SEQUENCE LISTING

<110> Sanofi

<120> Novel selection marker for cell transfection and protein production

<130> FR2014/014

<160> 4

<170> PatentIn version 3.5

<210> 1
<211> 1188
<212> DNA
<213> Cricetus cricetus

<400> 1
atggcttggc ggcagatgcg gaagagagcc ctggacgccg ctatcatcct gggaggcgga 60

ggcctgctgt tcacctctta cctgacagcc accggcgacg accacttcta cgccgagtac 120

ctgatgcctg ccctgcagag actgctggac cctgagtctg cccaccggct ggccatcaga 180

ttcacctccc tgggcctgct gcccagagcc accttccagg actccgacat gctggaagtg 240

cgggtgctgg gccacaagtt cagaaacccc gtgggaatcg ccgctggctt cgacaagcac 300

ggcgaggctg tggacggcct gtacaagctg ggcttcggct tcgtggaagt gggctccgtg 360

acaccccagc cccaggaagg caaccccaga cctagagtgt tccggctgcc tgaggaccag 420

gccgtgatca acagatacgg cttcaactcc cacggcctgt ccgtggtgga acaccggctg 480

agagccagac agcagaagca gaacaagctg accgccgacg gcctgcccct gggcatcaat 540

ctgggcaaga acaagacctc cgaggacgct gccgccgact acgtggaagg cgtgcgagtg 600

ctgggacctc tggccgatta cctggtcgtg aacgtgtcct cccccaacac cgctggcctg 660

agaagcctgc agggaaaggc cgagctgaga aggctgctgg ccaaggtgct gcaggaacgg 720

gacgctctga agggcgccca gaaacctgcc gtgctcgtga agatcgcccc tgacctgacc 780

gcccaggaca aagaggatat cgcctccgtg gccagagagc tgggcatcga cggactgatc 840

gtgaccaaca ccaccgtgtc tcggcctacc ggactgcagg gcgctctgag atctgagatg 900

ggcggcctgt ctggcaagcc tctgagggac ctgtccaccc agaccatcag agagatgtac 960

accctgaccc agggccggat ccccatcatt ggagtgggcg gagtgtcctc tggccaggac 1020

gccctggaaa agatccaggc tggcgcctct ctggtgcagc tgtataccgc cctgaccttt 1080

ctgggccctc ccgtggtggt gcgagtgaag agagaactgg aagccctgct gaaagagcgg 1140

ggcttcaaca ccgtgaccga ggccatcggc gctgaccaca gaagatga 1188

<210> 2
<211> 395
<212> PRT
<213> Cricetus cricetus

<400> 2

Met Ala Trp Arg Gln Met Arg Lys Arg Ala Leu Asp Ala Ala Ile Ile

1 5 10 15

Leu Gly Gly Gly Gly Leu Leu Phe Thr Ser Tyr Leu Thr Ala Thr Gly
20 25 30

Asp Asp His Phe Tyr Ala Glu Tyr Leu Met Pro Ala Leu Gln Arg Leu
35 40 45

Leu Asp Pro Glu Ser Ala His Arg Leu Ala Ile Arg Phe Thr Ser Leu
50 55 60

Gly Leu Leu Pro Arg Ala Thr Phe Gln Asp Ser Asp Met Leu Glu Val
65 70 75 80

Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala Gly
85 90 95

Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Leu Gly Phe
100 105 110

Gly Phe Val Glu Val Gly Ser Val Thr Pro Gln Pro Gln Glu Gly Asn
115 120 125

Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile Asn
130 135 140

Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg Leu
145 150 155 160

Arg Ala Arg Gln Gln Lys Gln Asn Lys Leu Thr Ala Asp Gly Leu Pro
165 170 175

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

Asp Tyr Val Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr Leu
195 200 205

Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu Gln
210 215 220

Gly Lys Ala Glu Leu Arg Arg Leu Leu Ala Lys Val Leu Gln Glu Arg
225 230 235 240

Asp Ala Leu Lys Gly Ala Gln Lys Pro Ala Val Leu Val Lys Ile Ala
245 250 255

Pro Asp Leu Thr Ala Gln Asp Lys Glu Asp Ile Ala Ser Val Ala Arg
260 265 270

Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser Arg

275 280 285

Pro Thr Gly Leu Gln Gly Ala Leu Arg Ser Glu Met Gly Gly Leu Ser
290 295 300

Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met Tyr
305 310 315 320

Thr Leu Thr Gln Gly Arg Ile Pro Ile Ile Gly Val Gly Gly Val Ser
325 330 335

Ser Gly Gln Asp Ala Leu Glu Lys Ile Gln Ala Gly Ala Ser Leu Val
340 345 350

Gln Leu Tyr Thr Ala Leu Thr Phe Leu Gly Pro Pro Val Val Val Arg
355 360 365

Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Arg Gly Phe Asn Thr
370 375 380

Val Thr Glu Ala Ile Gly Ala Asp His Arg Arg
385 390 395

<210> 3
<211> 1188
<212> DNA
<213> Homo sapiens

<400> 3
atggcttggc ggcacctgaa gaagagggcc caggacgccg tgatcatcct gggaggcgga 60

ggcctgctgt tcgcctctta cctgatggct accggcgacg agcggttcta cgccgagcat 120

ctgatgccca cactgcaggg cctgctggac cctgagtctg cccatagact ggccgtgcgg 180

ttcacctccc tgggactgct gcctagagcc cggttccagg actccgacat gctggaagtg 240

cgggtgctgg gccacaagtt cagaaacccc gtgggaatcg ccgctggctt cgacaagcac 300

ggcgaggctg tggacggcct gtacaagatg ggcttcggct tcgtggaaat cggctccgtg 360

acccccaagc cccaggaagg caaccccaga cctcgggtgt tcagactgcc tgaggaccag 420

gctgtgatca acagatacgg cttcaactcc cacggcctgt ccgtggtgga acaccggctg 480

agagccagac agcagaagca ggccaagctg accgaggatg gcctgcctct gggagtgaac 540

ctgggcaaga acaagacctc cgtggacgcc gccgaggatt acgctgaagg cgtgcgagtg 600

ctgggacccc tggctgatta cctggtcgtg aacgtgtcct cccccaacac cgctggcctg 660

agatctctgc agggcaaggc cgagctgcgg agactgctga caaaggtgct gcaggaacgc 720

gacggcctgc ggagagtgca tagacctgcc gtgctcgtga agatcgcccc cgacctgacc 780

agccaggaca aagaggatat cgcctccgtc gtgaaagagc tgggcatcga cggactgatc 840

gtgaccaaca ccaccgtgtc taggcctgcc ggactgcagg gggctctgag atctgaaacc 900

ggcggactgt ccggcaagcc tctgagggat ctgtccaccc agaccatcag agagatgtac 960

gccctgaccc agggccgggt gccaatcatt ggagtgggcg gagtgtcctc cggccaggat 1020

gccctggaaa agatcagagc cggcgcttcc ctggtgcagc tgtacaccgc tctgaccttt 1080

tggggccctc ccgtcgtggg caaagtgaag agagagctgg aagccctgct gaaagagcag 1140

ggatttggcg gcgtgaccga tgccatcggc gctgaccaca gaagatga 1188

<210> 4
<211> 395
<212> PRT
<213> Homo sapiens

<400> 4

Met Ala Trp Arg His Leu Lys Lys Arg Ala Gln Asp Ala Val Ile Ile
1 5 10 15

Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr Gly
20 25 30

Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly Leu
35 40 45

Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser Leu
50 55 60

Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu Val
65 70 75 80

Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala Gly
85 90 95

Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly Phe
100 105 110

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

Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile Asn
130 135 140

Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg Leu
145 150 155 160

Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu Pro
165 170 175

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

Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr Leu
195 200 205

```
Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu Gln
    210                 215                 220

Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu Arg
225                 230                 235                 240

Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile Ala
                245                 250                 255

Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val Lys
            260                 265                 270

Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser Arg
        275                 280                 285

Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu Ser
    290                 295                 300

Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met Tyr
305                 310                 315                 320

Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val Ser
                325                 330                 335

Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu Val
            340                 345                 350

Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly Lys
        355                 360                 365

Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly Gly
    370                 375                 380

Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
385                 390                 395
```