<110> GI Innovation,Inc.

<120> PHARMACEUTICAL COMPOSITION FOR TREATING CANCER COMPRISING FUSION PROTEIN COMPRISING IL-2 PROTEIN AND CD80 PROTEIN AND IMMUNE CHECKPOINT INHIBITOR

<130> POPB214529PCT

<150> KR 10-2019-0154632
<151> 2019-11-27

<160> 39

<170> KoPatentIn 3.0

<210> 1
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide (TPA)

<400> 1
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser His Ala
20 25

<210> 2
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> hB7-1:35-242

<400> 2
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr

```
 65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205
```

<210> 3
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge

<400> 3

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

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
             20                  25                  30
```

<210> 4
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> immunoglobulin fc

<400> 4

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

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln 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 Phe 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

Gly Leu Pro Ser Ser 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 Gln Glu Glu Met
        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 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
            180                 185                 190

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

Lys Ser Leu Ser Leu Ser Leu Gly
    210                 215
```

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

<220>
<223> linker

<400> 5
Gly Gly Gly Gly Ser
1 5

<210> 6
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL-2M

<400> 6
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

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

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr
130

<210> 7
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein comprising variants of IL-2 and fragments of CD80

<400> 7
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

```
  1               5                  10                  15

Ala Val Phe Val Ser Pro Ser His Ala Val Ile His Val Thr Lys Glu
             20                  25                  30

Val Lys Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu
         35                  40                  45

Glu Leu Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val
     50                  55                  60

Leu Thr Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn
 65                  70                  75                  80

Arg Thr Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala
                 85                  90                  95

Leu Arg Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr
            100                 105                 110

Glu Lys Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser
        115                 120                 125

Val Lys Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro
    130                 135                 140

Thr Ser Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro
145                 150                 155                 160

Glu Pro His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile
                165                 170                 175

Asn Thr Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser
            180                 185                 190

Ser Lys Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu
        195                 200                 205

Ile Lys Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr
    210                 215                 220

Thr Lys Gln Glu His Phe Pro Asp Asn Gly Ser Gly Gly Gly Gly Ser
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser Lys Tyr Gly
                245                 250                 255

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
            260                 265                 270

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Gln Leu Met Ile Ser Arg
        275                 280                 285

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
```

```
    290                 295                 300

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
305                 310                 315                 320

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
                325                 330                 335

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
            340                 345                 350

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
        355                 360                 365

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    370                 375                 380

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
385                 390                 395                 400

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                405                 410                 415

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            420                 425                 430

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
        435                 440                 445

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala
    450                 455                 460

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Gly
465                 470                 475                 480

Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
                485                 490                 495

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
            500                 505                 510

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe
        515                 520                 525

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
    530                 535                 540

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
545                 550                 555                 560

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
                565                 570                 575

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
```

```
            580                 585                 590

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
        595                 600                 605

Cys Gln Ser Ile Ile Ser Thr Leu Thr
    610                 615


<210>    8
<211>    1857
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    nucleotiedes coding fusion protein (GI101)


<400>    8
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tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc        120

tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa        180

aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac        240

cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct        300

gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag        360

cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac        420

ttcgagatcc ctacctccaa catccggcgg atcatctgtt ctacctctgg cggctttcct        480

gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg        540

tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc        600

accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtgaa ccagaccttc        660

aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct        720

ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct        780

ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct        840

aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtggtggt ggatgtgtct        900

caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc        960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc       1020

gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc       1080
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ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140

gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200

ctggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260

gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320

tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380

ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttggaggt 1440

ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500

ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa ccccaagctg 1560

accgccatgc tgaccgctaa gttctacatg cccaagaagg ccaccgagct gaagcacctc 1620

cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680

aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg 1740

aagggctccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800

tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac ctgatga 1857

<210> 9
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI101)

<400> 9
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

```
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
    290                 295                 300

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
```

```
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
            420                 425                 430

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

Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 10
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL-2

<400> 10

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Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
  1               5                  10                  15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
             20                  25                  30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
         35                  40                  45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
     50                  55                  60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 65                  70                  75                  80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                 85                  90                  95

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

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125

Ile Ser Thr Leu Thr
    130


<210>    11
<211>    288
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    CD80


<400>    11
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
  1               5                  10                  15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
             20                  25                  30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
         35                  40                  45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
     50                  55                  60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65                  70                  75                  80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
```

```
                85                  90                  95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
            100                 105                 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
        115                 120                 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
    130                 135                 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145                 150                 155                 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
                165                 170                 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
            180                 185                 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
        195                 200                 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
    210                 215                 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225                 230                 235                 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
                245                 250                 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
            260                 265                 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
        275                 280                 285
```

<210> 12
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> modified Fc

<400> 12

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Ser His Thr Gln Pro Leu Gly Val Phe Leu Phe Pro Pro Lys Pro Lys
  1               5                  10                  15
```

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
         35                  40                  45

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
     50                  55                  60

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

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

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
            100                 105                 110

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
        115                 120                 125

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
    210                 215


<210>    13
<211>    306
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    mCD80


<400>    13
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
  1               5                  10                  15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
```

```
            20                  25                  30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
         35                  40                  45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
     50                  55                  60

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65                  70                  75                  80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
                 85                  90                  95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
            100                 105                 110

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
        115                 120                 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
    130                 135                 140

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
145                 150                 155                 160

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
                165                 170                 175

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
            180                 185                 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
        195                 200                 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
    210                 215                 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225                 230                 235                 240

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

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
            260                 265                 270

Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
        275                 280                 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
    290                 295                 300

Phe Leu
```

305

<210> 14
<211> 1848
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (mGI101)

<400> 14
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ccttgccggt acaactctcc tcacgaggac gagtctgagg accggatcta ctggcagaaa 180

cacgacaagg tggtgctgtc cgtgatcgcc ggaaagctga aagtgtggcc tgagtacaag 240

aacaggaccc tgtacgacaa caccacctac agcctgatca tcctgggcct cgtgctgagc 300

gatagaggca cctattcttg cgtggtgcag aagaaagagc ggggcaccta cgaagtgaag 360

cacctggctc tggtcaagct gtccatcaag gccgacttca gcacccctaa catcaccgag 420

tctggcaacc cttccgccga caccaagaga atcacctgtt tcgcctctgg cggcttccct 480

aagcctcggt tctcttggct ggaaaacggc agagagctgc ccggcatcaa taccaccatt 540

tctcaggacc cagagtccga gctgtacacc atctccagcc agctcgactt taacaccacc 600

agaaaccaca ccatcaagtg cctgattaag tacggcgacg cccacgtgtc cgaggacttt 660

acttgggaga aacctcctga ggaccctcct gactctggat ctggcggcgg aggttctggc 720

ggaggtggaa gcggaggcgg aggatctgct gagtctaagt atggccctcc ttgtcctcca 780

tgtcctgctc cagaagctgc tggcggaccc tctgtgttcc tgtttcctcc aaagcctaag 840

gaccagctca tgatctctcg gacccctgaa gtgacctgcg tggtggtgga tgtgtctcaa 900

gaggaccctg aggtgcagtt caattggtac gtggacggcg tggaagtgca caacgccaag 960

accaagccta gagaggaaca gttcaactcc acctatagag tggtgtccgt gctgaccgtg 1020

ctgcaccagg attggctgaa cggcaaagag tacaagtgca aggtgtccaa caagggcctg 1080

ccttccagca tcgaaaagac catcagcaag gctaagggcc agcctaggga accccaggtt 1140

tacaccctgc ctccaagcca agaggaaatg accaagaacc aggtgtccct gacctgcctg 1200

gtcaagggct tctacccttc cgacattgcc gtggaatggg agtccaatgg ccagcctgag 1260

aacaactaca agaccacacc tcctgtgctg gactccgacg gctccttctt tctgtactct 1320

cgcctgaccg tggacaagtc taggtggcaa gagggcaacg tgttctcctg ctctgtgctg 1380

cacgaggctc tgcacaacca ctacacccag aagtccctgt ctctgtctct tggaggtggt 1440

ggcggttctg cccctacctc cagctctacc aagaaaaccc agctccagtt ggagcatctg 1500

ctgctggacc tccagatgat cctgaatggc atcaacaatt acaagaaccc caagctgacc 1560

gccatgctga ccgctaagtt ctacatgccc aagaaggcca ccgagctgaa gcacttgcag 1620

tgcctggaag aggaactgaa gcccctggaa gaagtgctga atctggccca gtccaagaac 1680

ttccacctga ggcctaggga cctgatctcc aacatcaacg tgatcgtgct ggaactgaaa 1740

ggctccgaga caaccttcat gtgcgagtac gccgacgaga cagccaccat cgtggaattt 1800

ctgaaccggt ggatcacctt ctgccagagc atcatctcca cactgacc 1848

<210> 15
<211> 616
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (mGI101)

<400> 15
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser His Ala Val Asp Glu Gln Leu Ser Lys
20 25 30

Ser Val Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His
35 40 45

Glu Asp Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val
50 55 60

Val Leu Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys
65 70 75 80

Asn Arg Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly
85 90 95

Leu Val Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys
100 105 110

Glu Arg Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser

```
        115                 120                 125

Ile Lys Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro
    130                 135                 140

Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro
145                 150                 155                 160

Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile
                165                 170                 175

Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser
            180                 185                 190

Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu
        195                 200                 205

Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys
    210                 215                 220

Pro Pro Glu Asp Pro Pro Asp Ser Gly Ser Gly Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser Lys Tyr Gly Pro
                245                 250                 255

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
            260                 265                 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Gln Leu Met Ile Ser Arg Thr
        275                 280                 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
    290                 295                 300

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
        355                 360                 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
```

```
                405                 410                 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
        435                 440                 445

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu
    450                 455                 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly
465                 470                 475                 480

Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                485                 490                 495

Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            500                 505                 510

Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr
        515                 520                 525

Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu
    530                 535                 540

Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
545                 550                 555                 560

Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                565                 570                 575

Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            580                 585                 590

Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
        595                 600                 605

Gln Ser Ile Ile Ser Thr Leu Thr
    610                 615


<210>    16
<211>    1437
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    nucleotiedes coding fusion protein (GI101C1)


<400>    16
atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg        60
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tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc 120

tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa 180

aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac 240

cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct 300

gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag 360

cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac 420

ttcgagatcc ctacctccaa catccggcgg atcatctgtt ctacctctgg cggctttcct 480

gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg 540

tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc 600

accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtgaa ccagaccttc 660

aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct 720

ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct 780

ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct 840

aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtggtggt ggatgtgtct 900

caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020

gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080

ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140

gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200

ctggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260

gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320

tctcgcctga ccgtggacaa gtctaggtgg caagagggca acgtgttctc ctgctctgtg 1380

ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc cctgggc 1437

<210> 17
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI101C1)

<400> 17

```
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
  1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
             20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
         35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
     50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
 65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                 85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

```
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
    290                 295                 300

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
            420                 425                 430

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

Leu Ser Leu Ser Leu Gly
    450
```

<210>  18
<211>  1176
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  nucleotiedes coding fusion protein (GI101C2)

<400>  18

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tctccatctc acgccgctga gtctaagtac ggccctcctt gtcctccatg tcctgctcca       120

gaagctgctg gcggaccctc tgtgttcctg tttcctccaa agcctaagga ccagctcatg       180

atctctcgga cccctgaagt gacctgcgtg gtggtggatg tgtctcaaga ggaccctgag       240
```

gtgcagttca attggtacgt ggacggcgtg gaagtgcaca acgccaagac caagcctaga 300

gaggaacagt tcaactccac ctacagagtg gtgtccgtgc tgaccgtgct gcaccaggat 360

tggctgaacg gcaaagagta caagtgcaag gtgtccaaca agggcctgcc ttccagcatc 420

gaaaagacca tctccaaggc taagggccag cctagggaac cccaggttta caccctgcct 480

ccaagccaag aggaaatgac caagaaccag gtgtccctga cctgcctggt caagggcttc 540

taccttccg acattgccgt ggaatgggag tccaatggcc agcctgagaa caactacaag 600

accacacctc ctgtgctgga ctccgacggc tccttctttc tgtactctcg cctgaccgtg 660

gacaagtcta ggtggcaaga gggcaacgtg ttctcctgct ctgtgctgca cgaggccctg 720

cacaatcact acacccagaa gtccctgtct ctgtctcttg gcggaggcgg aggatctgct 780

cctacctcca gctccaccaa gaaaacccag ctccagttgg agcatctgct gctggacctc 840

cagatgatcc tgaatggcat caacaattac aagaacccca agctgaccgc catgctgacc 900

gctaagttct acatgcccaa gaaggccacc gagctgaagc acctccagtg cctggaagag 960

gaactgaagc ccctggaaga agtgctgaat ctggcccagt ccaagaactt ccacctgagg 1020

cctagggacc tgatctccaa catcaacgtg atcgtgctgg aactgaaagg ctccgagaca 1080

accttcatgt gcgagtacgc cgacgagaca gccaccatcg tggaatttct gaaccggtgg 1140

atcaccttct gccagtccat catctccaca ctgacc 1176

<210> 19
<211> 367
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI101C2)

<400> 19
Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
1 5 10 15

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
20 25 30

Gln Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
35 40 45

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

```
     50                  55                  60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 65                  70                  75                  80

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

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

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

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

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

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
            180                 185                 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
        195                 200                 205

Ser Val Leu His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    210                 215                 220

Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser
225                 230                 235                 240

Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln
                245                 250                 255

Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Ala
            260                 265                 270

Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys
        275                 280                 285

His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
    290                 295                 300

Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
305                 310                 315                 320

Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr
                325                 330                 335

Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu
```

```
            340                 345                 350

Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
        355                 360                 365
```

<210> 20
<211> 1434
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (mGI101C1)

<400> 20

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atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg         60

tctccttctc acgctgtgga cgagcagctc tccaagtccg tgaaggataa ggtcctgctg        120

ccttgccggt acaactctcc tcacgaggac gagtctgagg accggatcta ctggcagaaa        180

cacgacaagg tggtgctgtc cgtgatcgcc ggaaagctga aagtgtggcc tgagtacaag        240

aacaggaccc tgtacgacaa caccacctac agcctgatca tcctgggcct cgtgctgagc        300

gatagaggca cctattcttg cgtggtgcag aagaaagagc ggggcaccta cgaagtgaag        360

cacctggctc tggtcaagct gtccatcaag gccgacttca gcacccctaa catcaccgag        420

tctggcaacc cttccgccga caccaagaga atcacctgtt tcgcctctgg cggcttccct        480

aagcctcggt tctcttggct ggaaaacggc agagagctgc ccggcatcaa taccaccatt        540

tctcaggacc cagagtccga gctgtacacc atctccagcc agctcgactt taacaccacc        600

agaaaccaca ccatcaagtg cctgattaag tacggcgacg cccacgtgtc cgaggacttt        660

acttgggaga aacctcctga ggaccctcct gactctggat ctggcggcgg aggttctggc        720

ggaggtggaa gcggaggcgg aggatctgct gagtctaagt atggccctcc ttgtcctcca        780

tgtcctgctc cagaagctgc tggcggaccc tctgtgttcc tgtttcctcc aaagcctaag        840

gaccagctca tgatctctcg gacccctgaa gtgacctgcg tggtggtgga tgtgtctcaa        900

gaggaccctg aggtgcagtt caattggtac gtggacggcg tggaagtgca caacgccaag        960

accaagccta gagaggaaca gttcaactcc acctatagag tggtgtccgt gctgaccgtg       1020

ctgcaccagg attggctgaa cggcaaagag tacaagtgca aggtgtccaa caagggcctg       1080
```

ccttccagca tcgaaaagac catcagcaag gctaagggcc agcctaggga accccaggtt 1140

tacaccctgc ctccaagcca agaggaaatg accaagaacc aggtgtccct gacctgcctg 1200

gtcaagggct tctacccttc cgacattgcc gtggaatggg agtccaatgg ccagcctgag 1260

aacaactaca agaccacacc tcctgtgctg gactccgacg gctccttctt tctgtactct 1320

cgcctgaccg tggacaagtc taggtggcaa gagggcaacg tgttctcctg ctctgtgctg 1380

cacgaggctc tgcacaacca ctacacccag aagtccctgt ctctgtccct gggc 1434

<210> 21
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (mGI101C1)

<400> 21

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Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
  1               5                  10                  15

Ala Val Phe Val Ser Pro Ser His Ala Val Asp Glu Gln Leu Ser Lys
             20                  25                  30

Ser Val Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His
         35                  40                  45

Glu Asp Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val
     50                  55                  60

Val Leu Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys
 65                  70                  75                  80

Asn Arg Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly
                 85                  90                  95

Leu Val Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys
            100                 105                 110

Glu Arg Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser
        115                 120                 125

Ile Lys Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro
    130                 135                 140

Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro
145                 150                 155                 160

Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile
```

```
                165                 170                 175

Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser
            180                 185                 190

Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu
        195                 200                 205

Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys
    210                 215                 220

Pro Pro Glu Asp Pro Pro Asp Ser Gly Ser Gly Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser Lys Tyr Gly Pro
                245                 250                 255

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
            260                 265                 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Gln Leu Met Ile Ser Arg Thr
        275                 280                 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
    290                 295                 300

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
        355                 360                 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
        435                 440                 445

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu
```

```
    450                 455                 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
465                 470                 475


<210>    22
<211>    133
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    variants of IL-2 (3M, M45)


<400>    22
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
  1               5                  10                  15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
             20                  25                  30

Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys
         35                  40                  45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
     50                  55                  60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 65                  70                  75                  80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                 85                  90                  95

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

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125

Ile Ser Thr Leu Thr
    130


<210>    23
<211>    133
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    variants of IL-2 (3M, M61)


<400>    23
```

```
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
  1               5                  10                  15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
             20                  25                  30

Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys
         35                  40                  45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Arg Glu Leu Lys
     50                  55                  60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 65                  70                  75                  80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
                 85                  90                  95

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

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125

Ile Ser Thr Leu Thr
    130


<210>    24
<211>    133
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    variants of IL-2 (3M, M72)


<400>    24
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
  1               5                  10                  15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
             20                  25                  30

Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys
         35                  40                  45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
     50                  55                  60

Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
 65                  70                  75                  80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
```

```
                85                  90                  95

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

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
        115                 120                 125

Ile Ser Thr Leu Thr
    130
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<210> 25
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (GI102-M45)

<400> 25

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atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg         60

tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc        120

tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa        180

aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac        240

cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct        300

gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag        360

cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac        420

ttcgagatcc ctacctccaa catccggcgg atcatctgtt ctacctctgg cggctttcct        480

gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg        540

tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc        600

accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtgaa ccagaccttc        660

aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct        720

ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct        780

ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct        840

aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtggtggt ggatgtgtct        900

caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc        960
```

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020

gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080

ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140

gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200

ctggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260

gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320

tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380

ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttggaggt 1440

ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500

ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa ccccaagctg 1560

accgccatgc tgaccgctaa gttcgccatg cccaagaagg ccaccgagct gaagcacctc 1620

cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680

aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg 1740

aagggctccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800

tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac c 1851

<210> 26
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI102-M45)

<400> 26
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr

```
 65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                 85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
    290                 295                 300

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
```

```
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
            420                 425                 430

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

Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Ala Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 27
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (GI102-M61)

<400> 27
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tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc 120

tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa 180

aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac 240

cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct 300

gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag 360

cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac 420

ttcgagatcc ctacctccaa catccggcgg atcatctgtt ctacctctgg cggctttcct 480

gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg 540

tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc 600

accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtgaa ccagaccttc 660

aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct 720

ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct 780

ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct 840

aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtggtggt ggatgtgtct 900

caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020

gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080

ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140

gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200

ctggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260

gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320

tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380

ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttggaggt 1440

ggtggcggtt ctgcccctac agctcctct accaagaaaa cccagctcca gttggagcat 1500

ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa ccccaagctg 1560

```
accgccatgc tgaccgctaa gttctacatg cccaagaagg ccaccgagct gaagcacctc       1620

cagtgcctgg aaagggaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag       1680

aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg       1740

aagggctccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa       1800

tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac c                1851
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<210> 28
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI102-M61)

<400> 28

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Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
  1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
             20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
         35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
     50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
 65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                 85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175
```

```
Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
    290                 295                 300

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
            420                 425                 430

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

Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460
```

```
Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Arg Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 29
<211> 1857
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (GI102-M72)

<400> 29

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tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc        120

tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa        180

aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac        240

cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct        300

gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag        360

cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac        420

ttcgagatcc ctacctccaa catccggcgg atcatctgtt ctacctctgg cggctttcct        480
```

gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg 540

tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc 600

accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtgaa ccagaccttc 660

aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct 720

ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct 780

ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct 840

aaggaccagc tcatgatctc tcggacaccc gaagtgacct gcgtggtggt ggatgtgtct 900

caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc 1020

gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1080

ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140

gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200

ctggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260

gagaacaact acaagaccac acctcctgtg ctggactccg acggctcctt ctttctgtac 1320

tctcgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1380

ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttggaggt 1440

ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500

ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa ccccaagctg 1560

accgccatgc tgaccgctaa gttctacatg cccaagaagg ccaccgagct gaagcacctc 1620

cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatggggc ccagtccaag 1680

aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg 1740

aagggctccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800

tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac ctgatga 1857

<210> 30
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI102-M72)

<400> 30

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Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
  1               5                  10                  15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
             20                  25                  30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
         35                  40                  45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
     50                  55                  60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
 65                  70                  75                  80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His
                 85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

```
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
    290                 295                 300

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
            420                 425                 430

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

Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Ala Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560
```

```
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 31
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (GI101w)

<400> 31

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tctccttctc acgctgtgat ccacgtgacc aaagaagtga aagaggtcgc cacactgtcc        120

tgcggccaca acgtttcagt ggaagaactg gcccagacca ggatctactg gcagaaagaa        180

aagaaaatgg tgctgaccat gatgtccggc gacatgaaca tctggcctga gtacaagaac        240

cggaccatct tcgacatcac caacaacctg tccatcgtga ttctggccct gaggccttct        300

gatgagggca cctatgagtg cgtggtgctg aagtacgaga aggacgcctt caagcgcgag        360

cacctggctg aagtgacact gtccgtgaag gccgactttc ccacaccttc catctccgac        420

ttcgagatcc ctacctccaa catccggcgg atcatctgtt ctacctctgg cggctttcct        480

gagcctcacc tgtcttggct ggaaaacggc gaggaactga acgccatcaa caccaccgtg        540

tctcaggacc ccgaaaccga gctgtacgct gtgtcctcca agctggactt caacatgacc        600

accaaccaca gcttcatgtg cctgattaag tacggccacc tgagagtgaa ccagaccttc        660

aactggaaca ccaccaagca agagcacttc cctgacaatg gatctggcgg cggaggttct        720

ggcggaggtg gaagcggagg cggaggatct gctgagtcta agtatggccc tccttgtcct        780

ccatgtcctg ctccagaagc tgctggcgga ccctctgtgt tcctgtttcc tccaaagcct        840

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caagaggacc ctgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc        960

aagaccaagc ctagagagga acagttcaac tccacctaca gagtggtgtc cgtgctgacc       1020

gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc       1080
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ctgccttcca gcatcgaaaa gaccatctcc aaggctaagg gccagcctag ggaaccccag 1140

gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1200

ctggtcaagg gcttctaccc ttccgacatt gccgtggaat gggagtccaa tggccagcct 1260

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ctgcacgagg ccctgcacaa tcactacacc cagaagtccc tgtctctgtc tcttggaggt 1440

ggtggcggtt ctgcccctac cagctcctct accaagaaaa cccagctcca gttggagcat 1500

ctgctgctgg acctccagat gattctgaac gggatcaaca actataagaa ccccaagctg 1560

acccgcatgc tgacctttaa gttctacatg cccaagaagg ccaccgagct gaagcacctc 1620

cagtgcctgg aagaagaact gaagcccctg gaagaggtgc tgaatctggc ccagtccaag 1680

aacttccacc tgaggccacg ggacctgatc agcaacatca acgtgatcgt gctggaactg 1740

aagggctccg agacaacctt tatgtgcgag tacgccgacg agacagccac catcgtggaa 1800

tttctgaacc ggtggatcac cttctgccag agcatcatct ccacactgac c 1851

<210> 32
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (GI101w)

<400> 32
Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys
1 5 10 15

Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp
20 25 30

Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn
35 40 45

Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn
50 55 60

Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr
65 70 75 80

Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His

```
                85                  90                  95

Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser
            100                 105                 110

Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys
        115                 120                 125

Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn
    130                 135                 140

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

Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr
                165                 170                 175

Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn
            180                 185                 190

Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
    290                 295                 300

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
```

```
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
            420                 425                 430

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

Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 33
<211> 1848
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotiedes coding fusion protein (mGI102-M61)

<400> 33

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ccttgccggt acaactctcc tcacgaggac gagtctgagg accggatcta ctggcagaaa 180

cacgacaagg tggtgctgtc cgtgatcgcc ggaaagctga aagtgtggcc tgagtacaag 240

aacaggaccc tgtacgacaa caccacctac agcctgatca tcctgggcct cgtgctgagc 300

gatagaggca cctattcttg cgtggtgcag aagaaagagc ggggcaccta cgaagtgaag 360

cacctggctc tggtcaagct gtccatcaag gccgacttca gcacccctaa catcaccgag 420

tctggcaacc cttccgccga caccaagaga atcacctgtt tcgcctctgg cggcttccct 480

aagcctcggt tctcttggct ggaaaacggc agagagctgc ccggcatcaa taccaccatt 540

tctcaggacc cagagtccga gctgtacacc atctccagcc agctcgactt taacaccacc 600

agaaaccaca ccatcaagtg cctgattaag tacggcgacg cccacgtgtc cgaggacttt 660

acttgggaga aacctcctga ggaccctcct gactctggat ctggcggcgg aggttctggc 720

ggaggtggaa gcggaggcgg aggatctgct gagtctaagt atggccctcc ttgtcctcca 780

tgtcctgctc cagaagctgc tggcggaccc tctgtgttcc tgtttcctcc aaagcctaag 840

gaccagctca tgatctctcg gacccctgaa gtgacctgcg tggtggtgga tgtgtctcaa 900

gaggaccctg aggtgcagtt caattggtac gtggacggcg tggaagtgca caacgccaag 960

accaagccta gagaggaaca gttcaactcc acctatagag tggtgtccgt gctgaccgtg 1020

ctgcaccagg attggctgaa cggcaaagag tacaagtgca aggtgtccaa caagggcctg 1080

ccttccagca tcgaaaagac catcagcaag gctaagggcc agcctaggga accccaggtt 1140

tacaccctgc ctccaagcca agaggaaatg accaagaacc aggtgtccct gacctgcctg 1200

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aacaactaca agaccacacc tcctgtgctg gactccgacg gctccttctt tctgtactct 1320

cgcctgaccg tggacaagtc taggtggcaa gagggcaacg tgttctcctg ctctgtgctg 1380

cacgaggctc tgcacaacca ctacacccag aagtccctgt ctctgtctct tggaggtggt 1440

ggcggttctg cccctacctc cagctctacc aagaaaaccc agctccagtt ggagcatctg 1500

ctgctggacc tccagatgat cctgaatggc atcaacaatt acaagaaccc caagctgacc 1560

gccatgctga ccgctaagtt ctacatgccc aagaaggcca ccgagctgaa gcacttgcag 1620

tgcctggaaa gggaactgaa gcccctggaa gaagtgctga atctggccca gtccaagaac 1680

ttccacctga ggcctaggga cctgatctcc aacatcaacg tgatcgtgct ggaactgaaa 1740

ggctccgaga caaccttcat gtgcgagtac gccgacgaga cagccaccat cgtggaattt 1800

ctgaaccggt ggatcacctt ctgccagagc atcatctcca cactgacc 1848

<210> 34
<211> 616
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein (mGI102-M61)

<400> 34

```
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
  1               5                  10                  15

Ala Val Phe Val Ser Pro Ser His Ala Val Asp Glu Gln Leu Ser Lys
             20                  25                  30

Ser Val Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His
         35                  40                  45

Glu Asp Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val
     50                  55                  60

Val Leu Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys
 65                  70                  75                  80

Asn Arg Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly
                 85                  90                  95

Leu Val Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys
            100                 105                 110

Glu Arg Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser
        115                 120                 125

Ile Lys Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro
    130                 135                 140

Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro
145                 150                 155                 160

Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile
                165                 170                 175

Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser
            180                 185                 190
```

```
Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu
        195                 200                 205

Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys
    210                 215                 220

Pro Pro Glu Asp Pro Pro Asp Ser Gly Ser Gly Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser Lys Tyr Gly Pro
                245                 250                 255

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
            260                 265                 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Gln Leu Met Ile Ser Arg Thr
        275                 280                 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
    290                 295                 300

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
        355                 360                 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
        435                 440                 445

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu
    450                 455                 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly
465                 470                 475                 480
```

```
Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln
                485                 490                 495

Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
            500                 505                 510

Asn Tyr Lys Asn Pro Lys Leu Thr Ala Met Leu Thr Ala Lys Phe Tyr
        515                 520                 525

Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Arg
    530                 535                 540

Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn
545                 550                 555                 560

Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val
                565                 570                 575

Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
            580                 585                 590

Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
        595                 600                 605

Gln Ser Ile Ile Ser Thr Leu Thr
    610                 615
```

<210> 35
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> wild type hIL-2

<400> 35

```
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
  1               5                  10                  15

Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
             20                  25                  30

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
         35                  40                  45

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
     50                  55                  60

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
 65                  70                  75                  80
```

```
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
                 85                  90                  95

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
            100                 105                 110

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
        115                 120                 125

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
    130                 135                 140

Cys Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 36
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-2 with signal sequence

<400> 36

```
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
  1               5                  10                  15

Ala Val Phe Val Ser Pro Ser His Ala Ala Pro Thr Ser Ser Ser Thr
             20                  25                  30

Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
         35                  40                  45

Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met
     50                  55                  60

Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His
 65                  70                  75                  80

Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
                 85                  90                  95

Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
            100                 105                 110

Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
        115                 120                 125

Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn
    130                 135                 140

Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
```

145 150 155

<210> 37
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence coding IL-2 with signal sequence

<400> 37
atggatgcta tgctgagagg cctgtgttgc gtgctgctgc tgtgtggcgc tgtgttcgtg 60

tctccttctc acgctgcccc taccagctcc tctaccaaga aaacccagct ccagttggag 120

catctgctgc tggacctcca gatgattctg aacgggatca acaactataa gaaccccaag 180

ctgacccgca tgctgacctt taagttctac atgcccaaga aggccaccga gctgaagcac 240

ctccagtgcc tggaagaaga actgaagccc ctggaagagg tgctgaatct ggcccagtcc 300

aagaacttcc acctgaggcc acgggacctg atcagcaaca tcaacgtgat cgtgctggaa 360

ctgaagggct ccgagacaac ctttatgtgc gagtacgccg acgagacagc caccatcgtg 420

gaatttctga accggtggat caccttctgc cagagcatca tctccacact gacc 474

<210> 38
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> mGI-101

<400> 38
Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp Lys Val Leu Leu Pro
1 5 10 15

Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser Glu Asp Arg Ile Tyr
20 25 30

Trp Gln Lys His Asp Lys Val Val Leu Ser Val Ile Ala Gly Lys Leu
35 40 45

Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu Tyr Asp Asn Thr Thr
50 55 60

Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser Asp Arg Gly Thr Tyr
65 70 75 80

```
Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr Tyr Glu Val Lys His
                 85                  90                  95

Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp Phe Ser Thr Pro Asn
            100                 105                 110

Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys
        115                 120                 125

Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn
    130                 135                 140

Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu
145                 150                 155                 160

Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg
                165                 170                 175

Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser
            180                 185                 190

Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Gly
        195                 200                 205

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

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

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

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

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

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
        355                 360                 365
```

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

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

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

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

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

Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser
    450                 455                 460

Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln
465                 470                 475                 480

Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Ala
                485                 490                 495

Met Leu Thr Ala Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys
            500                 505                 510

His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
        515                 520                 525

Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
    530                 535                 540

Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr
545                 550                 555                 560

Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu
                565                 570                 575

Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 39
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> TIGIT ECD

<400> 39

```
Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
  1               5                  10                  15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
             20                  25                  30

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
         35                  40                  45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
     50                  55                  60

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

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

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
            100                 105                 110

His Gly Ala Arg Phe Gln Ile Pro
        115                 120
```