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<120> ATTENUATED GLUTAMINE SYNTHETASE AS A SELECTION MARKER

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<151> 2016-11-16

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<170> PatentIn version 3.5

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Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
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Ser Glu Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
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Ser Ser Thr Leu Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu Val
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Pro Ala Ala Met Phe Arg Asp Pro Phe Arg Lys Asp Pro Asn Lys Leu
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Val Leu Cys Glu Val Phe Lys Tyr Asn Arg Arg Pro Ala Glu Thr Asn
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Leu Arg His Thr Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
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Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
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His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
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Tyr Tyr Cys Gly Val Gly Ala Asp Arg Ala Tyr Gly Arg Asp Ile Val
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Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Ala Gly
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Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
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Cys Glu Gly Ile Ser Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
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Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
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Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
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Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys Tyr Ile Glu Glu
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Ala Ile Glu Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
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Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
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Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
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Ala Ser Ile Arg Ile Pro Arg Thr Val Gly Gln Glu Lys Lys Gly Tyr
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Val Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
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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
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            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
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Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Thr Gly
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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
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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
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Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
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Ala Ser Ile Arg Ile Pro Arg Thr Val Gly Gln Glu Lys Lys Gly Tyr
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Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ala Val Thr
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Phe Gln Tyr Lys Asn
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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
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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
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Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
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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
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Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Tyr Ala Val Thr
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Phe Gln Tyr Lys Asn
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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
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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
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Cys Glu Gly Ile Arg Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
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Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
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Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
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Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Arg Cys Ile Glu Glu
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Ala Ile Asp Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
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        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
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<220>
<223> CMV Promoter

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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

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gcctccatct cctgcaggtc tagtaagagc ctcctgcata gtaatggaat cacctatttg 180

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tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 540

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agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 660

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tgttagtag 729

<210> 8
<211> 20
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<220>
<223> Wild type Internal Ribosome Entry Site

<400> 8
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<210> 9
<211> 1407
<212> DNA
<213> Artificial Sequence

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

<400> 9
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agcctctccc tgtctccggg taaatga 1407

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

<213> Artificial Sequence

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

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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
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ccccagggtg agaaagtcca agccatgtat atctgggttg atggtactgg agaaggactg 120

cgctgcaaaa cccgcaccct ggactgtgag cccaagtgtg tagaagagtt acctgagtgg 180

aattttgatg gctctagtac ctttcagtct gagggctcca acagtgacat gtatctcagc 240

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aagcccattc ctgggaactg gaatggtgca ggctgccata ccaactttag caccaaggcc 780

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ctcaatgaga ctggcgacga gcccttccaa tacaaaaact aa 1122

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<213> Artificial Sequence

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

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ataaagcatt tttttcactg cattctagtt gtggtttgtc caaactcatc aatgtatctt 120

atcatgtctg 130

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

<220>
<223> Tricistronic mAb GS

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

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gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

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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 ccccttttgca 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 aatagggggtt 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

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

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

<400> 89
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gcctccatct cctgcaggtc tagtaagagc ctcctgcata gtaatggaat cacctatttg 180

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aaaatcagca gagtggaggc tgaggatgtt ggggtttatt actgcgccca aaacctagag 360

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tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 540

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

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

<400> 92
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gccggtgtgc gtttgtctat atgttatttt ccaccatatt gccgtctttt ggcaatgtga 120

gggcccggaa acctggccct gtcttcttga cgagcattcc taggggtctt tcccctctcg 180

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ctcggtacac atgctttaca tgtgtttagt cgaggttaaa aaaacgtcta ggccccccga 540

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<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
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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

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cagtgggaat tccaaatagg accctgtgaa ggaatccgca tgggagatca tctctgggtg 660

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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
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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
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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
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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
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catatttgaa tgtatttaga aaaataaaca aatagggggtt ccgcgcacat ttccccgaaa 120

agtgccacct gacgtc 136

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

<400> 102
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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

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cttgcctgct tgtatgctgg ggtcaagatt acaggaacat atgctgaggt caagcatgcc 600

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gcccgtttca tcttgcatcg agtatgtaaa gactttgggg taatagcaac ctttgacccc 720

aagcccattc ctgggaactg gaatggtgca ggctgccata ccaactttag taccaagacc 780

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caccggtacc atattcgagc ctacgatccc aaggggggggc tggacaatgc ccgtcgtctg 900

actgggttcc acaaaacgtc caacatcaac gactttcag 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
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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

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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
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    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
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