eolf-seql
SEQUENCE LISTING

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<120> Means and methods for determination of Botulinum neurotoxin biological activity

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<170> PatentIn version 3.3

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Gly His  Phe Thr Leu Gly Cys  Val Leu Glu Glu Gln  Glu His Gln
   1070                1075                1080

Val Ala  Lys Glu Glu Arg Glu  Thr Pro Thr Thr Asp  Ser Met Pro
   1085                1090                1095

Pro Leu  Leu Lys Gln Ala Ile  Glu Leu Phe Asp Arg  Gln Gly Ala
   1100                1105                1110

Glu Pro  Ala Phe Leu Phe Gly  Leu Glu Leu Ile Ile  Cys Gly Leu
   1115                1120                1125

Glu Lys  Gln Leu Lys Cys Glu  Ser Gly Gly Pro Thr  Asp Ala Leu
   1130                1135                1140
```

Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp
1145 1150 1155

Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp
1160 1165 1170

Leu Asp Met Leu Pro Gly
1175

<210> 5
<211> 1725
<212> DNA
<213> artificial

<220>
<223> Cholinetransporter-SNAP25-tTA (1)(pCMV-Tet3G)

<400> 5
gaattcacca tggctttcca tgtggaagga ctgatagcta tcatcgtgtt ctaccttcta 60

attttgctgg ttggaatatg ggctgcctgg agaaccaaaa acagtggcag cgcagaagag 120

cgcagcgaag ccatcatagt tggtggccga gatattggtt tattggttgg tggatttacc 180

atgacagcta cctgggtcgg aggagggtat atcaatggca cagctgaagc agtttatgta 240

ccaggttatg gcctagcttg ggctcaggca ccaattggat attctcttag tctgatttta 300

ggtggcctgt tctttgcaaa acctatgcgt tcaaaggggt atgtgaccat gttagacccg 360

tttcagcaaa tctatggaaa acgcatgggc ggactcctgt ttattcctgc actgatggga 420

gaaatgttct gggctgcagc aattttctct gctttgggag ccaccatcag cgtgatcatc 480

gatgtggata tgcacatttc tgtcatcatc tctgcactca ttgccactct gtacacactg 540

gtgggagggc tctattctgt ggcctacact gatgtcgttc agctcttttg catttttgta 600

gggctgtgga tcagcgtccc ctttgcattg tcacatcctg cagtcgcaga catcgggttc 660

actgctgtgc atgccaaata ccaaaagccg tggctgggaa ctgttgactc atctgaagtc 720

tactcttggc ttgatagttt tctgttgttg atgctgggtg gaatcccatg gcaagcatac 780

tttcagaggg ttctctcttc ttcctcagcc acctatgctc aagtgctgtc cttcctggca 840

gctttcgggt gcctggtgat ggccatccca gccatactca ttggggccat tggagcatca 900

acagactgga accagactgc atatgggctt ccagatccca agactacaga agaggcagac 960

atgattttac caattgttct gcagtatctc tgccctgtgt atatttcttt ctttggtctt 1020

ggtgcagttt ctgctgctgt tatgtcatca gcagattctt ccatcttgtc agcaagttcc 1080

atgtttgcac ggaacatcta ccagctttcc ttcagacaaa atgcttcgga caaagaaatc 1140

gtttgggtta tgcgaatcac agtgtttgtg tttggagcat ctgcaacagc catggccttg 1200

ctgacgaaaa ctgtgtatgg gctctggtac ctcagttctg accttgttta catcgttatc 1260

ttcccccagc tgctttgtgt actctttgtt aagggaacca acacctatgg ggccgtggca 1320

ggttatgttt ctggcctctt cctgagaata actggagggg agccatatct gtatcttaac 1380

aagcttaaat caagtgatgc ttacaaaaaa gcctggggca ataatcagga cggagtggtg 1440

gccagccagc ctgctcgtgt agtggacgaa cgggagcaga tggccatcag tggcggcttc 1500

atccgcaggg taacaaatga tgcccgagaa aatgaaatgg atgaaaacct agagcaggtg 1560

agcggcatca tcgggaacct ccgtcacatg gccctggata tgggcaatga gatcgataca 1620

cagaatcgcc agatcgacag gatcatggag aaggctgatt ccaacaaaac cagaattgat 1680

gaggccaacc aacgtgcaac aaagatgctg ggaagtggtt ctaga 1725

<210> 6
<211> 817
<212> PRT
<213> artificial

<220>
<223> Cholinetransporter-SNAP25-tTA (1)(pCMV-Tet3G)

<400> 6

Met Ala Phe His Val Glu Gly Leu Ile Ala Ile Ile Val Phe Tyr Leu
1 5 10 15

Leu Ile Leu Leu Val Gly Ile Trp Ala Ala Trp Arg Thr Lys Asn Ser
20 25 30

Gly Ser Ala Glu Glu Arg Ser Glu Ala Ile Ile Val Gly Gly Arg Asp
35 40 45

Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
50 55 60

Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Val Pro Gly Tyr
65 70 75 80

Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
85 90 95

Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
100 105 110

Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
115 120 125

Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala
130 135 140

Ile Phe Ser Ala Leu Gly Ala Thr Ile Ser Val Ile Ile Asp Val Asp
145 150 155 160

Met His Ile Ser Val Ile Ile Ser Ala Leu Ile Ala Thr Leu Tyr Thr
165 170 175

Leu Val Gly Gly Leu Tyr Ser Val Ala Tyr Thr Asp Val Val Gln Leu

```
            180                 185                 190

Phe Cys Ile Phe Val Gly Leu Trp Ile Ser Val Pro Phe Ala Leu Ser
        195                 200                 205

His Pro Ala Val Ala Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr
    210                 215                 220

Gln Lys Pro Trp Leu Gly Thr Val Asp Ser Ser Glu Val Tyr Ser Trp
225                 230                 235                 240

Leu Asp Ser Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala
                245                 250                 255

Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val
            260                 265                 270

Leu Ser Phe Leu Ala Ala Phe Gly Cys Leu Val Met Ala Ile Pro Ala
        275                 280                 285

Ile Leu Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala
    290                 295                 300

Tyr Gly Leu Pro Asp Pro Lys Thr Thr Glu Glu Ala Asp Met Ile Leu
305                 310                 315                 320

Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly
                325                 330                 335

Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile
            340                 345                 350

Leu Ser Ala Ser Ser Met Phe Ala Arg Asn Ile Tyr Gln Leu Ser Phe
        355                 360                 365

Arg Gln Asn Ala Ser Asp Lys Glu Ile Val Trp Val Met Arg Ile Thr
    370                 375                 380

Val Phe Val Phe Gly Ala Ser Ala Thr Ala Met Ala Leu Leu Thr Lys
385                 390                 395                 400

Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Val
                405                 410                 415

Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Val Lys Gly Thr Asn Thr
            420                 425                 430

Tyr Gly Ala Val Ala Gly Tyr Val Ser Gly Leu Phe Leu Arg Ile Thr
        435                 440                 445

Gly Gly Glu Pro Tyr Leu Tyr Leu Asn Lys Leu Lys Ser Ser Asp Ala
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    450                 455                 460

Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln
465                 470                 475                 480

Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly
                485                 490                 495

Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp Glu
            500                 505                 510

Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg His Met Ala
        515                 520                 525

Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp Arg
    530                 535                 540

Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn
545                 550                 555                 560

Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ser Arg Leu Asp Lys Ser
                565                 570                 575

Lys Val Ile Asn Ser Ala Leu Glu Leu Leu Asn Gly Val Gly Ile Glu
            580                 585                 590

Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys Leu Gly Val Glu Gln Pro
        595                 600                 605

Thr Leu Tyr Trp His Val Lys Asn Lys Arg Ala Leu Leu Asp Ala Leu
    610                 615                 620

Pro Ile Glu Met Leu Asp Arg His His Thr His Ser Cys Pro Leu Glu
625                 630                 635                 640

Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn Asn Ala Lys Ser Tyr Arg
                645                 650                 655

Cys Ala Leu Leu Ser His Arg Asp Gly Ala Lys Val His Leu Gly Thr
            660                 665                 670

Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu Glu Asn Gln Leu Ala Phe
        675                 680                 685

Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn Ala Leu Tyr Ala Leu Ser
    690                 695                 700

Ala Val Gly His Phe Thr Leu Gly Cys Val Leu Glu Glu Gln Glu His
705                 710                 715                 720

Gln Val Ala Lys Glu Glu Arg Glu Thr Pro Thr Thr Asp Ser Met Pro
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eolf-seql

725 730 735

Pro Leu Leu Lys Gln Ala Ile Glu Leu Phe Asp Arg Gln Gly Ala Glu
740 745 750

Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile Ile Cys Gly Leu Glu Lys
755 760 765

Gln Leu Lys Cys Glu Ser Gly Gly Pro Thr Asp Ala Leu Asp Asp Phe
770 775 780

Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp
785 790 795 800

Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro
805 810 815

Gly

<210> 7
<211> 2370
<212> DNA
<213> artificial

<220>
<223> Cholinetransporter-SNAP25-tTA (3)(pCMV-Tet3G)

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cgcagcgaag ccatcatagt tggtggccga gatattggtt tattggttgg tggatttacc 180

atgacagcta cctgggtcgg aggagggtat atcaatggca cagctgaagc agtttatgta 240

ccaggttatg gcctagcttg ggctcaggca ccaattggat attctcttag tctgatttta 300

ggtggcctgt tctttgcaaa acctatgcgt tcaaaggggt atgtgaccat gttagacccg 360

tttcagcaaa tctatggaaa acgcatgggc ggactcctgt ttattcctgc actgatggga 420

gaaatgttct gggctgcagc aattttctct gctttgggag ccaccatcag cgtgatcatc 480

gatgtggata tgcacatttc tgtcatcatc tctgcactca ttgccactct gtacacactg 540

gtgggagggc tctattctgt ggcctacact gatgtcgttc agctcttttg catttttgta 600

gggctgtgga tcagcgtccc ctttgcattg tcacatcctg cagtcgcaga catcgggttc 660

actgctgtgc atgccaaata ccaaaagccg tggctgggaa ctgttgactc atctgaagtc 720

tactcttggc ttgatagttt tctgttgttg atgctgggtg gaatcccatg gcaagcatac 780

tttcagaggg ttctctcttc ttcctcagcc acctatgctc aagtgctgtc cttcctggca 840

gctttcgggt gcctggtgat ggccatccca gccatactca ttggggccat tggagcatca 900

acagactgga accagactgc atatgggctt ccagatccca agactacaga agaggcagac 960

atgattttac caattgttct gcagtatctc tgccctgtgt atatttcttt ctttggtctt 1020

ggtgcagttt ctgctgctgt tatgtcatca gcagattctt ccatcttgtc agcaagttcc 1080

atgtttgcac ggaacatcta ccagctttcc ttcagacaaa atgcttcgga caaagaaatc 1140

gtttgggtta tgcgaatcac agtgtttgtg tttggagcat ctgcaacagc catggccttg 1200

ctgacgaaaa ctgtgtatgg gctctggtac ctcagttctg accttgttta catcgttatc 1260

ttcccccagc tgctttgtgt actctttgtt aagggaacca acacctatgg ggccgtggca 1320

ggttatgttt ctggcctctt cctgagaata actggagggg agccatatct gtatcttcag 1380

cccttgatct tctaccctgg ctattaccct gatgataatg gtatatataa tcagaaattt 1440

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gccaagtatc tatttgaaag tggaaccttg ccacctaaat tagatgtatt tgatgctgtt 1560

gttgcaagac acagtgaaga aaacatggat aagacaattc ttgtcaaaaa tgaaaatatt 1620

aaattagatg aacttgcact tgtgaagcca cgacagagca tgaccctcag ctcaactttc 1680

accaataaag aggccttcct tgatgttgat tccagtccag aagggtctgg gactgaagat 1740

aatttacagg ccgaagacgc agacatgcgc aatgagctgg aggagatgca gcgaagggct 1800

gaccagttgg ctgatgagtc gctggaaagc acccgtcgta tgctgcaact ggttgaagag 1860

agtaaagatg ctggtatcag gactttggtt atgttggatg aacaaggaga acaactggaa 1920

cgcattgagg aagggatgga ccaaatcaat aaggacatga aagaagcaga aaagaatttg 1980

acggacctag gaaaattctg cgggctttgt gtgtgtccct gtaacaagct taaatcaagt 2040

gatgcttaca aaaaagcctg gggcaataat caggacggag tggtggccag ccagcctgct 2100

cgtgtagtgg acgaacggga gcagatggcc atcagtggcg gcttcatccg cagggtaaca 2160

aatgatgccc gagaaaatga aatggatgaa aacctagagc aggtgagcgg catcatcggg 2220

aacctccgtc acatggccct ggatatgggc aatgagatcg atacacagaa tcgccagatc 2280

gacaggatca tggagaaggc tgattccaac aaaaccagaa ttgatgaggc caaccaacgt 2340

gcaacaaaga tgctgggaag tggttctaga 2370

<210> 8
<211> 1032
<212> PRT
<213> artificial

<220>
<223> Cholinetransporter-SNAP25-tTA (3)(pCMV-Tet3G)

<400> 8

Met Ala Phe His Val Glu Gly Leu Ile Ala Ile Ile Val Phe Tyr Leu
1 5 10 15

Leu Ile Leu Leu Val Gly Ile Trp Ala Ala Trp Arg Thr Lys Asn Ser
20 25 30

Gly Ser Ala Glu Glu Arg Ser Glu Ala Ile Ile Val Gly Gly Arg Asp

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        35                  40                  45

Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
    50                  55                  60

Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Val Pro Gly Tyr
65                  70                  75                  80

Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
                85                  90                  95

Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
            100                 105                 110

Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
        115                 120                 125

Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala
    130                 135                 140

Ile Phe Ser Ala Leu Gly Ala Thr Ile Ser Val Ile Ile Asp Val Asp
145                 150                 155                 160

Met His Ile Ser Val Ile Ile Ser Ala Leu Ile Ala Thr Leu Tyr Thr
                165                 170                 175

Leu Val Gly Gly Leu Tyr Ser Val Ala Tyr Thr Asp Val Val Gln Leu
            180                 185                 190

Phe Cys Ile Phe Val Gly Leu Trp Ile Ser Val Pro Phe Ala Leu Ser
        195                 200                 205

His Pro Ala Val Ala Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr
    210                 215                 220

Gln Lys Pro Trp Leu Gly Thr Val Asp Ser Ser Glu Val Tyr Ser Trp
225                 230                 235                 240

Leu Asp Ser Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala
                245                 250                 255

Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val
            260                 265                 270

Leu Ser Phe Leu Ala Ala Phe Gly Cys Leu Val Met Ala Ile Pro Ala
        275                 280                 285

Ile Leu Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala
    290                 295                 300

Tyr Gly Leu Pro Asp Pro Lys Thr Thr Glu Glu Ala Asp Met Ile Leu
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305                 310                 315                 320

Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly
                325                 330                 335

Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile
            340                 345                 350

Leu Ser Ala Ser Ser Met Phe Ala Arg Asn Ile Tyr Gln Leu Ser Phe
        355                 360                 365

Arg Gln Asn Ala Ser Asp Lys Glu Ile Val Trp Val Met Arg Ile Thr
    370                 375                 380

Val Phe Val Phe Gly Ala Ser Ala Thr Ala Met Ala Leu Leu Thr Lys
385                 390                 395                 400

Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Val
                405                 410                 415

Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Val Lys Gly Thr Asn Thr
            420                 425                 430

Tyr Gly Ala Val Ala Gly Tyr Val Ser Gly Leu Phe Leu Arg Ile Thr
        435                 440                 445

Gly Gly Glu Pro Tyr Leu Tyr Leu Gln Pro Leu Ile Phe Tyr Pro Gly
    450                 455                 460

Tyr Tyr Pro Asp Asp Asn Gly Ile Tyr Asn Gln Lys Phe Pro Phe Lys
465                 470                 475                 480

Thr Leu Ala Met Val Thr Ser Phe Leu Thr Asn Ile Cys Ile Ser Tyr
                485                 490                 495

Leu Ala Lys Tyr Leu Phe Glu Ser Gly Thr Leu Pro Pro Lys Leu Asp
            500                 505                 510

Val Phe Asp Ala Val Val Ala Arg His Ser Glu Glu Asn Met Asp Lys
        515                 520                 525

Thr Ile Leu Val Lys Asn Glu Asn Ile Lys Leu Asp Glu Leu Ala Leu
    530                 535                 540

Val Lys Pro Arg Gln Ser Met Thr Leu Ser Ser Thr Phe Thr Asn Lys
545                 550                 555                 560

Glu Ala Phe Leu Asp Val Asp Ser Ser Pro Glu Gly Ser Gly Thr Glu
                565                 570                 575

Asp Asn Leu Gln Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu
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            580                 585                 590

Met Gln Arg Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr
        595                 600                 605

Arg Arg Met Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg
    610                 615                 620

Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu
625                 630                 635                 640

Glu Gly Met Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn
                645                 650                 655

Leu Thr Asp Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn
            660                 665                 670

Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln
        675                 680                 685

Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu
    690                 695                 700

Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala
705                 710                 715                 720

Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile
                725                 730                 735

Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr
            740                 745                 750

Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys
        755                 760                 765

Thr Arg Ile Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser
    770                 775                 780

Gly Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
785                 790                 795                 800

Leu Asn Gly Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
                805                 810                 815

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
            820                 825                 830

Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met Leu Asp Arg His His
        835                 840                 845

Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
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850 855 860

Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly
865 870 875 880

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
885 890 895

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
900 905 910

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
915 920 925

Val Leu Glu Glu Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
930 935 940

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu
945 950 955 960

Phe Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
965 970 975

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro
980 985 990

Thr Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala
995 1000 1005

Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp
1010 1015 1020

Asp Phe Asp Leu Asp Met Leu Pro Gly
1025 1030

<210> 9
<211> 603
<212> DNA
<213> artificial

<220>
<223> Synaptotagmin-SNAP25-tTA(pCMV-Tet3G)

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accaccgcca cgatgcccat tggacccgtg gacaactcca ctgagagtgg gggtgctggg 120

gagagccagg aggacatgtt tgccaaactg aaggagaagt tattcaatga gataaacaag 180

attcccttac caccctgggc actgatcgcc attgctgtgg ttgctgggct cctgcttctc 240

acctgctgct tctgcatcaa gcttaaatca agtgatgctt acaaaaaagc ctggggcaat 300

aatcaggacg gagtggtggc cagccagcct gctcgtgtag tggacgaacg ggagcagatg 360

gccatcagtg gcggcttcat ccgcagggta acaaatgatg cccgagaaaa tgaaatggat 420

gaaaacctag agcaggtgag cggcatcatc gggaacctcc gtcacatggc cctggatatg 480

ggcaatgaga tcgatacaca gaatcgccag atcgacagga tcatggagaa ggctgattcc 540

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aga 603

<210> 10
<211> 443
<212> PRT
<213> artificial

<220>
<223> Synaptotagmin-SNAP25-tTA(pCMV-Tet3G)

<400> 10

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Ile Gly Pro Val Asp Asn Ser Thr Glu
20 25 30

Ser Gly Gly Ala Gly Glu Ser Gln Glu Asp Met Phe Ala Lys Leu Lys
35 40 45

Glu Lys Leu Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro Trp Ala
50 55 60

Leu Ile Ala Ile Ala Val Val Ala Gly Leu Leu Leu Thr Cys Cys
65 70 75 80

Phe Cys Ile Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly
85 90 95

Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val Asp
100 105 110

Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Val Thr
115 120 125

Asn Asp Ala Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val Ser
130 135 140

Gly Ile Ile Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn Glu
145 150 155 160

Ile Asp Thr Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala Asp
165 170 175

Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln Arg Ala Thr Lys Met
180 185 190

Leu Gly Ser Gly Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala
195 200 205

Leu Glu Leu Leu Asn Gly Val Gly Ile Glu Gly Leu Thr Thr Arg Lys
210 215 220

Leu Ala Gln Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val
225 230 235 240

Lys Asn Lys Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met Leu Asp
245 250 255

Arg His His Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp
260 265 270

Phe Leu Arg Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His
275 280 285

Arg Asp Gly Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln
290 295 300

Tyr Glu Thr Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe
305 310 315 320

Ser Leu Glu Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr
325 330 335

Leu Gly Cys Val Leu Glu Glu Gln Glu His Gln Val Ala Lys Glu Glu
340 345 350

Arg Glu Thr Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Lys Gln Ala
355 360 365

Ile Glu Leu Phe Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly
370 375 380

Leu Glu Leu Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser
385 390 395 400

Gly Gly Pro Thr Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro
405 410 415

Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala
420 425 430

Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Gly
435 440

<210> 11
<211> 3600
<212> DNA

<213> artificial

<220>
<223> mAN02-SNAP25(pcDNA3.1)

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tgtgccgaca aagctcggga tggcgtctgt gatgaggcct gcaacagcca tgcctgccag 180

tgggatgggg gtgactgttc tctcaccatg gagaacccct gggccaactg ctcctcccca 240

cttccctgct gggattatat caacaaccag tgtgatgagc tgtgcaacac ggtcgagtgc 300

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gcagaccact tcaaagacaa ccactgtgac caggggtgca acagtgagga gtgtggttgg 420

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taccccctatt atggtgagaa gtcagctgct atgaagaaac agaggatgac acgcagatcc 660

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cgccagtgtg ttcaagactc agaccactgc ttcaagaaca cggatgcagc agcagctctc 780

ctggcctctc acgccataca ggggaccctg tcataccctc ttgtgtctgt cgtcagtgaa 840

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ctgtttatta ttctgctggg ggtaatcaac aagcttaaat caagtgatgc ttacaaaaaa 960

gcctggggca ataatcagga cggagtggtg gccagccagc ctgctcgtgt agtggacgaa 1020

cgggagcaga tggccatcag tggcggcttc atccgcaggg taacaaatga tgcccgagaa 1080

aatgaaatgg atgaaaacct agagcaggtg agcggcatca tcgggaacct ccgtcacatg 1140

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actcttcgcc gagatgcaag caatcacaag cgtcgtgagc cagtgggaca ggatgctgtg 1380

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gaacactggg tcgatgatga agggccccag ccaaagaaag taaaggctga agatgaggcc 1500

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ttgacttctg ctctctcacc tgtcatctgt gggcccaaca gatctttcct cagcctgaag 2460

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tggtcagatg tgaccaccag ccctacccct gggggtgctg gaggaggtca gcggggacct 3540

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<400> 12

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Thr Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg Asp Gly Val Cys
        35                  40                  45

Asp Glu Ala Cys Asn Ser His Ala Cys Gln Trp Asp Gly Gly Asp Cys
    50                  55                  60

Ser Leu Thr Met Glu Asn Pro Trp Ala Asn Cys Ser Ser Pro Leu Pro
65                  70                  75                  80

Cys Trp Asp Tyr Ile Asn Asn Gln Cys Asp Glu Leu Cys Asn Thr Val
                85                  90                  95

Glu Cys Leu Phe Asp Asn Phe Glu Cys Gln Gly Asn Ser Lys Thr Cys
            100                 105                 110

Lys Tyr Asp Lys Tyr Cys Ala Asp His Phe Lys Asp Asn His Cys Asp
        115                 120                 125

Gln Gly Cys Asn Ser Glu Glu Cys Gly Trp Asp Gly Leu Asp Cys Ala
    130                 135                 140

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

Leu Met Pro Pro Glu Gln Leu Leu Gln Asp Ala Arg Ser Phe Leu Arg
                165                 170                 175

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

Gln Gly Glu Leu Met Val Tyr Pro Tyr Tyr Gly Glu Lys Ser Ala Ala
        195                 200                 205

Met Lys Lys Gln Arg Met Thr Arg Arg Ser Leu Pro Gly Glu Gln Glu
    210                 215                 220

Gln Glu Val Ala Gly Ser Lys Val Phe Leu Glu Ile Asp Asn Arg Gln
225                 230                 235                 240

Cys Val Gln Asp Ser Asp His Cys Phe Lys Asn Thr Asp Ala Ala Ala
                245                 250                 255

Ala Leu Leu Ala Ser His Ala Ile Gln Gly Thr Leu Ser Tyr Pro Leu
            260                 265                 270
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Val Ser Val Val Ser Glu Ser Leu Thr Pro Glu Arg Thr Gln Leu Leu
        275                 280                 285

Tyr Leu Leu Ala Val Ala Val Val Ile Ile Leu Phe Ile Ile Leu Leu
    290                 295                 300

Gly Val Ile Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp
305                 310                 315                 320

Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val
                325                 330                 335

Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Val
            340                 345                 350

Thr Asn Asp Ala Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val
        355                 360                 365

Ser Gly Ile Ile Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn
    370                 375                 380

Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala
385                 390                 395                 400

Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln Arg Ala Thr Lys
                405                 410                 415

Met Leu Gly Ser Gly Met Ala Lys Arg Lys Arg Lys His Gly Ser Leu
            420                 425                 430

Trp Leu Pro Glu Gly Phe Thr Leu Arg Arg Asp Ala Ser Asn His Lys
        435                 440                 445

Arg Arg Glu Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser
    450                 455                 460

Val Gln Val Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His
465                 470                 475                 480

Trp Val Asp Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp
                485                 490                 495

Glu Ala Leu Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp
            500                 505                 510

Thr Gln Gln His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu
        515                 520                 525

Ala Leu Thr Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val
    530                 535                 540
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Asn Val Arg Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu
545                 550                 555                 560

Arg Gly Gly Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp
                565                 570                 575

Ser Ser Ala Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu
            580                 585                 590

Gln Ala Gln Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala
        595                 600                 605

Arg Tyr Ser Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala
    610                 615                 620

Asp Ala Asn Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala
625                 630                 635                 640

Val Ala Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg
                645                 650                 655

Val Thr Asp Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile
            660                 665                 670

Leu Ala Ala Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn
        675                 680                 685

Cys Gln Ala Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu
    690                 695                 700

His Trp Ala Ala Ala Val Asn Asn Val Glu Ala Thr Leu Leu Leu Leu
705                 710                 715                 720

Lys Asn Gly Ala Asn Arg Asp Met Gln Asp Asn Lys Glu Glu Thr Pro
                725                 730                 735

Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Ala Ala Lys Ile Leu
            740                 745                 750

Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu
        755                 760                 765

Pro Arg Asp Val Ala Arg Asp Arg Met His His Asp Ile Val Arg Leu
    770                 775                 780

Leu Asp Glu Tyr Asn Val Thr Pro Ser Pro Pro Gly Thr Val Leu Thr
785                 790                 795                 800

Ser Ala Leu Ser Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser
                805                 810                 815
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Leu Lys His Thr Pro Met Gly Lys Lys Ser Arg Arg Pro Ser Ala Lys
            820                 825                 830

Ser Thr Met Pro Thr Ser Leu Pro Asn Leu Ala Lys Glu Ala Lys Asp
        835                 840                 845

Ala Lys Gly Ser Arg Arg Lys Lys Ser Leu Ser Glu Lys Val Gln Leu
    850                 855                 860

Ser Glu Ser Ser Val Thr Leu Ser Pro Val Asp Ser Leu Glu Ser Pro
865                 870                 875                 880

His Thr Tyr Val Ser Asp Thr Thr Ser Ser Pro Met Ile Thr Ser Pro
                885                 890                 895

Gly Ile Leu Gln Ala Ser Pro Asn Pro Met Leu Ala Thr Ala Ala Pro
            900                 905                 910

Pro Ala Pro Val His Ala Gln His Ala Leu Ser Phe Ser Asn Leu His
        915                 920                 925

Glu Met Gln Pro Leu Ala His Gly Ala Ser Thr Val Leu Pro Ser Val
    930                 935                 940

Ser Gln Leu Leu Ser His His His Ile Val Ser Pro Gly Ser Gly Ser
945                 950                 955                 960

Ala Gly Ser Leu Ser Arg Leu His Pro Val Pro Val Pro Ala Asp Trp
                965                 970                 975

Met Asn Arg Met Glu Val Asn Glu Thr Gln Tyr Asn Glu Met Phe Gly
            980                 985                 990

Met Val Leu Ala Pro Ala Glu Gly  Thr His Pro Gly Ile  Ala Pro Gln
        995                 1000                1005

Ser Arg  Pro Pro Glu Gly Lys  His Ile Thr Thr Pro  Arg Glu Pro
    1010                1015                1020

Leu Pro  Pro Ile Val Thr Phe  Gln Leu Ile Pro Lys  Gly Ser Ile
    1025                1030                1035

Ala Gln  Pro Ala Gly Ala Pro  Gln Pro Gln Ser Thr  Cys Pro Pro
    1040                1045                1050

Ala Val  Ala Gly Pro Leu Pro  Thr Met Tyr Gln Ile  Pro Glu Met
    1055                1060                1065

Ala Arg  Leu Pro Ser Val Ala  Phe Pro Thr Ala Met  Met Pro Gln
    1070                1075                1080
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Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr His Pro
1085 1090 1095

Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln His
1100 1105 1110

Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser
1115 1120 1125

Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu
1130 1135 1140

Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp
1145 1150 1155

Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly
1160 1165 1170

Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn
1175 1180 1185

Asn Met Gln Val Tyr Ala
1190

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<213> artificial

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gagagtaaag atgctggtat caggactttg gttatgttgg atgaacaagg agaacaactg 180

gaacgcattg aggaagggat ggaccaaatc aataaggaca tgaaagaagc agaaaagaat 240

ttgacggacc taggaaaatt ctgcgggctt tgtgtgtgtc cctgtaacaa gcttaaatca 300

agtgatgctt acaaaaaagc ctggggcaat aatcaggacg gagtggtggc cagccagcct 360

gctcgtgtag tggacgaacg ggagcagatg gccatcagtg gcggcttcat ccgcagggta 420

acaaatgatg cccgagaaaa tgaaatggat gaaaacctag agcaggtgag cggcatcatc 480

gggaacctcc gtcacatggc cctggatatg ggcaatgaga tcgatacaca gaatcgccag 540

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cgtgcaacaa agatgctggg aagtggttct aga 633

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<213> artificial

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<400> 14

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1               5                  10                  15

Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30

Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45

Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60

Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80

Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95

Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110

Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125

Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140

Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160

Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175

Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190

Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ser Arg
        195                 200                 205

Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu Asn Gly
    210                 215                 220

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

Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg Ala Leu
```

eolf-seql

245 250 255

Leu Asp Ala Leu Pro Ile Glu Met Leu Asp Arg His His Thr His Ser
260 265 270

Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn Asn Ala
275 280 285

Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala Lys Val
290 295 300

His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu Glu Asn
305 310 315 320

Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn Ala Leu
325 330 335

Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val Leu Glu
340 345 350

Glu Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro Thr Thr
355 360 365

Asp Ser Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu Phe Asp Arg
370 375 380

Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile Ile Cys
385 390 395 400

Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro Thr Asp Ala
405 410 415

Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp
420 425 430

Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu
435 440 445

Asp Met Leu Pro Gly
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<212> DNA
<213> artificial

<220>
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ggtgataaat ggcgaaacaa aaagtttgaa ttgggtttgg agtttcccaa tcttccttat 180

tatattgatg gtgatgttaa attaacacag tctatggcca tcatacgtta tatagctgac 240

aagcacaaca tgttgggtgg ttgtccaaaa gagcgtgcag agatttcaat gcttgaagga 300

gcggttttgg atattagata cggtgtttcg agaattgcat atagtaaaga ctttgaaact 360

ctcaaagttg attttcttag caagctacct gaaatgctga aaatgttcga agatcgttta 420

tgtcataaaa catatttaaa tggtgatcat gtaacccatc ctgacttcat gttgtatgac 480

gctcttgatg ttgttttata catggaccca atgtgcctgg atgcgttccc aaaattagtt 540

tgttttaaaa aacgtattga agctatccca caaattgata agtacttgaa atccagcaag 600

tatatagcat ggcctttgca gggctggcaa gccacgtttg gtggtggcga ccatcctcca 660

aaatcggatg ccgaagacgc agacatgcgc aatgagctgg aggagatgca gcgaagggct 720

gaccagttgg ctgatgagtc gctggaaagc acccgtcgta tgctgcaact ggttgaagag 780

agtaaagatg ctggtatcag gactttggtt atgttggatg aacaaggaga acaactggaa 840

cgcattgagg aagggatgga ccaaatcaat aaggacatga aagaagcaga aaagaatttg 900

acggacctag gaaaattctg cgggctttgt gtgtgtccct gtaacaagct taaatcaagt 960

gatgcttaca aaaaagcctg gggcaataat caggacggag tggtggccag ccagcctgct 1020

cgtgtagtgg acgaacggga gcagatggcc atcagtggcg gcttcatccg cagggtaaca 1080

aatgatgccc gagaaaatga aatggatgaa aacctagagc aggtgagcgg catcatcggg 1140

aacctccgtc acatggccct ggatatgggc aatgagatcg atacacagaa tcgccagatc 1200

gacaggatca tggagaaggc tgattccaac aaaaccagaa ttgatgaggc caaccaacgt 1260

gcaacaaaga tgctgggaag tggttctaga 1290

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<211> 672
<212> PRT
<213> artificial

<220>
<223> GST-SNAP25-tTA (2)(pCMV-Tet3G)

<400> 16

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn

65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Ala Glu Asp Ala
210 215 220

Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg Arg Ala Asp Gln Leu
225 230 235 240

Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Gln Leu Val Glu
245 250 255

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

Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met Asp Gln Ile Asn Lys
275 280 285

Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp Leu Gly Lys Phe Cys
290 295 300

Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr
305 310 315 320

Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro
325 330 335

Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe

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            340                 345                 350

Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp Glu Asn
        355                 360                 365

Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg His Met Ala Leu
    370                 375                 380

Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp Arg Ile
385                 390                 395                 400

Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
                405                 410                 415

Arg Ala Thr Lys Met Leu Gly Ser Gly Ser Arg Leu Asp Lys Ser Lys
            420                 425                 430

Val Ile Asn Ser Ala Leu Glu Leu Leu Asn Gly Val Gly Ile Glu Gly
        435                 440                 445

Leu Thr Thr Arg Lys Leu Ala Gln Lys Leu Gly Val Glu Gln Pro Thr
    450                 455                 460

Leu Tyr Trp His Val Lys Asn Lys Arg Ala Leu Leu Asp Ala Leu Pro
465                 470                 475                 480

Ile Glu Met Leu Asp Arg His His Thr His Ser Cys Pro Leu Glu Gly
                485                 490                 495

Glu Ser Trp Gln Asp Phe Leu Arg Asn Asn Ala Lys Ser Tyr Arg Cys
            500                 505                 510

Ala Leu Leu Ser His Arg Asp Gly Ala Lys Val His Leu Gly Thr Arg
        515                 520                 525

Pro Thr Glu Lys Gln Tyr Glu Thr Leu Glu Asn Gln Leu Ala Phe Leu
    530                 535                 540

Cys Gln Gln Gly Phe Ser Leu Glu Asn Ala Leu Tyr Ala Leu Ser Ala
545                 550                 555                 560

Val Gly His Phe Thr Leu Gly Cys Val Leu Glu Glu Gln Glu His Gln
                565                 570                 575

Val Ala Lys Glu Glu Arg Glu Thr Pro Thr Thr Asp Ser Met Pro Pro
            580                 585                 590

Leu Leu Lys Gln Ala Ile Glu Leu Phe Asp Arg Gln Gly Ala Glu Pro
        595                 600                 605

Ala Phe Leu Phe Gly Leu Glu Leu Ile Ile Cys Gly Leu Glu Lys Gln
```

eolf-seql

610 615 620

Leu Lys Cys Glu Ser Gly Gly Pro Thr Asp Ala Leu Asp Asp Phe Asp
625 630 635 640

Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
645 650 655

Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Gly
660 665 670

<210> 17
<211> 2094
<212> DNA
<213> artificial

<220>
<223> GFP-SNAP25-tTA(pcDNA3.1)

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gatgctacat acggaaagct tacccttaaa tttatttgca ctactggaaa actacctgtt 180

ccatggccaa cacttgtcac tactttctct tatggtgttc aatgcttttc ccgttatccg 240

gatcatatga aacggcatga ctttttcaag agtgccatgc ccgaaggtta tgtacaggaa 300

cgcactatat ctttcaaaga tgacgggaac tacaagacgc gtgctgaagt caagtttgaa 360

ggtgataccc ttgttaatcg tatcgagtta aaaggtattg attttaaaga agatggaaac 420

attctcggac acaaactgga gtacaactat aactcacaca atgtatacat cacggcagac 480

aaacaaaaga atggaatcaa agctaacttc aaaattcgcc acaacattga agatggatcc 540

gttcaactag cagaccatta tcaacaaaat actccaattg gcgatggccc tgtcctttta 600

ccagacaacc attacctgtc gacacaatct gccctttcga aagatcccaa cgaaaagcgt 660

gaccacatgg tccttcttga gtttgtaact gctgctggga ttacacatgg catggatgag 720

ctctacaaag ccgaagacgc agacatgcgc aatgagctgg aggagatgca gcgaagggct 780

gaccagttgg ctgatgagtc gctggaaagc acccgtcgta tgctgcaact ggttgaagag 840

agtaaagatg ctggtatcag gactttggtt atgttggatg aacaaggaga acaactggaa 900

cgcattgagg aagggatgga ccaaatcaat aaggacatga aagaagcaga aaagaatttg 960

acggacctag gaaaattctg cgggctttgt gtgtgtccct gtaacaagct taaatcaagt 1020

gatgcttaca aaaaagcctg gggcaataat caggacggag tggtggccag ccagcctgct 1080

cgtgtagtgg acgaacggga gcagatggcc atcagtggcg gcttcatccg cagggtaaca 1140

aatgatgccc gagaaaatga aatggatgaa aacctagagc aggtgagcgg catcatcggg 1200

aacctccgtc acatggccct ggatatgggc aatgagatcg atacacagaa tcgccagatc 1260

gacaggatca tggagaaggc tgattccaac aaaaccagaa ttgatgaggc caaccaacgt 1320

gcaacaaaga tgctgggaag tggttctaga ctggacaaga gcaaagtcat aaactctgct 1380

ctggaattac tcaatggagt cggtatcgaa ggcctgacga caaggaaact cgctcaaaag 1440

ctgggagttg agcagcctac cctgtactgg cacgtgaaga acaagcgggc cctgctcgat 1500

gccctgccaa tcgagatgct ggacaggcat catacccact cctgcccccct ggaaggcgag 1560

tcatggcaag actttctgcg gaacaacgcc aagtcatacc gctgtgctct cctctcacat 1620

cgcgacgggg ctaaagtgca tctcggcacc cgcccaacag agaaacagta cgaaaccctg 1680

gaaaatcagc tcgcgttcct gtgtcagcaa ggcttctccc tggagaacgc actgtacgct 1740

ctgtccgccg tgggccactt tacactgggc tgcgtattgg aggaacagga gcatcaagta 1800

gcaaaagagg aaagagagac acctaccacc gattctatgc ccccacttct gaaacaagca 1860

attgagctgt tcgaccggca gggagccgaa cctgccttcc ttttcggcct ggaactaatc 1920

atatgtggcc tggagaaaca gctaaagtgc gaaagcggcg ggccgaccga cgcccttgac 1980

gattttgact tagacatgct cccagccgat gcccttgacg actttgacct tgatatgctg 2040

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<210> 18
<211> 691
<212> PRT
<213> artificial

<220>
<223> GFP-SNAP25-tTA(pcDNA3.1)

<400> 18

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

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

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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180                 185                 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala
225                 230                 235                 240

Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg Arg Ala
                245                 250                 255

Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Gln
            260                 265                 270

Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val Met Leu
        275                 280                 285

Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met Asp Gln
    290                 295                 300

Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp Leu Gly
305                 310                 315                 320

Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys Ser Ser
                325                 330                 335

Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala
            340                 345                 350

Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser
        355                 360                 365

Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met
    370                 375                 380

Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg His
385                 390                 395                 400
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Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile
                405                 410                 415

Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu
            420                 425                 430

Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ser Arg Leu Asp
        435                 440                 445

Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu Asn Gly Val Gly
    450                 455                 460

Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys Leu Gly Val Glu
465                 470                 475                 480

Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg Ala Leu Leu Asp
                485                 490                 495

Ala Leu Pro Ile Glu Met Leu Asp Arg His His Thr His Ser Cys Pro
            500                 505                 510

Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn Asn Ala Lys Ser
        515                 520                 525

Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala Lys Val His Leu
    530                 535                 540

Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu Glu Asn Gln Leu
545                 550                 555                 560

Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn Ala Leu Tyr Ala
                565                 570                 575

Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val Leu Glu Glu Gln
            580                 585                 590

Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro Thr Thr Asp Ser
        595                 600                 605

Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu Phe Asp Arg Gln Gly
    610                 615                 620

Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile Ile Cys Gly Leu
625                 630                 635                 640

Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro Thr Asp Ala Leu Asp
                645                 650                 655

Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp
            660                 665                 670
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Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
675 680 685

Leu Pro Gly
690

<210> 19
<211> 1731
<212> DNA
<213> artificial

<220>
<223> MBP-SNAP25-tTA (2)(pCMV-Tet3G)

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tacaacggcc tggccgaggt gggcaagaag ttcgagaagg acaccggcat caaggtgacc 120

gtggagcacc ccgacaagct ggaggagaag ttcccccagg tggccgccac cggcgacggc 180

cccgacatca tcttctgggc ccacgacaga ttcggcggct acgcccagag cggcctgctg 240

gccgagatca cccccgacaa ggccttccag gacaagctgt acccccttcac ctgggacgcc 300

gtgagataca acggcaagct gatcgcctac cccatcgccg tggaggccct gagcctgatc 360

tacaacaagg acctgctgcc caacccccccc aagacctggg aggagatccc cgccctggac 420

aaggagctga aggccaaggg caagagcgcc ctgatgttca acctgcagga gccctacttc 480

acctggcccc tgatcgccgc cgacggcggc tacgccttca agtacgagaa cggcaagtac 540

gacatcaagg acgtgggcgt ggacaacgcc ggcgccaagg ccggcctgac cttcctggtg 600

gacctgatca agaacaagca catgaacgcc gacaccgact acagcatcgc cgaggccgcc 660

ttcaacaagg gcgagaccgc catgaccatc aacggcccct gggcctggag caacatcgac 720

accagcaagg tgaactacgg cgtgaccgtg ctgcccacct tcaagggcca gcccagcaag 780

cccttcgtgg gcgtgctgag cgccggcatc aacgccgcca gccccaacaa ggagctggcc 840

aaggagttcc tggagaacta cctgctgacc gacgagggcc tggaggccgt gaacaaggac 900

aagcccctgg gcgccgtggc cctgaagagc tacgaggagg agctggccaa ggaccccaga 960

atcgccgcca ccatggagaa cgcccagaag ggcgagatca tgcccaacat cccccagatg 1020

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atgctgcaac tggttgaaga gagtaaagat gctggtatca ggactttggt tatgttggat 1260

gaacaaggag aacaactgga acgcattgag gaagggatgg accaaatcaa taaggacatg 1320

aaagaagcag aaaagaattt gacggaccta ggaaaattct gcgggctttg tgtgtgtccc 1380

tgtaacaagc ttaaatcaag tgatgcttac aaaaaagcct ggggcaataa tcaggacgga 1440

gtggtggcca gccagcctgc tcgtgtagtg gacgaacggg agcagatggc catcagtggc 1500

ggcttcatcc gcagggtaac aaatgatgcc cgagaaaatg aaatggatga aaacctagag 1560

caggtgagcg gcatcatcgg gaacctccgt cacatggccc tggatatggg caatgagatc 1620

gatacacaga atcgccagat cgacaggatc atggagaagg ctgattccaa caaaaccaga 1680

attgatgagg ccaaccaacg tgcaacaaag atgctgggaa gtggttctag a 1731

<210> 20
<211> 819
<212> PRT
<213> artificial

<220>
<223> MBP-SNAP25-tTA (2) (pCMV-Tet3G)

<400> 20

Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
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Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
100 105 110

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
130 135 140

Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
165 170 175

Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
180 185 190

Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp

195 200 205

Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
210 215 220

Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
225 230 235 240

Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
260 265 270

Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
275 280 285

Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
290 295 300

Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
305 310 315 320

Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
325 330 335

Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
340 345 350

Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Ala
355 360 365

Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg Arg Ala
370 375 380

Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Gln
385 390 395 400

Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val Met Leu
405 410 415

Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met Asp Gln
420 425 430

Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp Leu Gly
435 440 445

Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys Ser Ser
450 455 460

Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala

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465                 470                 475                 480

Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser
                485                 490                 495

Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met
            500                 505                 510

Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg His
        515                 520                 525

Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile
    530                 535                 540

Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu
545                 550                 555                 560

Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ser Arg Leu Asp
                565                 570                 575

Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu Asn Gly Val Gly
            580                 585                 590

Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys Leu Gly Val Glu
        595                 600                 605

Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg Ala Leu Leu Asp
    610                 615                 620

Ala Leu Pro Ile Glu Met Leu Asp Arg His His Thr His Ser Cys Pro
625                 630                 635                 640

Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn Asn Ala Lys Ser
                645                 650                 655

Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala Lys Val His Leu
            660                 665                 670

Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu Glu Asn Gln Leu
        675                 680                 685

Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn Ala Leu Tyr Ala
    690                 695                 700

Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val Leu Glu Glu Gln
705                 710                 715                 720

Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro Thr Thr Asp Ser
                725                 730                 735

Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu Phe Asp Arg Gln Gly
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eolf-seql

740 745 750

Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile Ile Cys Gly Leu
755 760 765

Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro Thr Asp Ala Leu Asp
770 775 780

Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp
785 790 795 800

Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
805 810 815

Leu Pro Gly

<210> 21
<211> 1089
<212> DNA
<213> artificial

<220>
<223> CLAT-SNAP25-tTA (1)(pCMV-Tet3G)

<400> 21
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gcgctgggga acggagtggc cggcgccggc gaagaagacc cggctgcggc cttcttggcg 120

cagcaagaga gcgagattgc gggcatcgag aacgacgagg ccttcgccat cctggacggc 180

ggcgcccccg ggccccagcc gcacggcgag ccgccggggg gtccggatgc tgttgatgga 240

gtaatgaatg gtgaatacta ccaggaaagt aatggtccaa cagacagtta tgcagctatt 300

tcacaagtgg atcgattgca gtcagagcct gaaagtatcc gtaaatggag agaagaacaa 360

atggaacgct tggaagccct tgatgccaat tctcggaagc aagaagcaga gtggaaagaa 420

aaggcaataa aggagctaga agaatggtat gcaagacagg acgagcagct acagaaaaca 480

aaagcaaaca acagggtggc agatgaagct ttctacaaac aacccttcgc tgacgtgatt 540

ggttatgtca caaacataaa ccatccttgc tacagcctag aacaggcagc agaagaagcc 600

tttgtaaatg acattgacga gtcgtcccca ggcactgagt gggaacgggt ggcccggctg 660

tgtgacttta accccaagtc tagcaagcag gccaaagatg tctcccgcat gcgctcagtc 720

ctcatctccc tcaagcaggc cccgctggtg cactcaagtg atgcttacaa aaaagcctgg 780

ggcaataatc aggacggagt ggtggccagc cagcctgctc gtgtagtgga cgaacgggag 840

cagatggcca tcagtggcgg cttcatccgc agggtaacaa atgatgcccg agaaaatgaa 900

atggatgaaa acctagagca ggtgagcggc atcatcggga acctccgtca catggccctg 960

gatatgggca atgagatcga tacacagaat cgccagatcg acaggatcat ggagaaggct 1020

gattccaaca aaaccagaat tgatgaggcc aaccaacgtg caacaaagat gctgggaagt 1080

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<210> 22
<211> 605
<212> PRT
<213> artificial

<220>
<223> CLAT-SNAP25-tTA (1)(pCMV-Tet3G)

<400> 22

Met Ala Glu Leu Asp Pro Phe Gly Ala Pro Ala Gly Ala Pro Gly Gly
1 5 10 15

Pro Ala Leu Gly Asn Gly Val Ala Gly Ala Gly Glu Glu Asp Pro Ala
20 25 30

Ala Ala Phe Leu Ala Gln Gln Glu Ser Glu Ile Ala Gly Ile Glu Asn
35 40 45

Asp Glu Ala Phe Ala Ile Leu Asp Gly Gly Ala Pro Gly Pro Gln Pro
50 55 60

His Gly Glu Pro Pro Gly Gly Pro Asp Ala Val Asp Gly Val Met Asn
65 70 75 80

Gly Glu Tyr Tyr Gln Glu Ser Asn Gly Pro Thr Asp Ser Tyr Ala Ala
85 90 95

Ile Ser Gln Val Asp Arg Leu Gln Ser Glu Pro Glu Ser Ile Arg Lys
100 105 110

Trp Arg Glu Glu Gln Met Glu Arg Leu Glu Ala Leu Asp Ala Asn Ser
115 120 125

Arg Lys Gln Glu Ala Glu Trp Lys Glu Lys Ala Ile Lys Glu Leu Glu
130 135 140

Glu Trp Tyr Ala Arg Gln Asp Glu Gln Leu Gln Lys Thr Lys Ala Asn
145 150 155 160

Asn Arg Val Ala Asp Glu Ala Phe Tyr Lys Gln Pro Phe Ala Asp Val
165 170 175

Ile Gly Tyr Val Thr Asn Ile Asn His Pro Cys Tyr Ser Leu Glu Gln
180 185 190

Ala Ala Glu Glu Ala Phe Val Asn Asp Ile Asp Glu Ser Ser Pro Gly
195 200 205

Thr Glu Trp Glu Arg Val Ala Arg Leu Cys Asp Phe Asn Pro Lys Ser
210 215 220

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Ser Lys Gln Ala Lys Asp Val Ser Arg Met Arg Ser Val Leu Ile Ser
225                 230                 235                 240

Leu Lys Gln Ala Pro Leu Val His Ser Ser Asp Ala Tyr Lys Lys Ala
                245                 250                 255

Trp Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val
            260                 265                 270

Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg
        275                 280                 285

Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln
    290                 295                 300

Val Ser Gly Ile Ile Gly Asn Leu Arg His Met Ala Leu Asp Met Gly
305                 310                 315                 320

Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys
                325                 330                 335

Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln Arg Ala Thr
            340                 345                 350

Lys Met Leu Gly Ser Gly Ser Arg Leu Asp Lys Ser Lys Val Ile Asn
        355                 360                 365

Ser Ala Leu Glu Leu Leu Asn Gly Val Gly Ile Glu Gly Leu Thr Thr
    370                 375                 380

Arg Lys Leu Ala Gln Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp
385                 390                 395                 400

His Val Lys Asn Lys Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met
                405                 410                 415

Leu Asp Arg His His Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp
            420                 425                 430

Gln Asp Phe Leu Arg Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu
        435                 440                 445

Ser His Arg Asp Gly Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu
    450                 455                 460

Lys Gln Tyr Glu Thr Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln
465                 470                 475                 480

Gly Phe Ser Leu Glu Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His
                485                 490                 495
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Phe Thr Leu Gly Cys Val Leu Glu Glu Gln Glu His Gln Val Ala Lys
500 505 510

Glu Glu Arg Glu Thr Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Lys
515 520 525

Gln Ala Ile Glu Leu Phe Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu
530 535 540

Phe Gly Leu Glu Leu Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys
545 550 555 560

Glu Ser Gly Gly Pro Thr Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
565 570 575

Leu Pro Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala
580 585 590

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Gly
595 600 605

<210> 23
<211> 3731
<212> DNA
<213> artificial

<220>
<223> tTA-SNAP25-SV2 (pCMV-Tet3G)

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cagcctaccc tgtactggca cgtgaagaac aagcgggccc tgctcgatgc cctgccaatc 180

gagatgctgg acaggcatca tacccactcc tgccccctgg aaggcgagtc atggcaagac 240

tttctgcgga acaacgccaa gtcataccgc tgtgctctcc tctcacatcg cgacggggct 300

aaagtgcatc tcggcacccg cccaacagag aaacagtacg aaaccctgga aaatcagctc 360

gcgttcctgt gtcagcaagg cttctccctg gagaacgcac tgtacgctct gtccgccgtg 420

ggccacttta cactgggctg cgtattggag gaacaggagc atcaagtagc aaaagaggaa 480

agagagacac ctaccaccga ttctatgccc ccacttctga aacaagcaat tgagctgttc 540

gaccggcagg gagccgaacc tgccttcctt ttcggcctgg aactaatcat atgtggcctg 600

gagaaacagc taaagtgcga aagcggcggg ccgaccgacg cccttgacga ttttgactta 660

gacatgctcc cagccgatgc ccttgacgac tttgaccttg atatgctgcc tgctgacgct 720

cttgacgatt ttgaccttga catgctcccc ggggccggcg ccggcagcgg agtggtggcc 780

agccagcctg ctcgtgtagt ggacgaacgg gagcagatgg ccatcagtgg cggcttcatc 840

cgcagggtaa caaatgatgc ccgagaaaat gaaatggatg aaaacctaga gcaggtgagc 900

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ggcatcatcg ggaacctccg tcacatggcc ctggatatgg gcaatgagat cgatacacag    960
aatcgccaga tcgacaggat catggagaag gctgattcca acaaaaccag aattgatgag   1020
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tacaaggata ggacttcact gatgaagggt gccaaggaca ttgccagaga ggtgaagaaa   1140
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ctcttctgtc gcttactttc tggattcggg attggaggag ccatacccac tgtgttctcg   1860
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Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met Leu Asp Arg His His
50 55 60

Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65 70 75 80

Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly
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Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu

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Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
    130                 135                 140

Val Leu Glu Glu Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145                 150                 155                 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu
                165                 170                 175

Phe Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
            180                 185                 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro
        195                 200                 205

Thr Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala
    210                 215                 220

Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp
225                 230                 235                 240

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

Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile
            260                 265                 270

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

Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg
    290                 295                 300

His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln
305                 310                 315                 320

Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp
                325                 330                 335

Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ala Gly Ala
            340                 345                 350

Gly Ser Glu Asp Ser Tyr Lys Asp Arg Thr Ser Leu Met Lys Gly Ala
        355                 360                 365

Lys Asp Ile Ala Arg Glu Val Lys Lys Gln Thr Val Lys Lys Val Asn
    370                 375                 380

Gln Ala Val Asp Arg Ala Gln Asp Glu Tyr Thr Gln Arg Ser Tyr Ser
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Arg Phe Gln Asp Glu Glu Asp Asp Asp Asp Tyr Tyr Pro Ala Gly Glu
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Thr Tyr Asn Gly Glu Ala Asn Asp Asp Glu Gly Ser Ser Glu Ala Thr
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Glu Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly Glu Tyr Gln Gly
435 440 445

Ile Pro Ser Met Asn Gln Ala Lys Asp Ser Ile Val Ser Val Gly Gln
450 455 460

Pro Lys Gly Asp Glu Tyr Lys Asp Arg Arg Glu Leu Glu Ser Glu Arg
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Arg Ala Asp Glu Glu Glu Leu Ala Gln Gln Tyr Glu Leu Ile Ile Gln
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Glu Cys Gly His Gly Arg Phe Gln Trp Ala Leu Phe Phe Val Leu Gly
500 505 510

Met Ala Leu Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val
515 520 525

Leu Pro Ser Ala Glu Thr Asp Leu Cys Ile Pro Asn Ser Gly Ser Gly
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Trp Leu Gly Ser Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Phe
545 550 555 560

Trp Gly Gly Leu Ala Asp Lys Val Gly Arg Lys Gln Ser Leu Leu Ile
565 570 575

Cys Met Ser Val Asn Gly Phe Phe Ala Phe Leu Ser Ser Phe Val Gln
580 585 590

Gly Tyr Gly Phe Phe Leu Phe Cys Arg Leu Leu Ser Gly Phe Gly Ile
595 600 605

Gly Gly Ala Ile Pro Thr Val Phe Ser Tyr Phe Ala Glu Val Leu Ala
610 615 620

Arg Glu Lys Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met
625 630 635 640

Ile Gly Gly Ile Tyr Ala Ser Ala Met Ala Trp Ala Ile Ile Pro His
645 650 655

Tyr Gly Trp Ser Phe Ser Met Gly Ser Ala Tyr Gln Phe His Ser Trp

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Arg Val Phe Val Ile Val Cys Ala Leu Pro Cys Val Ser Ser Val Val
        675                 680                 685

Ala Leu Thr Phe Met Pro Glu Ser Pro Arg Phe Leu Leu Glu Val Gly
    690                 695                 700

Lys His Asp Glu Ala Trp Met Ile Leu Lys Leu Ile His Asp Thr Asn
705                 710                 715                 720

Met Arg Ala Arg Gly Gln Pro Glu Lys Val Phe Thr Val Asn Lys Ile
                725                 730                 735

Lys Thr Pro Lys Gln Ile Asp Glu Leu Ile Glu Ile Glu Ser Asp Thr
            740                 745                 750

Gly Thr Trp Tyr Arg Arg Cys Phe Val Arg Ile Arg Thr Glu Leu Tyr
        755                 760                 765

Gly Ile Trp Leu Thr Phe Met Arg Cys Phe Asn Tyr Pro Val Arg Asp
    770                 775                 780

Asn Thr Ile Lys Leu Thr Ile Val Trp Phe Thr Leu Ser Phe Gly Tyr
785                 790                 795                 800

Tyr Gly Leu Ser Val Trp Phe Pro Asp Val Ile Lys Pro Leu Gln Ser
                805                 810                 815

Asp Glu Tyr Ala Leu Leu Thr Arg Asn Val Glu Arg Asp Lys Tyr Ala
            820                 825                 830

Asn Phe Thr Ile Asn Phe Thr Met Glu Asn Gln Ile His Thr Gly Met
        835                 840                 845

Glu Tyr Asp Asn Gly Arg Phe Ile Gly Val Lys Phe Lys Ser Val Thr
    850                 855                 860

Phe Lys Asp Ser Val Phe Lys Ser Cys Thr Phe Glu Asp Val Thr Ser
865                 870                 875                 880

Val Asn Thr Tyr Phe Lys Asn Cys Thr Phe Ile Asp Thr Val Phe Asp
                885                 890                 895

Asn Thr Asp Phe Glu Pro Tyr Lys Phe Ile Asp Ser Glu Phe Lys Asn
            900                 905                 910

Cys Ser Phe Phe His Asn Lys Thr Gly Cys Gln Ile Thr Phe Asp Asp
        915                 920                 925

Asp Tyr Ser Ala Tyr Trp Ile Tyr Phe Val Asn Phe Leu Gly Thr Leu
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eolf-seql

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Ala Val Leu Pro Gly Asn Ile Val Ser Ala Leu Leu Met Asp Arg Ile
945 950 955 960

Gly Arg Leu Thr Met Leu Gly Gly Ser Met Val Leu Ser Gly Ile Ser
965 970 975

Cys Phe Phe Leu Trp Phe Gly Thr Ser Glu Ser Met Met Ile Gly Met
980 985 990

Leu Cys Leu Tyr Asn Gly Leu Thr Ile Ser Ala Trp Asn Ser Leu Asp
995 1000 1005

Val Val Thr Val Glu Leu Tyr Pro Thr Asp Arg Arg Ala Thr Gly
1010 1015 1020

Phe Gly Phe Leu Asn Ala Leu Cys Lys Ala Ala Ala Val Leu Gly
1025 1030 1035

Asn Leu Ile Phe Gly Ser Leu Val Ser Ile Thr Lys Ser Ile Pro
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Leu Cys Leu Pro Asp Thr Arg Thr Gln Val Leu
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Leu Asn Gly Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
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Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met Leu Asp Arg His His
50 55 60

Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65 70 75 80

Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys

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

Phe Asp Leu Asp Met Leu Pro Gly Ala Gly Ala Gly Ser Gly Val Val
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Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile
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Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu
        275                 280                 285

Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg
    290                 295                 300

His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln
305                 310                 315                 320

Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp
                325                 330                 335

Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ala Gly Ala
            340                 345                 350

Gly Ser Gly Ala Gly Ala Gly Ser Ala Phe His Val Glu Gly Leu Ile
        355                 360                 365

Ala Ile Ile Val Phe Tyr Leu Leu Ile Leu Leu Val Gly Ile Trp Ala
    370                 375                 380

Ala Trp Arg Thr Lys Asn Ser Gly Ser Ala Glu Glu Arg Ser Glu Ala
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Ile Ile Val Gly Gly Arg Asp Ile Gly Leu Leu Val Gly Gly Phe Thr
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Met Thr Ala Thr Trp Val Gly Gly Gly Tyr Ile Asn Gly Thr Ala Glu
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Ala Val Tyr Val Pro Gly Tyr Gly Leu Ala Trp Ala Gln Ala Pro Ile
435 440 445

Gly Tyr Ser Leu Ser Leu Ile Leu Gly Gly Leu Phe Phe Ala Lys Pro
450 455 460

Met Arg Ser Lys Gly Tyr Val Thr Met Leu Asp Pro Phe Gln Gln Ile
465 470 475 480

Tyr Gly Lys Arg Met Gly Gly Leu Leu Phe Ile Pro Ala Leu Met Gly
485 490 495

Glu Met Phe Trp Ala Ala Ala Ile Phe Ser Ala Leu Gly Ala Thr Ile
500 505 510

Ser Val Ile Ile Asp Val Asp Met His Ile Ser Val Ile Ile Ser Ala
515 520 525

Leu Ile Ala Thr Leu Tyr Thr Leu Val Gly Gly Leu Tyr Ser Val Ala
530 535 540

Tyr Thr Asp Val Val Gln Leu Phe Cys Ile Phe Val Gly Leu Trp Ile
545 550 555 560

Ser Val Pro Phe Ala Leu Ser His Pro Ala Val Ala Asp Ile Gly Phe
565 570 575

Thr Ala Val His Ala Lys Tyr Gln Lys Pro Trp Leu Gly Thr Val Asp
580 585 590

Ser Ser Glu Val Tyr Ser Trp Leu Asp Ser Phe Leu Leu Leu Met Leu
595 600 605

Gly Gly Ile Pro Trp Gln Ala Tyr Phe Gln Arg Val Leu Ser Ser Ser
610 615 620

Ser Ala Thr Tyr Ala Gln Val Leu Ser Phe Leu Ala Ala Phe Gly Cys
625 630 635 640

Leu Val Met Ala Ile Pro Ala Ile Leu Ile Gly Ala Ile Gly Ala Ser
645 650 655

Thr Asp Trp Asn Gln Thr Ala Tyr Gly Leu Pro Asp Pro Lys Thr Thr
660 665 670

Glu Glu Ala Asp Met Ile Leu Pro Ile Val Leu Gln Tyr Leu Cys Pro

675 680 685

Val Tyr Ile Ser Phe Phe Gly Leu Gly Ala Val Ser Ala Ala Val Met
690 695 700

Ser Ser Ala Asp Ser Ser Ile Leu Ser Ala Ser Ser Met Phe Ala Arg
705 710 715 720

Asn Ile Tyr Gln Leu Ser Phe Arg Gln Asn Ala Ser Asp Lys Glu Ile
725 730 735

Val Trp Val Met Arg Ile Thr Val Phe Val Phe Gly Ala Ser Ala Thr
740 745 750

Ala Met Ala Leu Leu Thr Lys Thr Val Tyr Gly Leu Trp Tyr Leu Ser
755 760 765

Ser Asp Leu Val Tyr Ile Val Ile Phe Pro Gln Leu Leu Cys Val Leu
770 775 780

Phe Val Lys Gly Thr Asn Thr Tyr Gly Ala Val Ala Gly Tyr Val Ser
785 790 795 800

Gly Leu Phe Leu Arg Ile Thr Gly Gly Glu Pro Tyr Leu Tyr Leu Gln
805 810 815

Pro Leu Ile Phe Tyr Pro Gly Tyr Tyr Pro Asp Asp Asn Gly Ile Tyr
820 825 830

Asn Gln Lys Phe Pro Phe Lys Thr Leu Ala Met Val Thr Ser Phe Leu
835 840 845

Thr Asn Ile Cys Ile Ser Tyr Leu Ala Lys Tyr Leu Phe Glu Ser Gly
850 855 860

Thr Leu Pro Pro Lys Leu Asp Val Phe Asp Ala Val Val Ala Arg His
865 870 875 880

Ser Glu Glu Asn Met Asp Lys Thr Ile Leu Val Lys Asn Glu Asn Ile
885 890 895

Lys Leu Asp Glu Leu Ala Leu Val Lys Pro Arg Gln Ser Met Thr Leu
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Ser Ser Thr Phe Thr Asn Lys Glu Ala Phe Leu Asp Val Asp Ser Ser
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Pro Glu Gly Ser Gly Thr Glu Asp Asn Leu Gln
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catcctgact tcatgttgta tgacgctctt gatgttgttt tatacatgga cccaatgtgc 1560

ctggatgcgt tcccaaaatt agtttgtttt aaaaaacgta ttgaagctat cccacaaatt 1620

gataagtact tgaaatccag caagtatata gcatggcctt tgcagggctg gcaagccacg 1680

tttggtggtg gcgaccatcc tccaaaatcg gattaactaa gtaaggatcc agacatgata 1740

agatacattg atgagtttgg acaaaccaca actagaatgc agtgaaaaaa atgctttatt 1800

tgtgaaattt gtgatgctat tgctttattt gtaaccatta taagctgcaa taaacaagtt 1860

aacaacaaca attgcattca ttttatgttt caggttcagg gggaggtgtg ggaggttttt 1920

taaagcaagt aaaacctcta caaatgtggt atggctgatt atgatcctgc aagcctcgtc 1980

gtcctggccg gaccacgcta tctgtgcaag gtccccggcc ccggacgcgc gctccatgag 2040

cagagcgccc gccgccgagg cgaagactcg ggcggcgccc tgcccgtccc accaggtcaa 2100

caggcggtaa ccggcctctt catcgggaat gcgcgcgacc ttcagcatcg ccggcatgtc 2160

cccctggcgg acgggaagta tccagctcga ccaagctt 2198

<210> 28
<211> 569
<212> PRT
<213> artificial

<220>
<223> tTA-SNAP25-GST(pCMV-Tet3G)

<400> 28

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1 5 10 15

Leu Asn Gly Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met Leu Asp Arg His His
50 55 60

Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65 70 75 80

Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly
85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
130 135 140

Val Leu Glu Glu Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu
165 170 175

```
Phe Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
            180                 185                 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro
        195                 200                 205

Thr Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala
    210                 215                 220

Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp
225                 230                 235                 240

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

Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile
            260                 265                 270

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

Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg
    290                 295                 300

His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln
305                 310                 315                 320

Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp
                325                 330                 335

Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Met Ser Pro
            340                 345                 350

Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu
        355                 360                 365

Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg
    370                 375                 380

Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu
385                 390                 395                 400

Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln
                405                 410                 415

Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly
            420                 425                 430

Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val
        435                 440                 445
```

Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe
450 455 460

Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys
465 470 475 480

Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His
485 490 495

Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu
500 505 510

Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe
515 520 525

Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser
530 535 540

Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly
545 550 555 560

Gly Gly Asp His Pro Pro Lys Ser Asp
565

<210> 29
<211> 2255
<212> DNA
<213> artificial

<220>
<223> tTA-SNAP25-GFP(pCMV-Tet3G)

<400> 29
gaattcacca tgtctagact ggacaagagc aaagtcataa actctgctct ggaattactc 60

aatggagtcg gtatcgaagg cctgacgaca aggaaactcg ctcaaaagct gggagttgag 120

cagcctaccc tgtactggca cgtgaagaac aagcgggccc tgctcgatgc cctgccaatc 180

gagatgctgg acaggcatca tacccactcc tgccccctgg aaggcgagtc atggcaagac 240

tttctgcgga acaacgccaa gtcataccgc tgtgctctcc tctcacatcg cgacggggct 300

aaagtgcatc tcggcacccg cccaacagag aaacagtacg aaaccctgga aaatcagctc 360

gcgttcctgt gtcagcaagg cttctccctg gagaacgcac tgtacgctct gtccgccgtg 420

ggccacttta cactgggctg cgtattggag gaacaggagc atcaagtagc aaaagaggaa 480

agagagacac ctaccaccga ttctatgccc ccacttctga aacaagcaat tgagctgttc 540

gaccggcagg gagccgaacc tgccttcctt ttcggcctgg aactaatcat atgtggcctg 600

gagaaacagc taaagtgcga aagcggcggg ccgaccgacg cccttgacga ttttgactta 660

gacatgctcc cagccgatgc ccttgacgac tttgaccttg atatgctgcc tgctgacgct 720

cttgacgatt ttgaccttga catgctcccc ggggccggcg ccggcagcgg agtggtggcc 780

agccagcctg ctcgtgtagt ggacgaacgg gagcagatgg ccatcagtgg cggcttcatc 840

cgcagggtaa caaatgatgc ccgagaaaat gaaatggatg aaaacctaga gcaggtgagc 900

ggcatcatcg ggaacctccg tcacatggcc ctggatatgg gcaatgagat cgatacacag 960

aatcgccaga tcgacaggat catggagaag gctgattcca acaaaaccag aattgatgag 1020

gccaaccaac gtgcaacaaa gatgctggga agtggtgcca gcaaaggaga agaacttttc 1080

actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct 1140

gtcagtggag agggtgaagg tgatgctaca tacggaaagc ttacccttaa atttatttgc 1200

actactggaa aactacctgt tccatggcca acacttgtca ctactttctc ttatggtgtt 1260

caatgctttt cccgttatcc ggatcatatg aaacggcatg actttttcaa gagtgccatg 1320

cccgaaggtt atgtacagga acgcactata tctttcaaag atgacgggaa ctacaagacg 1380

cgtgctgaag tcaagtttga aggtgatacc cttgttaatc gtatcgagtt aaaaggtatt 1440

gattttaaag aagatggaaa cattctcgga cacaaactcg agtacaacta taactcacac 1500

aatgtataca tcacggcaga caaacaaaag aatggaatca aagctaactt caaaattcgc 1560

cacaacattg aagatggatc cgttcaacta gcagaccatt atcaacaaaa tactccaatt 1620

ggcgatggcc ctgtcctttt accagacaac cattacctgt cgacacaatc tgccctttcg 1680

aaagatccca acgaaaagcg tgaccacatg gtccttcttg agtttgtaac tgctgctggg 1740

attacacatg gcatggatga gctctacaaa taactaagta aggatccaga catgataaga 1800

tacattgatg agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt 1860

gaaatttgtg atgctattgc tttatttgta accattataa gctgcaataa acaagttaac 1920

aacaacaatt gcattcattt tatgtttcag gttcaggggg aggtgtggga ggtttttaa 1980

agcaagtaaa acctctacaa atgtggtatg gctgattatg atcctgcaag cctcgtcgtc 2040

ctggccggac cacgctatct gtgcaaggtc cccggccccg gacgcgcgct ccatgagcag 2100

agcgcccgcc gccgaggcga agactcgggc ggcgccctgc ccgtcccacc aggtcaacag 2160

gcggtaaccg gcctcttcat cgggaatgcg cgcgaccttc agcatcgccg gcatgtcccc 2220

ctggcggacg ggaagtatcc agctcgacca agctt 2255

<210> 30
<211> 696
<212> PRT
<213> artificial

<220>
<223> tTA-SNAP25-GFP(pCMV-Tet3G)

<400> 30

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1 5 10 15

Leu Asn Gly Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

```
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
        35                  40                  45

Arg Ala Leu Leu Asp Ala Leu Pro Ile Glu Met Leu Asp Arg His His
    50                  55                  60

Thr His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65                  70                  75                  80

Asn Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly
                85                  90                  95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
            100                 105                 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
        115                 120                 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
    130                 135                 140

Val Leu Glu Glu Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145                 150                 155                 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu
                165                 170                 175

Phe Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
            180                 185                 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro
        195                 200                 205

Thr Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala
    210                 215                 220

Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp
225                 230                 235                 240

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

Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile
            260                 265                 270

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

Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu Arg
    290                 295                 300
```

```
His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln
305                 310                 315                 320

Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp
                325                 330                 335

Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ala Ser Lys
            340                 345                 350

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
        355                 360                 365

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
    370                 375                 380

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
385                 390                 395                 400

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly
                405                 410                 415

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
            420                 425                 430

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser
        435                 440                 445

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
    450                 455                 460

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
465                 470                 475                 480

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
                485                 490                 495

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
            500                 505                 510

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
        515                 520                 525

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
    530                 535                 540

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
545                 550                 555                 560

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
                565                 570                 575
```

```
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala Glu Asp Ala Asp
            580                 585                 590

Met Arg Asn Glu Leu Glu Glu Met Gln Arg Arg Ala Asp Gln Leu Ala
        595                 600                 605

Asp Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Gln Leu Val Glu Glu
    610                 615                 620

Ser Lys Asp Ala Gly Ile Arg Thr Leu Val Met Leu Asp Glu Gln Gly
625                 630                 635                 640

Glu Gln Leu Glu Arg Ile Glu Glu Gly Met Asp Gln Ile Asn Lys Asp
                645                 650                 655

Met Lys Glu Ala Glu Lys Asn Leu Thr Asp Leu Gly Lys Phe Cys Gly
            660                 665                 670

Leu Cys Val Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys
        675                 680                 685

Lys Ala Trp Gly Asn Asn Gln Asp
    690                 695
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<210> 31
<211> 444
<212> PRT
<213> artificial

<220>
<223> SNAP110-pTET-tTAK

<400> 31

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Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
1               5                   10                  15

Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
            20                  25                  30

Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
        35                  40                  45

Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
    50                  55                  60

Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
65                  70                  75                  80

Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
                85                  90                  95

Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly Ser Arg
```

```
            100                 105                 110

Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu Asn Glu
        115                 120                 125

Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys Leu Gly
    130                 135                 140

Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg Ala Leu
145                 150                 155                 160

Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His Thr His Phe
                165                 170                 175

Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn Asn Ala
            180                 185                 190

Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala Lys Val
        195                 200                 205

His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu Glu Asn
    210                 215                 220

Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn Ala Leu
225                 230                 235                 240

Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val Leu Glu
                245                 250                 255

Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro Thr Thr
            260                 265                 270

Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu Phe Asp His
        275                 280                 285

Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile Ile Cys
    290                 295                 300

Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala Tyr Ser Arg
305                 310                 315                 320

Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly Leu Leu Asp
                325                 330                 335

Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala Ala Pro Arg
            340                 345                 350

Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser Thr Ala Pro
        355                 360                 365

Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp
```

370 375 380

Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
385 390 395 400

Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp Ser
405 410 415

Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met
420 425 430

Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
435 440

<210> 32
<211> 10
<212> PRT
<213> artificial

<220>
<223> leucine-rich nuclear export signal (NES)

<220>
<221> misc_feature
<222> (2)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (6)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 32

Leu Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Leu
1 5 10

<210> 33
<211> 247
<212> PRT
<213> artificial

<220>
<223> tetracycline dependent transactivator

<400> 33

Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu
1 5 10 15

Asn Gly Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys
20 25 30

Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg

35 40 45

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

His Ser Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn
65 70 75 80

Asn Ala Lys Ser Tyr Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala
85 90 95

Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu
100 105 110

Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn
115 120 125

Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val
130 135 140

Leu Glu Glu Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro
145 150 155 160

Thr Thr Asp Ser Met Pro Pro Leu Leu Lys Gln Ala Ile Glu Leu Phe
165 170 175

Asp Arg Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile
180 185 190

Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Gly Pro Thr
195 200 205

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu
210 215 220

Asp Asp Phe Asp Leu Asp Met Leu Pro Ala Asp Ala Leu Asp Asp Phe
225 230 235 240

Asp Leu Asp Met Leu Pro Gly
245

<210> 34
<211> 334
<212> PRT
<213> artificial

<220>
<223> tetracycline dependent transactivator

<400> 34

Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu
1 5 10 15

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Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys
            20                  25                  30

Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg
        35                  40                  45

Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His Thr
    50                  55                  60

His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn
65                  70                  75                  80

Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala
                85                  90                  95

Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu
            100                 105                 110

Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn
        115                 120                 125

Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val
    130                 135                 140

Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro
145                 150                 155                 160

Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu Phe
                165                 170                 175

Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile
            180                 185                 190

Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala Tyr
        195                 200                 205

Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly Leu
    210                 215                 220

Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala Ala
225                 230                 235                 240

Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser Thr
                245                 250                 255

Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly
            260                 265                 270

Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu
        275                 280                 285
```

Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
290 295 300

Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
305 310 315 320

Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
325 330

<210> 35
<211> 22
<212> DNA
<213> artificial

<220>
<223> forward primer Tet-element

<400> 35
agctgggagt tgagcagcct ac 22

<210> 36
<211> 22
<212> DNA
<213> artificial

<220>
<223> reverse primer Tet-element

<400> 36
ggtgccgaga tgcactttag cc 22

<210> 37
<211> 20
<212> DNA
<213> artificial

<220>
<223> forward primer Luciferase

<400> 37
gaagagatac gccctggttc 20

<210> 38
<211> 20
<212> DNA
<213> artificial

<220>
<223> reverse primer Luciferase

<400> 38
cgggaggtag atgagatgtg 20