SEQUENCE LISTING

<110> AGENCY FOR SCIENCE, TECHNOLOGY AND RESEARCH

<120> ATTENUATED GLUTAMINE SYNTHETASE AS A SELECTION MARKER

<130> 9869SG4731

<150> 10201609619S
<151> 2016-11-16

<160> 103

<170> PatentIn version 3.5

<210> 1
<211> 373
<212> PRT
<213> Homo sapiens

<400> 1

```
Met Thr Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Val
1               5                   10                  15


Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
            20                  25                  30


Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
        35                  40                  45


Ser Glu Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
    50                  55                  60


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


Pro Ala Ala Met Phe Arg Asp Pro Phe Arg Lys Asp Pro Asn Lys Leu
                85                  90                  95


Val Leu Cys Glu Val Phe Lys Tyr Asn Arg Arg Pro Ala Glu Thr Asn
            100                 105                 110
```

```
Leu Arg His Thr Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
        115                 120                 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
    130                 135                 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145                 150                 155                 160

Tyr Tyr Cys Gly Val Gly Ala Asp Arg Ala Tyr Gly Arg Asp Ile Val
                165                 170                 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Ala Gly
            180                 185                 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
        195                 200                 205

Cys Glu Gly Ile Ser Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
    210                 215                 220

Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
225                 230                 235                 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
                245                 250                 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys Tyr Ile Glu Glu
            260                 265                 270

Ala Ile Glu Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
        275                 280                 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
    290                 295                 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
305                 310                 315                 320
```

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


Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ser Val Thr
            340                 345                 350


Glu Ala Leu Ile Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
        355                 360                 365


Phe Gln Tyr Lys Asn
    370
```

<210> 2
<211> 373
<212> PRT
<213> Cricetulus griseus

<400> 2

```
Met Ala Thr Ser Ala Ser Ser His Leu Asn Lys Asn Ile Lys Gln Met
1               5                   10                  15


Tyr Leu Cys Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
            20                  25                  30


Val Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
        35                  40                  45


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


Ser Ser Thr Phe Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu Ser
65                  70                  75                  80


Pro Val Ala Met Phe Arg Asp Pro Phe Arg Arg Asp Pro Asn Lys Leu
                85                  90                  95


Val Phe Cys Glu Val Phe Lys Tyr Asn Arg Lys Pro Ala Glu Thr Asn
```

```
            100                 105                 110

Leu Arg His Ser Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
        115                 120                 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
    130                 135                 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145                 150                 155                 160

Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala Tyr Gly Arg Asp Ile Val
                165                 170                 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Thr Gly
            180                 185                 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
        195                 200                 205

Cys Glu Gly Ile Arg Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
    210                 215                 220

Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
225                 230                 235                 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
                245                 250                 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys His Ile Glu Glu
            260                 265                 270

Ala Ile Glu Lys Leu Ser Lys Arg His Arg Tyr His Ile Arg Ala Tyr
        275                 280                 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
    290                 295                 300
```

```
Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
305                 310                 315                 320


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


Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ala Val Thr
            340                 345                 350


Glu Ala Ile Val Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
        355                 360                 365


Phe Gln Tyr Lys Asn
    370


<210>  3
<211>  373
<212>  PRT
<213>  Mus musculus

<400>  3

Met Ala Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Met
1               5                   10                  15


Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
            20                  25                  30


Val Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
        35                  40                  45


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


Ser Ser Thr Phe Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu His
65                  70                  75                  80


Pro Val Ala Met Phe Arg Asp Pro Phe Arg Lys Asp Pro Asn Lys Leu
                85                  90                  95
```

```
Val Leu Cys Glu Val Phe Lys Tyr Asn Arg Lys Pro Ala Glu Thr Asn
            100                 105                 110

Leu Arg His Ile Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
        115                 120                 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
    130                 135                 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145                 150                 155                 160

Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala Tyr Gly Arg Asp Ile Val
                165                 170                 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Thr Gly
            180                 185                 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
        195                 200                 205

Cys Glu Gly Ile Arg Met Gly Asp His Leu Trp Ile Ala Arg Phe Ile
    210                 215                 220

Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
225                 230                 235                 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
                245                 250                 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys Cys Ile Glu Glu
            260                 265                 270

Ala Ile Asp Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
        275                 280                 285
```

```
Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
    290                 295                 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Gly
305                 310                 315                 320

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

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Tyr Ala Val Thr
            340                 345                 350

Glu Ala Ile Val Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
        355                 360                 365

Phe Gln Tyr Lys Asn
    370
```

<210> 4
<211> 373
<212> PRT
<213> Rattus norvegicus

<400> 4

```
Met Ala Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Met
1               5                   10                  15

Tyr Met Asn Leu Pro Gln Gly Glu Lys Ile Gln Leu Met Tyr Ile Trp
            20                  25                  30

Val Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
        35                  40                  45

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

Ser Ser Thr Phe Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu His
65                  70                  75                  80
```

```
Pro Val Ala Met Phe Arg Asp Pro Phe Arg Arg Asp Pro Asn Lys Leu
                85                  90                  95

Val Phe Cys Glu Val Phe Lys Tyr Asn Arg Lys Pro Ala Glu Thr Asn
            100                 105                 110

Leu Arg His Ser Cys Lys Arg Ile Met Asp Met Val Ser Ser Gln His
        115                 120                 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
    130                 135                 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145                 150                 155                 160

Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala Tyr Gly Arg Asp Ile Val
                165                 170                 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Ile Lys Ile Thr Gly
            180                 185                 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
        195                 200                 205

Cys Glu Gly Ile Arg Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
    210                 215                 220

Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
225                 230                 235                 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
                245                 250                 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Arg Cys Ile Glu Glu
            260                 265                 270

Ala Ile Asp Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
```

```
        275                 280                 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
    290                 295                 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
305                 310                 315                 320

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

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Tyr Ala Val Thr
            340                 345                 350

Glu Ala Ile Val Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
        355                 360                 365

Phe Gln Tyr Lys Asn
    370
```

<210> 5
<211> 8201
<212> DNA
<213> Artificial Sequence

<220>
<223> Biscistronic mAb GS

<400> 5

```
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg       60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
```

attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 900

gtttaaactt aagcttggta ccgagctcgg atccactagt ccagtgtggt ggaattctgc 960

agatatccag cacagtggcg gccgccacca tggacatgag ggtccctgct cagctcctgg 1020

ggctcctgct gctctggctc tcaggtgcca gatgtgacat tgtaatgaca cagaccccac 1080

tctccctgcc cgtcaccccc ggagagccgg cctccatctc ctgcaggtct agtaagagcc 1140

tcctgcatag taatggaatc acctatttgt actggtacct gcagaagcca gggcagtctc 1200

cacagctcct gatctatcag atgtctaatc tggtgtccgg ggtccctgac aggttcagtg 1260

gcagtggatc aggcacagat tttacactga aaatcagcag agtggaggct gaggatgttg 1320

gggtttatta ctgcgcccaa aacctagagc tgccctacac tttcggcgga gggaccaagg 1380

tggagatcaa acgtaccgtg gcggcgccat ctgtcttcat cttcccgcca tctgatgagc 1440

agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat cccagagagg 1500

ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag gagagtgtca 1560

cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg ctgagcaaag 1620

cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc 1680

ccgtcacaaa gagcttcaac aggggagagt gttagtagga tatcgtctag acccctctcc 1740

ctccccccccc cctaacgtta ctggccgaag ccgcttggaa taaggccggt gtgcgtttgt 1800

ctatatgtta ttttccacca tattgccgtc ttttggcaat gtgagggccc ggaaacctgg 1860

ccctgtcttc ttgacgagca ttcctagggg tctttcccct ctcgccaaag gaatgcaagg 1920

tctgttgaat gtcgtgaagg aagcagttcc tctggaagct tcttgaagac aaacaacgtc 1980

tgtagcgacc ctttgcaggc agcggaaccc cccacctggc gacaggtgcc tctgcggcca 2040

aaagccacgt gtataagata cacctgcaaa ggcggcacaa ccccagtgcc acgttgtgag 2100

ttggatagtt gtggaaagag tcaaatggct ctcctcaagc gtattcaaca aggggctgaa 2160

ggatgcccag aaggtacccc attgtatggg atctgatctg gggcctcggt acacatgctt 2220

tacatgtgtt tagtcgaggt taaaaaaacg tctaggcccc ccgaaccacg gggacgtggt 2280

tttcctttga aaaacacgat gataatatgg ccacaaccat ggagtttggg ctgagctggg 2340

ttttcctcgt tgctcttttt agaggtgtcc agtgtcaggt gcagctggtg cagtctgggg 2400

ctgaggtgaa gaagcctggg tcctccgtga aggtctcctg caaggcctct ggatacgcct 2460

tctcctactc ttggatcaac tgggtgcgac aggcccctgg acaagggctc gagtggatgg 2520

gacggatctt ccctggcgat ggtgacacag actacaacgg caagttcaag ggcagagtca 2580

ccatcaccgc cgacaagtcc acgagcacag cctacatgga actgagcagc ctgagatctg 2640

aggacacggc cgtctattac tgtgcacgaa acgtgttcga tggctattgg ctggtgtact 2700

ggggccaggg gaccctggtc accgtcagca gcgctagcac caagggccca tcggtcttcc 2760

ccctggcacc ctcctccaag agcacctctg ggggcacagc ggccctgggc tgcctggtca 2820

aggactactt ccccgaaccg gtgacggtgt catggaactc aggcgccctg accagcggcg 2880

tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc agcgtggtga 2940

ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat cacaagccca 3000

gcaacaccaa ggtggacaag aaagttgagc ccaaatcttg tgacaaaact cacacatgcc 3060

caccgtgccc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 3120

ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 3180

gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 3240

ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca 3300

ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 3360

ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac 3420

aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc agcctgacct 3480

gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc aatgggcagc 3540

cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttcctct 3600

acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg 3660

tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg tctccgggta 3720

aatgatcgag tctagagggc ccgtttaaac ccgctgatca gcctcgactg tgccttctag 3780

gcggccgctt gccagccatc tgttgtttgc ccctcccccg tgccttcctt gaccctggaa 3840

ggtgccactc ccactgtcct ttcctaataa aatgaggaaa ttgcatcgca ttgtctgagt 3900

aggtgtcatt ctattctggg gggtggggtg gggcaggaca gcaaggggga ggattgggaa 3960

gacaatagca ggcatgctgg ggatgcggtg ggctctatgg cttctgaggc ggaaagaacc 4020

agctggggct ctagggggta tccccacgcg ccctgtagcg gcgcattaag cgcggcgggt 4080

gtggtggtta cgcgcagcgt gaccgctaca cttgccagcg ccctagcgcc cgctcctttc 4140

gctttcttcc cttcctttct cgccacgttc gccggtctgt ggaatgtgtg tcagttaggg 4200

tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca tctcaattag 4260

tcagcaacca ggtgtggaaa gtccccaggc tccccagcag gcagaagtat gcaaagcatg 4320

catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc gcccctaact 4380

ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat ttatgcagag 4440

gccgaggccg cctctgcctc tgagctattc cagaagtagt gaggaggctt ttttggaggc 4500

ctaggctttt gcaaaaagct cccgggagct tgtatatcca ttttcggatc tgatcaagag 4560

acaggatgag gatcggccac catggccacc tcagcaagtt cccacttgaa caaaaacatc 4620

aagcaaatgt acttgtgcct gccccagggt gagaaagtcc aagccatgta tatctgggtt 4680

gatggtactg gagaaggact gcgctgcaaa acccgcaccc tggactgtga gcccaagtgt 4740

gtagaagagt tacctgagtg gaattttgat ggctctagta cctttcagtc tgagggctcc 4800

aacagtgaca tgtatctcag ccctgttgcc atgtttcggg acccccttccg cagagatccc 4860

aacaagctgg tgttctgtga agttttcaag tacaaccgga agcctgcaga gaccaattta 4920

aggcactcgt gtaaacggat aatggacatg gtgagcaacc agcacccctg gtttggaatg 4980

gaacaggagt atactctgat gggaacagat gggcaccctt ttggttggcc ttccaatggc 5040

tttcctgggc cccaaggtcc gtattactgt ggtgtgggcg cagacaaagc ctatggcagg 5100

gatatcgtgg aggctcacta ccgcgcctgc ttgtatgctg gggtcaagat tacaggaaca 5160

aatgctgagg tcatgcctgc ccagtgggaa ttccaaatag gaccctgtga aggaatccgc 5220

atgggagatc atctctgggt ggcccgtttc atcttgcatc gagtatgtga agactttggg 5280

gtaatagcaa cctttgaccc caagcccatt cctgggaact ggaatggtgc aggctgccat 5340

accaacttta gcaccaaggc catgcgggag gagaatggtc tgaagcacat cgaggaggcc 5400

atcgagaaac taagcaagcg gcaccggtac cacattcgag cctacgatcc caaggggggc 5460

ctggacaatg cccgtcgtct gactgggttc cacgaaacgt ccaacatcaa cgacttttct 5520

gctggtgtcg ccaatcgcag tgccagcatc cgcattcccc ggactgtcgg ccaggagaag 5580

aaaggttact ttgaagaccg ccgcccctct gccaattgtg acccctttgc agtgacagaa 5640

gccatcgtcc gcacatgcct tctcaatgag actggcgacg agcccttcca atacaaaaac 5700

taagcgggac tctggggttc gaaatgaccg accaagcgac gcccaacctg ccatcacgag 5760

atttcgattc caccgccgcc ttctatgaaa ggttgggctt cggaatcgtt ttccgggacg 5820

ccggctggat gatcctccag cgcggggatc tcatgctgga gttcttcgcc caccccaact 5880

tgtttattgc agcttataat ggttacaaat aaagcaatag catcacaaat ttcacaaata 5940

aagcattttt ttcactgcat tctagttgtg gtttgtccaa actcatcaat gtatcttatc 6000

atgtctgtat accgtcgacc tctagctaga gcttggcgta atcatggtca tagctgtttc 6060

ctgtgtgaaa ttgttatccg ctcacaattc cacacaacat acgagccgga agcataaagt 6120

gtaaagcctg gggtgcctaa tgagtgagct aactcacatt aattgcgttg cgctcactgc 6180

ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcggc caacgcgcgg 6240

ggagaggcgg tttgcgtatt gggcgctctt ccgcttcctc gctcactgac tcgctgcgct 6300

cggtcgttcg gctgcggcga gcggtatcag ctcactcaaa ggcggtaata cggttatcca 6360

cagaatcagg ggataacgca ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga 6420

accgtaaaaa ggccgcgttg ctggcgtttt tccataggct ccgcccccct gacgagcatc 6480

acaaaaatcg acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg 6540

cgtttccccc tggaagctcc ctcgtgcgct ctcctgttcc gaccctgccg cttaccggat 6600

acctgtccgc ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt 6660

atctcagttc ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa cccccgttc 6720

agcccgaccg ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg 6780

acttatcgcc actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg 6840

gtgctacaga gttcttgaag tggtggccta actacggcta cactagaaga acagtatttg 6900

gtatctgcgc tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg 6960

gcaaacaaac caccgctggt agcggttttt ttgtttgcaa gcagcagatt acgcgcagaa 7020

aaaaaggatc tcaagaagat cctttgatct tttctacggg gtctgacgct cagtggaacg 7080

aaaactcacg ttaagggatt ttggtcatga gattatcaaa aaggatcttc acctagatcc 7140

ttttaaatta aaaatgaagt tttaaatcaa tctaaagtat atatgagtaa acttggtctg 7200

acagttacca atgcttaatc agtgaggcac ctatctcagc gatctgtcta tttcgttcat 7260

ccatagttgc ctgactcccc gtcgtgtaga taactacgat acgggagggc ttaccatctg 7320

gccccagtgc tgcaatgata ccgcgagacc cacgctcacc ggctccagat ttatcagcaa 7380

taaaccagcc agccggaagg gccgagcgca gaagtggtcc tgcaacttta tccgcctcca 7440

tccagtctat taattgttgc cgggaagcta gagtaagtag ttcgccagtt aatagtttgc 7500

gcaacgttgt tgccattgct acaggcatcg tggtgtcacg ctcgtcgttt ggtatggctt 7560

cattcagctc cggttcccaa cgatcaaggc gagttacatg atcccccatg ttgtgcaaaa 7620

aagcggttag ctccttcggt cctccgatcg ttgtcagaag taagttggcc gcagtgttat 7680

cactcatggt tatggcagca ctgcataatt ctcttactgt catgccatcc gtaagatgct 7740

tttctgtgac tggtgagtac tcaaccaagt cattctgaga atagtgtatg cggcgaccga 7800

gttgctcttg cccggcgtca atacgggata ataccgcgcc acatagcaga actttaaaag 7860

tgctcatcat tggaaaacgt tcttcggggc gaaaactctc aaggatctta ccgctgttga 7920

gatccagttc gatgtaaccc actcgtgcac ccaactgatc ttcagcatct tttactttca 7980

ccagcgtttc tgggtgagca aaaacaggaa ggcaaaatgc cgcaaaaaag ggaataaggg 8040

cgacacggaa atgttgaata ctcatactct tccttttca atattattga agcatttatc 8100

agggttattg tctcatgagc ggatacatat ttgaatgtat ttagaaaaat aaacaaatag 8160

gggttccgcg cacatttccc cgaaaagtgc cacctgacgt c 8201

<210> 6
<211> 588
<212> DNA
<213> Artificial Sequence

<220>
<223> CMV Promoter

<400> 6
gttgacattg attattgact agttattaat agtaatcaat tacggggtca ttagttcata 60

gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc 120

ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180

ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgcccac ttggcagtac 240

atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg 300

cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360

tattagtcat cgctattacc atggtgatgc ggttttggca gtacatcaat gggcgtggat 420

agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt 480

tttggcacca aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc 540

aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctc 588

<210> 7
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain of antibody GA101 (LC 1-729)

<400> 7

atggacatga gggtccctgc tcagctcctg gggctcctgc tgctctggct ctcaggtgcc 60

agatgtgaca ttgtaatgac acagacccca ctctccctgc ccgtcacccc tggagagccg 120

gcctccatct cctgcaggtc tagtaagagc ctcctgcata gtaatggaat cacctatttg 180

tactggtacc tgcagaagcc agggcagtct ccacagctcc tgatctatca gatgtctaat 240

ctggtgtccg gggtccctga caggttcagt ggcagtggat caggcacaga ttttacactg 300

aaaatcagca gagtggaggc tgaggatgtt ggggtttatt actgcgccca aaacctagag 360

ctgccctaca ctttcggcgg agggaccaag gtggagatca aacgtaccgt ggcggcgcca 420

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 480

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 540

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 600

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 660

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 720

tgttagtag 729

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild type Internal Ribosome Entry Site

<400> 8
atgataatat ggccacaacc 20

<210> 9
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain of antibody GA101 (HC 1329-2747)

<400> 9
atggagtttg ggctgagctg ggttttcctc gttgctcttt ttagaggtgt ccagtgtcag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg ggtcctccgt gaaggtctcc 120

tgcaaggcct ctggatacgc cttctcctac tcttggatca actgggtgcg acaggcccct 180

ggacaagggc tcgagtggat gggacggatc ttccctggcg atggtgacac agactacaac 240

ggcaagttca agggcagagt caccatcacc gccgacaagt ccacgagcac agcctacatg 300

gaactgagca gcctgagatc tgaggacacg gccgtctatt actgtgcacg aaacgtgttc 360

gatggctatt ggctggtgta ctggggccag gggaccctgg tcaccgtcag cagcgctagc 420

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcatggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 720

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 840

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 960

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1080

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1140

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1200

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1320

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380

agcctctccc tgtctccggg taaatga 1407

<210> 10
<211> 232
<212> DNA

<213> Artificial Sequence

<220>
<223> Bovine Growth Hormone Polyadenylation signal (BGH pA)

<400> 10
tgtgccttct aggcggccgc ttgccagcca tctgttgttt gcccctcccc cgtgccttcc 60

ttgaccctgg aaggtgccac tcccactgtc ctttcctaat aaaatgagga attgcatcg 120

cattgtctga gtaggtgtca ttctattctg gggggtgggg tggggcagga cagcaagggg 180

gaggattggg aagacaatag caggcatgct ggggatgcgg tgggctctat gg 232

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 promoter

<400> 11
ctgtggaatg tgtgtca 17

<210> 12
<211> 1122
<212> DNA
<213> Artificial Sequence

<220>
<223> Glutamine Synthetase (GS); Wild Type Glutamine Synthetase from CHO cell

<400> 12
atggccacct cagcaagttc ccacttgaac aaaaacatca agcaaatgta cttgtgcctg 60

ccccagggtg agaaagtcca agccatgtat atctgggttg atggtactgg agaaggactg 120

cgctgcaaaa cccgcaccct ggactgtgag cccaagtgtg tagaagagtt acctgagtgg 180

aattttgatg gctctagtac ctttcagtct gagggctcca acagtgacat gtatctcagc 240

cctgttgcca tgtttcggga ccccttccgc agagatccca acaagctggt gttctgtgaa 300

gttttcaagt acaaccggaa gcctgcagag accaatttaa ggcactcgtg taaacggata 360

atggacatgg tgagcaacca gcacccctgg tttggaatgg aacaggagta tactctgatg 420

ggaacagatg ggcacccttt tggttggcct tccaatggct ttcctgggcc ccaaggtccg 480

tattactgtg gtgtgggcgc agacaaagcc tatggcaggg atatcgtgga ggctcactac 540

cgcgcctgct tgtatgctgg ggtcaagatt acaggaacaa atgctgaggt catgcctgcc 600

cagtgggaat tccaaatagg accctgtgaa ggaatccgca tgggagatca tctctgggtg 660

gcccgtttca tcttgcatcg agtatgtgaa gactttgggg taatagcaac ctttgacccc 720

aagcccattc ctgggaactg gaatggtgca ggctgccata ccaactttag caccaaggcc 780

atgcgggagg agaatggtct gaagcacatc gaggaggcca tcgagaaact aagcaagcgg 840

caccggtacc acattcgagc ctacgatccc aaggggggcc tggacaatgc ccgtcgtctg 900

actgggttcc acgaaacgtc caacatcaac gacttttctg ctggtgtcgc caatcgcagt 960

gccagcatcc gcattccccg gactgtcggc caggagaaga aaggttactt tgaagaccgc 1020

cgcccctctg ccaattgtga ccccttgca gtgacagaag ccatcgtccg cacatgcctt 1080

ctcaatgaga ctggcgacga gcccttccaa tacaaaaact aa 1122

<210> 13
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 pA terminator sequence (SV40pA)

<400> 13
acttgtttat tgcagcttat aatggttaca ataaagcaa tagcatcaca aatttcacaa 60

ataaagcatt tttttcactg cattctagtt gtggtttgtc caaactcatc aatgtatctt 120

atcatgtctg 130

<210> 14
<211> 7985
<212> DNA
<213> Artificial Sequence

<220>
<223> Tricistronic mAb GS

<400> 14
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg 60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac tcgagtcctt agggagcgat ccagcacgag gagaggccgg gaggggcgg 660

gacggggcgg ggcctctggg agagtgggtt gcggggaggc tggcttttgg caggaagtaa 720

cgcatttgct ggactcgagt gatgcggttt tggcagtaca tcaatgggcg tggatagcgg 780

tttgactcac ggggatttcc aagtctccac cccattgacg tcaatgggag tttgttttgg 840

caccaaaatc aacgggactt tccaaaatgt cgtaacaact ccgccccatt gacgcaaatg 900

ggcggtaggc gtgtacggtg ggaggtctat ataagcagag ctctctggct agcgtttaaa 960

cttaagcttg gtaccgagct cggatccaga attcgccaca atggacatga gggtccctgc 1020

tcagctcctg gggctcctgc tgctctggct ctcaggtgcc agatgtgaca ttgtaatgac 1080

acagacccca ctctccctgc ccgtcacccc tggagagccg gcctccatct cctgcaggtc 1140

tagtaagagc ctcctgcata gtaatggaat cacctatttg tactggtacc tgcagaagcc 1200

agggcagtct ccacagctcc tgatctatca gatgtctaat ctggtgtccg gggtccctga 1260

caggttcagt ggcagtggat caggcacaga ttttacactg aaaatcagca gagtggaggc 1320

tgaggatgtt ggggtttatt actgcgccca aaacctagag ctgccctaca ctttcggcgg 1380

agggaccaag gtggagatca aacgtaccgt ggcggcgcca tctgtcttca tcttcccgcc 1440

atctgatgag cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta 1500

tcccagagag gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca 1560

ggagagtgtc acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac 1620

gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg 1680

cctgagctcg cccgtcacaa agagcttcaa caggggagag tgttagtagg atatcgtcta 1740

gacccctctc cctccccccc ccctaacgtt actggccgaa gccgcttgga ataaggccgg 1800

tgtgcgtttg tctatatgtt attttccacc atattgccgt cttttggcaa tgtgagggcc 1860

cggaaacctg gccctgtctt cttgacgagc attcctaggg gtctttcccc tctcgccaaa 1920

ggaatgcaag gtctgttgaa tgtcgtgaag gaagcagttc ctctggaagc ttcttgaaga 1980

caaacaacgt ctgtagcgac cctttgcagg cagcggaacc ccccacctgg cgacaggtgc 2040

ctctgcggcc aaaagccacg tgtataagat acacctgcaa aggcggcaca accccagtgc 2100

cacgttgtga gttggatagt tgtggaaaga gtcaaatggc tctcctcaag cgtattcaac 2160

aaggggctga aggatgccca gaaggtaccc cattgtatgg gatctgatct ggggcctcgg 2220

tacacatgct ttacatgtgt ttagtcgagg ttaaaaaaac gtctaggccc cccgaaccac 2280

ggggacgtgg ttttcctttg aaaaacacga tgataatatg gccacaacca tggagtttgg 2340

gctgagctgg gttttcctcg ttgctctttt tagaggtgtc cagtgtcagg tgcagctggt 2400

gcagtctggg gctgaggtga agaagcctgg gtcctccgtg aaggtctcct gcaaggcctc 2460

tggatacgcc ttctcctact cttggatcaa ctgggtgcga caggcccctg gacaagggct 2520

cgagtggatg ggacggatct tccctggcga tggtgacaca gactacaacg gcaagttcaa 2580

gggcagagtc accatcaccg ccgacaagtc cacgagcaca gcctacatgg aactgagcag 2640

cctgagatct gaggacacgg ccgtctatta ctgtgcacga aacgtgttcg atggctattg 2700

gctggtgtac tggggccagg ggaccctggt caccgtcagc agcgctagca ccaagggccc 2760

atcggtcttc cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg 2820

ctgcctggtc aaggactact tccccgaacc ggtgacggtg tcatggaact caggcgccct 2880

gaccagcggc gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag 2940

cagcgtggtg accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa 3000

tcacaagccc agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac 3060

tcacacatgc ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt 3120

ccccccaaaa cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt 3180

ggtggacgtg agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga 3240

ggtgcataat gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt 3300

cagcgtcctc accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt 3360

ctccaacaaa gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc 3420

ccgagaacca caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt 3480

cagcctgacc tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag 3540

caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc 3600

cttcttcctc tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt 3660

ctcatgctcc gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct 3720

gtctccgggt aaatgaatcg atgcctgcag gtggccggcc acaccggtgc ccctctccct 3780

ccccccccccc taacgttact ggccgaagcc gcttggaata aggccggtgt gcgtttgtct 3840

atatgttatt ttccaccata ttgccgtctt ttggcaatgt gagggcccgg aaacctggcc 3900

ctgtcttctt gacgagcatt cctaggggtc tttcccctct cgccaaagga atgcaaggtc 3960

tgttgaatgt cgtgaaggaa gcagttcctc tggaagcttc ttgaagacaa acaacgtctg 4020

tagcgaccct ttgcaggcag cggaaccccc cacctggcga caggtgcctc tgcggccaaa 4080

agccacgtgt ataagataca cctgcaaagg cggcacaacc ccagtgccac gttgtgagtt 4140

ggatagttgt ggaaagagtc aaatggctct cctcaagcgt attcaacaag gggctgaagg 4200

atgcccagaa ggtaccccat tgtatgggat ctgatctggg gcctcggtac acatgcttta 4260

catgtgttta gtcgaggtta aaaaaacgtc taggcccccc gaaccacggg gacgtggttt 4320

tcctttgaaa aacacgatga taagcttgcc acaaccccgg gagatgagga tcgtttcgca 4380

tggccacctc agcaagttcc cacttgaaca aaaacatcaa gcaaatgtac ttgtgcctgc 4440

cccagggtga gaaagtccaa gccatgtata tctgggttga tggtactgga gaaggactgc 4500

gctgcaaaac ccgcaccctg gactgtgagc ccaagtgtgt agaagagtta cctgagtgga 4560

attttgatgg ctctagtacc tttcagtctg agggctccaa cagtgacatg tatctcagcc 4620

ctgttgccat gtttcgggac cccttccgca gagatcccaa caagctggtg ttctgtgaag 4680

ttttcaagta caaccggaag cctgcagaga ccaatttaag gcactcgtgt aaacggataa 4740

tggacatggt gagcaaccag cacccctggt ttggaatgga acaggagtat actctgatgg 4800

gaacagatgg gcacccttttt ggttggcctt ccaatggctt tcctgggccc caaggtccgt 4860

attactgtgg tgtgggcgca gacaaagcct atggcaggga tatcgtggag gctcactacc 4920

gcgcctgctt gtatgctggg gtcaagatta caggaacaaa tgctgaggtc atgcctgccc 4980

agtgggaatt ccaaatagga ccctgtgaag gaatccgcat gggagatcat ctctgggtgg 5040

cccgtttcat cttgcatcga gtatgtgaag actttggggt aatagcaacc tttgacccca 5100

agcccattcc tgggaactgg aatggtgcag gctgccatac caactttagc accaaggcca 5160

tgcgggagga gaatggtctg aagcacatcg aggaggccat cgagaaacta agcaagcggc 5220

accggtacca cattcgagcc tacgatccca agggggggcct ggacaatgcc cgtcgtctga 5280

ctgggttcca cgaaacgtcc aacatcaacg acttttctgc tggtgtcgcc aatcgcagtg 5340

ccagcatccg cattccccgg actgtcggcc aggagaagaa aggttacttt gaagaccgcc 5400

gcccctctgc caattgtgac ccctttgcag tgacagaagc catcgtccgc acatgccttc 5460

tcaatgagac tggcgacgag cccttccaat acaaaaacta attcgaaatg accgaccaag 5520

cgacgcccaa cctgccatca cgagatttcg attccaccgc cgccttctat gaaaggttgg 5580

gcttcggaat cgttttccgg gacgccggct ggatgatcct ccagcgcggg gatctcatgc 5640

tggagttctt cgcccacccc aacttgttta ttgcagctta taatggttac aaataaagca 5700

atagcatcac aaatttcaca aataaagcat ttttttcact gcattctagt tgtggtttgt 5760

ccaaactcat caatgtatct tatcatgtct gtataccgtc gacctctagc tagagcttgg 5820

cgtaatcatg gtcatagctg tttcctgtgt gaaattgtta tccgctcaca attccacaca 5880

acatacgagc cggaagcata aagtgtaaag cctggcgcgc ctaatgagtg agctaactca 5940

cattaattgc gttgcgctca ctgcccgctt tccagtcggg aaacctgtcg tgccagctgc 6000

attaatgaat cggcgatcgc gcggggagag gcggtttgcg tattgggcgc tcttccgctt 6060

cctcgctcac tgactcgctg cgctcggtcg ttcggctgcg gcgagcggta tcagctcact 6120

caaaggcggt aatacggtta tccacagaat caggggataa cgcaggaaag aacatgtgag 6180

caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc gttgctggcg tttttccata 6240

ggctccgccc ccctgacgag catcacaaaa atcgacgctc aagtcagagg tggcgaaacc 6300

cgacaggact ataaagatac caggcgtttc cccctggaag ctccctcgtg cgctctcctg 6360

ttccgaccct gccgcttacc ggatacctgt ccgcctttct cccttcggga agcgtggcgc 6420

tttctcatag ctcacgctgt aggtatctca gttcggtgta ggtcgttcgc tccaagctgg 6480

gctgtgtgca cgaacccccc gttcagcccg accgctgcgc cttatccggt aactatcgtc 6540

ttgagtccaa cccggtaaga cacgacttat cgccactggc agcagccact ggtaacagga 6600

ttagcagagc gaggtatgta ggcggtgcta cagagttctt gaagtggtgg cctaactacg 6660

gctacactag aagaacagta tttggtatct gcgctctgct gaagccagtt accttcggaa 6720

aaagagttgg tagctcttga tccggcaaac aaaccaccgc tggtagcggt ttttttgttt 6780

gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta 6840

cggggtctga cgctcagtgg aacgaaaact cacgttaagg gattttggtc atgagattat 6900

caaaaaggat cttcacctag atccttttaa attaaaaatg aagttttaaa tcaatctaaa 6960

gtatatatga gtaaacttgg tctgacagtt accaatgctt aatcagtgag gcacctatct 7020

cagcgatctg tctatttcgt tcatccatag ttgcctgact ccccgtcgtg tagataacta 7080

cgatacggga gggcttacca tctggcccca gtgctgcaat gataccgcga gacccacgct 7140

caccggctcc agatttatca gcaataaacc agccagccgg aagggccgag cgcagaagtg 7200

gtcctgcaac tttatccgcc tccatccagt ctattaattg ttgccgggaa gctagagtaa 7260

gtagttcgcc agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt 7320

cacgctcgtc gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta 7380

catgatcccc catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg atcgttgtca 7440

gaagtaagtt ggccgcagtg ttatcactca tggttatggc agcactgcat aattctctta 7500

ctgtcatgcc atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct 7560

gagaatagtg tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg 7620

cgccacatag cagaacttta aaagtgctca tcattggaaa acgttcttcg gggcgaaaac 7680

tctcaaggat cttaccgctg ttgagatcca gttcgatgta acccactcgt gcacccaact 7740

gatcttcagc atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa 7800

atgccgcaaa aaagggaata agggcgacac ggaaatgttg aatactcata ctcttccttt 7860

ttcaatatta ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat 7920

gtatttagaa aaataaacaa ataggggttc cgcgcacatt tccccgaaaa gtgccacctg 7980

acgtc 7985

<210> 15
<211> 712
<212> DNA
<213> Artificial Sequence

<220>
<223> CMV Promoter

<400> 15
gttgacattg attattgact agttattaat agtaatcaat tacggggtca ttagttcata 60

gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc 120

ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180

ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgcccac ttggcagtac 240

atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg 300

cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360

tattagtcat cgctattact cgagtcctta gggagcgatc cagcacgagg agaggccggg 420

agggggcggg acggggcggg gcctctggga gagtgggttg cggggaggct ggcttttggc 480

aggaagtaac gcatttgctg gactcgagtg atgcggtttt ggcagtacat caatgggcgt 540

ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt caatgggagt 600

ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactc cgccccattg 660

acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc tc 712

<210> 16
<211> 128
<212> DNA
<213> Artificial Sequence

<220>
<223> Part of hamster’s Aprt (Adenine phosphoribosyltransferase) exon2 complementary strand

<400> 16
tcgagtcctt agggagcgat ccagcacgag gagaggccgg gaggggggcgg gacggggcgg 60

ggcctctggg agagtgggtt gcggggaggc tggcttttgg caggaagtaa cgcatttgct 120

ggactcga 128

<210> 17
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Multiple Cloning Site (MCS)

<400> 17
gctagcgttt aaacttaagc ttggtaccga gctcggatcc a 41

<210> 18
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain of antibody GA101 (LC 1-729)

<400> 18
atggacatga gggtccctgc tcagctcctg gggctcctgc tgctctggct ctcaggtgcc 60

agatgtgaca ttgtaatgac acagacccca ctctccctgc ccgtcacccc tggagagccg 120

gcctccatct cctgcaggtc tagtaagagc ctcctgcata gtaatggaat cacctatttg 180

tactggtacc tgcagaagcc agggcagtct ccacagctcc tgatctatca gatgtctaat 240

ctggtgtccg gggtccctga caggttcagt ggcagtggat caggcacaga ttttacactg 300

aaaatcagca gagtggaggc tgaggatgtt ggggtttatt actgcgccca aaacctagag 360

ctgccctaca ctttcggcgg agggaccaag gtggagatca aacgtaccgt ggcggcgcca 420

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 480

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 540

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 600

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 660

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 720

tgttagtag 729

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild type Internal Ribosome Entry Site

<400> 19
atgataatat ggccacaacc 20

<210> 20
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain of antibody GA101 (HC 1329-2747)

<400> 20
atggagtttg ggctgagctg ggttttcctc gttgctcttt ttagaggtgt ccagtgtcag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg ggtcctccgt gaaggtctcc 120

tgcaaggcct ctggatacgc cttctcctac tcttggatca actgggtgcg acaggcccct 180

ggacaagggc tcgagtggat gggacggatc ttccctggcg atggtgacac agactacaac 240

ggcaagttca agggcagagt caccatcacc gccgacaagt ccacgagcac agcctacatg 300

gaactgagca gcctgagatc tgaggacacg gccgtctatt actgtgcacg aaacgtgttc 360

gatggctatt ggctggtgta ctggggccag gggaccctgg tcaccgtcag cagcgctagc 420

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcatggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 720

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 840

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 960

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1080

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1140

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1200

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1320

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380

agcctctccc tgtctccggg taaatga 1407

<210> 21
<211> 594
<212> DNA
<213> Artificial Sequence

<220>
<223> Attenuated Internal Ribosome Entry Site (IRESatt)

<400> 21
accggtgccc ctctccctcc ccccccccta acgttactgg ccgaagccgc ttggaataag 60

gccggtgtgc gtttgtctat atgttatttt ccaccatatt gccgtctttt ggcaatgtga 120

gggcccggaa acctggccct gtcttcttga cgagcattcc taggggtctt tcccctctcg 180

ccaaaggaat gcaaggtctg ttgaatgtcg tgaaggaagc agttcctctg gaagcttctt 240

gaagacaaac aacgtctgta gcgacccttt gcaggcagcg gaaccccca cctggcgaca 300

ggtgcctctg cggccaaaag ccacgtgtat aagatacacc tgcaaaggcg gcacaacccc 360

agtgccacgt tgtgagttgg atagttgtgg aaagagtcaa atggctctcc tcaagcgtat 420

tcaacaaggg gctgaaggat gcccagaagg taccccattg tatgggatct gatctggggc 480

ctcggtacac atgctttaca tgtgtttagt cgaggttaaa aaaacgtcta ggccccccga 540

accacgggga cgtggttttc ctttgaaaaa cacgatgata agcttgccac aacc 594

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Attenuation stretch

<400> 22
ccgggagatg aggatcgttt cgc 23

<210> 23
<211> 1122
<212> DNA
<213> Artificial Sequence

<220>
<223> Glutamine Synthetase (GS); Wild Type Glutamine Synthetase from CHO cell

<400> 23
atggccacct cagcaagttc ccacttgaac aaaaacatca agcaaatgta cttgtgcctg 60

ccccagggtg agaaagtcca agccatgtat atctgggttg atggtactgg agaaggactg 120

cgctgcaaaa cccgcaccct ggactgtgag cccaagtgtg tagaagagtt acctgagtgg 180

aattttgatg gctctagtac ctttcagtct gagggctcca acagtgacat gtatctcagc 240

cctgttgcca tgtttcggga ccccttccgc agagatccca acaagctggt gttctgtgaa 300

gttttcaagt acaaccggaa gcctgcagag accaatttaa ggcactcgtg taaacggata 360

atggacatgg tgagcaacca gcacccctgg tttggaatgg aacaggagta tactctgatg 420

ggaacagatg ggcacccttt tggttggcct tccaatggct ttcctgggcc ccaaggtccg 480

tattactgtg gtgtgggcgc agacaaagcc tatggcaggg atatcgtgga ggctcactac 540

cgcgcctgct tgtatgctgg ggtcaagatt acaggaacaa atgctgaggt catgcctgcc 600

cagtgggaat tccaaatagg accctgtgaa ggaatccgca tgggagatca tctctgggtg 660

gcccgtttca tcttgcatcg agtatgtgaa gactttgggg taatagcaac ctttgacccc 720

aagcccattc ctgggaactg gaatggtgca ggctgccata ccaactttag caccaaggcc 780

atgcgggagg agaatggtct gaagcacatc gaggaggcca tcgagaaact aagcaagcgg 840

caccggtacc acattcgagc ctacgatccc aaggggggcc tggacaatgc ccgtcgtctg 900

actgggttcc acgaaacgtc caacatcaac gacttttctg ctggtgtcgc caatcgcagt 960

gccagcatcc gcattccccg gactgtcggc caggagaaga aaggttactt tgaagaccgc 1020

cgcccctctg ccaattgtga ccccttgca gtgacagaag ccatcgtccg cacatgcctt 1080

ctcaatgaga ctggcgacga gcccttccaa tacaaaaact aa 1122

<210> 24
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> pcDNA sequence between neo and SV40pA

<400> 24
ttcgaaatga ccgaccaagc gacgcccaac ctgccatcac gagatttcga ttccaccgcc 60

gccttctatg aaaggttggg cttcggaatc gttttccggg acgccggctg gatgatcctc 120

cagcgcgggg atctcatgct ggagttcttc gcccacccc 159

<210> 25
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 pA terminator sequence (SV40pA)

<400> 25
aacttgttta ttgcagctta taatggttac aaataaagca atagcatcac aaatttcaca 60

aataaagcat ttttttcact gcattctagt tgtggtttgt ccaaactcat caatgtatct 120

tatcatgtct g 131

<210> 26
<211> 382
<212> DNA
<213> Artificial Sequence

<220>
<223> Corresponding region with pcDNA3.1

<400> 26
tataccgtcg acctctagct agagcttggc gtaatcatgg tcatagctgt ttcctgtgtg 60

aaattgttat ccgctcacaa ttccacacaa catacgagcc ggaagcataa agtgtaaagc 120

ctggcgcgcc taatgagtga gctaactcac attaattgcg ttgcgctcac tgcccgcttt 180

ccagtcggga aacctgtcgt gccagctgca ttaatgaatc ggcgatcgcg cggggagagg 240

cggtttgcgt attgggcgct cttccgcttc ctcgctcact gactcgctgc gctcggtcgt 300

tcggctgcgg cgagcggtat cagctcactc aaaggcggta atacggttat ccacagaatc 360

aggggataac gcaggaaaga ac 382

<210> 27
<211> 671
<212> DNA
<213> Artificial Sequence

<220>
<223> pUC origin

<400> 27
atgtgagcaa aaggccagca aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt 60

ttccataggc tccgcccccc tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg 120

cgaaacccga caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc 180

tctcctgttc cgaccctgcc gcttaccgga tacctgtccg cctttctccc ttcgggaagc 240

gtggcgcttt ctcatagctc acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc 300

aagctgggct gtgtgcacga acccccccgtt cagcccgacc gctgcgcctt atccggtaac 360

tatcgtcttg agtccaaccc ggtaagacac gacttatcgc cactggcagc agccactggt 420

aacaggatta gcagagcgag gtatgtaggc ggtgctacag agttcttgaa gtggtggcct 480

aactacggct acactagaag aacagtattt ggtatctgcg ctctgctgaa gccagttacc 540

ttcggaaaaa gagttggtag ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtttt 600

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 660

ttttctacgg g 671

<210> 28
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Corresponding region with pcDNA3.1

<400> 28
gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatga gattatcaaa 60

aaggatcttc acctagatcc ttttaaatta aaaatgaagt tttaaatcaa tctaaagtat 120

atatgagtaa acttggtctg acag 144

<210> 29
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> Ampicillin (Amp) resistance gene on complementary strand

<400> 29
ttaccaatgc ttaatcagtg aggcacctat ctcagcgatc tgtctatttc gttcatccat 60

agttgcctga ctccccgtcg tgtagataac tacgatacgg gagggcttac catctggccc 120

cagtgctgca atgataccgc gagacccacg ctcaccggct ccagatttat cagcaataaa 180

ccagccagcc ggaagggccg agcgcagaag tggtcctgca actttatccg cctccatcca 240

gtctattaat tgttgccggg aagctagagt aagtagttcg ccagttaata gtttgcgcaa 300

cgttgttgcc attgctacag gcatcgtggt gtcacgctcg tcgtttggta tggcttcatt 360

cagctccggt tcccaacgat caaggcgagt tacatgatcc cccatgttgt gcaaaaaagc 420

ggttagctcc ttcggtcctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact 480

catggttatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgcttttc 540

tgtgactggt gagtactcaa ccaagtcatt ctgagaatag tgtatgcggc gaccgagttg 600

ctcttgcccg gcgtcaatac gggataatac cgcgccacat agcagaactt taaaagtgct 660

catcattgga aaacgttctt cggggcgaaa actctcaagg atcttaccgc tgttgagatc 720

cagttcgatg taacccactc gtgcacccaa ctgatcttca gcatctttta ctttcaccag 780

cgtttctggg tgagcaaaaa caggaaggca aaatgccgca aaaaagggaa taagggcgac 840

acggaaatgt tgaatactca t 861

<210> 30
<211> 136
<212> DNA
<213> Artificial Sequence

<220>
<223> beta-Lactamase (bla) promoter

<400> 30
actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata 60

catatttgaa tgtatttaga aaaataaaca aatagggttt ccgcgcacat ttccccgaaa 120

agtgccacct gacgtc 136

<210> 31
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSsmaUP

<400> 31
gtgtgacccg ggagatgagg atcgtttcgc atggccacct cagcaagttc ccacttg 57

<210> 32
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSBstBILP

<400> 32
gaattcttcg aattagtttt tgtattcgaa gggctcgtcg cc 42

<210> 33
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSSMASV4UP

<400> 33
gtgctcccgg gagcttgtat atccattttc ggatctgatc aagagacagg atgaggatcg 60

gccaccatgg ccacctcagc aagttcccac ttgaac 96

<210> 34
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSBSTBISV4LP

<400> 34
ggtcatttcg aaccccagag tcccgcttag tttttgtatt ggaagggctc gtcg 54

<210> 35
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R324CFP

<400> 35
cgcagtgcca gcatctgcat tccccggact gtcggc 36

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

<220>
<223> primer R324CLP

<400> 36
gccgacagtc cggggaatgc agatgctggc actgcg 36

<210> 37
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R341CFP

<400> 37
ggttactttg aagaccgctg cccctctgcc aattgtgac 39

<210> 38
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R341CLP

<400> 38
gtcacaattg gcagaggggc agcggtcttc aaagtaacc 39

<210> 39
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R324AUP

<400> 39
cgcagtgcca gcatcgccat tccccggact gtc 33

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R324ALP

<400> 40
gacagtccgg ggaatggcga tgctggcact gcg 33

<210> 41
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R341AUP

<400> 41
tactttgaag accgcgcccc ctctgccaat tgt 33

<210> 42
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer R341ALP

<400> 42
acaattggca gaggggcgc ggtcttcaaa gta 33

<210> 43
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM1 UP

<400> 43
cctgagtgga attttgctgg ctctagtacc tttcag 36

<210> 44
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM1 LP

<400> 44
ctgaaaggta ctagtgccag caaaattcca ctcagg 36

<210> 45
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM2 UP

<400> 45
tggaattttg atggctctgc tacctttcag tctgagggc 39

<210> 46
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM2 LP

<400> 46
gccctcagac tgaaaggtag cagagccatc aaaattcca 39

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM4 UP

<400> 47
caccctggt ttggaatggc acaggagtat actctg 36

<210> 48
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM4 LP

<400> 48
cagagtatac tcctgtgcca ttccaaacca ggggtg 36

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM5 UP

<400> 49
tggtttggaa tggaacaggc gtatactctg atgggaaca 39

<210> 50
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM5 LP

<400> 50
tgttcccatc agagtatacg cctgttccat tccaaacca 39

<210> 51
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM6 UP

<400> 51
ccccaaggtc cgtatgcctg tggtgtgggc gcagac 36

<210> 52
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM6 LP

<400> 52
gtctgcgccc acaccacagg catacggacc ttgggg 36

<210> 53
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM8 UP

<400> 53
ggggtcaaga ttacagcaac aaatgctgag gtc 33

<210> 54
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM8 LP

<400> 54
gacctcagca tttgttgctg taatcttgac ccc 33

<210> 55
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM9 UP

<400> 55
acaggaacaa atgctgcggt catgcctgcc cag 33

<210> 56
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> primer GSM9 LP

<400> 56
ctgggcaggc atgaccgcag catttgttcc tgt 33

<210> 57
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM10 UP

<400> 57
atgcctgccc agtgggcatt ccaaatagga ccc 33

<210> 58
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM10 LP

<400> 58
gggtcctatt tggaatgccc actgggcagg cat 33

<210> 59
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM12 UP

<400> 59
attcctggga actgggcagg tgcaggctgc catacc 36

<210> 60
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM12 LP

<400> 60
ggtatggcag cctgcacctg cccagttccc aggaat 36

<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM13 UP

<400> 61
cctgggaact ggaatgctgc aggctgccat acc 33

<210> 62
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM13 LP

<400> 62
ggtatggcag cctgcagcat tccagttccc agg 33

<210> 63
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM14 UP

<400> 63
aatggtgcag gctgcgcaac caactttagc acc 33

<210> 64
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM14 LP

<400> 64
ggtgctaaag ttggttgcgc agcctgcacc att 33

<210> 65
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM15 UP

<400> 65
gcaggctgcc ataccgcatt tagcaccaag gcc 33

<210> 66
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM15 LP

<400> 66
ggccttggtg ctaaatgcgg tatggcagcc tgc 33

<210> 67
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM16 UP

<400> 67
ggctgccata ccaactttgc aaccaaggcc atgcgg 36

<210> 68
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM16 LP

<400> 68
ccgcatggcc ttggttgcaa agttggtatg gcagcc 36

<210> 69
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM17 UP

<400> 69
agcaccaagg ccatggcgga ggagaatggt ctg 33

<210> 70
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM17 LP

<400> 70
cagaccattc tcctccgcca tggccttggt gct 33

<210> 71
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM18 UP

<400> 71
ctggacaatg cccgtgctct gactgggttc cac 33

<210> 72
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM18 LP

<400> 72
gtggaaccca gtcagagcac gggcattgtc cag 33

<210> 73
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM19 UP

<400> 73
ctgactgggt tccacgcaac gtccaacatc aac 33

<210> 74
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM19 LP

<400> 74
gttgatgttg gacgttgcgt ggaacccagt cag 33

<210> 75
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM20 UP

<400> 75
gctggtgtcg ccaatgccag tgccagcatc cgc 33

<210> 76
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM20 LP

<400> 76
gcggatgctg gcactggcat tggcgacacc agc 33

<210> 77
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM21 UP

<400> 77
caggagaaga aaggtgcttt tgaagaccgc cgc 33

<210> 78
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM21 LP

<400> 78
gcggcggtct tcaaaagcac ctttcttctc ctg 33

<210> 79
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM22 UP

<400> 79
aagaaaggtt actttgcaga ccgccgcccc tctgcc 36

<210> 80
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM22 LP

<400> 80
ggcagagggg cggcggtctg caaagtaacc tttctt 36

<210> 81
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> primer GSM23 UP

<400> 81
actgtcggcc aggaggcgaa aggttacttt gaa 33

<210> 82
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM23 LP

<400> 82
ttcaaagtaa cctttcgcct cctggccgac agt 33

<210> 83
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM24 UP

<400> 83
ggttactttg aagacgcccg cccctctgcc aat 33

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer GSM24 LP

<400> 84
attggcagag gggcgggcgt cttcaaagta acc 33

<210> 85
<211> 7985
<212> DNA
<213> Artificial Sequence

<220>
<223> Tricistronic GA101 GS R324C

<400> 85
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg 60

ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac tcgagtcctt agggagcgat ccagcacgag gagaggccgg gaggggcgg 660

gacggggcgg ggcctctggg agagtgggtt gcggggaggc tggcttttgg caggaagtaa 720

cgcatttgct ggactcgagt gatgcggttt tggcagtaca tcaatgggcg tggatagcgg 780

tttgactcac ggggatttcc aagtctccac cccattgacg tcaatgggag tttgttttgg 840

caccaaaatc aacgggactt tccaaaatgt cgtaacaact ccgccccatt gacgcaaatg 900

ggcggtaggc gtgtacggtg ggaggtctat ataagcagag ctctctggct agcgtttaaa 960

cttaagcttg gtaccgagct cggatccaga attcgccaca atggacatga gggtccctgc 1020

tcagctcctg gggctcctgc tgctctggct ctcaggtgcc agatgtgaca ttgtaatgac 1080

acagacccca ctctccctgc ccgtcacccc tggagagccg gcctccatct cctgcaggtc 1140

tagtaagagc ctcctgcata gtaatggaat cacctatttg tactggtacc tgcagaagcc 1200

agggcagtct ccacagctcc tgatctatca gatgtctaat ctggtgtccg gggtccctga 1260

caggttcagt ggcagtggat caggcacaga ttttacactg aaaatcagca gagtggaggc 1320

tgaggatgtt ggggtttatt actgcgccca aaacctagag ctgccctaca ctttcggcgg 1380

agggaccaag gtggagatca aacgtaccgt ggcggcgcca tctgtcttca tcttcccgcc 1440

atctgatgag cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta 1500

tcccagagag gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca 1560

ggagagtgtc acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac 1620

gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg 1680

cctgagctcg cccgtcacaa agagcttcaa caggggagag tgttagtagg atatcgtcta 1740

gacccctctc cctccccccc ccctaacgtt actggccgaa gccgcttgga ataaggccgg 1800

tgtgcgtttg tctatatgtt attttccacc atattgccgt cttttggcaa tgtgagggcc 1860

cggaaacctg gccctgtctt cttgacgagc attcctaggg gtctttcccc tctcgccaaa 1920

ggaatgcaag gtctgttgaa tgtcgtgaag gaagcagttc ctctggaagc ttcttgaaga 1980

caaacaacgt ctgtagcgac cctttgcagg cagcggaacc ccccacctgg cgacaggtgc 2040

ctctgcggcc aaaagccacg tgtataagat acacctgcaa aggcggcaca accccagtgc 2100

cacgttgtga gttggatagt tgtggaaaga gtcaaatggc tctcctcaag cgtattcaac 2160

aaggggctga aggatgccca gaaggtaccc cattgtatgg gatctgatct ggggcctcgg 2220

tacacatgct ttacatgtgt ttagtcgagg ttaaaaaaac gtctaggccc cccgaaccac 2280

ggggacgtgg ttttcctttg aaaaacacga tgataatatg gccacaacca tggagtttgg 2340

gctgagctgg gttttcctcg ttgctctttt tagaggtgtc cagtgtcagg tgcagctggt 2400

gcagtctggg gctgaggtga agaagcctgg gtcctccgtg aaggtctcct gcaaggcctc 2460

tggatacgcc ttctcctact cttggatcaa ctgggtgcga caggcccctg gacaagggct 2520

cgagtggatg ggacggatct tccctggcga tggtgacaca gactacaacg gcaagttcaa 2580

gggcagagtc accatcaccg ccgacaagtc cacgagcaca gcctacatgg aactgagcag 2640

cctgagatct gaggacacgg ccgtctatta ctgtgcacga aacgtgttcg atggctattg 2700

gctggtgtac tggggccagg ggaccctggt caccgtcagc agcgctagca ccaagggccc 2760

atcggtcttc cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg 2820

ctgcctggtc aaggactact tccccgaacc ggtgacggtg tcatggaact caggcgccct 2880

gaccagcggc gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag 2940

cagcgtggtg accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa 3000

tcacaagccc agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac 3060

tcacacatgc ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt 3120

ccccccaaaa cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt 3180

ggtggacgtg agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga 3240

ggtgcataat gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt 3300

cagcgtcctc accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt 3360

ctccaacaaa gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc 3420

ccgagaacca caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt 3480

cagcctgacc tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag 3540

caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc 3600

cttcttcctc tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt 3660

ctcatgctcc gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct 3720

gtctccgggt aaatgaatcg atgcctgcag gtggccggcc acaccggtgc ccctctccct 3780

ccccccccccc taacgttact ggccgaagcc gcttggaata aggccggtgt gcgtttgtct 3840

atatgttatt ttccaccata ttgccgtctt ttggcaatgt gagggcccgg aaacctggcc 3900

ctgtcttctt gacgagcatt cctaggggtc tttcccctct cgccaaagga atgcaaggtc 3960

tgttgaatgt cgtgaaggaa gcagttcctc tggaagcttc ttgaagacaa acaacgtctg 4020

tagcgaccct ttgcaggcag cggaaccccc cacctggcga caggtgcctc tgcggccaaa 4080

agccacgtgt ataagataca cctgcaaagg cggcacaacc ccagtgccac gttgtgagtt 4140

ggatagttgt ggaaagagtc aaatggctct cctcaagcgt attcaacaag gggctgaagg 4200

atgcccagaa ggtaccccat tgtatgggat ctgatctggg gcctcggtac acatgcttta 4260

catgtgttta gtcgaggtta aaaaaacgtc taggcccccc gaaccacggg gacgtggttt 4320

tcctttgaaa aacacgatga taagcttgcc acaaccccgg gagatgagga tcgtttcgca 4380

tggccacctc agcaagttcc cacttgaaca aaaacatcaa gcaaatgtac ttgtgcctgc 4440

cccagggtga gaaagtccaa gccatgtata tctgggttga tggtactgga gaaggactgc 4500

gctgcaaaac ccgcaccctg gactgtgagc ccaagtgtgt agaagagtta cctgagtgga 4560

attttgatgg ctctagtacc tttcagtctg agggctccaa cagtgacatg tatctcagcc 4620

ctgttgccat gtttcgggac cccttccgca gagatcccaa caagctggtg ttctgtgaag 4680

ttttcaagta caaccggaag cctgcagaga ccaatttaag gcactcgtgt aaacggataa 4740

tggacatggt gagcaaccag cacccctggt ttggaatgga acaggagtat actctgatgg 4800

gaacagatgg gcacccttttt ggttggcctt ccaatggctt tcctgggccc caaggtccgt 4860

attactgtgg tgtgggcgca gacaaagcct atggcaggga tatcgtggag gctcactacc 4920

gcgcctgctt gtatgctggg gtcaagatta caggaacaaa tgctgaggtc atgcctgccc 4980

agtgggaatt ccaaatagga ccctgtgaag gaatccgcat gggagatcat ctctgggtgg 5040

cccgtttcat cttgcatcga gtatgtgaag actttggggt aatagcaacc tttgacccca 5100

agcccattcc tgggaactgg aatggtgcag gctgccatac caactttagc accaaggcca 5160

tgcgggagga gaatggtctg aagcacatcg aggaggccat cgagaaacta agcaagcggc 5220

accggtacca cattcgagcc tacgatccca agggggggcct ggacaatgcc cgtcgtctga 5280

ctgggttcca cgaaacgtcc aacatcaacg acttttctgc tggtgtcgcc aatcgcagtg 5340

ccagcatctg cattccccgg actgtcggcc aggagaagaa aggttacttt gaagaccgcc 5400

gcccctctgc caattgtgac ccctttgcag tgacagaagc catcgtccgc acatgccttc 5460

tcaatgagac tggcgacgag cccttccaat acaaaaacta attcgaaatg accgaccaag 5520

cgacgcccaa cctgccatca cgagatttcg attccaccgc cgccttctat gaaaggttgg 5580

gcttcggaat cgttttccgg gacgccggct ggatgatcct ccagcgcggg gatctcatgc 5640

tggagttctt cgcccacccc aacttgttta ttgcagctta taatggttac aaataaagca 5700

atagcatcac aaatttcaca aataaagcat ttttttcact gcattctagt tgtggtttgt 5760

ccaaactcat caatgtatct tatcatgtct gtataccgtc gacctctagc tagagcttgg 5820

cgtaatcatg gtcatagctg tttcctgtgt gaaattgtta tccgctcaca attccacaca 5880

acatacgagc cggaagcata aagtgtaaag cctggcgcgc ctaatgagtg agctaactca 5940

cattaattgc gttgcgctca ctgcccgctt tccagtcggg aaacctgtcg tgccagctgc 6000

attaatgaat cggcgatcgc gcggggagag gcggtttgcg tattgggcgc tcttccgctt 6060

cctcgctcac tgactcgctg cgctcggtcg ttcggctgcg gcgagcggta tcagctcact 6120

caaaggcggt aatacggtta tccacagaat caggggataa cgcaggaaag aacatgtgag 6180

caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc gttgctggcg tttttccata 6240

ggctccgccc ccctgacgag catcacaaaa atcgacgctc aagtcagagg tggcgaaacc 6300

cgacaggact ataaagatac caggcgtttc cccctggaag ctccctcgtg cgctctcctg 6360

ttccgaccct gccgcttacc ggatacctgt ccgcctttct cccttcggga agcgtggcgc 6420

tttctcatag ctcacgctgt aggtatctca gttcggtgta ggtcgttcgc tccaagctgg 6480

gctgtgtgca cgaacccccc gttcagcccg accgctgcgc cttatccggt aactatcgtc 6540

ttgagtccaa cccggtaaga cacgacttat cgccactggc agcagccact ggtaacagga 6600

ttagcagagc gaggtatgta ggcggtgcta cagagttctt gaagtggtgg cctaactacg 6660

gctacactag aagaacagta tttggtatct gcgctctgct gaagccagtt accttcggaa 6720

aaagagttgg tagctcttga tccggcaaac aaaccaccgc tggtagcggt ttttttgttt 6780

gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta 6840

cggggtctga cgctcagtgg aacgaaaact cacgttaagg gattttggtc atgagattat 6900

caaaaaggat cttcacctag atccttttaa attaaaaatg aagttttaaa tcaatctaaa 6960

gtatatatga gtaaacttgg tctgacagtt accaatgctt aatcagtgag gcacctatct 7020

cagcgatctg tctatttcgt tcatccatag ttgcctgact ccccgtcgtg tagataacta 7080

cgatacggga gggcttacca tctggcccca gtgctgcaat gataccgcga gacccacgct 7140

caccggctcc agatttatca gcaataaacc agccagccgg aagggccgag cgcagaagtg 7200

gtcctgcaac tttatccgcc tccatccagt ctattaattg ttgccgggaa gctagagtaa 7260

gtagttcgcc agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt 7320

cacgctcgtc gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta 7380

catgatcccc catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg atcgttgtca 7440

gaagtaagtt ggccgcagtg ttatcactca tggttatggc agcactgcat aattctctta 7500

ctgtcatgcc atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct 7560

gagaatagtg tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg 7620

cgccacatag cagaacttta aaagtgctca tcattggaaa acgttcttcg gggcgaaaac 7680

tctcaaggat cttaccgctg ttgagatcca gttcgatgta acccactcgt gcacccaact 7740

gatcttcagc atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa 7800

atgccgcaaa aaagggaata agggcgacac ggaaatgttg aatactcata ctcttccttt 7860

ttcaatatta ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat 7920

gtatttagaa aaataaacaa atagggggttc cgcgcacatt tccccgaaaa gtgccacctg 7980

acgtc 7985

<210> 86
<211> 128
<212> DNA
<213> Artificial Sequence

<220>
<223> Part of hamster’s Aprt (Adenine phosphoribosyltransferase) exon2 complementary strand

<400> 86
tcgagtcctt agggagcgat ccagcacgag gagaggccgg gaggggcgg gacggggcgg 60

ggcctctggg agagtgggtt gcggggaggc tggcttttgg caggaagtaa cgcatttgct 120

ggactcga 128

<210> 87
<211> 205
<212> DNA
<213> Artificial Sequence

<220>
<223> Second portion of CMV promoter

<400> 87
gtgatgcggt tttggcagta catcaatggg cgtggatagc ggtttgactc acggggattt 60

ccaagtctcc accccattga cgtcaatggg agtttgtttt ggcaccaaaa tcaacgggac 120

tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa tgggcggtag gcgtgtacgg 180

tgggaggtct atataagcag agctc 205

<210> 88
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Multiple Cloning Site (MCS)

<400> 88
gctagcgttt aaacttaagc ttggtaccga gctcggatcc a 41

<210> 89
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain of antibody GA101 (LC 1-729)

<400> 89
atggacatga gggtccctgc tcagctcctg gggctcctgc tgctctggct ctcaggtgcc 60

agatgtgaca ttgtaatgac acagacccca ctctccctgc ccgtcacccc tggagagccg 120

gcctccatct cctgcaggtc tagtaagagc ctcctgcata gtaatggaat cacctatttg 180

tactggtacc tgcagaagcc agggcagtct ccacagctcc tgatctatca gatgtctaat 240

ctggtgtccg gggtccctga caggttcagt ggcagtggat caggcacaga ttttacactg 300

aaaatcagca gagtggaggc tgaggatgtt ggggtttatt actgcgccca aaacctagag 360

ctgccctaca ctttcggcgg agggaccaag gtggagatca aacgtaccgt ggcggcgcca 420

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 480

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 540

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 600

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 660

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 720

tgttagtag 729

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild type Internal Ribosome Entry Site (IRES)

<400> 90
atgataatat ggccacaacc 20

<210> 91
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain of antibody GA101 (HC 1329-2747)

<400> 91
atggagtttg ggctgagctg ggttttcctc gttgctcttt ttagaggtgt ccagtgtcag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg ggtcctccgt gaaggtctcc 120

tgcaaggcct ctggatacgc cttctcctac tcttggatca actgggtgcg acaggcccct 180

ggacaagggc tcgagtggat gggacggatc ttccctggcg atggtgacac agactacaac 240

ggcaagttca agggcagagt caccatcacc gccgacaagt ccacgagcac agcctacatg 300

gaactgagca gcctgagatc tgaggacacg gccgtctatt actgtgcacg aaacgtgttc 360

gatggctatt ggctggtgta ctggggccag gggaccctgg tcaccgtcag cagcgctagc 420

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcatggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 720

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 840

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 960

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1080

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1140

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1200

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1320

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380

agcctctccc tgtctccggg taaatga 1407

<210> 92
<211> 594
<212> DNA
<213> Artificial Sequence

<220>
<223> Attenuated Internal Ribosome Entry Site (attIRES)

<400> 92
accggtgccc ctctccctcc ccccccccta acgttactgg ccgaagccgc ttggaataag 60

gccggtgtgc gtttgtctat atgttatttt ccaccatatt gccgtctttt ggcaatgtga 120

gggcccggaa acctggccct gtcttcttga cgagcattcc taggggtctt tcccctctcg 180

ccaaaggaat gcaaggtctg ttgaatgtcg tgaaggaagc agttcctctg gaagcttctt 240

gaagacaaac aacgtctgta gcgacccttt gcaggcagcg gaaccccca cctggcgaca 300

ggtgcctctg cggccaaaag ccacgtgtat aagatacacc tgcaaaggcg gcacaacccc 360

agtgccacgt tgtgagttgg atagttgtgg aaagagtcaa atggctctcc tcaagcgtat 420

tcaacaaggg gctgaaggat gcccagaagg taccccattg tatgggatct gatctggggc 480

ctcggtacac atgctttaca tgtgtttagt cgaggttaaa aaaacgtcta ggccccccga 540

accacgggga cgtggttttc ctttgaaaaa cacgatgata agcttgccac aacc 594

<210> 93
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Attenuation stretch

<400> 93
ccgggagatg aggatcgttt cgc 23

<210> 94
<211> 1122
<212> DNA
<213> Artificial Sequence

<220>
<223> Glutamine Synthetase (GS) having R324C mutation

<400> 94
atggccacct cagcaagttc ccacttgaac aaaaacatca agcaaatgta cttgtgcctg 60

ccccagggtg agaaagtcca agccatgtat atctgggttg atggtactgg agaaggactg 120

cgctgcaaaa cccgcaccct ggactgtgag cccaagtgtg tagaagagtt acctgagtgg 180

aattttgatg gctctagtac ctttcagtct gagggctcca acagtgacat gtatctcagc 240

cctgttgcca tgtttcggga ccccttccgc agagatccca acaagctggt gttctgtgaa 300

gttttcaagt acaaccggaa gcctgcagag accaatttaa ggcactcgtg taaacggata 360

atggacatgg tgagcaacca gcacccctgg tttggaatgg aacaggagta tactctgatg 420

ggaacagatg ggcacccttt tggttggcct tccaatggct ttcctgggcc ccaaggtccg 480

tattactgtg gtgtgggcgc agacaaagcc tatggcaggg atatcgtgga ggctcactac 540

cgcgcctgct tgtatgctgg ggtcaagatt acaggaacaa atgctgaggt catgcctgcc 600

cagtgggaat tccaaatagg accctgtgaa ggaatccgca tgggagatca tctctgggtg 660

gcccgtttca tcttgcatcg agtatgtgaa gactttgggg taatagcaac ctttgacccc 720

aagcccattc ctgggaactg gaatggtgca ggctgccata ccaactttag caccaaggcc 780

atgcgggagg agaatggtct gaagcacatc gaggaggcca tcgagaaact aagcaagcgg 840

caccggtacc acattcgagc ctacgatccc aaggggggcc tggacaatgc ccgtcgtctg 900

actgggttcc acgaaacgtc caacatcaac gacttttctg ctggtgtcgc caatcgcagt 960

gccagcatct gcattccccg gactgtcggc caggagaaga aaggttactt tgaagaccgc 1020

cgcccctctg ccaattgtga ccccttttgca gtgacagaag ccatcgtccg cacatgcctt 1080

ctcaatgaga ctggcgacga gcccttccaa tacaaaaact aa 1122

<210> 95
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> pcDNA sequence between neo and SV40pA

<400> 95
ttcgaaatga ccgaccaagc gacgcccaac ctgccatcac gagatttcga ttccaccgcc 60

gccttctatg aaaggttggg cttcggaatc gttttccggg acgccggctg gatgatcctc 120

cagcgcgggg atctcatgct ggagttcttc gcccacccc 159

<210> 96
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 pA terminator sequence (SV40pA)

<400> 96
aacttgttta ttgcagctta taatggttac aaataaagca atagcatcac aaatttcaca 60

aataaagcat ttttttcact gcattctagt tgtggtttgt ccaaactcat caatgtatct 120

tatcatgtct g 131

<210> 97
<211> 382
<212> DNA
<213> Artificial Sequence

<220>
<223> Corresponding region with pcDNA3.1

<400> 97
tataccgtcg acctctagct agagcttggc gtaatcatgg tcatagctgt ttcctgtgtg 60

aaattgttat ccgctcacaa ttccacacaa catacgagcc ggaagcataa agtgtaaagc 120

ctggcgcgcc taatgagtga gctaactcac attaattgcg ttgcgctcac tgcccgcttt 180

ccagtcggga aacctgtcgt gccagctgca ttaatgaatc ggcgatcgcg cggggagagg 240

cggtttgcgt attgggcgct cttccgcttc ctcgctcact gactcgctgc gctcggtcgt 300

tcggctgcgg cgagcggtat cagctcactc aaaggcggta atacggttat ccacagaatc 360

aggggataac gcaggaaaga ac 382

<210> 98
<211> 671
<212> DNA
<213> Artificial Sequence

<220>
<223> PUC origin

<400> 98
atgtgagcaa aaggccagca aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt 60

ttccataggc tccgcccccc tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg 120

cgaaacccga caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc 180

tctcctgttc cgaccctgcc gcttaccgga tacctgtccg cctttctccc ttcgggaagc 240

gtggcgcttt ctcatagctc acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc 300

aagctgggct gtgtgcacga acccccgtt cagcccgacc gctgcgcctt atccggtaac 360

tatcgtcttg agtccaaccc ggtaagacac gacttatcgc cactggcagc agccactggt 420

aacaggatta gcagagcgag gtatgtaggc ggtgctacag agttcttgaa gtggtggcct 480

aactacggct acactagaag aacagtattt ggtatctgcg ctctgctgaa gccagttacc 540

ttcggaaaaa gagttggtag ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtttt 600

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 660

ttttctacgg g 671

<210> 99
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Corresponding region with pcDNA3.1

<400> 99
gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatga gattatcaaa 60

aaggatcttc acctagatcc ttttaaatta aaaatgaagt tttaaatcaa tctaaagtat 120

atatgagtaa acttggtctg acag 144

<210> 100
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> Ampicillin (Amp) resistance gene on complementary strand

<400> 100
ttaccaatgc ttaatcagtg aggcacctat ctcagcgatc tgtctatttc gttcatccat 60

agttgcctga ctccccgtcg tgtagataac tacgatacgg gagggcttac catctggccc 120

cagtgctgca atgataccgc gagacccacg ctcaccggct ccagatttat cagcaataaa 180

ccagccagcc ggaagggccg agcgcagaag tggtcctgca actttatccg cctccatcca 240

gtctattaat tgttgccggg aagctagagt aagtagttcg ccagttaata gtttgcgcaa 300

cgttgttgcc attgctacag gcatcgtggt gtcacgctcg tcgtttggta tggcttcatt 360

cagctccggt tcccaacgat caaggcgagt tacatgatcc cccatgttgt gcaaaaaagc 420

ggttagctcc ttcggtcctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact 480

catggttatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgcttttc 540

tgtgactggt gagtactcaa ccaagtcatt ctgagaatag tgtatgcggc gaccgagttg 600

ctcttgcccg gcgtcaatac gggataatac cgcgccacat agcagaactt taaaagtgct 660

catcattgga aaacgttctt cggggcgaaa actctcaagg atcttaccgc tgttgagatc 720

cagttcgatg taacccactc gtgcacccaa ctgatcttca gcatctttta ctttcaccag 780

cgtttctggg tgagcaaaaa caggaaggca aaatgccgca aaaaagggaa taagggcgac 840

acggaaatgt tgaatactca t 861

<210> 101
<211> 136
<212> DNA
<213> Artificial Sequence

<220>
<223> beta-Lactamase (bla) promoter

<400> 101
actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata 60

catatttgaa tgtatttaga aaaataaaca aatagggttt ccgcgcacat ttccccgaaa 120

agtgccacct gacgtc 136

<210> 102
<211> 1122
<212> DNA
<213> Cricetulus griseus

<400> 102
atggccacct cagcaagttc ccacttgaac aaaggcatca agcaaatgta catgtccctg 60

ccccagggtg agaaagtcca agccatgtat atctgggttg atggtaccgg agaaggactg 120

cgctgcaaaa cccgcaccct ggactgtgag cccaagtgtg tagaagagtt acctgagtgg 180

aattttgatg gctctagtac ctttcagtct gagggctcca acagtgacat gtatctcagc 240

cctgttgcca tgtttcggga ccccttccgc aaagagccca acaagctggt gttctgtgaa 300

gtcttcaagt acaaccggaa gcctgcagag accaatttaa gacacacgtg taaacggata 360

atggacatgg tgagcaacca gcacccctgg tttggaatgg aacaggagta tactctcttg 420

ggaacagatg ggcacccttt tggttggcct tccgatggct tccctgggcc ccaaggtctg 480

tattactgtg gtgtgggcgc agacaaagcc tatcgcaggg atatcatgga ggctcactac 540

cttgcctgct tgtatgctgg ggtcaagatt acaggaacat atgctgaggt caagcatgcc 600

cagtgggaat tccaaatagg accctgtgaa ggaatccgca tgggagatca tctgtgggtg 660

gcccgtttca tcttgcatcg agtatgtaaa gactttgggg taatagcaac ctttgacccc 720

aagcccattc ctgggaactg gaatggtgca ggctgccata ccaactttag taccaagacc 780

atgcgggagg agaatggtct gaagcacatc aaggaggcca ttgagaaact aagcaagcgg 840

caccggtacc atattcgagc ctacgatccc aaggggggggc tggacaatgc ccgtcgtctg 900

actgggttcc acaaaacgtc caacatcaac gacttttcag ctggcgtcgc cgatcgcagt 960

gccagcatcc gcattccccg gactgtcggc caggagaaga aaggttactt tgaagcccgc 1020

tgcccctctg ccaattgtga ccccttgca gtgacagaag ccatcgtccg cacatgcctt 1080

ctcaatgaga ctggcgacga gcccttccaa tacaaaaact aa 1122

<210> 103
<211> 373
<212> PRT
<213> Cricetulus griseus

<400> 103

Met Ala Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Met
1 5 10 15

Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
20 25 30

Val Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
35 40 45

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

Ser Ser Thr Phe Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu Ser
65 70 75 80

Pro Val Ala Met Phe Arg Asp Pro Phe Arg Lys Glu Pro Asn Lys Leu
85 90 95

```
Val Phe Cys Glu Val Phe Lys Tyr Asn Arg Lys Pro Ala Glu Thr Asn
            100                 105                 110

Leu Arg His Thr Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
        115                 120                 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Leu Gly Thr Asp Gly
    130                 135                 140

His Pro Phe Gly Trp Pro Ser Asp Gly Phe Pro Gly Pro Gln Gly Leu
145                 150                 155                 160

Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala Tyr Arg Arg Asp Ile Met
                165                 170                 175

Glu Ala His Tyr Leu Ala Cys Leu Tyr Ala Gly Val Lys Ile Thr Gly
            180                 185                 190

Thr Tyr Ala Glu Val Lys His Ala Gln Trp Glu Phe Gln Ile Gly Pro
        195                 200                 205

Cys Glu Gly Ile Arg Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
    210                 215                 220

Leu His Arg Val Cys Lys Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
225                 230                 235                 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
                245                 250                 255

Ser Thr Lys Thr Met Arg Glu Glu Asn Gly Leu Lys His Ile Lys Glu
            260                 265                 270

Ala Ile Glu Lys Leu Ser Lys Arg His Arg Tyr His Ile Arg Ala Tyr
        275                 280                 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
```

```
    290                 295                 300

Lys Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asp Arg Ser
305                 310                 315                 320

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

Phe Glu Ala Arg Cys Pro Ser Ala Asn Cys Asp Pro Phe Ala Val Thr
            340                 345                 350

Glu Ala Ile Val Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
        355                 360                 365

Phe Gln Tyr Lys Asn
    370
```