140                 145                 150

acc acc cca cct ggc cac agt gtc cct gtg cca gcc aca gag ctg ggc   533
Thr Thr Pro Pro Gly His Ser Val Pro Val Pro Ala Thr Glu Leu Gly
    155                 160                 165

tcc act gaa ctg gtg acc acc aag acg gcc ggc cct gag caa caa       578
Ser Thr Glu Leu Val Thr Thr Lys Thr Ala Gly Pro Glu Gln Gln
170                 175                 180

tagcaggg                                                         586

<210> 4
<211> 184
<212> PRT
<213> homo sapiens

<400> 4
Met Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala Pro
 1               5                  10                  15
Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys
            20                  25                  30
Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala
        35                  40                  45
Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly
    50                  55                  60
Ala Gly Ala Gly Glu Ala Ala Leu Pro Leu Pro Gly Leu Leu Phe Gly
65                  70                  75                  80
Ala Pro Ala Leu Leu Gly Leu Ala Leu Val Leu Ala Leu Val Leu Val
                85                  90                  95
Gly Leu Val Ser Trp Arg Arg Arg Gln Arg Arg Leu Arg Gly Ala Ser
            100                 105                 110
Ser Ala Glu Ala Pro Asp Gly Asp Lys Asp Ala Pro Glu Pro Leu Asp
        115                 120                 125
Lys Val Ile Ile Leu Ser Pro Gly Ile Ser Asp Ala Thr Ala Pro Ala
    130                 135                 140
Trp Pro Pro Pro Gly Glu Asp Pro Gly Thr Thr Pro Pro Gly His Ser
145                 150                 155                 160
Val Pro Val Pro Ala Thr Glu Leu Gly Ser Thr Glu Leu Val Thr Thr
                165                 170                 175
Lys Thr Ala Gly Pro Glu Gln Gln
            180


<210> 5
<211> 995
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (219)...(770)

<400> 5
aagactcaaa cttagaaact tgaattagat gtggtattca aatccttacg tgccgcgaag 60
acacagacag cccccgtaag aacccacgaa gcaggcgaag ttcattgttc tcaacattct 120
agctgctctt gctgcatttg ctctggaatt cttgtagaga tattacttgt ccttccaggc 180
tgttctttct gtagctccct tgttttcttt ttgtgatc atg ttg cag atg gct ggg 236
                                        Met Leu Gln Met Ala Gly
```

```
                                                  1               5

cag tgc tcc caa aat gaa tat ttt gac agt ttg ttg cat gct tgc ata   284
Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile
            10                  15                  20

cct tgt caa ctt cga tgt tct tct aat act cct cct cta aca tgt cag   332
Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln
        25                  30                  35

cgt tat tgt aat gca agt gtg acc aat tca gtg aaa gga acg aat gcg   380
Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
    40                  45                  50

att ctc tgg acc tgt ttg gga ctg agc tta ata att tct ttg gca gtt   428
Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val
55                  60                  65                  70

ttc gtg cta atg ttt ttg cta agg aag ata agc tct gaa cca tta aag   476
Phe Val Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys
                75                  80                  85

gac gag ttt aaa aac aca gga tca ggt ctc ctg ggc atg gct aac att   524
Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile
            90                  95                  100

gac ctg gaa aag agc agg act ggt gat gaa att att ctt ccg aga ggc   572
Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly
        105                 110                 115

ctc gag tac acg gtg gaa gaa tgc acc tgt gaa gac tgc atc aag agc   620
Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser
    120                 125                 130

aaa ccg aag gtc gac tct gac cat tgc ttt cca ctc cca gct atg gag   668
Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu
135                 140                 145                 150

gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag   716
Glu Gly Ala Thr Ile Leu Val Thr Thr Lys Thr Asn Asp Tyr Cys Lys
                155                 160                 165

agc ctg cca gct gct ttg agt gct acg gag ata gag aaa tca att tct   764
Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu Ile Glu Lys Ser Ile Ser
            170                 175                 180

gct agg taattaacca tttcgactcg agcagtgcca ctttaaaaat cttttgtcag   820
Ala Arg


aatagatgat gtgtcagatc tctttaggat gactgtattt ttcagttgcc gatacagctt 880
tttgtcctct aactgtggaa actctttatg ttagatatat ttctctaggt tactgttggg 940
agcttaatgg tagaaacttc cttggtttca tgattaaagt ctttttttt cctga       995

<210> 6
<211> 184
<212> PRT
<213> homo sapiens

<400> 6
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
 1               5                  10                  15
Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
            20                  25                  30
Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        35                  40                  45
Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
    50                  55                  60
```

```
Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65                  70                  75                  80
Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
                85                  90                  95
Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
            100                 105                 110
Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
        115                 120                 125
Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
    130                 135                 140
Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
145                 150                 155                 160
Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
                165                 170                 175
Ile Glu Lys Ser Ile Ser Ala Arg
            180
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<210> 7
<211> 1149
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (173)...(1023)

<400> 7

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gaattcggca cgaggcagaa aggagaaaat tcaggataac tctcctgagg ggtgagccaa 60
gccctgccat gtagtgcacg caggacatca acaaacacag ataacaggaa atgatccatt 120
ccctgtggtc acttattcta aaggccccaa ccttcaaagt tcaagtagtg at atg gat 178
                                                        Met Asp
                                                         1

gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt aag aaa   226
Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu Lys Lys
          5                  10                  15

aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca cgg aag   274
Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys
     20                  25                  30

gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg gct gca   322
Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala
 35                  40                  45                  50

acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg tct ttc   370
Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe
                55                  60                  65

tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg gca gag   418
Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
            70                  75                  80

ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga gcc ccc   466
Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro
          85                  90                  95

aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg aaa atc   514
Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
    100                 105                 110

ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac agc aga   562
Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg
115                 120                 125                 130

aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa gac tgc   610
Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys
```

```
                135                 140                 145

ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa gga tct   658
Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
            150                 155                 160

tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta   706
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
        165                 170                 175

gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt   754
Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
    180                 185                 190

ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat   802
Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
195                 200                 205                 210

cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg   850
Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
                215                 220                 225

gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat   898
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
            230                 235                 240

aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa   946
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
        245                 250                 255

ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga   994
Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
    260                 265                 270

gat gtc aca ttt ttt ggt gca ttg aaa ct gctgtgacct acttacacca      1043
Asp Val Thr Phe Phe Gly Ala Leu Lys
275                 280

tgtctgtagc tattttcctc cctttctctg tacctctaag aagaaagaat ctaactgaaa 1103
ataccaaaaa aaaaaaaaaa aaaaaaaaaa ccctcgagcg gccgcc                 1149

<210> 8
<211> 283
<212> PRT
<213> homo sapiens

<400> 8
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1               5                  10                  15
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
            20                  25                  30
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
        35                  40                  45
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
    50                  55                  60
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65                  70                  75                  80
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
                85                  90                  95
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
            100                 105                 110
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
        115                 120                 125
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
    130                 135                 140
Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
145                 150                 155                 160
Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
```

```
                 165                 170                 175
Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
            180                 185                 190
Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
        195                 200                 205
Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
    210                 215                 220
Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225                 230                 235                 240
Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
                245                 250                 255
Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
            260                 265                 270
Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys
        275                 280


<210> 9
<211> 1680
<212> DNA
<213> mus musculus

<220>
<221> CDS
<222> (164)...(1093)

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ccatgctctg agggcagtct cccaggacac agatgacagg aaatgaccca cccctgtggt 120
cacttactcc aaaggcctag accttcaaag tgctcctcgt gga atg gat gag tct   175
                                              Met Asp Glu Ser
                                               1

gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc tcc gag aaa gga   223
Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys Ser Glu Lys Gly
 5                  10                  15                  20

gaa gat atg aaa gtg gga tat gat ccc atc act ccg cag aag gag gag   271
Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro Gln Lys Glu Glu
                25                  30                  35

ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg ctg gct gct acc   319
Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu Leu Ala Ala Thr
            40                  45                  50

ctc ctg ctg gcc ctg ttg tcc agc agt ttc aca gcg atg tcc ttg tac   367
Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala Met Ser Leu Tyr
        55                  60                  65

cag ttg gct gcc ttg caa gca gac ctg atg aac ctg cgc atg gag ctg   415
Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu Arg Met Glu Leu
    70                  75                  80

cag agc tac cga ggt tca gca aca cca gcc gcc gcg ggt gct cca gag   463
Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala Gly Ala Pro Glu
 85                  90                  95                 100

ttg acc gct gga gtc aaa ctc ctg aca ccg gca gct cct cga ccc cac   511
Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala Pro Arg Pro His
                105                 110                 115

aac tcc agc cgc ggc cac agg aac aga cgc gct ttc cag gga cca gag   559
Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe Gln Gly Pro Glu
            120                 125                 130

gaa aca gaa caa gat gta gac ctc tca gct cct cct gca cca tgc ctg   607
Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu
        135                 140                 145
```

```
cct gga tgc cgc cat tct caa cat gat gat aat gga atg aac ctc aga   655
Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg
    150                 155                 160

aac atc att caa gac tgt ctg cag ctg att gca gac agc gac acg ccg   703
Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp Thr Pro
165                 170                 175                 180

act ata cga aaa gga act tac aca ttt gtt cca tgg ctt ctc agc ttt   751
Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe
                185                 190                 195

aaa aga gga aat gcc ttg gag gag aaa gag aac aaa ata gtg gtg agg   799
Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg
            200                 205                 210

caa aca ggc tat ttc ttc atc tac agc cag gtt cta tac acg gac ccc   847
Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro
        215                 220                 225

atc ttt gct atg ggt cat gtc atc cag agg aag aaa gta cac gtc ttt   895
Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe
    230                 235                 240

ggg gac gag ctg agc ctg gtg acc ctg ttc cga tgt att cag aat atg   943
Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met
245                 250                 255                 260

ccc aaa aca ctg ccc aac aat tcc tgc tac tcg gct ggc atc gcg agg   991
Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg
                265                 270                 275

ctg gaa gaa gga gat gag att cag ctt gca att cct cgg gag aat gca   1039
Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala
            280                 285                 290

cag att tca cgc aac gga gac gac acc ttc ttt ggt gcc cta aaa ctg   1087
Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu
        295                 300                 305

ctg taa ctcacttgct ggagtgcgtg atccccttcc ctcgtcttct ctgtacctcc    1143
Leu  *


gagggagaaa cagacgactg gaaaaactaa aagatgggga aagccgtcag cgaaagtttt 1203
ctcgtgaccc gttgaatctg atccaaacca ggaaatataa cagacagcca caaccgaagt 1263
gtgccatgtg agttatgaga aacggagccc gcgctcagaa agaccggatg aggaagaccg 1323
ttttctccag tcctttgcca acacgcaccg caaccttgct ttttgccttg ggtgacacat 1383
gttcagaatg cagggagatt tccttgtttt gcgatttgcc atgagaagag ggcccacaac 1443
tgcaggtcac tgaagcattc acgctaagtc tcaggattta ctctcccttc tcatgctaag 1503
tacacacacg ctcttttcca ggtaatacta tgggatacta tggaaaggtt gtttgttttt 1563
aaatctagaa gtcttgaact ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata 1623
aacttaatta aaaaggtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa    1680

<210> 10
<211> 309
<212> PRT
<213> mus musculus

<400> 10
Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
 1               5                  10                  15
Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
            20                  25                  30
Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
        35                  40                  45
Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
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     50                  55                  60
Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
65                  70                  75                  80
Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
                85                  90                  95
Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
            100                 105                 110
Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
        115                 120                 125
Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
    130                 135                 140
Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
145                 150                 155                 160
Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
                165                 170                 175
Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
            180                 185                 190
Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
        195                 200                 205
Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
    210                 215                 220
Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
225                 230                 235                 240
Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
                245                 250                 255
Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala
            260                 265                 270
Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
        275                 280                 285
Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
    290                 295                 300
Ala Leu Lys Leu Leu
305
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<210> 11
<211> 185
<212> PRT
<213> homo sapiens

<400> 11

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Met Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala Pro
 1               5                  10                  15
Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys
            20                  25                  30
Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala
        35                  40                  45
Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro Gln Glu Ser Val
    50                  55                  60
Gly Ala Gly Ala Gly Glu Ala Ala Leu Pro Leu Pro Gly Leu Leu Phe
65                  70                  75                  80
Gly Ala Pro Ala Leu Leu Gly Leu Ala Leu Val Leu Ala Leu Val Leu
                85                  90                  95
Val Gly Leu Val Ser Trp Arg Arg Arg Gln Arg Arg Leu Arg Gly Ala
            100                 105                 110
Ser Ser Ala Glu Ala Pro Asp Gly Asp Lys Asp Ala Pro Glu Pro Leu
        115                 120                 125
Asp Lys Val Ile Ile Leu Ser Pro Gly Ile Ser Asp Ala Thr Ala Pro
    130                 135                 140
Ala Trp Pro Pro Pro Gly Glu Asp Pro Gly Thr Thr Pro Pro Gly His
145                 150                 155                 160
Ser Val Pro Val Pro Ala Thr Glu Leu Gly Ser Thr Glu Leu Val Thr
                165                 170                 175
Thr Lys Thr Ala Gly Pro Glu Gln Gln
            180                 185
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<210> 12

<211> 247
<212> PRT
<213> homo sapiens

<400> 12
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1   5   10   15
Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
            20   25   30
Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
        35   40   45
Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
    50   55   60
Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
65   70   75   80
Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
                85   90   95
Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
            100   105   110
Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val
        115   120   125
Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly
    130   135   140
Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala
145   150   155   160
Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr
                165   170   175
Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg
            180   185   190
Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr
        195   200   205
Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro
    210   215   220
Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala
225   230   235   240
Gln Glu Gly Gly Pro Gly Ala
                245

<210> 13
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BLyS binding polypeptide

<400> 13
Glu Cys Phe Asp Leu Leu Val Arg Ala Trp Val Pro Cys Ser Val Leu
 1   5   10   15
Lys

<210> 14
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BLyS binding polypeptide

<400> 14
Glu Cys Phe Asp Leu Leu Val Arg His Trp Val Pro Cys Gly Leu Leu
 1   5   10   15
Arg

<210> 15
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BLyS binding polypeptide

<400> 15
Glu Cys Phe Asp Leu Leu Val Arg Arg Trp Val Pro Cys Glu Met Leu
1 5 10 15
Gly

<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BLyS binding polypeptide

<400> 16
Glu Cys Phe Asp Leu Leu Val Arg Ser Trp Val Pro Cys His Met Leu
1 5 10 15
Arg

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

<220>
<223> BLyS binding polypeptide

<400> 17
Glu Cys Phe Asp Leu Leu Val Arg His Trp Val Ala Cys Gly Leu Leu
1 5 10 15
Arg

<210> 18
<211> 1214
<212> DNA
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<221> CDS
<222> (17)...(1192)

<400> 18
tattaggccg gccacc atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg 52
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu
1 5 10

ctg ctg tgt ggc gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc 100
Leu Leu Cys Gly Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala
15 20 25

gag ttg aga cgc ttc cgt aga gct atg aga tcc tgc ccc gaa gag cag 148
Glu Leu Arg Arg Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln

30 35 40

tac tgg gat cct ctg ctg ggt acc tgc atg tcc tgc aaa acc att tgc 196
Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
45 50 55 60

aac cat cag agc cag cgc acc tgt gca gcc ttc tgc agg tca ctc agc 244
Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
65 70 75

tgc cgc aag gag caa ggc aag ttc tat gac cat ctc ctg agg gac tgc 292
Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
80 85 90

atc agc tgt gcc tcc atc tgt gga cag cac cct aag caa tgt gca tac 340
Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
95 100 105

ttc tgt gag aac aag ctc agg agc cca gtg aac ctt cca cca gag ctc 388
Phe Cys Glu Asn Lys Leu Arg Ser Pro Val Asn Leu Pro Pro Glu Leu
110 115 120

agg aga cag cgg agt gga gaa gtt gaa aac aat tca gac aac tcg gga 436
Arg Arg Gln Arg Ser Gly Glu Val Glu Asn Asn Ser Asp Asn Ser Gly
125 130 135 140

agg tac caa gga ttg gag cac aga ggc tca gaa gca agt cca gct ctc 484
Arg Tyr Gln Gly Leu Glu His Arg Gly Ser Glu Ala Ser Pro Ala Leu
145 150 155

cca ggt ctc aag gag ccc aaa tct tca gac aaa act cac aca tgc cca 532
Pro Gly Leu Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
160 165 170

ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc 580
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
175 180 185

ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc 628
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
190 195 200

aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc 676
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
205 210 215 220

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg 724
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
225 230 235

cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc 772
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
240 245 250

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc 820
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
255 260 265

tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc 868
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
270 275 280

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg 916
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
285 290 295 300

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 964
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

305 310 315

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 1012
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
320 325 330

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 1060
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
335 340 345

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1108
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
350 355 360

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1156
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
365 370 375 380

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taatctagag 1202
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390

gcgcgccaat ta 1214

<210> 19
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<400> 19
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30
Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro
35 40 45
Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser
50 55 60
Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu
65 70 75 80
Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala
85 90 95
Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn
100 105 110
Lys Leu Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg
115 120 125
Ser Gly Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly
130 135 140
Leu Glu His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys
145 150 155 160
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
165 170 175
Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
180 185 190
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
195 200 205
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
210 215 220
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
225 230 235 240
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
245 250 255
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
260 265 270
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

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        275                 280                 285
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    290                 295                 300
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
305                 310                 315                 320
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                325                 330                 335
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            340                 345                 350
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        355                 360                 365
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    370                 375                 380
Ser Leu Ser Leu Ser Pro Gly Lys
385                 390


<210> 20
<211> 1070
<212> DNA
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<221> CDS
<222> (17)...(1048)

<400> 20
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                  Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu
                   1               5                  10

ctg ctg tgt ggc gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc   100
Leu Leu Cys Gly Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala
          15                  20                  25

gag ttg aga cgc ttc cgt aga gct atg aga tcc tgc ccc gaa gag cag   148
Glu Leu Arg Arg Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln
      30                  35                  40

tac tgg gat cct ctg ctg ggt acc tgc atg tcc tgc aaa acc att tgc   196
Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
 45                  50                  55                  60

aac cat cag agc cag cgc acc tgt gca gcc ttc tgc agg tca ctc agc   244
Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
                 65                  70                  75

tgc cgc aag gag caa ggc aag ttc tat gac cat ctc ctg agg gac tgc   292
Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
             80                  85                  90

atc agc tgt gcc tcc atc tgt gga cag cac cct aag caa tgt gca tac   340
Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
         95                  100                 105

ttc tgt gag aac gag ccc aaa tct tca gac aaa act cac aca tgc cca   388
Phe Cys Glu Asn Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
    110                 115                 120

ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc   436
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
125                 130                 135                 140

ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc   484
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                145                 150                 155
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aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc   532
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            160                 165                 170

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg   580
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        175                 180                 185

cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc   628
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    190                 195                 200

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc   676
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
205                 210                 215                 220

tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc   724
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                225                 230                 235

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg   772
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            240                 245                 250

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc   820
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        255                 260                 265

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg   868
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    270                 275                 280

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc   916
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
285                 290                 295                 300

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag   964
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                305                 310                 315

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac   1012
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            320                 325                 330

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taatctagag        1058
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        335                 340

gcgcgccaat ta                                                    1070
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<210> 21
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<400> 21

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1               5                  10                  15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
            20                  25                  30
Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro
        35                  40                  45
Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser
    50                  55                  60
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Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu
65                  70                  75                  80
Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala
                85                  90                  95
Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn
            100                 105                 110
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        115                 120                 125
Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    130                 135                 140
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
145                 150                 155                 160
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                165                 170                 175
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            180                 185                 190
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        195                 200                 205
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    210                 215                 220
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
225                 230                 235                 240
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                245                 250                 255
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            260                 265                 270
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        275                 280                 285
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    290                 295                 300
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
305                 310                 315                 320
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                325                 330                 335
Ser Leu Ser Leu Ser Pro Gly Lys
            340
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<210> 22
<211> 1082
<212> DNA
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<221> CDS
<222> (17)...(1060)

<400> 22

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                  Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu
                   1               5                  10

ctg ctg tgt ggc gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc   100
Leu Leu Cys Gly Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala
         15                  20                  25

gag ttg aga cgc ttc cgt aga gct atg aga tcc tgc ccc gaa gag cag   148
Glu Leu Arg Arg Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln
     30                  35                  40

tac tgg gat cct ctg ctg ggt acc tgc atg tcc tgc aaa acc att tgc   196
Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
 45                  50                  55                  60

aac cat cag agc cag cgc acc tgt gca gcc ttc tgc agg tca ctc agc   244
Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
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65 70 75

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tgc cgc aag gag caa ggc aag ttc tat gac cat ctc ctg agg gac tgc   292
Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
                80                  85                  90

atc agc tgt gcc tcc atc tgt gga cag cac cct aag caa tgt gca tac   340
Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
            95                 100                 105

ttc tgt gag aac aag ctc agg agc gag ccc aaa tct tca gac aaa act   388
Phe Cys Glu Asn Lys Leu Arg Ser Glu Pro Lys Ser Ser Asp Lys Thr
        110                 115                 120

cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca   436
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser
125                 130                 135                 140

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg   484
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                145                 150                 155

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct   532
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            160                 165                 170

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc   580
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        175                 180                 185

aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc   628
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    190                 195                 200

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac   676
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
205                 210                 215                 220

aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc   724
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr
                225                 230                 235

atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg   772
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            240                 245                 250

ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc   820
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        255                 260                 265

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc   868
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    270                 275                 280

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac   916
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
285                 290                 295                 300

tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc   964
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                305                 310                 315

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct   1012
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            320                 325                 330

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa   1060
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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335 340 345

taatctagag gcgcgccaat ta 1082

<210> 23
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<400> 23
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30
Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro
35 40 45
Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser
50 55 60
Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu
65 70 75 80
Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala
85 90 95
Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn
100 105 110
Lys Leu Arg Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
115 120 125
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
130 135 140
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
145 150 155 160
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
165 170 175
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
180 185 190
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
195 200 205
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
210 215 220
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
225 230 235 240
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
245 250 255
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
260 265 270
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
275 280 285
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
290 295 300
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
305 310 315 320
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
325 330 335
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345

<210> 24
<211> 1109
<212> DNA
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<221> CDS

<222> (17)...(1090)

<400> 24

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tattaggccg gccacc atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg 52
                  Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu
                   1               5                  10

ctg ctg tgt ggc gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc   100
Leu Leu Cys Gly Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala
          15                  20                  25

gag ttg aga cgc ttc cgt aga gct atg aga tcc tgc ccc gaa gag cag   148
Glu Leu Arg Arg Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln
      30                  35                  40

tac tgg gat cct ctg ctg ggt acc tgc atg tcc tgc aaa acc att tgc   196
Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys
  45                  50                  55                  60

aac cat cag agc cag cgc acc tgt gca gcc ttc tgc agg tca ctc agc   244
Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser
                  65                  70                  75

tgc cgc aag gag caa ggc aag ttc tat gac cat ctc ctg agg gac tgc   292
Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys
              80                  85                  90

atc agc tgt gcc tcc atc tgt gga cag cac cct aag caa tgt gca tac   340
Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr
          95                  100                 105

ttc tgt gag aac aag ctc agg agc cca gtg aac ctt cca cca gag ctc   388
Phe Cys Glu Asn Lys Leu Arg Ser Pro Val Asn Leu Pro Pro Glu Leu
     110                 115                 120

agg gag ccc aaa tct tca gac aaa act cac aca tgc cca ccg tgc cca   436
Arg Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
125                 130                 135                 140

gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa   484
Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
                145                 150                 155

ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg   532
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            160                 165                 170

gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac   580
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        175                 180                 185

gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag   628
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    190                 195                 200

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac   676
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
205                 210                 215                 220

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa   724
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                225                 230                 235

gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag   772
Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            240                 245                 250

ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg   820
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```
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        255                 260                 265

acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc   868
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    270                 275                 280

agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac   916
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
285                 290                 295                 300

tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc   964
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                305                 310                 315

tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc   1012
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            320                 325                 330

ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag   1060
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        335                 340                 345

aag agc ctc tcc ctg tct ccg ggt aaa taa tctagaggcg cgccaatta      1109
Lys Ser Leu Ser Leu Ser Pro Gly Lys  *
    350                 355
```

<210> 25
<211> 357
<212> PRT
<213> Artificial Sequence

<220>
<223> TACI-Fc fusion protein

<400> 25

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1               5                  10                  15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
            20                  25                  30
Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro
        35                  40                  45
Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser
    50                  55                  60
Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu
65                  70                  75                  80
Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala
                85                  90                  95
Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn
            100                 105                 110
Lys Leu Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg 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
Glu 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 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser
225                 230                 235                 240
Ser 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 Lys
        355
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<210> 26
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> BAFF-R-Fc fusion protein

<400> 26

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

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 27
tattaggccg gccaccatgg atgcaatga 29

<210> 28
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 28
tgaagatttg ggctccttga gacctggga 29

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

<220>
<223> Primer sequence

<400> 29
tcccaggtct caaggagccc aaatcttca 29

<210> 30
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 30
taattggcgc gcctctagat tatttacccg gagaca 36

<210> 31
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 31
tgaagatttg ggctcgttct cacagaagta 30

<210> 32
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 32
atacttctgt gagaacgagc ccaaatcttc a 31

<210> 33
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 33
tttgggctcg ctcctgagct tgttctcaca 30

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 34
ctcaggagcg agcccaaatc ttcagaca 28

<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 35
tttgggctcc ctgagctctg gtggaa 26

<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 36
gagctcaggg agcccaaatc ttcagaca 28

<210> 37
<211> 1216
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (141)...(890)

<400> 37
gaattcggct cgagcctttt tatttctcct tgcgtaacaa ccttcttccc ttctgcacca 60
ctgcccgtac ccttacccgc cccgccacct ccttgctacc ccactcttga aaccacagct 120
gttggcaggg tccccagctc atg cca gcc tca tct cct ttc ttg cta gcc ccc 173
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro
1 5 10

aaa ggg cct cca ggc aac atg ggg ggc cca gtc aga gag ccg gca ctc 221
Lys Gly Pro Pro Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu
15 20 25

tca gtt gcc ctc tgg ttg agt tgg ggg gca gct ctg ggg gcc gtg gct 269
Ser Val Ala Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala
30 35 40

tgt gcc atg gct ctg ctg acc caa caa aca gag ctg cag agc ctc agg 317
Cys Ala Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg

```
45                  50                  55

aga gag gtg agc cgg ctg cag ggg aca gga ggc ccc tcc cag aat ggg   365
Arg Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 60                  65                  70                  75

gaa ggg tat ccc tgg cag agt ctc ccg gag cag agt tcc gat gcc ctg   413
Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu
                 80                  85                  90

gaa gcc tgg gag aat ggg gag aga tcc cgg aaa agg aga gca gtg ctc   461
Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu
            95                 100                 105

acc caa aaa cag aag aag cag cac tct gtc ctg cac ctg gtt ccc att   509
Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile
        110                 115                 120

aac gcc acc tcc aag gat gac tcc gat gtg aca gag gtg atg tgg caa   557
Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln
    125                 130                 135

cca gct ctt agg cgt ggg aga ggc cta cag gcc caa gga tat ggt gtc   605
Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val
140                 145                 150                 155

cga atc cag gat gct gga gtt tat ctg ctg tat agc cag gtc ctg ttt   653
Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe
                160                 165                 170

caa gac gtg act ttc acc atg ggt cag gtg gtg tct cga gaa ggc caa   701
Gln Asp Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln
            175                 180                 185

gga agg cag gag act cta ttc cga tgt ata aga agt atg ccc tcc cac   749
Gly Arg Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His
        190                 195                 200

ccg gac cgg gcc tac aac agc tgc tat agc gca ggt gtc ttc cat tta   797
Pro Asp Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu
    205                 210                 215

cac caa ggg gat att ctg agt gtc ata att ccc cgg gca agg gcg aaa   845
His Gln Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys
220                 225                 230                 235

ctt aac ctc tct cca cat gga acc ttc ctg ggg ttt gtg aaa ctg       890
Leu Asn Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu
                240                 245                 250

tgattgtgtt ataaaaagtg gctcccagct tggaagacca gggtgggtac atactggaga 950
cagccaagag ctgagtatat aaaggagagg gaatgtgcag gaacagaggc gtcttcctgg 1010
gtttggctcc ccgttcctca cttttccctt ttcattccca ccccctagac tttgatttta 1070
cggatatctt gcttctgttc cccatggagc tccgaattct tgcgtgtgtg tagatgaggg 1130
gcgggggacg ggcgccaggc attgttcaga cctggtcggg gcccactgga agcatccaga 1190
acagcaccac catctagcgg ccgccg                                      1216

<210> 38
<211> 250
<212> PRT
<213> homo sapiens

<400> 38
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
 1               5                  10                  15
Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
            20                  25                  30
Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
```

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

<210> 39
<211> 762
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (7)...(759)

<400> 39

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ggatcc atg aag cac ctg tgg ttc ttc ctc ctg ctg gtg gcg gct ccc    48
       Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro
        1               5                   10

aga tgg gtc ctg tcc gag ccc aaa tct tgt gac aaa act cac aca tgc    96
Arg Trp Val Leu Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 15                  20                  25                  30

cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc   144
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
                35                  40                  45

ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag   192
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
            50                  55                  60

gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag   240
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
        65                  70                  75

ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag   288
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
    80                  85                  90

ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc   336
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 95                  100                 105                 110

acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag   384
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```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                115                 120                 125

gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa   432
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
            130                 135                 140

gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc   480
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
        145                 150                 155

cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa   528
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
    160                 165                 170

ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag   576
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
175                 180                 185                 190

ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc   624
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                195                 200                 205

tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag   672
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
            210                 215                 220

cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac   720
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
        225                 230                 235

cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga           762
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    240                 245                 250
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<210> 40
<211> 251
<212> PRT
<213> homo sapiens

<400> 40

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
210 215 220
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
225 230 235 240
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
245 250

<210> 41
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Optimized tPA leader

<400> 41
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30
Phe Arg Arg
35