SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research Organisation

<120> Measuring G protein coupled receptor activation

<130> 508883

<150> 61/148,271
<151> 2009-01-29

<160> 56

<170> PatentIn version 3.5

<210> 1
<211> 339
<212> PRT
<213> Caenorhabditis elegans

<400> 1

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Gly Val Thr Leu Thr Phe Cys Val Asn Ile Val Leu Leu Gly Leu Leu
            20                  25                  30

Lys Thr Arg Gly Lys Asn Leu Gly Thr Tyr Lys Tyr Leu Met Ala Phe
        35                  40                  45

Phe Ser Val Phe Ser Ile Phe Tyr Ala Ile Ile Glu Phe Ile Leu Arg
    50                  55                  60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys
65                  70                  75                  80

Arg Phe Asn Tyr Ser Thr Lys Leu Gly Lys Ile Asn Ser Ala Phe Tyr
                85                  90                  95

Cys Ala Cys Phe Ala Thr Ser Phe Val Val Ser Gly Val His Phe Val
            100                 105                 110

Tyr Arg Tyr Phe Ala Thr Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
        115                 120                 125

Leu Pro Thr Leu Leu Leu Trp Pro Leu Gly Cys Ser Val Pro Val Thr
    130                 135                 140

Met Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145                 150                 155                 160
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Glu Ala Ala Val Thr Asn Val Leu Asn Asn His Tyr Asn Trp Ile Lys
165 170 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
180 185 190

Gly Val Arg His Ile Tyr Leu Lys Asn Leu Leu Gly Cys Phe Val His
195 200 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Met Phe Tyr Cys Gly Tyr
210 215 220

Ala Thr Trp Lys Thr Met Asn Glu His Lys Asp Val Ser Asp Arg Thr
225 230 235 240

Arg Ala Leu Gln Lys Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Leu
245 250 255

Ile Pro Thr Ile Phe Met Tyr Ala Pro Thr Gly Val Met Phe Ile Ala
260 265 270

Pro Phe Phe Asp Val Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe
275 280 285

Cys Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Leu Ile
290 295 300

Ile Arg Asp Phe Arg Arg Thr Ile Phe Asn Phe Leu Cys Gly Lys Lys
305 310 315 320

Asn Ser Val Asp Glu Ser Arg Ser Thr Thr Arg Ala Asn Leu Ser Gln
325 330 335

Val Pro Thr

<210> 2
<211> 346
<212> PRT
<213> Caenorhabditis elegans

<400> 2

Met Ser Gly Gln Leu Trp Leu Ala Leu Val Asp Ala Ala Asp Met Val
1 5 10 15

Gly Phe Thr Leu Thr Ile Ser Ile Asn Ile Ile Leu Leu Gly Leu Ile
20 25 30

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Arg Thr Arg Gly Lys Thr Leu Gly Thr Tyr Lys Tyr Leu Met Ser Phe
        35                  40                  45

Phe Ser Phe Phe Ser Ile Phe Tyr Ala Ile Val Glu Ser Ile Leu Arg
    50                  55                  60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys
65                  70                  75                  80

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

Cys Ala Cys Phe Ala Thr Ser Phe Val Leu Ser Ala Val His Phe Val
            100                 105                 110

Tyr Arg Tyr Phe Ala Ala Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
        115                 120                 125

Leu Pro His Leu Leu Leu Trp Pro Leu Met Cys Ser Ile Pro Val Thr
    130                 135                 140

Ala Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145                 150                 155                 160

Glu Ala Ala Val Thr Tyr Val Leu Lys Thr His Tyr Glu Val Ile Lys
                165                 170                 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
            180                 185                 190

Gly Glu Arg His Ile Tyr Ile Lys Asn Leu Leu Gly Cys Phe Val His
        195                 200                 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Val Phe Tyr Cys Gly Phe
    210                 215                 220

Ser Thr Trp Trp Thr Ile Arg Glu His Arg Gly Ala Ser Asp Arg Thr
225                 230                 235                 240

Arg His Leu His Arg Gln Leu Phe Lys Ala Leu Val Phe Gln Thr Leu
                245                 250                 255

Val Pro Ser Ile Phe Met Tyr Ile Pro Thr Gly Val Met Phe Ile Ala
            260                 265                 270

Pro Phe Phe Asp Ile Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe
        275                 280                 285
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Cys Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Phe Ile
    290                 295                 300

Ile Arg Glu Phe Arg Val Thr Ile Leu Asn Ile Ile Arg Gly Asn Glu
305                 310                 315                 320

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

Ser Gln Pro Ala Ala Val Asn Leu Ser Gly
            340                 345
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<210> 3
<211> 341
<212> PRT
<213> Caenorhabditis elegans

<400> 3

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Met Ser Asp Arg His Trp Leu Asp Ile Thr Thr Tyr Ser Asp His Ile
1               5                   10                  15

Gly Phe Thr Ile Ser Thr Ile Ala Asn Phe Val Leu Ile Leu Leu Leu
            20                  25                  30

Val Phe Arg Pro Thr Lys Ser Tyr Gly Ser Tyr Lys Tyr Leu Met Ile
        35                  40                  45

Thr Phe Cys Val Phe Ser Leu Phe Tyr Thr Ser Ile Glu Thr Phe Leu
    50                  55                  60

Arg Pro Leu Ile His Ile Tyr Asp Asn Thr Ile Phe Val Ile Gln Arg
65                  70                  75                  80

Lys Arg Phe Gln Tyr Ser Glu Gly Thr Ala Arg Ala Ile Ser Ser Thr
                85                  90                  95

Tyr Cys Gly Cys Tyr Ala Met Ser Phe Thr Leu Phe Ala Val His Phe
            100                 105                 110

Val Tyr Arg Tyr Tyr Ala Ala Cys Lys Pro Asp Asn Leu Arg Tyr Phe
        115                 120                 125

Gln Gly Cys Tyr Phe Val Ala Trp Val Phe Gly Ala Met Ala Val Ala
    130                 135                 140

Ala Ser Trp Gly Phe Ala Ala Phe Ile Leu Tyr Pro Glu Thr Glu Arg
145                 150                 155                 160
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Thr Arg Thr Ala Leu Ile His Val Ile Gln Thr Ser Tyr Glu Leu Asp
                165                 170                 175

Pro Glu Trp Val Gly Asn Val Pro Tyr Ser Tyr Trp Arg Thr Glu Asn
            180                 185                 190

Gly Val Glu Tyr Leu Asn Pro Arg Asn Val Ile Gly Ile Phe Gln His
        195                 200                 205

Gly Val Ile Met Ile Leu Ser Phe Gly Thr Val Phe Tyr Cys Gly Phe
    210                 215                 220

Asn Thr Tyr Lys Thr Leu Asn Gly Ser Leu Gly Val Ser Glu Lys Thr
225                 230                 235                 240

Lys Glu Met His Thr Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Ile
                245                 250                 255

Ile Pro Thr Thr Leu Met Tyr Ile Pro Thr Thr Met Leu Phe Val Thr
            260                 265                 270

Pro Phe Val Gly Leu Asn Ile Gly Cys Tyr Gly Asn Ile Thr Thr Ala
        275                 280                 285

Thr Val His Leu Tyr Pro Gly Ile Asp Pro Val Val Leu Ile Phe Ile
    290                 295                 300

Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe Arg Cys Phe Tyr
305                 310                 315                 320

Arg Ser Asn Ser Val Glu Asn Thr Ala Thr Ile Arg Gln Tyr Gln Gln
                325                 330                 335

Ser Ser Ser Lys Gly
            340
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<210> 4
<211> 348
<212> PRT
<213> Caenorhabditis elegans

<400> 4

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Met Ser Asp Ile Tyr Trp Ile Gln Ile Thr Glu Val Cys Ser Phe Val
1               5                  10                  15

Gly Phe Met Leu Ser Val Leu Gly Asn Ser Thr Leu Leu Val Leu Leu
            20                  25                  30
```

```
Ser Gly Lys Ser Ile Asp Gly Ile Gly Thr Tyr Arg Tyr Leu Met Ile
        35                  40                  45

Thr Phe Cys Val Phe Ser Leu Leu Phe Thr Ile Leu Glu Asp Phe Ile
    50                  55                  60

Arg Pro Leu Met His His Tyr Asn Asn Thr Ile Ile Val Leu Gln Arg
65                  70                  75                  80

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

Tyr Cys Gly Cys Phe Ala Met Cys Phe Val Met Phe Ala Val His Phe
            100                 105                 110

Ile Tyr Arg Tyr Leu Val Ala Cys His Pro Thr Lys Leu His Tyr Phe
        115                 120                 125

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

Gly Ser Trp Val Ala Ile Ala Tyr Val Phe Phe Gln Glu Asp Leu Glu
145                 150                 155                 160

Thr Arg Thr Asp Leu Val Phe Ile Leu Ser Thr Cys Tyr Asn Leu Thr
                165                 170                 175

Pro Asp Asp Val Gly His Val Pro Tyr Ala Phe Tyr Lys Thr Gln Gly
            180                 185                 190

Asn Thr Arg Val Ile Arg Trp Asp Asn Met Ile Gly Val Ile His His
        195                 200                 205

Met Ile Val Met Thr Ile Ser Ile Ser Ala Val Phe Tyr Phe Gly Ile
    210                 215                 220

Lys Thr Tyr Thr Arg Ile Met Ser Phe Lys Gly Lys Ser Gln Lys Thr
225                 230                 235                 240

Lys Asp Leu Gln Asn Gln Phe Phe Thr Ala Leu Val Ala Gln Thr Val
                245                 250                 255

Val Pro Leu Ile Phe Met Phe Ile Pro Asn Met Val Leu Thr Thr Ala
            260                 265                 270

Ala Leu Ile Asp Gly Thr Phe Gly Ser Trp Ala Asn Ile Thr Val Val
        275                 280                 285
```

Met Asn His Leu Tyr Pro Ala Ala Asp Pro Phe Val Ile Leu Phe Ile
290 295 300

Ile Lys Gly Phe Arg Asn Ser Ile Arg Asn Val Ile Tyr Arg Cys Thr
305 310 315 320

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

Gln Ser Lys Lys Gln Ser Phe Ser Arg Val Asp Ile
340 345

<210> 5
<211> 334
<212> PRT
<213> Caenorhabditis elegans

<400> 5

Met Thr Asp Gln His Trp Val Ile Ile Thr Asp Ile Ala Gly Pro Ile
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Gly Phe Ser Met Ser Ile Phe Ser Asn Ser Ile Leu Leu Phe Leu Ile
20 25 30

Phe Ser His Ser Ser Pro Ile Lys Gly Pro Tyr Lys Arg Met Leu Ile
35 40 45

Val Phe Cys Ile Phe Thr Val Phe Tyr Ser Phe Val Glu Val Met Leu
50 55 60

Gln Pro Leu Ile His Ile Tyr Asp Asp Thr Leu Phe Leu Ile His Arg
65 70 75 80

Lys Arg Ile Asp Leu Pro Lys Trp Leu Thr Arg Leu Val Pro Thr Thr
85 90 95

Tyr Cys Trp Cys Tyr Ala Met Ser Phe Ser Leu Phe Ala Leu Gln Phe
100 105 110

Leu Tyr Arg Tyr Val Ala Val Cys Lys Pro Gln Tyr Val Asp Leu Phe
115 120 125

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

Thr Ser Trp Gly Leu Thr Ala Ala Phe Met Phe Pro Gln Thr Asp Arg
145 150 155 160

```
Thr Thr Glu Ile Phe Leu His Ile Ile Tyr Ser Ser Tyr Asp Leu Glu
                165                 170                 175

Pro Tyr Trp Thr Asp Tyr Val Ala Tyr Lys Tyr Phe Asp Thr Asp Glu
            180                 185                 190

Asn Asn Val Arg Trp Val Asn Val Leu Ser Phe Phe Gly Val Leu Gln
        195                 200                 205

His Gly Ile Val Ile Thr Leu Ser Phe Gly Thr Leu Tyr Tyr Cys Gly
    210                 215                 220

Ile Asn Thr Tyr Leu Lys Ile Lys Lys His Thr Gly Thr Ser Asn Arg
225                 230                 235                 240

Thr Arg Cys Ile Gln Leu Gln Leu Phe Arg Ala Leu Val Ala Gln Thr
                245                 250                 255

Ile Leu Pro Met Phe Met Met Tyr Ile Pro Val Gly Phe Met Phe Ala
            260                 265                 270

Cys Pro Tyr Phe Asp Leu Gln Leu Gly Ala Tyr Thr Asn Tyr Gln Thr
        275                 280                 285

Val Met Ala Gln Leu Tyr Pro Gly Ile Asp Pro Phe Val Met Leu Phe
    290                 295                 300

Leu Ile Asp Ser Tyr Arg Ile Thr Ile Phe Gly Trp Leu Cys Pro Arg
305                 310                 315                 320

Phe Val Tyr Val Lys Pro Met His Ser Thr Tyr Thr Leu Thr
                325                 330
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<210> 6
<211> 350
<212> PRT
<213> Caenorhabditis elegans

<400> 6

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Met Thr Asp Arg Arg Trp Val Ala Ile Thr Asp Ile Ala Gly Pro Ile
1               5                   10                  15

Gly Phe Thr Met Ser Ile Phe Ser Asn Ser Val Leu Leu Ser Leu Ile
            20                  25                  30

Phe Ser Ser Ser Ser Pro Ile Lys Gly Ala Tyr Lys Asn Met Leu Ile
        35                  40                  45
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Val Leu Cys Ile Phe Thr Met Phe Tyr Ser Phe Val Glu Ile Met Leu
50 55 60

Gln Pro Leu Ile His Ile Tyr Asp Asp Thr Leu Phe Leu Ile His Arg
65 70 75 80

Lys Arg Phe Asp Leu Ser Lys Gly Ile Thr Arg Leu Ile Pro Thr Thr
85 90 95

Tyr Cys Trp Cys Tyr Ala Met Ser Phe Ser Leu Phe Ala Leu Gln Phe
100 105 110

Leu Tyr Arg Tyr Val Ala Val Cys Lys Pro His Leu Val Val Phe Phe
115 120 125

Thr Gly Cys Tyr Phe Tyr Tyr Trp Leu Ala Leu Ile Leu Ser Leu Ala
130 135 140

Thr Ser Trp Gly Leu Thr Ala Ala Phe Met Phe Pro Gln Thr Asn Arg
145 150 155 160

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

Pro Tyr Trp Thr Asp Tyr Val Ala Tyr Lys Tyr Phe Asp Thr Asp Glu
180 185 190

Asn His Val Arg Trp Val Asn Val Leu Ser Leu Phe Gly Val Leu Gln
195 200 205

His Gly Leu Val Ile Thr Leu Ser Phe Gly Thr Leu Phe Tyr Cys Gly
210 215 220

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

Thr Arg Ser Leu Gln Leu Gln Leu Phe Arg Ala Leu Val Ala Gln Thr
245 250 255

Cys Leu Pro Met Leu Met Met Tyr Met Pro Ile Gly Phe Met Phe Ser
260 265 270

Cys Pro Tyr Phe Asp Leu Gln Leu Gly Ala Val Thr Asn Tyr Gln Thr
275 280 285

Val Met Ala Gln Leu Tyr Pro Gly Ile Asp Pro Phe Met Leu Leu Phe

290 295 300

Leu Ile Asn Ala Tyr Arg Lys Thr Val Leu Ser Leu Ile Cys Pro Asn
305 310 315 320

Phe Ile Gln Lys Lys Tyr Val Gln Thr Ala Thr Thr Arg Asp Gly Thr
325 330 335

Asp Ala Ser Ala Thr Met Asn Ser Val Lys Ser Thr Gln Leu
340 345 350

<210> 7
<211> 1020
<212> DNA
<213> Caenorhabditis elegans

<400> 7
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accttctgtg tcaacattgt tcttctcgga cttctgaaaa cacgtggaaa aaacttgggc 120

acttataaat atctcatggc gtttttctca gtattctcga ttttttacgc catcatcgag 180

ttcatattac gacctataat gcatattgag aacaccactt tctttttgat ctcaaggaaa 240

agattcaact actccaccaa acttggaaaa atcaactctg cgttttactg tgcttgtttt 300

gccaccagtt ttgttgtctc aggagttcac tttgtttatc gatattttgc aacttgcaaa 360

ccgaatctac ttcgtttgtt caacttgcca actcttctac tttggccact tggttgcagt 420

gtacccgtga caatgtgggc tagtgtctca tatttttgt atccagatac cgagtacacg 480

gaagcggctg tcaccaatgt actaaataac cactataact ggatcaaaaa ggagaatgta 540

tcgtacattg catacgtcta ttaccaatac gaaaacggag taaggcatat ctacctcaaa 600

aacttgcttg gatgctttgt tcattacttt gtcatgtcga tgacgtttgt tgtgatgttc 660

tactgcggat atgccacgtg gaaaactatg aatgaacaca aggatgtatc tgatagaact 720

cgagcgctac agaaacaact tttcaaagct ttagttcttc agacactcat cccaactatc 780

ttcatgtacg ccccaactgg agtcatgttc atcgcaccgt tttttgacgt gaatttgaat 840

gcaaacgcca atttcattgt gttttgctca tttctgtacc cgggactcga tccactcatt 900

ctgattttga tcattcgtga tttccgaaga acaatattca atttcttgtg tggaaagaaa 960

aacagtgttg atgaatcccg ctcgacaaca agagccaatt tgtctcaagt tccgacgtga 1020

<210> 8
<211> 1040
<212> DNA
<213> Caenorhabditis elegans

<400> 8
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acgtacaaat acttgatgag cttcttctcg ttcttctcaa tcttttatgc aatcgttgaa 180

tctattttga gaccaataat gcatatcgaa aacacgacgt tctttctgat ttctcggaaa 240

cgcttcgatt actcaactcg ccttggtaaa atcaactctg ctttctactg tgcttgtttt 300

gccacgagtt ttgtcctgtc tgcggtacac tttgtgtatc ggtactttgc cgcttgcaaa 360

ccgaatctgc tacgcttgtt taaccttccg catcttttac tgtggccttt gatgtgttcg 420

attcctgtga ctgcgtgggc aagtgtttct tacttttgt acccagacac cgagtacact 480

gaagcagcag ttacatatgt tctgaaaaca cactacgagg tgatcaaaaa agaaaatgta 540

tcttatatcg catacgtata ctatcaatat gaaaatgggg agcgtcacat ctacataaaa 600

aatttgcttg gctgctttgt acactacttc gttatgtcaa tgacatttgt agttgtgttt 660

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ctcattttta tcattcgcga attcgggtca ctattttgaa tatcatcaga ggaaatgagc 960

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<210> 9
<211> 1026
<212> DNA
<213> Caenorhabditis elegans

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ggttcataca agtacctgat gatcacattc tgcgtgttca gcctctttta cacctccatt 180

gaaacttttt tgagacctct catccatatc tacgacaata cgatcttcgt gattcagcgc 240

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aacgtcatcg ggatctttca acacggcgtc atcatgatcc tctccttcgg aacagtcttc 660

tactgcggat tcaacactta taagactttg aacggaagtc tgggggtgtc tgaaaaaaca 720

aaagaaatgc acacccaatt gttcaaggcc ttggttctac agactatcat ccctactaca 780

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<210> 10
<211> 1047
<212> DNA
<213> Caenorhabditis elegans

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ttcgcgatgt gcttcgtgat gttcgccgtt catttcatct atcgatatct agttgcttgt 360

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ttattcatag caggaagctg ggttgcaatt gcatatgtct tttttcaaga agacctagaa 480

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tactttggca ttaaaaccta cactcgaata atgagtttca agggaaaatc ccagaaaacc 720

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tcatgggcca atattactgt agttatgaat catttgtatc cggctgccga tccattcgtt 900

atactgttca ttattaaggg gttccggaat agtattagaa atgttatata tcgctgcaca 960

aaaacgaaaa aagcatcggt tagctcagtg gtccgtggta ttgaggctca aagcaagaaa 1020

caatcttttt ctcgagttga tatttaa 1047

<210> 11
<211> 1005
<212> DNA
<213> Caenorhabditis elegans

<400> 11
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ggtccataca aacgaatgct catagtattt tgcatattta ccgtattcta ctcatttgtc 180
gaagtcatgc ttcagccact aatccatatt tacgacgaca ctttattttt gattcatcga 240
aagagaatag acttgccaaa atggttaaca cgtttggttc ctactaccta ttgttggtgt 300
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<211> 1053
<212> DNA
<213> Caenorhabditis elegans

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ggagcttaca aaaatatgtt gatagtgttg tgtatattca ctatgttcta ctcttttgtt 180
gaaataatgc ttcaaccgtt gattcatatt tatgatgaca cgctgttctt gatccaccgg 240
aaaagatttg acctgtctaa aggaattaca cgtttgatac ctacaacata ttgttggtgt 300
tatgcaatga gtttctcatt attcgccctc cagtttttgt acagatatgt ggcagtttgc 360
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ttatcacttg ctacaagttg ggggcttact gcagctttta tgttcccgca aaccaatcga 480
acaactgaaa gcttcaacta cgtaataaaa acttcttatg acttagatcc ttattggacg 540
gattatgttg cctataaata ttttgacacc gatgagaatc atgtgagatg ggtgaatgtt 600

cttagtttat ttggagtctt gcagcacgga ttagtaatta cgttgagttt tggaacctta 660

ttctactgtg gaattaaaac ttatctcagc attactgaac atgttggaat gtccagcaag 720

acccgaagtc ttcaacttca actattccgt gctttagttg ctcagacatg tcttccaatg 780

ctcatgatgt acatgccaat aggattcatg ttttcttgcc cttactttga tttgcaactt 840

ggagcagtca caaactatca aaccgtcatg gcacagttat acccaggaat cgacccattt 900

atgttgctat ttcttattaa cgcctacaga aagacagtgt taagcttgat ctgtcctaat 960

tttatccaga aaaaatatgt tcaaacggca actactcgtg atggcacaga tgcctcggca 1020

acaatgaatt ctgttaaatc tacacagtta taa 1053

<210> 13
<211> 889
<212> PRT
<213> Artificial Sequence

<220>
<223> BRET construct

<400> 13

Met Ser Gly Glu Leu Trp Ile Thr Leu Val Asp Thr Ala Asp Ile Val
1 5 10 15

Gly Val Thr Leu Thr Phe Cys Val Asn Ile Val Leu Leu Gly Leu Leu
20 25 30

Lys Thr Arg Gly Lys Asn Leu Gly Thr Tyr Lys Tyr Leu Met Ala Phe
35 40 45

Phe Ser Val Phe Ser Ile Phe Tyr Ala Ile Ile Glu Phe Ile Leu Arg
50 55 60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys
65 70 75 80

Arg Phe Asn Tyr Ser Thr Lys Leu Gly Lys Ile Asn Ser Ala Phe Tyr
85 90 95

Cys Ala Cys Phe Ala Thr Ser Phe Val Val Ser Gly Val His Phe Val
100 105 110

Tyr Arg Tyr Phe Ala Thr Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
115 120 125

Leu Pro Thr Leu Leu Leu Trp Pro Leu Gly Cys Ser Val Pro Val Thr
130 135 140

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Met Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145                 150                 155                 160

Glu Ala Ala Val Thr Asn Val Leu Asn Asn His Tyr Asn Trp Ile Lys
                165                 170                 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
            180                 185                 190

Gly Val Arg His Ile Tyr Leu Lys Asn Leu Leu Gly Cys Phe Val His
        195                 200                 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Met Phe Tyr Cys Gly Tyr
    210                 215                 220

Ala Thr Trp Lys Thr Met Asn Glu His Lys Asp Val Ser Asp Arg Thr
225                 230                 235                 240

Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
                245                 250                 255

Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
            260                 265                 270

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
        275                 280                 285

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
    290                 295                 300

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
305                 310                 315                 320

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                325                 330                 335

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
            340                 345                 350

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        355                 360                 365

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
    370                 375                 380

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
385                 390                 395                 400
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Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
405 410 415

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
420 425 430

Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
435 440 445

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
450 455 460

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
465 470 475 480

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
485 490 495

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
500 505 510

Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
515 520 525

Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
530 535 540

Arg Val Leu Lys Asn Glu Gln Arg Ala Leu Gln Lys Gln Leu Phe Lys
545 550 555 560

Ala Leu Val Leu Gln Thr Leu Ile Pro Thr Ile Phe Met Tyr Ala Pro
565 570 575

Thr Gly Val Met Phe Ile Ala Pro Phe Phe Asp Val Asn Leu Asn Ala
580 585 590

Asn Ala Asn Phe Ile Val Phe Cys Ser Phe Leu Tyr Pro Gly Leu Asp
595 600 605

Pro Leu Ile Leu Ile Leu Ile Ile Arg Asp Phe Arg Arg Thr Ile Phe
610 615 620

Asn Phe Leu Cys Gly Lys Lys Asn Ser Val Asp Glu Ser Arg Ser Thr
625 630 635 640

Thr Arg Ala Asn Leu Ser Gln Val Pro Thr Met Val Ser Lys Gly Glu
645 650 655

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
660 665 670

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
675 680 685

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
690 695 700

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly Val Gln
705 710 715 720

Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
725 730 735

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
740 745 750

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
755 760 765

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
770 775 780

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
785 790 795 800

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
805 810 815

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
820 825 830

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
835 840 845

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
850 855 860

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
865 870 875 880

Thr Leu Gly Met Asp Glu Leu Tyr Lys
885

<210> 14

<211> 2670
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding BRET construct of SEQ ID NO:13

<400> 14
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accttctgtg tcaacattgt tcttctcgga cttctgaaaa cacgtggaaa aaacttgggc 120

acttataaat atctcatggc gtttttctca gtattctcga ttttttacgc catcatcgag 180

ttcatattac gacctataat gcatattgag aacaccactt tctttttgat ctcaaggaaa 240

agattcaact actccaccaa acttggaaaa atcaactctg cgttttactg tgcttgtttt 300

gccaccagtt ttgttgtctc aggagttcac tttgtttatc gatattttgc aacttgcaaa 360

ccgaatctac ttcgtttgtt caacttgcca actcttctac tttggccact tggttgcagt 420

gtacccgtga caatgtgggc tagtgtctca tatttttgt atccagatac cgagtacacg 480

gaagcggctg tcaccaatgt actaaataac cactataact ggatcaaaaa ggagaatgta 540

tcgtacattg catacgtcta ttaccaatac gaaaacggag taaggcatat ctacctcaaa 600

aacttgcttg gatgctttgt tcattacttt gtcatgtcga tgacgtttgt tgtgatgttc 660

tactgcggat atgccacgtg gaaaactatg aatgaacaca aggatgtatc tgatagaact 720

atgaccagca aggtgtacga ccccgagcag aggaagagga tgatcaccgg cccccagtgg 780

tgggccaggt gcaagcagat gaacgtgctg gacagcttca tcaactacta cgacagcgag 840

aagcacgccg agaacgccgt gatcttcctg cacggcaacg ccgctagcag ctacctgtgg 900

aggcacgtgg tgccccacat cgagcccgtg gccaggtgca tcatccccga tctgatcggc 960

atgggcaaga gcggcaagag cggcaacggc agctacaggc tgctggacca ctacaagtac 1020

ctgaccgcct ggttcgagct cctgaacctg cccaagaaga tcatcttcgt gggccacgac 1080

tggggcgcct gcctggcctt ccactacagc tacgagcacc aggacaagat caaggccatc 1140

gtgcacgccg agagcgtggt ggacgtgatc gagagctggg acgagtggcc agacatcgag 1200

gaggacatcg ccctgatcaa gagcgaggag ggcgagaaga tggtgctgga gaacaacttc 1260

ttcgtggaga ccatgctgcc cagcaagatc atgagaaagc tggagcccga ggagttcgcc 1320

gcctacctgg agcccttcaa ggagaagggc gaggtgagaa gacccaccct gagctggccc 1380

agagagatcc ccctggtgaa gggcggcaag cccgacgtgg tgcagatcgt gagaaactac 1440

aacgcctacc tgagagccag cgacgacctg cccaagatgt tcatcgagag cgaccccggc 1500

ttcttcagca acgccatcgt ggagggcgcc aagaagttcc ccaacaccga gttcgtgaag 1560

gtgaagggcc tgcacttcag ccaggaggac gcccccgacg agatgggcaa gtacatcaag 1620

agcttcgtgg agagagtgct gaagaacgag cagcgagcgc tacagaaaca acttttcaaa 1680

gctttagttc ttcagacact catcccaact atcttcatgt acgccccaac tggagtcatg 1740

ttcatcgcac cgtttttga cgtgaatttg aatgcaaacg ccaatttcat tgtgttttgc 1800

tcatttctgt acccgggact cgatccactc attctgattt tgatcattcg tgatttccga 1860

agaacaatat tcaatttctt gtgtggaaag aaaaacagtg ttgatgaatc ccgctcgaca 1920

acaagagcca atttgtctca agttccgacg atggtgagca agggcgagga gctgttcacc 1980

ggggtggtgc ccatcctggt cgagctggac ggcgacgtaa acggccacaa gttcagcgtg 2040

tccggcgagg gcgagggcga tgccacctac ggcaagctga ccctgaagtt catctgcacc 2100

accggcaagc tgcccgtgcc ctggcccacc ctcgtgacca ccctgagcta cggcgtgcag 2160

tgcttcagcc gctaccccga ccacatgaag cagcacgact tcttcaagtc cgccatgccc 2220

gaaggctacg tccaggagcg caccatcttc ttcaaggacg acggcaacta caagacccgc 2280

gccgaggtga agttcgaggg cgacaccctg gtgaaccgca tcgagctgaa gggcatcgac 2340

ttcaaggagg acggcaacat cctggggcac aagctggagt acaactacaa cagccacaac 2400

gtctatatca tggccgacaa gcagaagaac ggcatcaagg tgaacttcaa gatccgccac 2460

aacatcgagg acggcagcgt gcagctcgcc gaccactacc agcagaacac ccccatcggc 2520

gacggccccg tgctgctgcc cgacaaccac tacctgagca cccagtccgc cctgagcaaa 2580

gaccccaacg agaagcgcga tcacatggtc ctgctggagt tcgtgaccgc cgccgggatc 2640

actctcggca tggacgagct gtacaagtaa 2670

<210> 15
<211> 889
<212> PRT
<213> Artificial Sequence

<220>
<223> BRET construct

<400> 15

Met Ser Gly Glu Leu Trp Ile Thr Leu Val Asp Thr Ala Asp Ile Val
1 5 10 15

Gly Val Thr Leu Thr Phe Cys Val Asn Ile Val Leu Leu Gly Leu Leu
20 25 30

Lys Thr Arg Gly Lys Asn Leu Gly Thr Tyr Lys Tyr Leu Met Ala Phe
35 40 45

Phe Ser Val Phe Ser Ile Phe Tyr Ala Ile Ile Glu Phe Ile Leu Arg
50 55 60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys

65 70 75 80

Arg Phe Asn Tyr Ser Thr Lys Leu Gly Lys Ile Asn Ser Ala Phe Tyr
85 90 95

Cys Ala Cys Phe Ala Thr Ser Phe Val Val Ser Gly Val His Phe Val
100 105 110

Tyr Arg Tyr Phe Ala Thr Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
115 120 125

Leu Pro Thr Leu Leu Leu Trp Pro Leu Gly Cys Ser Val Pro Val Thr
130 135 140

Met Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145 150 155 160

Glu Ala Ala Val Thr Asn Val Leu Asn Asn His Tyr Asn Trp Ile Lys
165 170 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
180 185 190

Gly Val Arg His Ile Tyr Leu Lys Asn Leu Leu Gly Cys Phe Val His
195 200 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Met Phe Tyr Cys Gly Tyr
210 215 220

Ala Thr Trp Lys Thr Met Asn Glu His Lys Asp Val Ser Asp Arg Thr
225 230 235 240

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
245 250 255

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
260 265 270

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
275 280 285

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
290 295 300

Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
305 310 315 320

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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                325                 330                 335

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            340                 345                 350

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        355                 360                 365

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    370                 375                 380

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
385                 390                 395                 400

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                405                 410                 415

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            420                 425                 430

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        435                 440                 445

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    450                 455                 460

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg
465                 470                 475                 480

Ala Leu Gln Lys Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Leu Ile
                485                 490                 495

Pro Thr Ile Phe Met Tyr Ala Pro Thr Gly Val Met Phe Ile Ala Pro
            500                 505                 510

Phe Phe Asp Val Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe Cys
        515                 520                 525

Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Leu Ile Ile
    530                 535                 540

Arg Asp Phe Arg Arg Thr Ile Phe Asn Phe Leu Cys Gly Lys Lys Asn
545                 550                 555                 560

Ser Val Asp Glu Ser Arg Ser Thr Thr Arg Ala Asn Leu Ser Gln Val
                565                 570                 575
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Pro Thr Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met
            580                 585                 590

Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu
        595                 600                 605

Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala
    610                 615                 620

Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His
625                 630                 635                 640

Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu
                645                 650                 655

Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu
            660                 665                 670

Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu
        675                 680                 685

Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala
    690                 695                 700

Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His
705                 710                 715                 720

Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp
                725                 730                 735

Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met
            740                 745                 750

Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile
        755                 760                 765

Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe
    770                 775                 780

Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu
785                 790                 795                 800

Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg
                805                 810                 815

Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe
            820                 825                 830
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Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala
835 840 845

Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe
850 855 860

Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe
865 870 875 880

Val Glu Arg Val Leu Lys Asn Glu Gln
885

<210> 16
<211> 2670
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding BRET construct of SEQ ID NO:15

<400> 16
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accttctgtg tcaacattgt tcttctcgga cttctgaaaa cacgtggaaa aaacttgggc 120

acttataaat atctcatggc gtttttctca gtattctcga ttttttacgc catcatcgag 180

ttcatattac gacctataat gcatattgag aacaccactt tctttttgat ctcaaggaaa 240

agattcaact actccaccaa acttggaaaa atcaactctg cgttttactg tgcttgtttt 300

gccaccagtt ttgttgtctc aggagttcac tttgtttatc gatattttgc aacttgcaaa 360

ccgaatctac ttcgtttgtt caacttgcca actcttctac tttggccact tggttgcagt 420

gtacccgtga caatgtgggc tagtgtctca tatttttgt atccagatac cgagtacacg 480

gaagcggctg tcaccaatgt actaaataac cactataact ggatcaaaaa ggagaatgta 540

tcgtacattg catacgtcta ttaccaatac gaaaacggag taaggcatat ctacctcaaa 600

aacttgcttg gatgctttgt tcattacttt gtcatgtcga tgacgtttgt tgtgatgttc 660

tactgcggat atgccacgtg gaaaactatg aatgaacaca aggatgtatc tgatagaact 720

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 780

ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 840

ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 900

ctcgtgacca ccctgagcta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 960

cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 1020

ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 1080

gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 1140

aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 1200

ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 1260

gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 1320

tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 1380

ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagcga 1440

gcgctacaga aacaactttt caaagcttta gttcttcaga cactcatccc aactatcttc 1500

atgtacgccc caactggagt catgttcatc gcaccgtttt ttgacgtgaa tttgaatgca 1560

aacgccaatt tcattgtgtt ttgctcattt ctgtacccgg gactcgatcc actcattctg 1620

attttgatca ttcgtgattt ccgaagaaca atattcaatt tcttgtgtgg aaagaaaaac 1680

agtgttgatg aatcccgctc gacaacaaga gccaatttgt ctcaagttcc gacgatgacc 1740

agcaaggtgt acgaccccga gcagaggaag aggatgatca ccggccccca gtggtgggcc 1800

aggtgcaagc agatgaacgt gctggacagc ttcatcaact actacgacag cgagaagcac 1860

gccgagaacg ccgtgatctt cctgcacggc aacgccgcta gcagctacct gtggaggcac 1920

gtggtgcccc acatcgagcc cgtggccagg tgcatcatcc ccgatctgat cggcatgggc 1980

aagagcggca agagcggcaa cggcagctac aggctgctgg accactacaa gtacctgacc 2040

gcctggttcg agctcctgaa cctgcccaag aagatcatct tcgtgggcca cgactggggc 2100

gcctgcctgg ccttccacta cagctacgag caccaggaca agatcaaggc catcgtgcac 2160

gccgagagcg tggtggacgt gatcgagagc tgggacgagt ggccagacat cgaggaggac 2220

atcgccctga tcaagagcga ggagggcgag aagatggtgc tggagaacaa cttcttcgtg 2280

gagaccatgc tgcccagcaa gatcatgaga aagctggagc ccgaggagtt cgccgcctac 2340

ctggagccct tcaaggagaa gggcgaggtg agaagaccca ccctgagctg gcccagagag 2400

atccccctgg tgaagggcgg caagcccgac gtggtgcaga tcgtgagaaa ctacaacgcc 2460

tacctgagag ccagcgacga cctgcccaag atgttcatcg agagcgaccc cggcttcttc 2520

agcaacgcca tcgtggaggg cgccaagaag ttccccaaca ccgagttcgt gaaggtgaag 2580

ggcctgcact tcagccagga ggacgccccc gacgagatgg gcaagtacat caagagcttc 2640

gtggagagag tgctgaagaa cgagcagtaa 2670

<210> 17
<211> 650
<212> PRT
<213> Artificial Sequence

<220>
<223> BRET construct

<400> 17

Met Ser Gly Glu Leu Trp Ile Thr Leu Val Asp Thr Ala Asp Ile Val
1 5 10 15

Gly Val Thr Leu Thr Phe Cys Val Asn Ile Val Leu Leu Gly Leu Leu
20 25 30

Lys Thr Arg Gly Lys Asn Leu Gly Thr Tyr Lys Tyr Leu Met Ala Phe
35 40 45

Phe Ser Val Phe Ser Ile Phe Tyr Ala Ile Ile Glu Phe Ile Leu Arg
50 55 60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys
65 70 75 80

Arg Phe Asn Tyr Ser Thr Lys Leu Gly Lys Ile Asn Ser Ala Phe Tyr
85 90 95

Cys Ala Cys Phe Ala Thr Ser Phe Val Val Ser Gly Val His Phe Val
100 105 110

Tyr Arg Tyr Phe Ala Thr Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
115 120 125

Leu Pro Thr Leu Leu Leu Trp Pro Leu Gly Cys Ser Val Pro Val Thr
130 135 140

Met Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145 150 155 160

Glu Ala Ala Val Thr Asn Val Leu Asn Asn His Tyr Asn Trp Ile Lys
165 170 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
180 185 190

Gly Val Arg His Ile Tyr Leu Lys Asn Leu Leu Gly Cys Phe Val His
195 200 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Met Phe Tyr Cys Gly Tyr
210 215 220

Ala Thr Trp Lys Thr Met Asn Glu His Lys Asp Val Ser Asp Arg Thr
225 230 235 240

Arg Ala Leu Gln Lys Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Leu

245 250 255

Ile Pro Thr Ile Phe Met Tyr Ala Pro Thr Gly Val Met Phe Ile Ala
260 265 270

Pro Phe Phe Asp Val Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe
275 280 285

Cys Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Leu Ile
290 295 300

Ile Arg Asp Phe Arg Arg Thr Ile Phe Asn Phe Leu Cys Gly Lys Lys
305 310 315 320

Asn Ser Val Asp Glu Ser Arg Ser Thr Thr Arg Ala Asn Leu Ser Gln
325 330 335

Val Pro Thr Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
340 345 350

Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
355 360 365

Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
370 375 380

Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
385 390 395 400

His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
405 410 415

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

Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn
435 440 445

Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu
450 455 460

Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
465 470 475 480

His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
485 490 495

Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
500 505 510

Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
515 520 525

Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
530 535 540

Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
545 550 555 560

Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
565 570 575

Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
580 585 590

Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
595 600 605

Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
610 615 620

Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
625 630 635 640

Phe Val Glu Arg Val Leu Lys Asn Glu Gln
645 650

<210> 18
<211> 1953
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding BRET construct of SEQ ID NO:17

<400> 18
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accttctgtg tcaacattgt tcttctcgga cttctgaaaa cacgtggaaa aaacttgggc 120

acttataaat atctcatggc gtttttctca gtattctcga ttttttacgc catcatcgag 180

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gtacccgtga caatgtgggc tagtgtctca tatttttgt atccagatac cgagtacacg 480

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ttcagcaacg ccatcgtgga gggcgccaag aagttcccca acaccgagtt cgtgaaggtg 1860

aagggcctgc acttcagcca ggaggacgcc cccgacgaga tgggcaagta catcaagagc 1920

ttcgtggaga gagtgctgaa gaacgagcag taa 1953

<210> 19
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> BRET construct

<400> 19

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            20                  25                  30

Lys Thr Arg Gly Lys Asn Leu Gly Thr Tyr Lys Tyr Leu Met Ala Phe
        35                  40                  45

Phe Ser Val Phe Ser Ile Phe Tyr Ala Ile Ile Glu Phe Ile Leu Arg
    50                  55                  60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys
65                  70                  75                  80

Arg Phe Asn Tyr Ser Thr Lys Leu Gly Lys Ile Asn Ser Ala Phe Tyr
                85                  90                  95

Cys Ala Cys Phe Ala Thr Ser Phe Val Val Ser Gly Val His Phe Val
            100                 105                 110

Tyr Arg Tyr Phe Ala Thr Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
        115                 120                 125

Leu Pro Thr Leu Leu Leu Trp Pro Leu Gly Cys Ser Val Pro Val Thr
    130                 135                 140

Met Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145                 150                 155                 160

Glu Ala Ala Val Thr Asn Val Leu Asn Asn His Tyr Asn Trp Ile Lys
                165                 170                 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
            180                 185                 190

Gly Val Arg His Ile Tyr Leu Lys Asn Leu Leu Gly Cys Phe Val His
        195                 200                 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Met Phe Tyr Cys Gly Tyr
    210                 215                 220

Ala Thr Trp Lys Thr Met Asn Glu His Lys Asp Val Ser Asp Arg Thr
225                 230                 235                 240

Arg Ala Leu Gln Lys Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Leu
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Ile Pro Thr Ile Phe Met Tyr Ala Pro Thr Gly Val Met Phe Ile Ala
260 265 270

Pro Phe Phe Asp Val Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe
275 280 285

Cys Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Leu Ile
290 295 300

Ile Arg Asp Phe Arg Arg Thr Ile Phe Asn Phe Leu Cys Gly Lys Lys
305 310 315 320

Asn Ser Val Asp Glu Ser Arg Ser Thr Thr Arg Ala Asn Leu Ser Gln
325 330 335

Val Pro Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
385 390 395 400

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

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
435 440 445

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

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
465 470 475 480

Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

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

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

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

Tyr Lys

<210> 20
<211> 1737
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding BRET construct of SEQ ID NO:19

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ttcatattac gacctataat gcatattgag aacaccactt tctttttgat ctcaaggaaa 240

agattcaact actccaccaa acttggaaaa atcaactctg cgttttactg tgcttgtttt 300

gccaccagtt ttgttgtctc aggagttcac tttgtttatc gatattttgc aacttgcaaa 360

ccgaatctac ttcgtttgtt caacttgcca actcttctac tttggccact tggttgcagt 420

gtacccgtga caatgtgggc tagtgtctca tatttttttgt atccagatac cgagtacacg 480

gaagcggctg tcaccaatgt actaaataac cactataact ggatcaaaaa ggagaatgta 540

tcgtacattg catacgtcta ttaccaatac gaaaacggag taaggcatat ctacctcaaa 600

aacttgcttg gatgctttgt tcattacttt gtcatgtcga tgacgtttgt tgtgatgttc 660

tactgcggat atgccacgtg gaaaactatg aatgaacaca aggatgtatc tgatagaact 720

cgagcgctac agaaacaact tttcaaagct ttagttcttc agacactcat cccaactatc 780

ttcatgtacg ccccaactgg agtcatgttc atcgcaccgt tttttgacgt gaatttgaat 840

gcaaacgcca atttcattgt gttttgctca tttctgtacc cgggactcga tccactcatt 900

ctgattttga tcattcgtga tttccgaaga acaatattca atttcttgtg tggaaagaaa 960

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gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 1140

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gtgaccaccc tgagctacgg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260

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atcaaggtga acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560

cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 1620

ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680

ctggagttcg tgaccgccgc cgggatcact ctcggcatgg acgagctgta caagtaa 1737

<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 21
agtctagaat gtcgggagaa ttgtggatta 30

<210> 22
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 22
ggggacaagt ttgtacaaaa aagcaggctt catcacgtcg gaacttgag 49

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 23
aaccatgtcg ggagaattgt g 21

<210> 24
<211> 29
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<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 24
tgtagcgctc gcttgtacag ctcgtccat 29

<210> 25
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<212> DNA
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<220>
<223> Oligonucleotide primer

<400> 25
gagctgtaca agcgagcgct acagaaacaa 30

<210> 26
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 26
cttgctggtc atcgtcggaa cttgagaca 29

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 27
caagttccga cgatgaccag caaggtgta 29

<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 28
gttactgctc gttcttca 18

<210> 29
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 29
gagctgtaca agcgagcgct acagaaacaa 30

<210> 30
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 30
gttactgctc gttcttca 18

<210> 31
<211> 21
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<220>
<223> Oligonucleotide primer

<400> 31
aaccatgtcg ggagaattgt g 21

<210> 32
<211> 18
<212> DNA
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<220>
<223> Oligonucleotide primer

<400> 32
gttactgctc gttcttca 18

<210> 33
<211> 21
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<220>
<223> Oligonucleotide primer

<400> 33
aaccatgtcg ggagaattgt g 21

<210> 34
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 34
ctgtagcgct cgctgctcgt tcttcag 27

<210> 35
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 35
aagaacgagc agcgagcgct acagaaaca 29

<210> 36
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 36
cttgctcacc atcgtcggaa cttgagaca 29

<210> 37
<211> 29
<212> DNA
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<220>
<223> Oligonucleotide primer

<400> 37
caagttccga cgatggtgag caagggcga 29

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 38
gttacttgta cagctcgtc 19

<210> 39
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 39

aagaacgagc agcgagcgct acagaaaca 29

<210> 40
<211> 19
<212> DNA
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<223> Oligonucleotide primer

<400> 40
gttacttgta cagctcgtc 19

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 41
aaccatgtcg ggagaattgt g 21

<210> 42
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 42
gttacttgta cagctcgtc 19

<210> 43
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<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 43
caccagtttt gttgtctcag gagtttattt tgtttatcga tattttgcaa ctt 53

<210> 44
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 44
aagttgcaaa atatcgataa acaaaataaa ctcctgagac aacaaaactg gtg 53

<210> 45
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> mCitrine derivative

<400> 45

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

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

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

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

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

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

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

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

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

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

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

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

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

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val

210 215 220

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

<210> 46
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> mCFP derivative

<400> 46

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1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 47
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized ORF encoding SEQ ID NO:45

<400> 47
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aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180

gtcactactt taggttatgg tttgatgtgt tttgctagat acccagatca tatgaaacaa 240

catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300

aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360

aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420

ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480

atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540

cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600

ttatcctatc aatctagatt atccaaagat ccaaacgaaa agagagacca catggtcttg 660

ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaataa 717

<210> 48
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized ORF encoding SEQ ID NO:46

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gatgttaatg gtcacaaatt ttctgtctcc ggtgaaggtg aaggtgatgc tacttacggt 120

aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180

gtcactactt taacttgggg tgttcaatgt ttttctagat acccagatca tatgaaacaa 240

catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300

aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360

aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420

ttggaataca tttataactc tcacaatgtt tacatcactg ctgacaaaca aaagaatggt 480

atcaaagcta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540

cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600

ttatccactc aatctagatt atccaaagat ccaaacgaaa agagagacca catggtcttg 660

ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaataa 717

<210> 49
<211> 2448
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding FRET construct

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acttataaat atctcatggc gtttttctca gtattctcga ttttttacgc catcatcgag 180

ttcatattac gacctataat gcatattgag aacaccactt tctttttgat ctcaaggaaa 240

agattcaact actccaccaa acttggaaaa atcaactctg cgttttactg tgcttgtttt 300

gccaccagtt ttgttgtctc aggagttcac tttgtttatc gatattttgc aacttgcaaa 360

ccgaatctac ttcgtttgtt caacttgcca actcttctac tttggccact tggttgcagt 420

gtacccgtga caatgtgggc tagtgtctca tatttttgt atccagatac cgagtacacg 480

gaagcggctg tcaccaatgt actaaataac cactataact ggatcaaaaa ggagaatgta 540

tcgtacattg catacgtcta ttaccaatac gaaaacggag taaggcatat ctacctcaaa 600

aacttgcttg gatgctttgt tcattacttt gtcatgtcga tgacgtttgt tgtgatgttc 660

tactgcggat atgccacgtg gaaaactatg aatgaacaca aggatgtatc tgatagaact 720

atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 780

gatgttaatg gtcacaaatt ttctgtctcc ggtgaaggtg aaggtgatgc tacttacggt 840

aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 900

gtcactactt taacttgggg tgttcaatgt ttttctagat acccagatca tatgaaacaa 960

catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 1020

aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 1080

aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 1140

ttggaataca tttataactc tcacaatgtt tacatcactg ctgacaaaca aaagaatggt 1200

atcaaagcta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 1260

cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 1320

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tacgccccaa ctggagtcat gttcatcgca ccgtttttg acgtgaattt gaatgcaaac 1560

gccaatttca ttgtgttttg ctcatttctg tacccgggac tcgatccact cattctgatt 1620

ttgatcattc gtgatttccg aagaacaata ttcaatttct tgtgtggaaa gaaaaacagt 1680

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ggtgaagaat tattcactgg tgttgtccca attttggttg aattagatgg tgatgttaat 1800

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ttcaagtctg ccatgccaga aggttatgtt caagaaagaa ctatttttt caaagatgac 2040

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gaattaaaag gtattgattt taaagaagat ggtaacattt taggtcacaa attggaatac 2160

aactataact ctcacaatgt ttacatcatg gctgacaaac aaaagaatgg tatcaaagtt 2220

aacttcaaaa ttagacacaa cattgaagat ggttctgttc aattagctga ccattatcaa 2280

caaaatactc caattggtga tggtccagtc ttgttaccag acaaccatta cttatcctat 2340

caatctagat tatccaaaga tccaaacgaa aagagagacc acatggtctt gttagaattt 2400

gttactgctg ctggtattac ccatggtatg gatgaattgt acaaataa 2448

<210> 50
<211> 815
<212> PRT
<213> Artificial Sequence

<220>
<223> FRETConstruct

<400> 50

Met Ser Gly Glu Leu Trp Ile Thr Leu Val Asp Thr Ala Asp Ile Val
1 5 10 15

Gly Val Thr Leu Thr Phe Cys Val Asn Ile Val Leu Leu Gly Leu Leu

20 25 30

Lys Thr Arg Gly Lys Asn Leu Gly Thr Tyr Lys Tyr Leu Met Ala Phe
35 40 45

Phe Ser Val Phe Ser Ile Phe Tyr Ala Ile Ile Glu Phe Ile Leu Arg
50 55 60

Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg Lys
65 70 75 80

Arg Phe Asn Tyr Ser Thr Lys Leu Gly Lys Ile Asn Ser Ala Phe Tyr
85 90 95

Cys Ala Cys Phe Ala Thr Ser Phe Val Val Ser Gly Val His Phe Val
100 105 110

Tyr Arg Tyr Phe Ala Thr Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
115 120 125

Leu Pro Thr Leu Leu Leu Trp Pro Leu Gly Cys Ser Val Pro Val Thr
130 135 140

Met Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
145 150 155 160

Glu Ala Ala Val Thr Asn Val Leu Asn Asn His Tyr Asn Trp Ile Lys
165 170 175

Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
180 185 190

Gly Val Arg His Ile Tyr Leu Lys Asn Leu Leu Gly Cys Phe Val His
195 200 205

Tyr Phe Val Met Ser Met Thr Phe Val Val Met Phe Tyr Cys Gly Tyr
210 215 220

Ala Thr Trp Lys Thr Met Asn Glu His Lys Asp Val Ser Asp Arg Thr
225 230 235 240

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
245 250 255

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
260 265 270

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        275                 280                 285

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    290                 295                 300

Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
305                 310                 315                 320

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                325                 330                 335

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            340                 345                 350

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        355                 360                 365

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Ile
    370                 375                 380

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
385                 390                 395                 400

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                405                 410                 415

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            420                 425                 430

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Arg Leu Ser
        435                 440                 445

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    450                 455                 460

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Arg Ala
465                 470                 475                 480

Leu Gln Lys Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Leu Ile Pro
                485                 490                 495

Thr Ile Phe Met Tyr Ala Pro Thr Gly Val Met Phe Ile Ala Pro Phe
            500                 505                 510

Phe Asp Val Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe Cys Ser
        515                 520                 525
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Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Leu Ile Ile Arg
530 535 540

Asp Phe Arg Arg Thr Ile Phe Asn Phe Leu Cys Gly Lys Lys Asn Ser
545 550 555 560

Val Asp Glu Ser Arg Ser Thr Thr Arg Ala Asn Leu Ser Gln Val Pro
565 570 575

Thr Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
580 585 590

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
595 600 605

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
610 615 620

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
625 630 635 640

Leu Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
645 650 655

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
660 665 670

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
675 680 685

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
690 695 700

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
705 710 715 720

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
725 730 735

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
740 745 750

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
755 760 765

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Arg Leu
770 775 780

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
785 790 795 800

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
805 810 815

<210> 51
<211> 2694
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding BRET construct

<400> 51
atgggttctg gtcaattatg gttggcttta gttgatgctg cagatatggt tggttttact 60

ttgacaatct caattaatat cattttgtta ggtttgatta gaactagagg taaaaccttg 120

ggtacttaca agtacttgat gtctttcttt tctttctttt ctattttcta tgcaatcgtt 180

gaatctatct tgagaccaat catgcatatc gaaaacacta cattttttctt aatctccaga 240

aagagattcg attacagtac tagattgggt aaaattaatt cagctttcta ctgtgcttgt 300

ttcgcaacat ccttcgtttt gagtgcagtt catttcgttt acagatactt cgctgcttgt 360

aagcctaatt tgttgagatt gtttaactta cctcatttgt tattgtggcc attgatgtgt 420

tcaattcctg ttactgcttg ggcatctgtt tcatactttt tgtacccaga tacagaatat 480

accgaagctg cagttaccta tgttttgaag actcattacg aagttattaa aaaggaaaac 540

gtttcttaca ttgcttacgt ttactaccaa tacgaaaacg gtgaaagaca tatctatatt 600

aaaaacttat tgggttgttt cgttcattac ttcgttatgt ctatgacatt cgttgttgtt 660

ttctattgtg gtttctcaac ttggtggaca attagagaac atagaggtgc ttccgataga 720

acaatggtta gtaagggtga agaattattc accggtgttg ttccaatttt ggttgaatta 780

gatggtgacg ttaatggtca taaattttcc gttagtggtg aaggtgaagg tgacgcaaca 840

tacggtaaat tgaccttgaa gtttatttgt accactggta aattgccagt tccttggcca 900

accttggtta caaccttaac ttatggtgtt caatgttttt ccagataccc tgatcatatg 960

aagcaacatg atttctttaa gagtgctatg ccagaaggtt acgttcaaga aagaacaatt 1020

ttctttaagg atgatggtaa ctacaagact agagcagagg ttaagttcga aggtgacaca 1080

ttggttaaca gaatcgaatt gaagggtatc gatttcaagg aagatggtaa catcttgggt 1140

cataagttgg aatacaatta caactcccat aacgtttaca tcatggctga taagcaaaag 1200

aatggtatta aagttaactt caagatcaga cataacatcg aagatggttc agttcaattg 1260

gcagatcatt accaacaaaa cacccctatt ggtgacggtc ctgttttgtt gccagataac 1320

cattacttat caactcaatc cgctttgagt aaggatccaa acgaaaagag agatcatatg 1380

gttttgttgg aattcgttac tgctgcaggt atcacattgg gtatggatga attgtacaag 1440

agacatttgc atagacaatt gtttaaagct ttggttttcc aaaccttggt tccatcaatt 1500

tttatgtaca tccctactgg tgttatgttc atcgcaccat ttttcgatat caatttgaac 1560

gctaacgcaa acttcatcgt tttctgttca tttttgtatc ctggtttgga tccattgatc 1620

ttgattttca ttatcagaga attcagagtt acaattttaa acattattcg tggtaatgaa 1680

cgtggtaacg ctgttggtga agcatactct acctcaagaa ttaaatcttc acaaccagct 1740

gcagttaatt tgtctggtat gacatcaaag gtttacgatc ctgaacaaag aaaaagaatg 1800

attaccggtc cacaatggtg ggctcgttgt aagcaaatga acgttttgga ttctttcatt 1860

aactactacg attcagaaaa gcatgctgaa aacgctgtta ttttcttgca tggtaacgct 1920

gcatccagtt atttgtggag acatgttgtt cctcatattg aaccagttgc tagatgtatc 1980

atccctgatt tgatcggtat gggtaaatct ggtaaatctg gtaacggttc ttacagattg 2040

ttggatcatt acaagtactt aactgcatgg ttcgaattgt tgaatttgcc aaagaaaatt 2100

atcttcgttg gtcatgattg gggtgcttgt ttggcatttc attactctta cgaacatcaa 2160

gataaaatta aggctatcgt tcatgcagaa tccgttgttg atgttattga aagttgggat 2220

gaatggccag atatcgaaga agatatcgct ttaattaagt ccgaagaagg tgaaaagatg 2280

gttttggaaa acaacttttt cgttgaaact atgttgccta gtaagatcat gagaaagttg 2340

gaacctgaag aatttgctgc atatttggaa ccattcaaag aaaagggtga agttagaaga 2400

cctacattat cttggcctag agaaattcca ttggttaaag gtggtaaacc agatgttgtt 2460

caaatcgtta gaaactacaa cgcttactta agagcatctg atgatttgcc aaagatgttc 2520

atcgaatctg atcctggttt cttttctaat gctattgttg aaggtgctaa gaaattccct 2580

aacacagaat tcgttaaggt taagggtttg catttctctc aagaagatgc tccagatgaa 2640

atgggtaaat acatcaagtc atttgttgaa agagttttga aaaatgaaca ataa 2694

<210> 52
<211> 897
<212> PRT
<213> Artificial Sequence

<220>
<223> BRET Construct

<400> 52

Met Gly Ser Gly Gln Leu Trp Leu Ala Leu Val Asp Ala Ala Asp Met
1 5 10 15

Val Gly Phe Thr Leu Thr Ile Ser Ile Asn Ile Ile Leu Leu Gly Leu
20 25 30

```
Ile Arg Thr Arg Gly Lys Thr Leu Gly Thr Tyr Lys Tyr Leu Met Ser
        35                  40                  45

Phe Phe Ser Phe Phe Ser Ile Phe Tyr Ala Ile Val Glu Ser Ile Leu
    50                  55                  60

Arg Pro Ile Met His Ile Glu Asn Thr Thr Phe Phe Leu Ile Ser Arg
65                  70                  75                  80

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

Tyr Cys Ala Cys Phe Ala Thr Ser Phe Val Leu Ser Ala Val His Phe
            100                 105                 110

Val Tyr Arg Tyr Phe Ala Ala Cys Lys Pro Asn Leu Leu Arg Leu Phe
        115                 120                 125

Asn Leu Pro His Leu Leu Leu Trp Pro Leu Met Cys Ser Ile Pro Val
    130                 135                 140

Thr Ala Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr
145                 150                 155                 160

Thr Glu Ala Ala Val Thr Tyr Val Leu Lys Thr His Tyr Glu Val Ile
                165                 170                 175

Lys Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu
            180                 185                 190

Asn Gly Glu Arg His Ile Tyr Ile Lys Asn Leu Leu Gly Cys Phe Val
        195                 200                 205

His Tyr Phe Val Met Ser Met Thr Phe Val Val Val Phe Tyr Cys Gly
    210                 215                 220

Phe Ser Thr Trp Trp Thr Ile Arg Glu His Arg Gly Ala Ser Asp Arg
225                 230                 235                 240

Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
                245                 250                 255

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
            260                 265                 270

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

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
290 295 300

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
305 310 315 320

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
325 330 335

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
340 345 350

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
355 360 365

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
370 375 380

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
385 390 395 400

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
405 410 415

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
420 425 430

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
435 440 445

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
450 455 460

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
465 470 475 480

Arg His Leu His Arg Gln Leu Phe Lys Ala Leu Val Phe Gln Thr Leu
485 490 495

Val Pro Ser Ile Phe Met Tyr Ile Pro Thr Gly Val Met Phe Ile Ala
500 505 510

Pro Phe Phe Asp Ile Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe
515 520 525

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Cys Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Phe Ile
    530                 535                 540

Ile Arg Glu Phe Arg Val Thr Ile Leu Asn Ile Ile Arg Gly Asn Glu
545                 550                 555                 560

Arg Gly Asn Ala Val Gly Glu Ala Tyr Ser Thr Ser Arg Ile Lys Ser
                565                 570                 575

Ser Gln Pro Ala Ala Val Asn Leu Ser Gly Met Thr Ser Lys Val Tyr
            580                 585                 590

Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala
        595                 600                 605

Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp
    610                 615                 620

Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala
625                 630                 635                 640

Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile Glu Pro Val
                645                 650                 655

Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys
            660                 665                 670

Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr
        675                 680                 685

Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly
    690                 695                 700

His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr Ser Tyr Glu His Gln
705                 710                 715                 720

Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser Val Val Asp Val Ile
                725                 730                 735

Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile
            740                 745                 750

Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val
        755                 760                 765

Glu Thr Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu
    770                 775                 780
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Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg
785 790 795 800

Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys
805 810 815

Pro Asp Val Val Gln Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala
820 825 830

Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe
835 840 845

Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe
850 855 860

Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu
865 870 875 880

Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu
885 890 895

Gln

<210> 53
<211> 2673
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF encoding 2A adrenergic receptor-BRET construct

<400> 53
atgggttatc cttacgatgt tccagattat gcttcaatgg gttccttaca accagatgct 60

ggtaattctt catggaacgg tacagaagct ccaggtggtg gtaccagagc aactccatac 120

tcattgcaag ttacattgac cttagtttgt ttggctggtt tgttgatgtt gtttactgtt 180

ttcggtaacg ttttggttat tatcgcagtt tttacatcta gagctttgaa ggcaccacaa 240

aatttgttct tagttagttt ggcttctgca gatatcttgg ttgctacatt agttattcct 300

ttttctttgg caaacgaagt tatgggttat tggtacttcg gtaaagtttg gtgtgaaata 360

tatttggctt tggatgtttt gttttgtact tccagtatcg ttcatttgtg tgctatctct 420

ttggatagat actggtcaat cacacaagca atcgaataca atttgaagag aaccccaaga 480

agaattaaag ctatcatcgt tactgtttgg gttatttccg cagttattag ttttccacct 540

ttgatttcca ttgaaaagaa aggtgctggt ggtggtcaac aacctgcaga accaagttgt 600

aagattaatg atcaaaagtg gtatgttatt tcttcatcca ttggttcttt ctttgctcca 660

tgtttgatca tgatcttggt ttacgttaga atctatcaaa tcgctaagag aagaactaga 720

gttccacctt ctagaagagg tccagatgca atggtttcaa aaggtgaaga attgtttact 780

ggtgttgttc ctattttggt tgaattagat ggtgacgtta atggtcataa gtttagtgtt 840

tctggtgaag gtgaaggtga cgctacatac ggtaaattga ccttgaagtt tatttgtact 900

actggtaaat tgccagttcc ttggccaacc ttggttacca ctttaactta tggtgttcaa 960

tgtttttcca gatacccaga tcatatgaag caacatgatt tctttaagag tgctatgcct 1020

gaaggttacg ttcaagaaag aactattttc tttaaggatg atggtaacta caagacaaga 1080

gcagaggtta agtttgaagg tgacaccttg gttaacagaa tcgaattgaa gggtatcgat 1140

ttcaaggaag atggtaacat cttgggtcat aagttggaat acaattacaa ctcccataac 1200

gtttacatca tggctgataa gcaaaagaat ggtattaaag ttaacttcaa gatcagacat 1260

aacatcgaag atggttcagt tcaattggca gatcattacc aacaaaacac accaattggt 1320

gacggtcctg ttttgttacc agataaccat tacttgtcaa cccaatccgc tttaagtaaa 1380

gatcctaacg aaaagagaga tcatatggtt ttgttggaat tcgttactgc tgcaggtatc 1440

acattgggta tggatgaatt gtacaagaga tggagaggta gacaaaacag agaaaagaga 1500

ttcactttcg ttttggctgt tgttattggt gttttcgttg tttgttggtt cccatttttc 1560

tttacttaca cattgatcgc agttggttgt cctgttccat ctcaattgtt caacttcttt 1620

ttctggttcg gttactgtaa cagttctttg aacccagtta tatatactat tttcaatcat 1680

gatttcagaa gagcttttaa aaagattttg tgtagaggtg acagaaagag aatcgttatg 1740

acctctaagg tttacgatcc agaacaaaga aagagaatga ttactggtcc tcaatggtgg 1800

gcacgttgta agcaaatgaa cgttttggat tcttttatta actactacga ttcagaaaag 1860

catgctgaaa acgcagttat tttcttgcat ggtaacgctg catcatccta tttgtggaga 1920

catgttgttc ctcatattga accagttgct agatgtatca tcccagattt gatcggtatg 1980

ggtaaatctg gtaaatctgg taacggttct tacagattgt tggatcatta caagtacttg 2040

acagcatggt tcgaattgtt gaatttgcca aagaaaatta tcttcgttgg tcatgattgg 2100

ggtgcttgtt tggcattcca ttactcatac gaacatcaag ataaaattaa ggctatcgtt 2160

catgcagaat ccgttgttga tgttattgaa agttgggatg aatggccaga tatcgaagaa 2220

gatatcgctt taattaagtc tgaagaaggt gaaaagatgg ttttggaaaa caacttttc 2280

gttgaaacca tgttgccttc aaagatcatg agaaagttgg aaccagaaga attcgctgca 2340

tatttggaac cttttaaaga aaagggtgaa gttagaagac caactttgtc atggcctaga 2400

gaaattccat tagttaaagg tggtaaacct gatgttgttc aaatcgttag aaactacaac 2460

gcttacttga gagcatctga tgatttgcct aagatgttca tcgaatccga tccaggtttc 2520

ttttctaatg ctattgttga aggtgctaag aaattcccaa acactgaatt cgttaaggtt 2580

aagggtttgc atttctctca agaagatgct cctgatgaaa tgggtaaata catcaagtca 2640

ttcgttgaaa gagttttgaa aaatgaacaa taa 2673

<210> 54
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> 2A adrenergic receptor-BRET construct

<400> 54

Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Met Gly Ser Leu
1 5 10 15

Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly
20 25 30

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
35 40 45

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
65 70 75 80

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

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
115 120 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
210 215 220

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

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Met Val Ser Lys Gly Glu
245 250 255

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
260 265 270

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
275 280 285

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
290 295 300

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
305 310 315 320

Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
325 330 335

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
340 345 350

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
355 360 365

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

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
385 390 395 400

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
405 410 415

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
420 425 430

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp

435 440 445

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
450 455 460

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
465 470 475 480

Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Trp Arg Gly Arg Gln Asn
485 490 495

Arg Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe
500 505 510

Val Val Cys Trp Phe Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val
515 520 525

Gly Cys Pro Val Pro Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly
530 535 540

Tyr Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His
545 550 555 560

Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys
565 570 575

Arg Ile Val Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
580 585 590

Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
595 600 605

Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
610 615 620

Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
625 630 635 640

His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
645 650 655

Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
660 665 670

Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn
675 680 685

Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu
690 695 700

Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
705 710 715 720

His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
725 730 735

Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
740 745 750

Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
755 760 765

Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
770 775 780

Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
785 790 795 800

Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
805 810 815

Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
820 825 830

Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
835 840 845

Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
850 855 860

Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
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Phe Val Glu Arg Val Leu Lys Asn Glu Gln
885 890

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Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
35 40 45

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Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
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Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
65                  70                  75                  80

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

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
            100                 105                 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
        115                 120                 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
    130                 135                 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
145                 150                 155                 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
                165                 170                 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
            180                 185                 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
        195                 200                 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
    210                 215                 220

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

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly
                245                 250                 255

Gly Ala Asp Arg Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly
            260                 265                 270

Pro Thr Gly Ala Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala
        275                 280                 285

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

Gly Pro Gly Ala Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly
        355                 360                 365

Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe
    370                 375                 380

Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe
385                 390                 395                 400

Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val Gly Cys Pro Val Pro
                405                 410                 415

Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser
            420                 425                 430

Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala
        435                 440                 445

Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val
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