G00002

163163

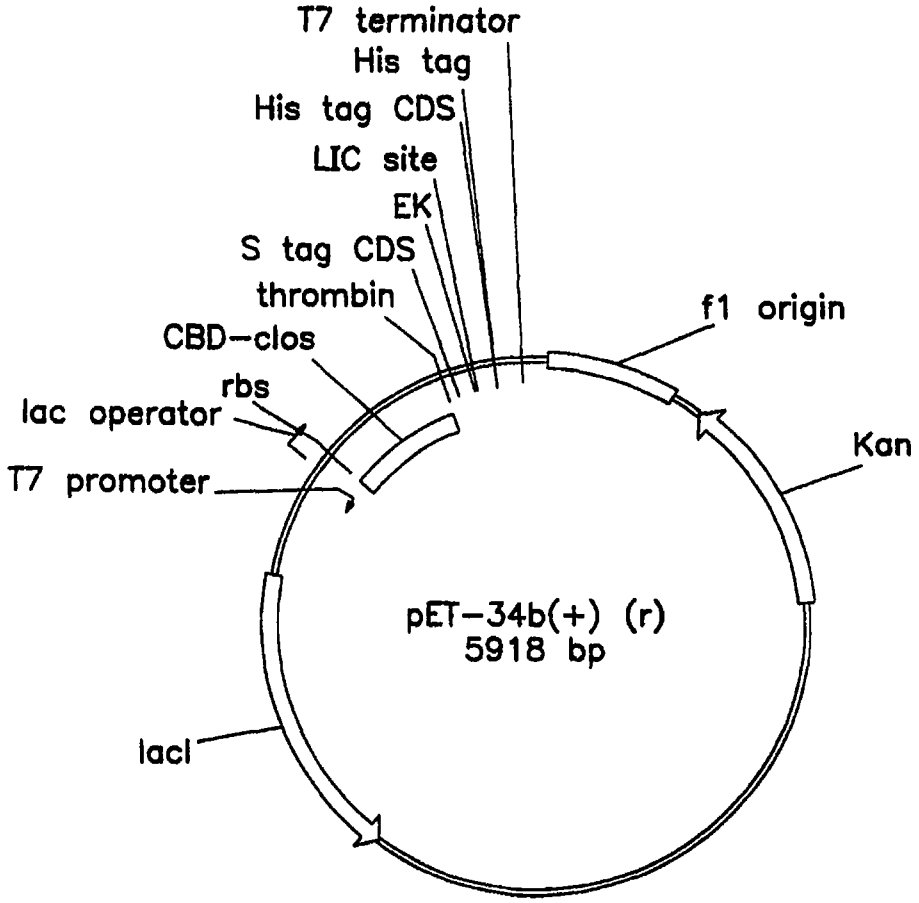


FIG. 1

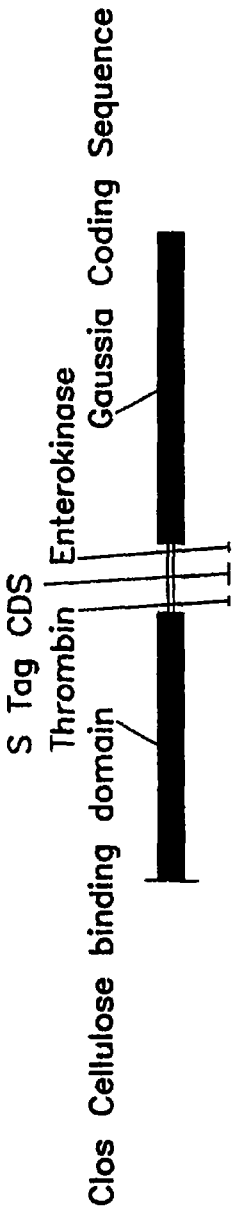

Clos Cellulose binding domain
S Tag CDS
Thrombin
Enterokinase
Gaussia Coding Sequence
CBD—Gaussia luciferase fusion protein
1146 bp

FIG. 2

SUBSTITUTE SHEET (RULE 26)

```
R. reniformis            MDLAKLGLKEVMPTKINLEGLVGDHAFSMEGVGEGNILEG   VKIS
                           |    | |||  | ||||  |  | | |||  | ||||  |   | |
R. mullerei            1 MSKQILKNTCLQEVMSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIR

R. reniformis              VTKGAPLPFAFDIVSVAF     AYTGYPEEIS  DYFLQSFPEGFTYErG
                           |||||||||||||||| ||       | ||  ||  ||| |||| || |||
R. mullerei           51 VTKGAPLPFAFDIVSPAFQYGNRTFTKYPNDIS--DYFIQSFPAGFMYER

R. reniformis              NIrYQDGGTAIvKS
                              | |||     |
R. mullerei           99 TLRYEDGGLVEIRSDINLIEDKFVYRVEYKGSNFPDDGPVMQKTILGIEP

R. reniformis            eSMY TNVTSVIGqIIAFKL QTGKHFTYHMRTVYKSKKPVETMPLYH
                         | ||  |   |   |   ||   ||    ||| |  |||  |   | ||
R. mullerei          149 SFEAMYMNNGVLVGEVILVYKL-NSGKYYSCHMKTLMKSKGVVKEFPSYH

R. reniformis              FIQHRL  VKTNVDTASGYVVQHETAIAAHSTIKKIEgaar
                           ||||||   || |    | | |||||||    | |
R. mullerei           198 FIQHRL--EKTYVED-GGFVEQHETAIAQMTSIGKPLGSLHEWV
```

FIG. 3

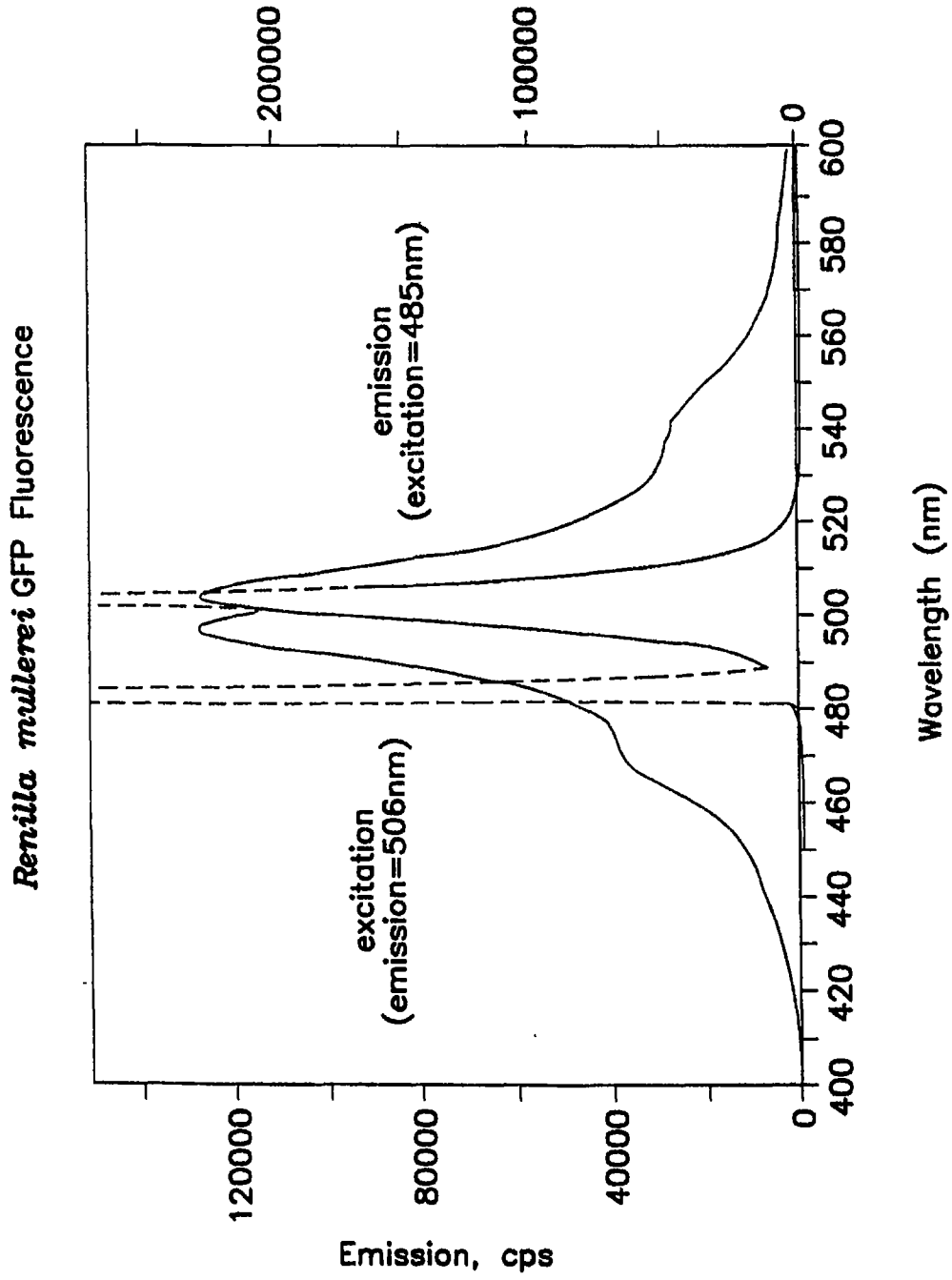

Renilla mulleri GFP Fluorescence
emission
(excitation=485nm)
excitation
(emission=506nm)
Emission, cps
Wavelength (nm)
200000
100000
0
120000
80000
40000
0
400
420
440
460
480
500
520
540
560
580
600

FIG. 4

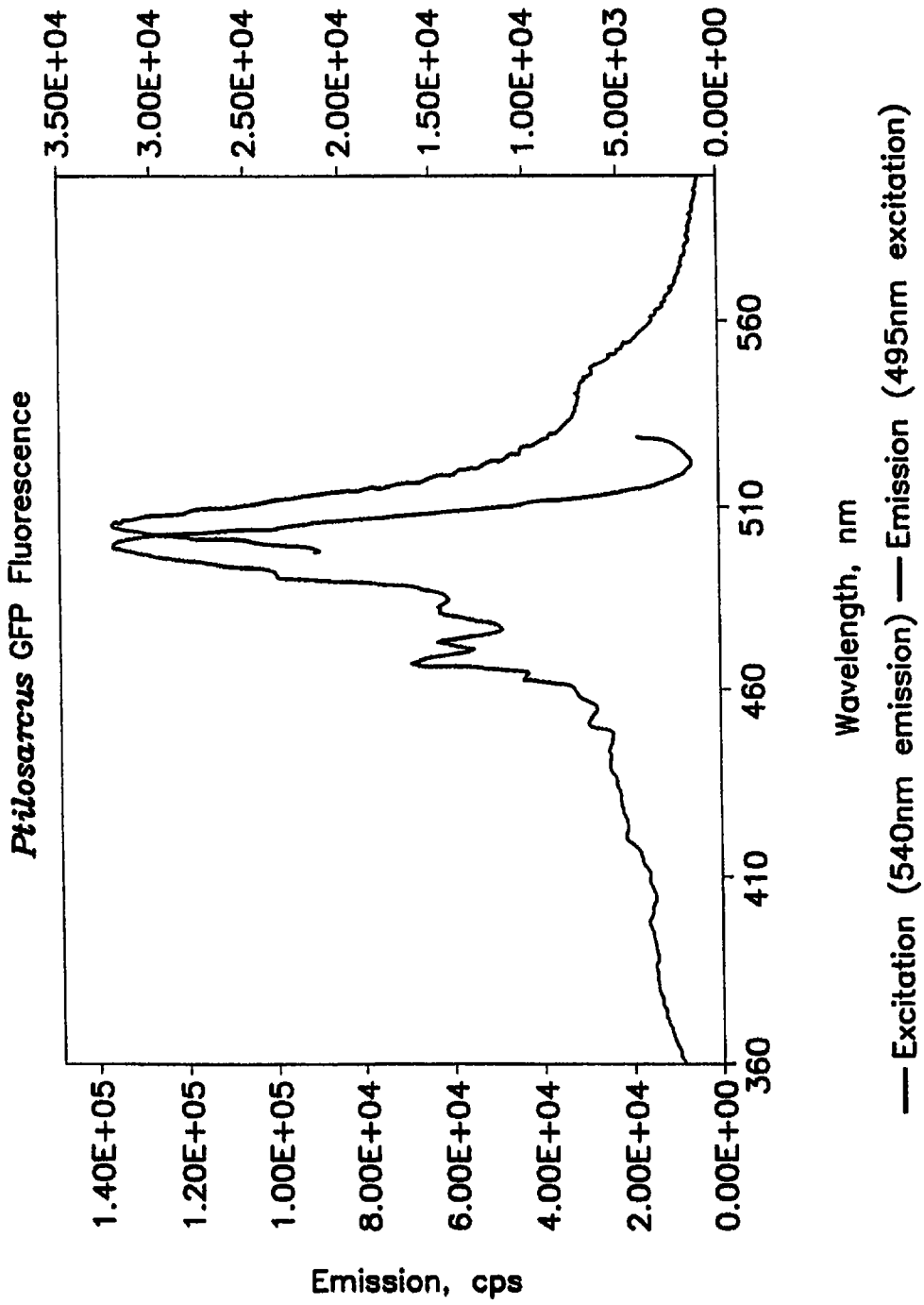

Ptilosarcus GFP Fluorescence
Emission, cps
1.40E+05
1.20E+05
1.00E+05
8.00E+04
6.00E+04
4.00E+04
2.00E+04
0.00E+00
3.50E+04
3.00E+04
2.50E+04
2.00E+04
1.50E+04
1.00E+04
5.00E+03
0.00E+00
360
410
460
510
560
Wavelength, nm
— Excitation (540nm emission) — Emission (495nm excitation)

FIG. 5

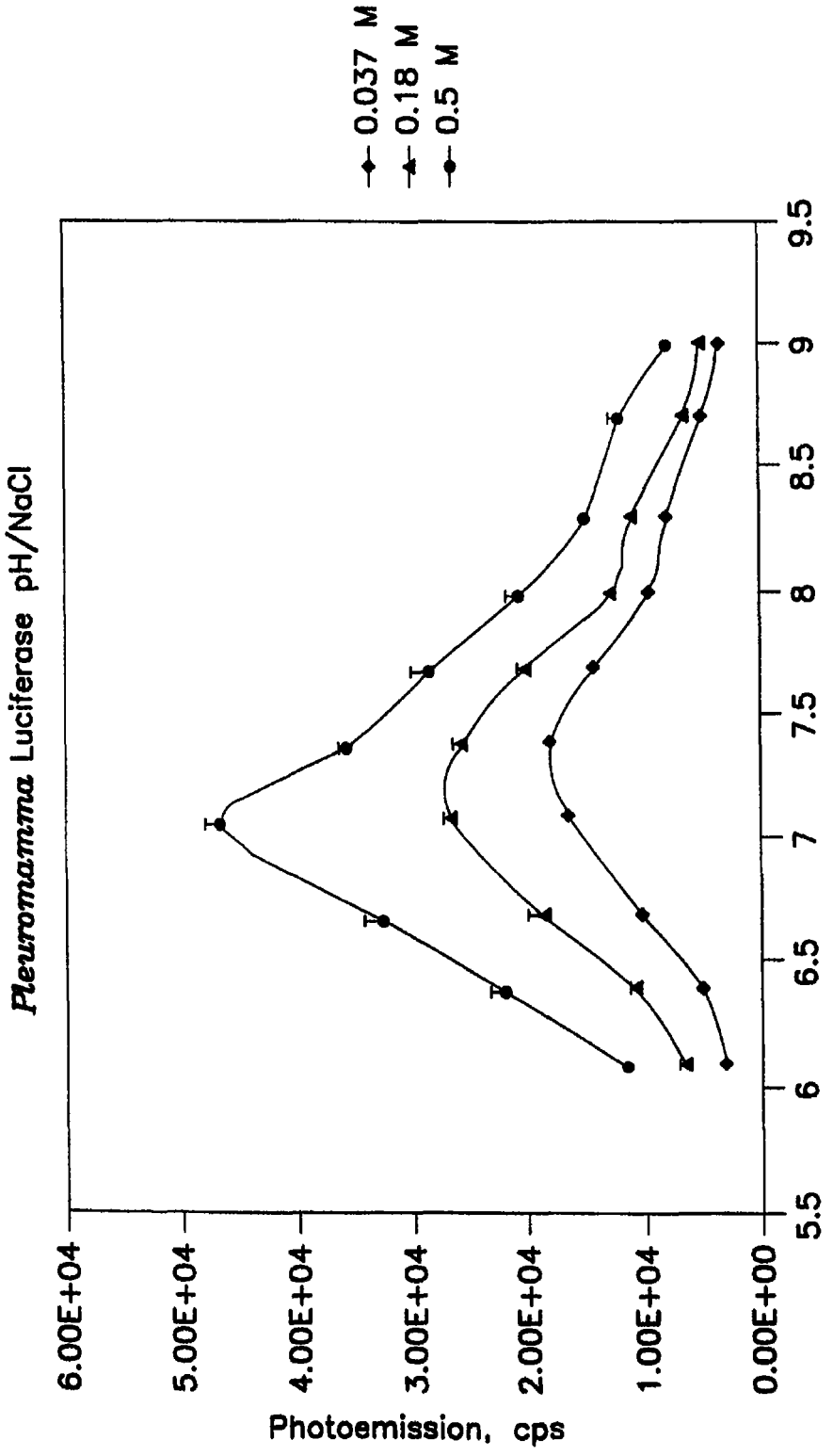

0.037 M
0.18 M
0.5 M
Pleuromamma Luciferase pH/NaCl
Photoemission, cps
6.00E+04
5.00E+04
4.00E+04
3.00E+04
2.00E+04
1.00E+04
0.00E+00
5.5
6
6.5
7
7.5
8
8.5
9
9.5
pH

FIG. 6

17 SEP 2002

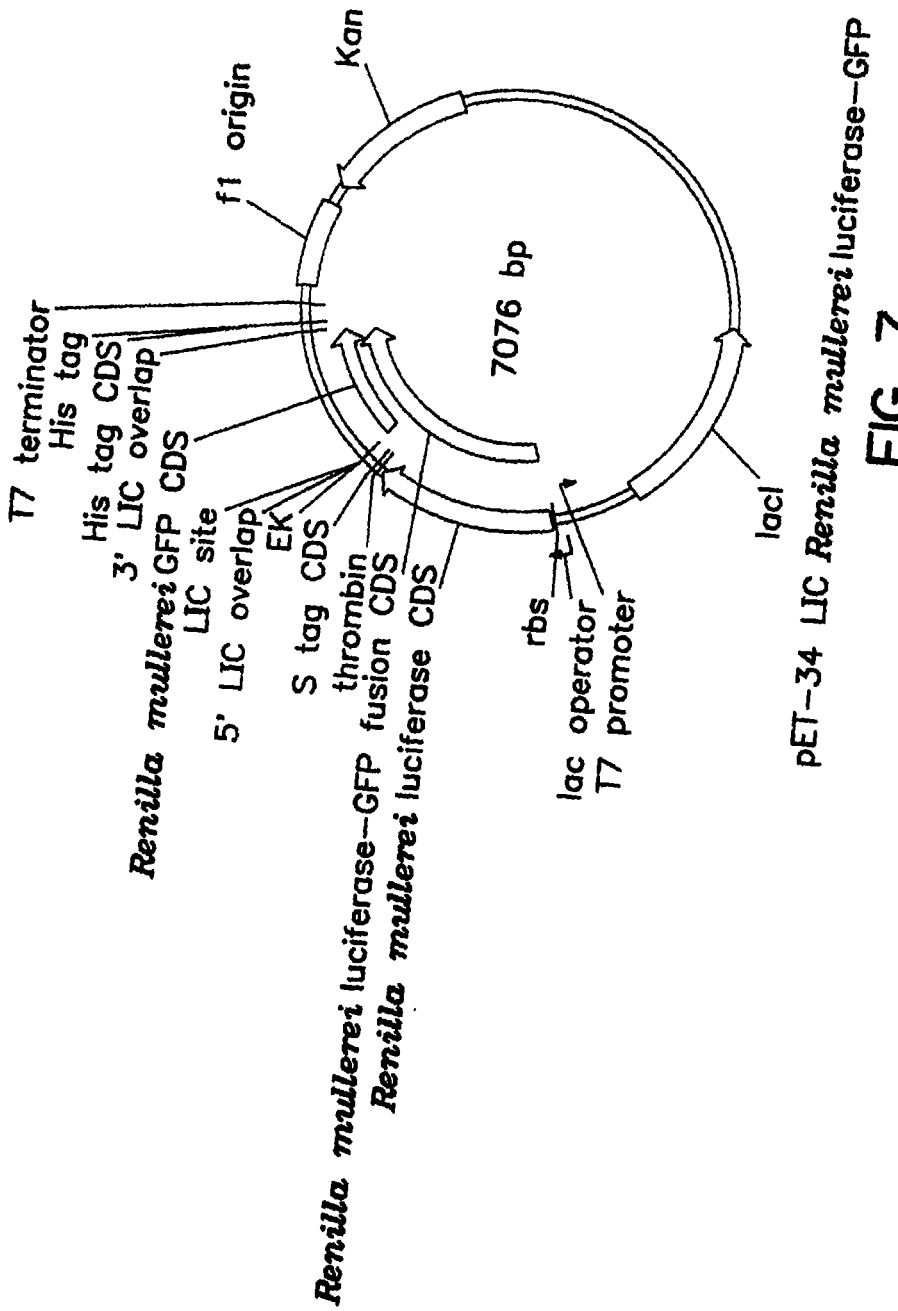


FIG. 7

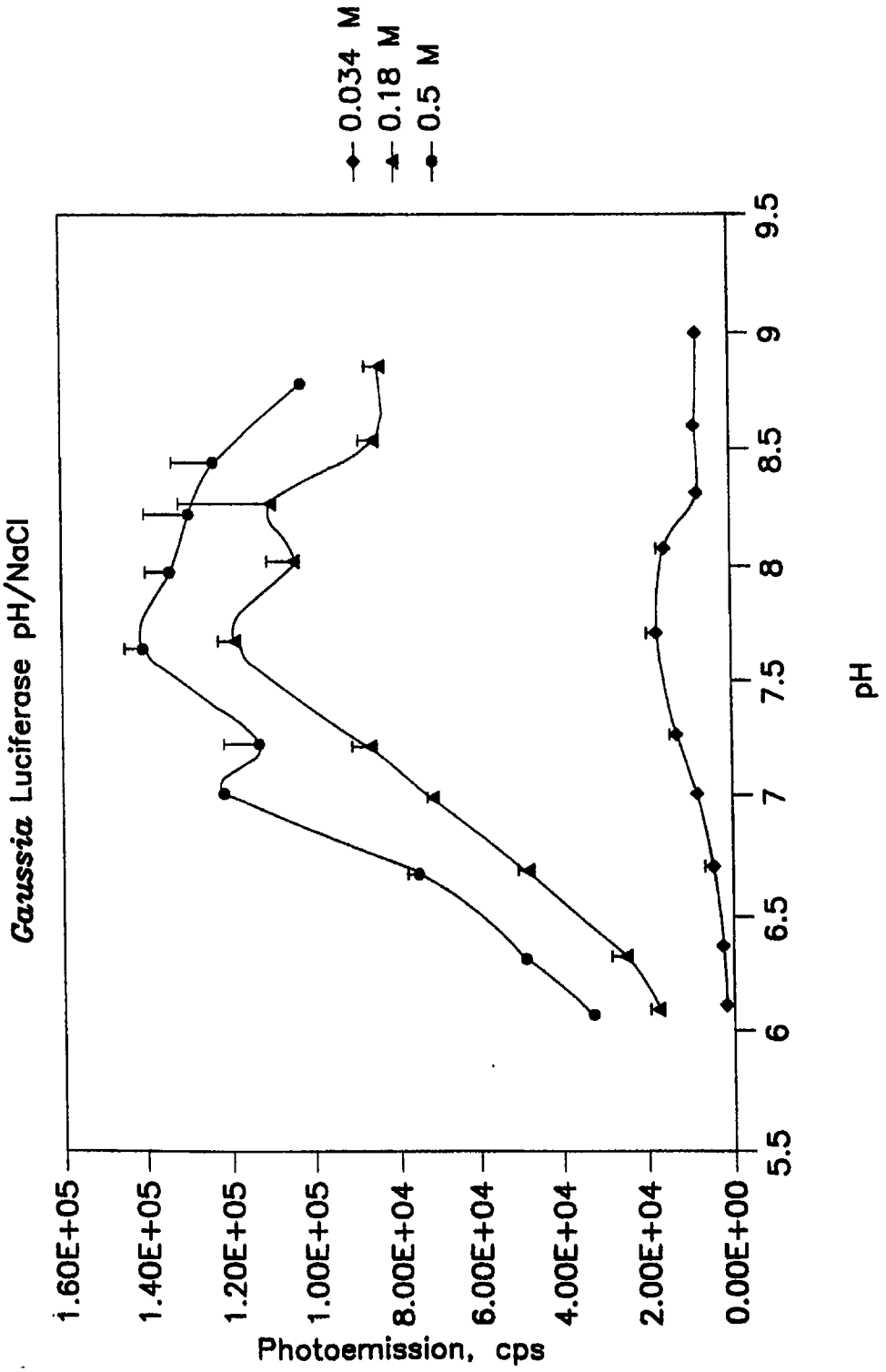

0.034 M
0.18 M
0.5 M
Gaussia Luciferase pH/NaCl
Photoemission, cps
1.60E+05
1.40E+05
1.20E+05
1.00E+05
8.00E+04
6.00E+04
4.00E+04
2.00E+04
0.00E+00
5.5
6
6.5
7
7.5
8
8.5
9
9.5
pH

FIG. 8

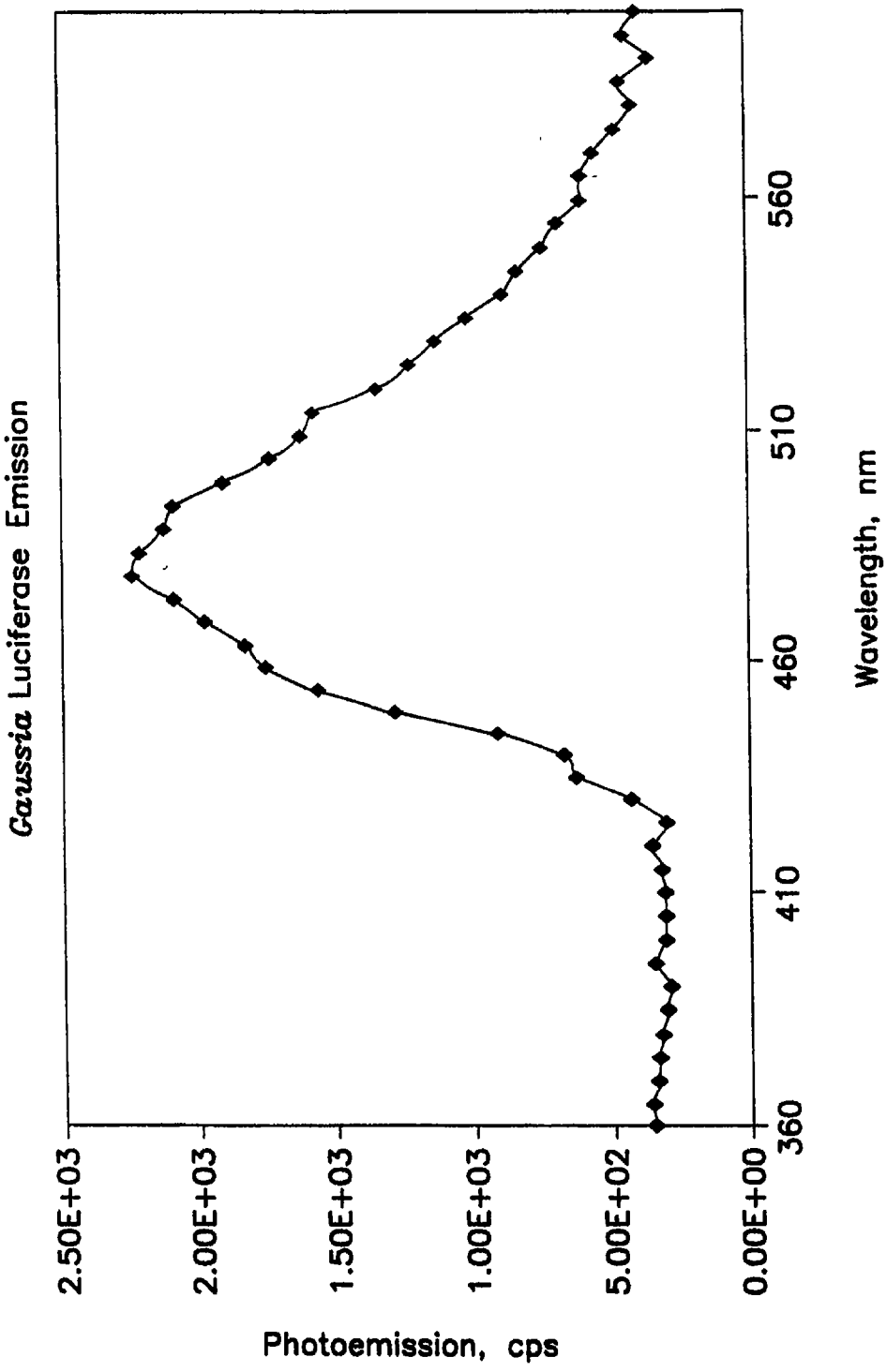

Gaussia Luciferase Emission
Photoemission, cps
2.50E+03
2.00E+03
1.50E+03
1.00E+03
5.00E+02
0.00E+00
360
410
460
510
560
Wavelength, nm

FIG. 9

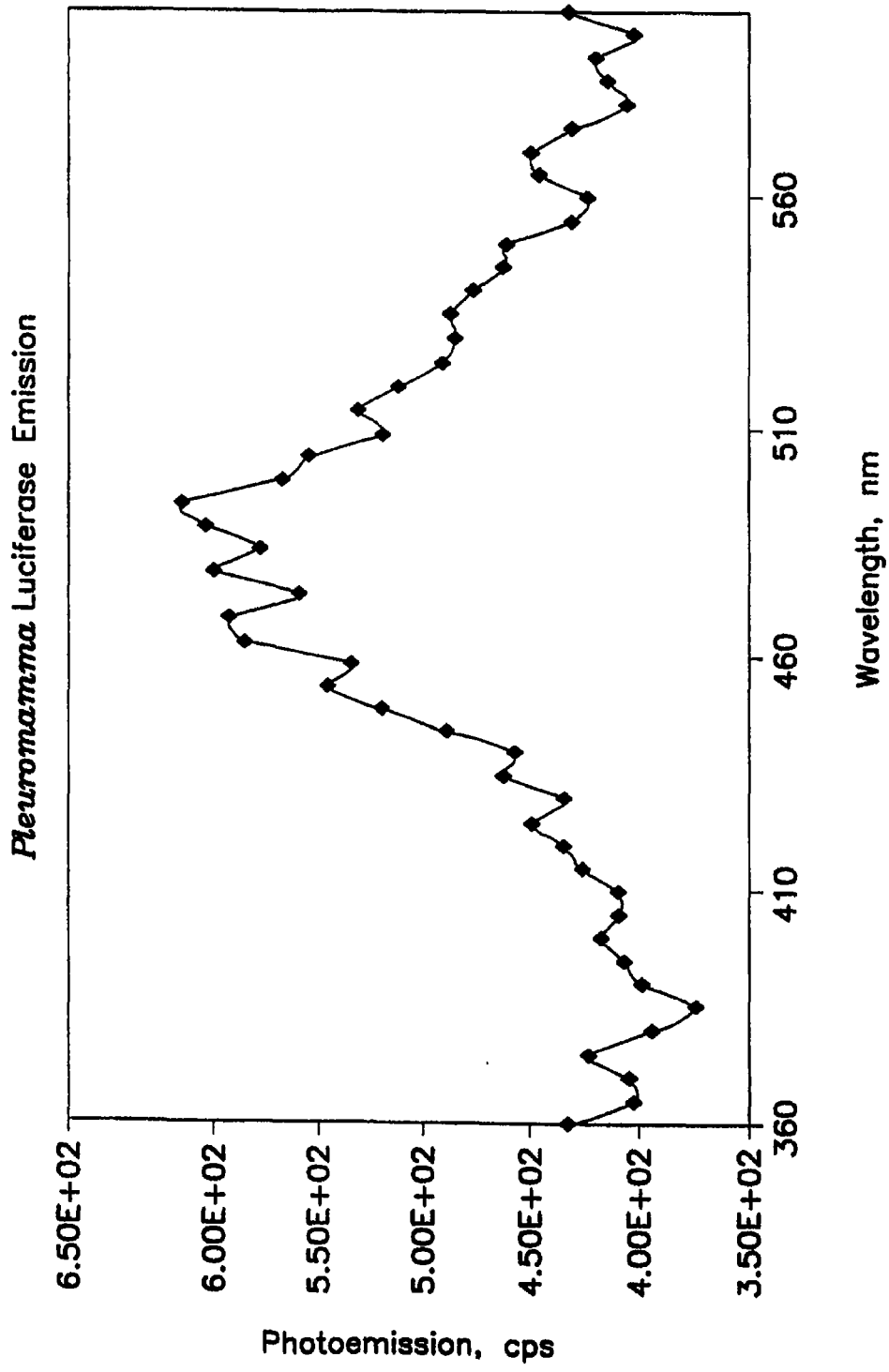

Pleuromamma Luciferase Emission
6.50E+02
6.00E+02
5.50E+02
5.00E+02
4.50E+02
4.00E+02
3.50E+02
Photoemission, cps
360
410
460
510
560
Wavelength, nm

FIG. 10

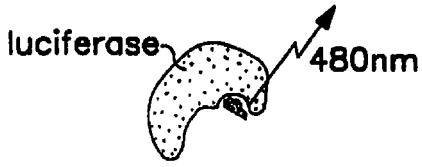


FIG. 11A

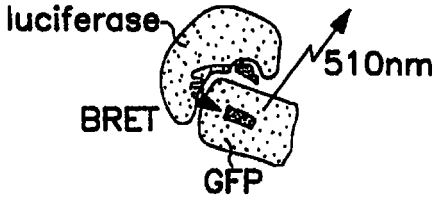


FIG. 11C

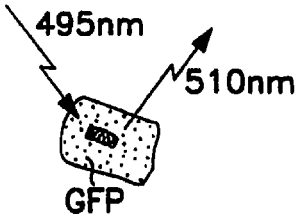


FIG. 11B

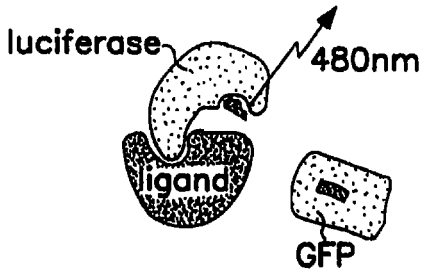


FIG. 11D

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT:
(A) NAME: PROLUME, LTD.
(B) STREET: 1085 William Pitt Way
(D) STATE: Pennsylvania
(D) COUNTRY: USA
(E) POSTAL CODE (ZIP): 15236

(i) INVENTOR/APPLICANT:
(A) NAME: Bryan, Bruce
(B) STREET: 716 Arden Drive
(C) CITY: Beverly Hills
(D) STATE: California
(D) COUNTRY: USA
(E) POSTAL CODE (ZIP): 90210

(i) INVENTOR/APPLICANT:
(A) NAME: Szent-Gyorgyi, Christopher
(B) STREET: 719 Duncan Avenue
(C) CITY: Pittsburgh
(D) STATE: Pennsylvania
(D) COUNTRY: USA
(E) POSTAL CODE (ZIP): 15237

(ii) TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCIFERASES AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH THROUGHPUT SCREENING AND NOVELTY ITEMS

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4250 Executive Square, 7th Floor
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE:
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5 and ASCII

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 26-MAR-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/102,939
(B) FILING DATE: 01-OCT-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/089,367
(B) FILING DATE: 15-JUNE-1998

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:60/079,624
(B) FILING DATE: 27-MAR-1998

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24729-P121

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619 450-8400
(B) TELEFAX: 619-450-8499
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...942
(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG      48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
 1               5                  10                  15

ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT      96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
            20                  25                  30

CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT     144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
        35                  40                  45

GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA     192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
    50                  55                  60

CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT     240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
65                  70                  75                  80
```

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CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG      288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
                85                  90                  95

TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT      336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
            100                 105                 110

TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG      384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
        115                 120                 125

GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT      432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
    130                 135                 140

CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT      480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
145                 150                 155                 160

GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA      528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
                165                 170                 175

ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA      576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
            180                 185                 190

ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA      624
Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
        195                 200                 205

TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT      672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
    210                 215                 220

GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT      720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
225                 230                 235                 240

AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG      768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
                245                 250                 255

TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC      816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
            260                 265                 270

GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT      864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
        275                 280                 285

TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG      912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
    290                 295                 300

TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA TTACTTTGGT TTTTTATTTA    965
Phe Val Glu Arg Val Leu Lys Asn Glu Gln
305                 310

CATTTTTCCC GGGTTTAATA ATATAAATGT CATTTTCAAC AATTTTATTT TAACTGAATA   1025
```

```
TTTCACAGGG AACATTCATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC  1085
ATTTTGGAAT ATTACCTCTT TCAATGAAAC TTTATAAACA GTGGTTCAAT TAATTAATAT  1145
ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTTA TTATAAAAAA A           1196
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1665
(D) OTHER INFORMATION: Cypridina hilgendorfii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC      48
Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val
 1               5                  10                  15

AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA      96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
            20                  25                  30

CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT     144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
        35                  40                  45

ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT     192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
    50                  55                  60

GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTA ATT     240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
65                  70                  75                  80

GAA TCC AGA GTA GAA GCT GCT GGA TAT TTT AGA ACG TTT TAC GCC AAA     288
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
                85                  90                  95

AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT CGA GGA ACC     336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
            100                 105                 110

AAG GGT GGC GAC TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA     384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
        115                 120                 125

CAG AAG GGA GCT GTA CTG ACT AAG ACA ACA CTG GAG GTA GTA GGA GAC     432
Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp
    130                 135                 140
```

```
GTA ATA GAC ATT ACT CAA GCT ACT GCA GAT CCT ATC ACA GTT AAC GGA      480
Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
145                 150                 155                 160

GGA GCT GAC CCA GTT ATC GCT AAC CCG TTC ACA ATT GGT GAG GTG ACC      528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
                165                 170                 175

ATT GCT GTT GTC GAA ATA CCC GGC TTC AAT ATT ACA GTC ATC GAA TTC      576
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
            180                 185                 190

TTT AAA CTA ATC GTG ATA GAT ATT CTG GGA GGA AGA TCT GTG AGA ATT      624
Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
        195                 200                 205

GCT CCA GAC ACA GCA AAC AAA GGA CTG ATA TCT GGT ATC TGT GGT AAT      672
Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
    210                 215                 220

CTG GAG ATG AAT GAC GCT GAT GAC TTT ACT ACA GAC GCA GAT CAG CTG      720
Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
225                 230                 235                 240

GCG ATC CAA CCC AAC ATA AAC AAA GAG TTC GAC GGC TGC CCA TTC TAC      768
Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr
                245                 250                 255

GGG AAT CCT TCT GAT ATC GAA TAC TGC AAA GGT CTC ATG GAG CCA TAC      816
Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
            260                 265                 270

AGA GCT GTA TGT CGT AAC AAT ATC AAC TTC TAC TAT TAC ACT CTG TCC      864
Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
        275                 280                 285

TGC GCC TTC GCT TAC TGT ATG GGA GGA GAA GAA AGA GCT AAA CAC GTC      912
Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
    290                 295                 300

CTT TTC GAC TAT GTT GAG ACA TGC GCT GCA CCG GAA ACG AGA GGA ACG      960
Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr
305                 310                 315                 320

TGT GTT TTA TCA GGA CAT ACT TTC TAT GAC ACA TTC GAC AAA GCC AGA     1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg
                325                 330                 335

TAT CAA TTC CAG GGC CCA TGC AAA GAG CTT CTG ATG GCC GCA GAC TGT     1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Leu Leu Met Ala Ala Asp Cys
            340                 345                 350

TAC TGG AAC ACA TGG GAT GTA AAG GTT TCA CAT AGA GAT GTT GAG TCA     1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
        355                 360                 365

TAC ACT GAG GTA GAG AAA GTA ACA ATC AGG AAA CAG TCA ACT GTA GTA     1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
    370                 375                 380

GAT TTG ATT GTG GAT GGC AAG CAG GTC AAG GTT GGA GGA GTG GAT GTA     1200
```

```
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
385                 390                 395                 400

TCT ATC CCG TAC AGT TCT GAG AAC ACA TCC ATA TAC TGG CAG GAT GGA    1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
                405                 410                 415

GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC    1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
            420                 425                 430

AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GGA    1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly
        435                 440                 445

AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT    1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
    450                 455                 460

TTC TTT GAC GCA GAA GGA GCA TGC GCT CTG ACC CCC AAT CCC CCA GGA    1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
465                 470                 475                 480

TGT ACA GAG GAG CAG AAA CCA GAA GCT GAG CGA CTC TGC AAT AGT CTA    1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu
                485                 490                 495

TTT GAT AGT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC    1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
            500                 505                 510

CGT ATT GCA CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAG CAA GGA    1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
        515                 520                 525

TTC TGT GAC CAT GCT TGG GAG TTC AAA AAA GAA TGC TAC ATA AAG CAT    1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
    530                 535                 540

GGA GAC ACT CTA GAA GTA CCA CCT GAA TGC CAA TAA ATGAACAAAG         1678
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
545                 550                 555

ATACAGAAGC TAAGACTACT ACAGCAGAAG ATAAAAGAGA AGCTGTAGTT CTTCAAAAAC  1738
AGTATATTTT GATGTACTCA TTGTTTACTT ACATAAAAAT AAATTGTTAT TATCATAACG  1798
TAAAGAAAAA AAAAAAAAAA AAAA                                        1822
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1644

(D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)

(x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATG GAA AAC ATG GAA AAC GAT GAA AAT ATT GTA GTT GGA CCT AAA CCG      48
Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Val Gly Pro Lys Pro
 1               5                  10                  15

TTT TAC CCT ATC GAA GAG GGA TCT GCT GGA ACA CAA TTA CGC AAA TAC      96
Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg Lys Tyr
            20                  25                  30

ATG GAG CGA TAT GCA AAA CTT GGC GCA ATT GCT TTT ACA AAT GCA GTT     144
Met Glu Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Val
        35                  40                  45

ACT GGT GTT GAT TAT TCT TAC GCC GAA TAC TTG GAG AAA TCA TGT TGT     192
Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
    50                  55                  60

CTA GGA AAA GCT TTG CAA AAT TAT GGT TTG GTT GTT GAT GGC AGA ATT     240
Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
65                  70                  75                  80

GCG TTA TGC AGT GAA AAC TGT GAA GAA TTT TTT ATT CCT GTA ATA GCC     288
Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Ile Ala
                85                  90                  95

GGA CTG TTT ATA GGT GTA GGT GTT GCA CCC ACT AAT GAG ATT TAC ACT     336
Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
            100                 105                 110

TTA CGT GAA CTG GTT CAC AGT TTA GGT ATC TCT AAA CCA ACA ATT GTA     384
Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
        115                 120                 125

TTT AGT TCT AAA AAA GGC TTA GAT AAA GTT ATA ACA GTA CAG AAA ACA     432
Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
    130                 135                 140

GTA ACT ACT ATT AAA ACC ATT GTT ATA CTA GAT AGC AAA GTT GAT TAT     480
Val Thr Thr Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
145                 150                 155                 160

CGA GGA TAT CAA TGT CTG GAC ACC TTT ATA AAA AGA AAC ACT CCA CCA     528
Arg Gly Tyr Gln Cys Leu Asp Thr Phe Ile Lys Arg Asn Thr Pro Pro
                165                 170                 175

GGT TTT CAA GCA TCC AGT TTC AAA ACT GTG GAA GTT GAC CGT AAA GAA     576
Gly Phe Gln Ala Ser Ser Phe Lys Thr Val Glu Val Asp Arg Lys Glu
            180                 185                 190

CAA GTT GCT CTT ATA ATG AAC TCT TCG GGT TCT ACC GGT TTG CCA AAA     624
Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
        195                 200                 205

GGC GTA CAA CTT ACT CAC GAA AAT ACA GTC ACT AGA TTT TCT CAT GCT     672
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Gly Val Gln Leu Thr His Glu Asn Thr Val Thr Arg Phe Ser His Ala
    210                 215                 220

AGA GAT CCG ATT TAT GGT AAC CAA GTT TCA CCA GGC ACC GCT GTT TTA      720
Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Val Leu
225                 230                 235                 240

ACT GTC GTT CCA TTC CAT CAT GGT TTT GGT ATG TTC ACT ACT CTA GGG      768
Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
                245                 250                 255

TAT TTA ATT TGT GGT TTT CGT GTT GTA ATG TTA ACA AAA TTC GAT GAA      816
Tyr Leu Ile Cys Gly Phe Arg Val Val Met Leu Thr Lys Phe Asp Glu
            260                 265                 270

GAA ACA TTT TTA AAA ACT CTA CAA GAT TAT AAA TGT ACA AGT GTT ATT      864
Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Thr Ser Val Ile
        275                 280                 285

CTT GTA CCG ACC TTG TTT GCA ATT CTC AAC AAA AGT GAA TTA CTC AAT      912
Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Lys Ser Glu Leu Leu Asn
    290                 295                 300

AAA TAC GAT TTG TCA AAT TTA GTT GAG ATT GCA TCT GGC GGA GCA CCT      960
Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
305                 310                 315                 320

TTA TCA AAA GAA GTT GGT GAA GCT GTT GCT AGA CGC TTT AAT CTT CCC     1008
Leu Ser Lys Glu Val Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
                325                 330                 335

GGT GTT CGT CAA GGT TAT GGT TTA ACA GAA ACA ACA TCT GCC ATT ATT     1056
Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
            340                 345                 350

ATT ACA CCA GAA GGA GAC GAT AAA CCA GGA GCT TCT GGA AAA GTC GTG     1104
Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
        355                 360                 365

CCG TTG TTT AAA GCA AAA GTT ATT GAT CTT GAT ACC AAA AAA TCT TTA     1152
Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Ser Leu
    370                 375                 380

GGT CCT AAC AGA CGT GGA GAA GTT TGT GTT AAA GGA CCT ATG CTT ATG     1200
Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
385                 390                 395                 400

AAA GGT TAT GTA AAT AAT CCA GAA GCA ACA AAA GAA CTT ATT GAC GAA     1248
Lys Gly Tyr Val Asn Asn Pro Glu Ala Thr Lys Glu Leu Ile Asp Glu
                405                 410                 415

GAA GGT TGG CTG CAC ACC GGA GAT ATT GGA TAT TAT GAT GAA GAA AAA     1296
Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
            420                 425                 430

CAT TTC TTT ATT GTC GAT CGT TTG AAG TCT TTA ATC AAA TAC AAA GGA     1344
His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
        435                 440                 445

TAC CAA GTA CCA CCT GCC GAA TTA GAA TCC GTT CTT TTG CAA CAT CCA     1392
Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
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    450                 455                 460

TCT ATC TTT GAT GCT GGT GTT GCC GGC GTT CCT GAT CCT GTA GCT GGC    1440
Ser Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly
465                 470                 475                 480

GAG CTT CCA GGA GCC GTT GTT GTA CTG GAA AGC GGA AAA AAT ATG ACC    1488
Glu Leu Pro GLy Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr
                485                 490                 495

GAA AAA GAA GTA ATG GAT TAT GTT GCA AGT CAA GTT TCA AAT GCA AAA    1536
Glu Lys Glu Val Met Asp Tyr Val Als Ser Gln Val Ser Asn Ala Lys
            500                 505                 510

CGT TTA CGT GGT GGT GTT CGT TTT GTG GAT GAA GTA CCT AAA GGT CTT    1584
Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
        515                 520                 525

ACT GGA AAA ATT GAC GGC AGA GCA ATT AGA GAA ATC CTT AAG AAA CCA    1632
Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro
    530                 535                 540

GTT GCT AAG ATG                                                    1644
Val Ala Lys Met
545
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1820 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1664
(D) OTHER INFORMATION: Vargula (cypridina) luciferase

(x) PUBLICATION INFORMATION:
JP 3-30678 Osaka (Tsuji)
(A) AUTHORS: Thompson et al.
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
(D) VOLUME: 86
(F) PAGES: 1326-1332
(G) DATE: (1989)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ATG AAG ATA ATA ATT CTG TCT GTT ATA TTG GCC TAC TGT GTC ACC GAC      48
Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp
 1               5                  10                  15

AAC TGT CAA GAT GCA TGT CCT GTA GAA GCG GAA CCG CCA TCA AGT ACA      96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
            20                  25                  30

CCA ACA GTT CCA ACT TCT TGT GAA GCT AAA GAA GGA GAA TGT ATA GAT     144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
```

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        35                  40                  45

ACC AGA TGC GCA ACA TGT AAA CGA GAT ATA CTA TCA GAT GGA CTG TGT     192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
    50                  55                  60

GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTG ATT     240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
65                  70                  75                  80

GAA TGC AGA GTA GAA GCA GCT GGT TAT TTT AGA ACG TTT TAC GGC AAA     288
Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys
                85                  90                  95

AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT AGG GGA ACC     336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
            100                 105                 110

AAG GGT GGC GAT TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA     384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
        115                 120                 125

CAG AAG GGA GCT GTG CTG ACT AAG ACA ACA CTG GAG GTT GCA GGA GAC     432
Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp
    130                 135                 140

GTA ATA GAC ATT ACT CAA GCT ACT GCA GAT CCT ATC ACA GTT AAC GGA     480
Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
145                 150                 155                 160

GGA GCT GAC CCA GTT ATC GCT AAC CCG TTC ACA ATT GGT GAG GTG ACC     528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
                165                 170                 175

ATT GCT GTT GTT GAA ATA CCG GGC TTC AAT ATC ACA GTC ATC GAA TTC     576
Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
            180                 185                 190

TTT AAA CTA ATC GTG ATT GAT ATT CTG GGA GGA AGA TCT GTC AGA ATT     624
Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
        195                 200                 205

GCT CCA GAC ACA GCA AAC AAA GGA CTG ATA TCT GGT ATC TGT GGT AAT     672
Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
    210                 215                 220

CTG GAG ATG AAT GAC GCT GAT GAC TTT ACT ACA GAT GCA GAT CAG CTG     720
Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
225                 230                 235                 240

GCG ATC CAA CCC AAC ATA AAC AAA GAG TTC GAC GGC TGC CCA TTC TAT     768
Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr
                245                 250                 255

GGC AAT CCT TCT GAT ATC GAA TAC TGC AAA GGT CTG ATG GAG CCA TAC     816
Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
            260                 265                 270

AGA GCT GTA TGT CGT AAC AAT ATC AAC TTC TAC TAT TAC ACT CTA TCC     864
Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
        275                 280                 285
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TGT GCC TTC GCT TAC TGT ATG GGA GGA GAA GAA AGA GCT AAA CAC GTC      912
Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
    290                 295                 300

CTT TTC GAC TAT GTT GAG ACA TGC GCT GCG CCG GAA ACG AGA GGA ACG      960
Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr
305                 310                 315                 320

TGT GTT TTA TCA GGA CAT ACT TTC TAT GAC ACA TTC GAC AAA GCA AGA     1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg
                325                 330                 335

TAT CAA TTC CAG GGC CCA TGC AAG GAG ATT CTG ATG GCC GCA GAC TGT     1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys
            340                 345                 350

TAC TGG AAC ACA TGG GAT GTA AAG GTT TCA CAT AGA GAC GTC GAA TCA     1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
        355                 360                 365

TAC ACT GAG GTA GAG AAA GTA ACA ATC AGG AAA CAG TCA ACT GTA GTA     1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
    370                 375                 380

GAT CTC ATT GTG GAT GGC AAG CAG GTC AAG GTT GGA GGA GTG GAT GTA     1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
385                 390                 395                 400

TCT ATC CCG TAC AGC TCT GAG AAC ACT TCC ATA TAC TGG CAG GAT GGA     1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly
                405                 410                 415

GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC     1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe
            420                 425                 430

AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GCA     1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Ala
        435                 440                 445

AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT     1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp
    450                 455                 460
TTC TTT GAC GCA GAA GGA GCA TGC GCT CTA ACC CCC AAC CCC CCA GGA     1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
465                 470                 475                 480

TGT ACA GAG GAA CAG AAA CCA GAA GCT GAG CGA CTT TGC AAT AAT CTC     1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu
                485                 490                 495

TTT GAT TCT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC     1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
            500                 505                 510

CGG ATT GCC CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAA CAA GGA     1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
        515                 520                 525

TTT TGT GAC CAT GCT TGG GAG TTC AAG AAA GAA TGC TAC ATA AAA CAT     1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
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    530                 535                 540

GGA GAC ACT CTA GAA GTA CCA CCT GAA TGT CAA TAA ACGTACAAAG          1678
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
545                 550                 555

ATACAGAAGC TAAGGCTACT ACAGCAGAAG ATAAAAAAGA AACTGTAGTT CCTTCAAAAA 1738
CCGTGTATTT TATGTACTCA TTGTTTAATT AGAGCAAAAT AAATTGTTAT TATCATAACT 1798
TAAACTAAAA AAAAAAAAAA AA                                          1820
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 958 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 115...702
(D) OTHER INFORMATION: apoaequorin-encoding gene

(x) PUBLICATION INFORMATION:
PATENT NO.: 5,093,240
(A) AUTHORS: Inouye et al.
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
(D) VOLUME: 82
(F) PAGES: 3154-3158
(G) DATE: (1985)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGAATGCAA TTCATCTTTG CATCAAAGAA    60

TTACATCAAA TCTCTAGTTG ATCAACTAAA TTGTCTCGAC AACAACAAGC AAAC ATG     117
                                                            Met
                                                             1

ACA AGC AAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC CCA     165
Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro
          5                  10                  15

AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC AAC     213
Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn
     20                  25                  30

CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT GAT     261
His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp
35                  40                  45

ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA CAC     309
Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His
50                  55                  60                  65
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AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT      357
Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly
                70                  75                  80

GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG GCT      405
Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala
            85                  90                  95

ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC CGT      453
Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg
        100                 105                 110

ATA TGG GGT GAT GCT TTG TTT GAT ATC GTT GAC AAA GAT CAA AAT GGA      501
Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly
    115                 120                 125

GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT ATC      549
Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile
130                 135                 140                 145

ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT      597
Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile
                150                 155                 160

GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA      645
Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu
            165                 170                 175

GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA      693
Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly
        180                 185                 190

GCT GTC CCC TAAGAAGCTC TACGGTGGTG  ATGCACCCTA GGAAGATGAT GTGATTTTGA 752
Ala Val Pro
    195

ATAAAACACT GATGAATTCA ATCAAAATTT TCCAAATTTT TGAACGATTT CAATCGTTTG   812
TGTTGATTTT TGTAATTAGG AACAGATTAA ATCGAATGAT TAGTTGTTTT TTTAATCAAC   872
AGAACTTACA AATCGAAAAA GTAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA   932
AAAAAAAAAA AAAAAAAAAA AAAAAA                                        958
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 591 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

  (A) NAME/KEY: Coding Sequence
  (B) LOCATION: 1...588
  (D) OTHER INFORMATION: Recombinant Aequorin AEQ1

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.
(B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
(C) JOURNAL: Biochemistry
(D) VOLUME: 26
(F) PAGES: 1326-1332
(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1               5                  10                  15

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC      96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30

AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC     144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
        35                  40                  45

GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
65                  70                  75                  80

GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG     288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT     336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
            100                 105                 110

CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT GAC AAA GAC CAA AAT     384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn
        115                 120                 125

GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GAT GGC     432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly
    130                 135                 140

ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160

ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT     528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT     576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180                 185                 190

GGA GCT GTC CCC TAA                                                591
Gly Ala Val Pro  *
        195
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...588
(D) OTHER INFORMATION: Recombinant Aequorin AEQ2

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.
(B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
(C) JOURNAL: Biochemistry
(D) VOLUME: 26
(F) PAGES: 1326-1332
(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn
 1               5                  10                  15

CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC      96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30

AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT     144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
        35                  40                  45

GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
65                  70                  75                  80

GGT GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG     288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu
                85                  90                  95

GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC     336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile
            100                 105                 110

CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT     384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn
```

```
        115                 120                 125

GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT     432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
    130                 135                 140

ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160

ATT GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT     528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT     576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180                 185                 190

GGA GCT GTC CCC TAA                                                 591
Gly Ala Val Pro  *
        195
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 591 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

  (A) NAME/KEY: Coding Sequence
  (B) LOCATION: 1...588
  (D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

  (A) AUTHORS: Prasher et al.
  (B) TITLE: Sequence Comparisons of Complementary
        DNAs Encoding Aequorin Isotypes
  (C) JOURNAL: Biochemistry
  (D) VOLUME: 26
  (F) PAGES: 1326-1332
  (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn
 1               5                  10                  15

CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC      96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30
```

```
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT     144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
        35                  40                  45

GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

CAC AAA GAT GCT GTA GGA GAC TTC TTC GGA GGA GCT GGA ATG AAA TAT     240
His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr
65                  70                  75                  80

GGT GTG GAA ACT GAT TGG CCT GCA TAC ATT GAA GGA TGG AAA AAA TTG     288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu
                85                  90                  95

GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC     336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile
            100                 105                 110

CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT     384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn
        115                 120                 125

GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT     432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
    130                 135                 140

ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160

ATT GAT GAA AAT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT     528
Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT     576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180                 185                 190

GGA GCT GTC CCC TAA                                                 591
Gly Ala Val Pro  *
        195
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...567

(D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Charbonneau et al.
(B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin
(C) JOURNAL: Am. Chem. Soc.
(D) VOLUME: 24
(E) ISSUE: 24
(F) PAGES: 6762-6771
(G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC      48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1               5                  10                  15

AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT      96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
            20                  25                  30

CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT     144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
        35                  40                  45

GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC     192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
    50                  55                  60

TTC TTC GGA GGA GCT GCA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT     240
Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
65                  70                  75                  80

GAA TAC ATC GAA GGA TGG AAA AGA CTG GCT TCC GAG GAA TTG AAA AGG     288
Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg
                85                  90                  95

TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG     336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
            100                 105                 110

TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT TCA CTG GAT GAA     384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu
        115                 120                 125

TGG AAA GCA TAC ACC AAA TCT GCT GGC ATC ATC CAA TCG TCA GAA GAT     432
Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp
    130                 135                 140

TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC     480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
145                 150                 155                 160

GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG     528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
                165                 170                 175

GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA GCT GTC CCC                 567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
```

180 185

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...588
(D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 10:
Asp 124 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1               5                  10                  15

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC      96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30

AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC     144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
        35                  40                  45

GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
65                  70                  75                  80

GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG     288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT     336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
            100                 105                 110

CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT     384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
```

```
        115                 120                 125

GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC     432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly
    130                 135                 140

ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145             150                 155                 160

ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT     528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT     576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180                 185                 190

GGA GCT GTC CCC                                                    588
Gly Ala Val Pro
        195
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...588
(D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 11:
Glu 135 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1               5                  10                  15

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC      96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30

AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC     144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
```

```
        35                  40                  45

GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
65                  70                  75                  80

GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG     288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT     336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
            100                 105                 110

CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT     384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
        115                 120                 125

GGA GCT ATT TCA CTG GAT TCA TGG AAA GCA TAC ACC AAA TCT GCT GGC     432
Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly
    130                 135                 140

ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160

ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT     528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT     576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180                 185                 190

GGA GCT GTC CCC                                                    588
Gly Ala Val Pro
        195
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 588 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

  (A) NAME/KEY: Coding Sequence
  (B) LOCATION: 1...588
  (D) OTHER INFORMATION: Recombinant site-directed
      Aequorin mutant w/increased biolum. activity

(x) PUBLICATION INFORMATION:
PATENT NO.: 5,360,728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC      48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn
 1               5                  10                  15

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC      96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
            20                  25                  30

AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC     144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
        35                  40                  45

GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT     192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
    50                  55                  60

CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT     240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr
65                  70                  75                  80

GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG     288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu
                85                  90                  95

GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT     336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile
            100                 105                 110

CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT     384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn
        115                 120                 125

GCA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC     432
Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly
    130                 135                 140

ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT     480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
145                 150                 155                 160

ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT     528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
                165                 170                 175

TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT     576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
            180                 185                 190

GGA GCT GTC CCC                                                    588
Gly Ala Val Pro
        195
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...567
(D) OTHER INFORMATION: Recombinant apoaequorin (AQUALITE®)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC      48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His
 1               5                  10                  15

AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT      96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser
            20                  25                  30

CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT     144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
        35                  40                  45

GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC     192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
    50                  55                  60

TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT     240
Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro
65                  70                  75                  80

GAA TAC ATC GAA GGA TGG AAA AAA CTG GCT TCC GAG GAA TTG AAA AGG     288
Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg
                85                  90                  95

TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG     336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu
            100                 105                 110

TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT CTG TCA GAT GAA     384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu
        115                 120                 125

TGG AAA GCA TAC ACC AAA TCT GAT GGC ATC ATC CAA TCG TCA GAA GAT     432
Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Gln Ser Ser Glu Asp
    130                 135                 140

TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC     480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
145                 150                 155                 160

GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG     528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
                165                 170                 175
```

```
GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA GCT GTC CCC                    567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:
PATENT NO.: 5,484,723

(ix) FEATURE:
(D) OTHER INFORMATION: Vibrio fisheri Flavin reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn
 1               5                  10                  15

Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala
            20                  25                  30

Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
        35                  40                  45

Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His
    50                  55                  60

Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser
65                  70                  75                  80

Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro
                85                  90                  95

His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu
            100                 105                 110

Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
        115                 120                 125

Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly
    130                 135                 140

Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala
145                 150                 155                 160

Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu
                165                 170                 175

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

Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
        195                 200                 205
```

```
Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys
    210                 215                 220

Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1079 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 259...975
(D) OTHER INFORMATION: *Renilla mulleri* GFP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
GGTTATACAC AAGTGTATCG CGTATCTGCA GACGCATCTA GTGGGATTAT TCGAGCGGTA     60
GTATTTACGT CAGACCTGTC TAATCGAAAC CACAACAAAC TCTTAAAATA AGCCACATTT    120
ACATAATATC TAAGAGACGC CTCATTTAAG AGTAGTAAAA ATATAATATA TGATAGAGTA    180
TACAACTCTC GCCTTAGACA GACAGTGTGC AACAGAGTAA CTCTTGTTAA TGCAATCGAA    240
AGCGTCAAGA GAGATAAG ATG AGT AAA CAA ATA TTG AAG AAC ACT TGT TTA       291
                    Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
                     1               5                  10

CAA GAA GTA ATG TCG TAT AAA GTA AAT CTG GAA GGA ATT GTA AAC AAC       339
Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn
            15                  20                  25

CAT GTT TTT ACA ATG GAG GGT TGC GGC AAA GGG AAT ATT TTA TTC GGC      387
His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly
        30                  35                  40

AAT CAA CTG GTT CAG ATT CGT GTC ACG AAA GGG GCC CCA CTG CCT TTT      435
Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe
    45                  50                  55

GCA TTT GAT ATT GTG TCA CCA GCT TTT CAA TAT GGC AAC CGT ACT TTC      483
Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe
60                  65                  70                  75

ACG AAA TAT CCG AAT GAT ATA TCA GAT TAT TTT ATA CAA TCA TTT CCA      531
Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro
                80                  85                  90

GCA GGA TTT ATG TAT GAA CGA ACA TTA CGT TAC GAA GAT GGC GGA CTT      579
Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu
            95                  100                 105

GTT GAA ATT CGT TCA GAT ATA AAT TTA ATA GAA GAC AAG TTC GTC TAC      627
Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr
```

```
        110                 115                 120

AGA GTG GAA TAC AAA GGT AGT AAC TTC CCA GAT GAT GGT CCC GTC ATG     675
Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met
    125                 130                 135

CAG AAG ACT ATC TTA GGA ATA GAG CCT TCA TTT GAA GCC ATG TAC ATG     723
Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
140                 145                 150                 155

AAT AAT GGC GTC TTG GTC GGC GAA GTA ATT CTT GTC TAT AAA CTA AAC     771
Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
                160                 165                 170

TCT GGG AAA TAT TAT TCA TGT CAC ATG AAA ACA TTA ATG AAG TCG AAA     819
Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
            175                 180                 185

GGT GTA GTA AAG GAG TTT CCT TCG TAT CAT TTT ATT CAA CAT CGT TTG     867
Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
        190                 195                 200

GAA AAG ACT TAC GTA GAA GAC GGG GGG TTC GTT GAA CAG CAT GAG ACT     915
Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
    205                 210                 215

GCT ATT GCT CAA ATG ACA TCT ATA GGA AAA CCA CTA GGA TCC TTA CAC     963
Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
220                 225                 230                 235

GAA TGG GTT TAA ACACAGTTAC ATTACTTTTT CCAATTCGTG TTTCATGTCA AATAAT  1021
Glu Trp Val  *

AATTTTTTAA ACAATTATCA ATGTTTTGTG ATATGTTTGT AAAAAAAAAA AAAAAAAA     1079
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 238 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu Gln Glu Val Met Ser
 1               5                  10                  15
Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
            20                  25                  30
Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
        35                  40                  45
Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
    50                  55                  60
Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
```

```
65                  70                  75                  80
Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
                85                  90                  95
Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
            100                 105                 110
Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
        115                 120                 125
Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
    130                 135                 140
Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
145                 150                 155                 160
Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
                165                 170                 175
Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
            180                 185                 190
Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
        195                 200                 205
Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
    210                 215                 220
Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 31...963
(D) OTHER INFORMATION: *Renilla mulleri* luciferase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
CGGCACGAGG TTTAAGAATC AATAAAAAAA  ATG ACG TCA AAA GTT TAC GAT CCT     54
                                  Met Thr Ser Lys Val Tyr Asp Pro
                                   1               5

GAA TTA AGA AAA CGC ATG ATT ACT GGT CCA CAA TGG TGG GCA AGA TGT     102
Glu Leu Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys
    10                  15                  20


AAA CAA ATG AAT GTT CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA     150
Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu
25                  30                  35                  40

AAA CAT GCA GAA AAT GCA GTT ATA TTT TTA CAT GGT AAT GCA GCA TCT     198
Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser
                45                  50                  55

TCT TAT TTA TGG CGT CAT GTT GTA CCA CAT GTT GAA CCA GTG GCG CGA     246
```

```
Ser Tyr Leu Trp Arg His Val Val Pro His Val Glu Pro Val Ala Arg
            60                  65                  70

TGT ATT ATA CCA GAT CTT ATA GGT ATG GGT AAA TCA GGC AAG TCT GGT     294
Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly
        75                  80                  85

AAT GGT TCC TAT AGA TTA CTA GAT CAT TAC AAA TAT CTT ACT GAA TGG     342
Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Glu Trp
    90                  95                  100

TTC AAA CAT CTT AAT TTA CCA AAG AAG ATC ATT TTT GTC GGT CAT GAT     390
Phe Lys His Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp
105                 110                 115                 120

TGG GGT GCT TGT TTA GCA TTT CAT TAT TGC TAT GAA CAT CAG GAT CGC     438
Trp Gly Ala Cys Leu Ala Phe His Tyr Cys Tyr Glu His Gln Asp Arg
                125                 130                 135

ATC AAA GCA GTT GTT CAT GCT GAA AGT GTA GTA GAT GTG ATT GAA TCG     486
Ile Lys Ala Val Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser
            140                 145                 150

TGG GAC GAA TGG CCT GAT ATT GAA GAA GAT ATT GCT TTG ATT AAA TCT     534
Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser
        155                 160                 165

GAA GAA GGA GAA AAA ATG GTT TTA GAG AAT AAC TTC TTC GTG GAA ACC     582
Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr
    170                 175                 180

ATG TTG CCA TCA AAA ATC ATG AGA AAG TTG GAA CCA GAG GAA TTT GCT     630
Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala
185                 190                 195                 200

GCT TAT CTT GAA CCA TTT AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA     678
Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr
                205                 210                 215

TTA TCA TGG CCT CGT GAA ATC CCT TTG GTA AAA GGT GGT AAA CCG GAT     726
Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp
            220                 225                 230

GTA GTA GAA ATT GTC AGG AAT TAT AAT GCT TAT CTT CGT GCA AGT CAT     774
Val Val Glu Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser His
        235                 240                 245

GAT TTA CCA AAA ATG TTT ATT GAA TCT GAT CCA GGA TTC TTT TCC AAT     822
Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn
    250                 255                 260

GCT ATT GTT GAA GGT GCT AAG AAA TTC CCT AAT ACT GAA TTT GTT AAA     870
Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys
265                 270                 275                 280

GTC AAA GGT CTT CAT TTT TCA CAA GAA GAT GCA CCT GAT GAA ATG GGA     918
Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly
                285                 290                 295

AAT TAT ATA AAA TCG TTT GTT GAG CGT GTT CTT AAA AAT GAA CAA TAAACT   969
Asn Tyr Ile Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln
```

```
            300                 305                 310

ACCAGGTTTC CATGTTGCCA CTTTAGCTGG GTTTAATAAA TTTCACTATC AATTTGAACA   1029
ATTTCACATT AATTTTAACT ATTAAAAAAT TATGGACACA GGGATTATAT CAGATGATTA   1089
ATTTAGTTGG GAACAATGAA TACCGAATAT TATGAATTCT CTTTAGCTAT TTATAATAAT   1149
CACATTCTTA TGTAATAAAA CTTTGTTTTA ATAAATTAAT GATTCAGAAA AAAAAAAAAA   1209
AAAAAAAA                                                           1217
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Thr Ser Lys Val Tyr Asp Pro Glu Leu Arg Lys Arg Met Ile Thr
 1               5                  10                  15
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
            20                  25                  30
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
        35                  40                  45
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
    50                  55                  60
Pro His Val Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
65                  70                  75                  80
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                85                  90                  95
His Tyr Lys Tyr Leu Thr Glu Trp Phe Lys His Leu Asn Leu Pro Lys
            100                 105                 110
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        115                 120                 125
Tyr Cys Tyr Glu His Gln Asp Arg Ile Lys Ala Val Val His Ala Glu
    130                 135                 140
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                 150                 155                 160
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165                 170                 175
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180                 185                 190
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
        195                 200                 205
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
    210                 215                 220
Leu Val Lys Gly Gly Lys Pro Asp Val Val Glu Ile Val Arg Asn Tyr
225                 230                 235                 240
Asn Ala Tyr Leu Arg Ala Ser His Asp Leu Pro Lys Met Phe Ile Glu
                245                 250                 255
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
            260                 265                 270
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
        275                 280                 285
Glu Asp Ala Pro Asp Glu Met Gly Asn Tyr Ile Lys Ser Phe Val Glu
```

```
    290                 295                 300
Arg Val Leu Lys Asn Glu Gln
305                 310
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 37...594
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
GCACGAGGGT ACTCAAAGTA TCTTCTGGCA GGGAAA ATG GGA GTG AAA GTT CTT      54
                                        Met Gly Val Lys Val Leu
                                         1               5

TTT GCC CTT ATT TGT ATT GCT GTG GCC GAG GCC AAA CCA ACT GAA AAC     102
Phe Ala Leu Ile Cys Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn
            10                  15                  20

AAT GAA GAT TTC AAC ATT GTA GCT GTA GCT AGC AAC TTT GCT ACA ACG     150
Asn Glu Asp Phe Asn Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr
        25                  30                  35

GAT CTC GAT GCT GAC CGT GGT AAA TTG CCC GGA AAA AAA TTA CCA CTT     198
Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu
    40                  45                  50

GAG GTA CTC AAA GAA ATG GAA GCC AAT GCT AGG AAA GCT GGC TGC ACT     246
Glu Val Leu Lys Glu Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr
55                  60                  65                  70

AGG GGA TGT CTG ATA TGC CTG TCA CAC ATC AAG TGT ACA CCC AAA ATG     294
Arg Gly Cys Leu Ile Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met
                75                  80                  85

AAG AAG TTT ATC CCA GGA AGA TGC CAC ACC TAT GAA GGA GAC AAA GAA     342
Lys Lys Phe Ile Pro Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu
            90                  95                  100

AGT GCA CAG GGA GGA ATA GGA GAG GCT ATT GTT GAC ATT CCT GAA ATT     390
Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile
        105                 110                 115

CCT GGG TTT AAG GAT TTG GAA CCC ATG GAA CAA TTC ATT GCA CAA GTT     438
Pro Gly Phe Lys Asp Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val
    120                 125                 130
```

```
GAC CTA TGT GTA GAC TGC ACA ACT GGA TGC CTC AAA GGT CTT GCC AAT     486
Asp Leu Cys Val Asp Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn
135                 140                 145                 150

GTG CAA TGT TCT GAT TTA CTC AAG AAA TGG CTG CCA CAA AGA TGT GCA     534
Val Gln Cys Ser Asp Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala
                155                 160                 165

ACT TTT GCT AGC AAA ATT CAA GGC CAA GTG GAC AAA ATA AAG GGT GCC     582
Thr Phe Ala Ser Lys Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala
            170                 175                 180

GGT GGT GAT TAA TCCTAATAGA ATACTGCATA ACTGGATGAT GATATACTAG CTTATT   640
Gly Gly Asp  *
        185

GCTCATAAAA TGGCCATTTT TTGTAACAAA TCGAGTCTAT GTAATTCAAA ATACCTAATT    700
AATTGTTAAT ACATATGTAA TTCCTATAAA TATAATTTAT GCAATCCAAA AAAAAAAAAA    760
AAAAA                                                               765
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
 1               5                  10                  15
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175
Asp Lys Ile Lys Gly Ala Gly Gly Asp
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:
(A) NAME/KEY: CBD Coding Sequence
(B) LOCATION: 1...1146
(D) OTHER INFORMATION: DNA encoding a CBD-*Gaussia* luciferase fusion protein

(ix) FEATURE:
(A) NAME/KEY: CBD Coding Sequence
(B) LOCATION: 1...591
(ix) FEATURE:
(A) NAME/KEY: Gaussia luciferase
(B) LOCATION: 591-1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
ATG TCA GTT GAA TTT TAC AAC TCT AAC AAA TCA GCA CAA ACA AAC TCA      48
Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
 1               5                  10                  15

ATT ACA CCA ATA ATC AAA ATT ACT AAC ACA TCT GAC AGT GAT TTA AAT      96
Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
            20                  25                  30

TTA AAT GAC GTA AAA GTT AGA TAT TAT TAC ACA AGT GAT GGT ACA CAA     144
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
        35                  40                  45

GGA CAA ACT TTC TGG TGT GAC CAT GCT GGT GCA TTA TTA GGA AAT AGC     192
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
    50                  55                  60

TAT GTT GAT AAC ACT AGC AAA GTG ACA GCA AAC TTC GTT AAA GAA ACA     240
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
65                  70                  75                  80

GCA AGC CCA ACA TCA ACC TAT GAT ACA TAT GTT GAA TTT GGA TTT GCA     288
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
                85                  90                  95

AGC GGA GCA GCT ACT CTT AAA AAA GGA CAA TTT ATA ACT ATT CAA GGA     336
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
            100                 105                 110

AGA ATA ACA AAA TCA GAC TGG TCA AAC TAC ACT CAA ACA AAT GAC TAT     384
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
        115                 120                 125

TCA TTT GAT GCA AGT AGT TCA ACA CCA GTT GTA AAT CCA AAA GTT ACA     432
```

```
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
    130                 135                 140

GGA TAT ATA GGT GGA GCT AAA GTT CTT GGT ACA GCA CCA GGT TCC GCG      480
Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
145                 150                 155                 160

GGT CTG GTG CCA CGC GGT AGT ACT GCA ATT GGT ATG AAA GAA ACC GCT      528
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
                165                 170                 175

GCT GCT AAA TTC GAA CGC CAG CAC ATG GAC AGC CCA GAT CTG GGT ACC      576
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
            180                 185                 190

GAT GAC GAC GAC AAG ATG GGA GTG AAA GTT CTT TTT GCC CTT ATT TGT      624
Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
        195                 200                 205

ATT GCT GTG GCC GAG GCC AAA CCA ACT GAA AAC AAT GAA GAT TTC AAC      672
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
    210                 215                 220

ATT GTA GCT GTA GCT AGC AAC TTT GCT ACA ACG GAT CTC GAT GCT GAC      720
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
225                 230                 235                 240

CGT GGT AAA TTG CCC GGA AAA AAA TTA CCA CTT GAG GTA CTC AAA GAA      768
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
                245                 250                 255

ATG GAA GCC AAT GCT AGG AAA GCT GGC TGC ACT AGG GGA TGT CTG ATA      816
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
            260                 265                 270

TGC CTG TCA CAC ATC AAG TGT ACA CCC AAA ATG AAG AAG TTT ATC CCA      864
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
        275                 280                 285

GGA AGA TGC CAC ACC TAT GAA GGA GAC AAA GAA AGT GCA CAG GGA GGA      912
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
    290                 295                 300

ATA GGA GAG GCT ATT GTT GAC ATT CCT GAA ATT CCT GGG TTT AAG GAT      960
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
305                 310                 315                 320

TTG GAA CCC ATG GAA CAA TTC ATT GCA CAA GTT GAC CTA TGT GTA GAC     1008
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
                325                 330                 335

TGC ACA ACT GGA TGC CTC AAA GGT CTT GCC AAT GTG CAA TGT TCT GAT     1056
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
            340                 345                 350

TTA CTC AAG AAA TGG CTG CCA CAA AGA TGT GCA ACT TTT GCT AGC AAA     1104
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
        355                 360                 365

ATT CAA GGC CAA GTG GAC AAA ATA AAG GGT GCC GGT GGT GAT             1146
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
```

370 375 380

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE: CBD-*Gaussia* luciferase fusion protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Met Ser Val Glu Phe Tyr Asn Ser Asn Lys Ser Ala Gln Thr Asn Ser
 1               5                  10                  15
Ile Thr Pro Ile Ile Lys Ile Thr Asn Thr Ser Asp Ser Asp Leu Asn
            20                  25                  30
Leu Asn Asp Val Lys Val Arg Tyr Tyr Tyr Thr Ser Asp Gly Thr Gln
        35                  40                  45
Gly Gln Thr Phe Trp Cys Asp His Ala Gly Ala Leu Leu Gly Asn Ser
    50                  55                  60
Tyr Val Asp Asn Thr Ser Lys Val Thr Ala Asn Phe Val Lys Glu Thr
65                  70                  75                  80
Ala Ser Pro Thr Ser Thr Tyr Asp Thr Tyr Val Glu Phe Gly Phe Ala
                85                  90                  95
Ser Gly Ala Ala Thr Leu Lys Lys Gly Gln Phe Ile Thr Ile Gln Gly
            100                 105                 110
Arg Ile Thr Lys Ser Asp Trp Ser Asn Tyr Thr Gln Thr Asn Asp Tyr
        115                 120                 125
Ser Phe Asp Ala Ser Ser Ser Thr Pro Val Val Asn Pro Lys Val Thr
    130                 135                 140
Gly Tyr Ile Gly Gly Ala Lys Val Leu Gly Thr Ala Pro Gly Ser Ala
145                 150                 155                 160
Gly Leu Val Pro Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala
                165                 170                 175
Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp Leu Gly Thr
            180                 185                 190
Asp Asp Asp Asp Lys Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys
        195                 200                 205
Ile Ala Val Ala Glu Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn
    210                 215                 220
Ile Val Ala Val Ala Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp
225                 230                 235                 240
Arg Gly Lys Leu Pro Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu
                245                 250                 255
Met Glu Ala Asn Ala Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile
            260                 265                 270
Cys Leu Ser His Ile Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro
        275                 280                 285
Gly Arg Cys His Thr Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly
    290                 295                 300
Ile Gly Glu Ala Ile Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp
305                 310                 315                 320
Leu Glu Pro Met Glu Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp
                325                 330                 335
```

```
Cys Thr Thr Gly Cys Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp
            340                 345                 350
Leu Leu Lys Lys Trp Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys
        355                 360                 365
Ile Gln Gly Gln Val Asp Lys Ile Lys Gly Ala Gly Gly Asp
    370                 375                 380
```

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: Amino-terminal *Renilla reniformis* GFP peptide (Identity of residue #5 unknown)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Met Asp Leu Ala Xaa Lys Leu Gly Leu Lys Glu Val Met Pro Thr Lys
 1               5                  10                  15

Ile Asn Leu Glu Gly Leu Val Gly Asp His Ala Phe Ser Met Glu Gly
            20                  25                  30

Val Gly Glu Gly Asn Ile Leu Glu Gly
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Val Lys Ile Ser Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile
 1               5                  10                  15
Val Ser Val Ala Phe
        20
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: *Renilla reniformis* GFP peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Ala Tyr Thr Gly Tyr Pro Glu Glu Ile Ser Asp Tyr Phe Leu Gln Ser Phe
 1               5                  10                  15

Pro Glu Gly Phe Thr Tyr Glu Arg Gly Asn Ile Arg Tyr Gln Asp Gly Gly
        20                  25                  30

Thr Ala Ile Val Lys Ser
35                  40
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: *Renilla reniformis* GFP peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Ile Val Gly Met Gln Pro Ser Tyr Glu Ser Met Tyr
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: Carboxyl-terminal *Renilla reniformis* GFP peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

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

Thr Gly Lys His Phe Thr Tyr His Met Arg Thr Val Tyr Lys Ser Lys
            20                  25                  30

Lys Pro Val Glu Thr Met Pro Leu Tyr His Phe Ile Gln His Arg Leu
        35                  40                  45

Val Lys Thr Asn Val Asp Thr Ala Ser Gly Tyr Val Val Gln His Glu
    50                  55                  60

Thr Ala Ile Ala Ala His Ser Thr Ile Lys Lys Ile Glu Gly Ala Ala
65                  70                  75                  80

Arg
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE: Pleuromamma

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 148...741
(D) OTHER INFORMATION: Pleuromamma luciferase

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
CGGCACGAGA TTTTGTCTGT GGTGATTGGG ATTGTCTGTC TCTCAGGTCA AGCAGAAAGT  60
TCGCTGAAAG GTGATTTCTG TAGTGATGTT TCCTTCTGGG ATGTGATCAA GTACAACACT  120
GAGAGTCGAC AATGCTGTGA CACAAAA ATG CTT AGA AAT TGC GCT AGG AAG CAA  174
                              Met Leu Arg Asn Cys Ala Arg Lys Gln
                               1               5

 GAG CAA GTT TGC GCC GAT GTG ACC GAG ATG AAA TGC CAA GCA GTT GCT    222
 Glu Gln Val Cys Ala Asp Val Thr Glu Met Lys Cys Gln Ala Val Ala
  10                  15                  20                  25

 TGG GCC GAC TGT GGA CCC AGA TTT GAT TCC ACT GGC AGG AAT AGA TGC    270
```

```
Trp Ala Asp Cys Gly Pro Arg Phe Asp Ser Thr Gly Arg Asn Arg Cys
                  30                  35                  40

CAA GTT CAA TAC AAG GAC TAC GCG TAC AAG TCC TGC GTG GAA GTT GAT    318
Gln Val Gln Tyr Lys Asp Tyr Ala Tyr Lys Ser Cys Val Glu Val Asp
              45                  50                  55

TAC ACT GTA CCG CAC AGG AAG CAA GTT CCA GAG TGC AAA CAA GTC ACT    366
Tyr Thr Val Pro His Arg Lys Gln Val Pro Glu Cys Lys Gln Val Thr
          60                  65                  70

AAA GAT AAC TGC GTT ACT GAT TGG GAA GTT GAC GCC AAT GGC AAC AAG    414
Lys Asp Asn Cys Val Thr Asp Trp Glu Val Asp Ala Asn Gly Asn Lys
      75                  80                  85

GTT TGG GGT GGT ACC GAG AAA TGC ACT CCT GTC ACT TGG GAA GAA TGT    462
Val Trp Gly Gly Thr Glu Lys Cys Thr Pro Val Thr Trp Glu Glu Cys
90                  95                  100                 105

AAT ATC GTG GAG AAA GAT GTA GAT TTT CCA ACT GTC AAG ACG GAA TGC    510
Asn Ile Val Glu Lys Asp Val Asp Phe Pro Thr Val Lys Thr Glu Cys
                  110                 115                 120

GGC ATC CTG TCT CAC CTT AAG TAT GCA GAC TTC ATA GAG GGA CCT TCC    558
Gly Ile Leu Ser His Leu Lys Tyr Ala Asp Phe Ile Glu Gly Pro Ser
              125                 130                 135

CAC TCT TTG TCT ATG AGA ACC AAT TGT CAG GTC AAG AGT TCA TTG GAC    606
His Ser Leu Ser Met Arg Thr Asn Cys Gln Val Lys Ser Ser Leu Asp
              140                 145                 150


TGC CGG CCT GTT AAG ACC AGG AAG TGT GCA ACG GTC GAG TAC CAC GAA    654
Cys Arg Pro Val Lys Thr Arg Lys Cys Ala Thr Val Glu Tyr His Glu
          155                 160                 165

TGC AGC ATG AAG CCC CAA GAA GAC TGC AGC CCA GTC ACT GTT CAT ATT    702
Cys Ser Met Lys Pro Gln Glu Asp Cys Ser Pro Val Thr Val His Ile
170                 175                 180                 185

CCT GAC CAG GAG AAA GTT CAC CAG AAG AAG TGC CTC ACA TAA            744
Pro Asp Gln Glu Lys Val His Gln Lys Lys Cys Leu Thr
                  190                 195

ATGTTATCAA TTTTAGCTCT TACTAATTTA AACATAATAA ATATCACATC GAAGCCCTTT  804
ATTTTATAGA AGTGTAATGC TTGAATAAAT CTAGTGAATA AAAAAAAAAA AAAAAAA    861
```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: polypeptide
(C) STRANDEDNESS: N/A
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(A) NAME/KEY: Pleuromamma luciferase
(B) LOCATION:
(D) OTHER INFORMATION: Pleuromamma luciferase

(vi) ORIGINAL SOURCE: Pleuromamma

(x) PUBLICATION INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Met Leu Arg Asn Cys Ala Arg Lys Gln Glu Gln Val Cys Ala Asp Val
 1               5                  10                  15

Thr Glu Met Lys Cys Gln Ala Val Ala Trp Ala Asp Cys Gly Pro Arg
            20                  25                  30

Phe Asp Ser Thr Gly Arg Asn Arg Cys Gln Val Gln Tyr Lys Asp Thr
        35                  40                  45

Ala Tyr Lys Ser Cys Val Glu Val Asp Tyr Thr Val Pro His Arg Lys
    50                  55                  60

Gln Val Pro Glu Cys Lys Gln Val Thr Lys Asp Asn Cys Val Thr Asp
65                  70                  75                  80

Trp Glu Val Asp Ala Asn Gly Asn Lys Val Trp Gly Gly Thr Glu Lys
                85                  90                  95

Cys Thr Pro Val Thr Trp Glu Glu Cys Asn Ile Val Glu Lys Asp Val
            100                 105                 110

Asp Phe Pro Thr Val Lys Thr Glu Cys Gly Ile Leu Ser His Leu Lys
        115                 120                 125

Tyr Ala Asp Phe Ile Glu Gly Pro Ser His Ser Leu Ser Met Arg Thr
    130                 135                 140

Asn Cys Gln Val Lys Ser Ser Leu Asp Cys Arg Pro Val Lys Thr Arg
145                 150                 155                 160

Lys Cys Ala Thr Val Glu Tyr His Glu Cys Ser Met Lys Pro Gln Glu
                165                 170                 175

Asp Cys Ser Pro Val Thr Val His Ile Pro Asp Gln Glu Lys Val His
            180                 185                 190

Gln Lys Lys Cys Leu Thr
        195
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE: Ptilosarcus gurneyi

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence (Insert A)

(B) LOCATION: 34...747
(D) OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP)

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
TCGGCACGAG CTGGCCTCCA CACTTTAGAC AAA ATG AAC CGC AAC GTA TTA AAG     54
                                      Met Asn Arg Asn Val Leu Lys
                                       1               5

AAC ACT GGA CTG AAA GAG ATT ATG TCG GCA AAA GCT AGC GTT GAA GGA     102
Asn Thr Gly Leu Lys Glu Ile Met Ser Ala Lys Ala Ser Val Glu Gly
        10                  15                  20

ATC GTG AAC AAT CAC GTT TTT TCC ATG GAA GGA TTT GGA AAA GGC AAT     150
Ile Val Asn Asn His Val Phe Ser Met Glu Gly Phe Gly Lys Gly Asn
    25                  30                  35

GTA TTA TTT GGA AAC CAA TTG ATG CAA ATC CGG GTT ACA AAG GGA GGT     198
Val Leu Phe Gly Asn Gln Leu Met Gln Ile Arg Val Thr Lys Gly Gly
40                  45                  50                  55

CCG TTG CCA TTC GCT TTC GAT ATT GTT TCC ATA GCT TTC CAA TAC GGG     246
Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Ile Ala Phe Gln Tyr Gly
                60                  65                  70

AAT CGC ACT TTC ACG AAA TAC CCA GAC GAC ATT GCG GAC TAC TTT GTT     294
Asn Arg Thr Phe Thr Lys Tyr Pro Asp Asp Ile Ala Asp Tyr Phe Val
            75                  80                  85

CAA TCA TTC CCG GCT GGA TTT TTC TAC GAA AGA AAT CTA CGC TTT GAA     342
Gln Ser Phe Pro Ala Gly Phe Phe Tyr Glu Arg Asn Leu Arg Phe Glu
        90                  95                  100

GAT GGC GCC ATT GTT GAC ATT CGT TCA GAT ATA AGT TTA GAA GAT GAT     390
Asp Gly Ala Ile Val Asp Ile Arg Ser Asp Ile Ser Leu Glu Asp Asp
    105                 110                 115

AAG TTC CAC TAC AAA GTG GAG TAT AGA GGC AAC GGT TTC CCT AGT AAC     438
Lys Phe His Tyr Lys Val Glu Tyr Arg Gly Asn Gly Phe Pro Ser Asn
120                 125                 130                 135

GGA CCC GTG ATG CAA AAA GCC ATC CTC GGC ATG GAG CCA TCG TTT GAG     486
Gly Pro Val Met Gln Lys Ala Ile Leu Gly Met Glu Pro Ser Phe Glu
                140                 145                 150

GTG GTC TAC ATG AAC AGC GGC GTT CTG GTG GGC GAA GTA GAT CTC GTT     534
Val Val Tyr Met Asn Ser Gly Val Leu Val Gly Glu Val Asp Leu Val
            155                 160                 165

TAC AAA CTC GAG TCA GGG AAC TAT TAC TCG TGC CAC ATG AAA ACG TTT     582
Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr Ser Cys His Met Lys Thr Phe
        170                 175                 180

TAC AGA TCC AAA GGT GGA GTG AAA GAA TTC CCG GAA TAT CAC TTT ATC     630
Tyr Arg Ser Lys Gly Gly Val Lys Glu Phe Pro Glu Tyr His Phe Ile
    185                 190                 195
```

```
CAT CAT CGT CTG GAG AAA ACC TAC GTG GAA GAA GGA AGC TTC GTG GAA    678
His His Arg Leu Glu Lys Thr Tyr Val Glu Glu Gly Ser Phe Val Glu
200                 205                 210                 215

CAA CAC GAG ACG GCC ATT GCA CAA CTG ACC ACA ATT GGA AAA CCT CTG    726
Gln His Glu Thr Ala Ile Ala Gln Leu Thr Thr Ile Gly Lys Pro Leu
                    220                 225                 230

GGC TCC CTT CAT GAA TGG GTG TAG AAAATGACCA ATATACTGGG GAAACCGATA   780
Gly Ser Leu His Glu Trp Val
                235
ACCGTTTGGA AGCTTGTGTA TACAAATTAT TTGGGGTCAT TTTGTAATGT GTATGTGTGT  840
TGTATGATCA ATAGACGTCG TCATTCATAG CTTGAATCCT TCAGCAAAAG AAACCTCGAA  900
GCATATTGAA ACCTCGAAGC ATATTGAAAC CTCGACGGAG AGCGTAAAGA GACCGCACAA  960
ATTAACGCGT TTCAACCAGC AGTTGGAATC TTTAAACCGA TCAAAACTAT TAATATAAAT 1020
ATATATACCC TGTATAACTT ATATATATCT ATATAGTTTG ATATTGATTA AATCTGTTCT 1080
TGATCAAAAA AAAAAAAAAA AAAA                                        1104
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE: Ptilosarcus gurneyi

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence (Insert B)
(B) LOCATION: 7...720
(D) OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP)

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
                              GACAAA ATG AAC CGC AAC GTA TTA AAG    27
                                     Met Asn Arg Asn Val Leu Lys
                                       1               5

AAC ACT GGA CTG AAA GAG ATT ATG TCG GCA AAA GCT AGC GTT GAA GGA     75
Asn Thr Gly Leu Lys Glu Ile Met Ser Ala Lys Ala Ser Val Glu Gly
            10                  15                  20

ATC GTG AAC AAT CAC GTT TTT TCC ATG GAA GGA TTT GGA AAA GGC AAT    123
Ile Val Asn Asn His Val Phe Ser Met Glu Gly Phe Gly Lys Gly Asn
    25                  30                  35

GTA TTA TTT GGA AAC CAA TTG ATG CAA ATC CGG GTT ACA AAG GGA GGT    171
Val Leu Phe Gly Asn Gln Leu Met Gln Ile Arg Val Thr Lys Gly Gly
40                  45                  50                  55

CCG TTG CCA TTC GCT TTC GAC ATT GTT TCC ATA GCT TTC CAA TAC GGG    219
```

```
Pro Leu Pro Phe Ala Phe Asp Ile Val Ser Ile Ala Phe Gln Tyr Gly
                60                  65                  70

AAT CGC ACT TTC ACG AAA TAC CCA GAC GAC ATT GCG GAC TAC TTT GTT    267
Asn Arg Thr Phe Thr Lys Tyr Pro Asp Asp Ile Ala Asp Tyr Phe Val
            75                  80                  85

CAA TCA TTT CCG GCT GGA TTT TTC TAC GAA AGA AAT CTA CGC TTT GAA    315
Gln Ser Phe Pro Ala Gly Phe Phe Tyr Glu Arg Asn Leu Arg Phe Glu
        90                  95                  100

GAT GGC GCC ATT GTT GAC ATT CGT TCA GAT ATA AGT TTA GAA GAT GAT    363
Asp Gly Ala Ile Val Asp Ile Arg Ser Asp Ile Ser Leu Glu Asp Asp
    105                 110                 115

AAG TTC CAC TAC AAA GTG GAG TAT AGA GGC AAC GGT TTC CCT AGT AAC    411
Lys Phe His Tyr Lys Val Glu Tyr Arg Gly Asn Gly Phe Pro Ser Asn
120                 125                 130                 135

GGA CCC GTG ATG CAA AAA GCC ATC CTC GGC ATG GAG CCA TCG TTT GAG    459
Gly Pro Val Met Gln Lys Ala Ile Leu Gly Met Glu Pro Ser Phe Glu
                140                 145                 150

GTG GTC TAC ATG AAC AGC GGC GTT CTG GTG GGC GAA GTA GAT CTC GTT    507
Val Val Tyr Met Asn Ser Gly Val Leu Val Gly Glu Val Asp Leu Val
            155                 160                 165

TAC AAA CTC GAG TCA GGG AAC TAT TAC TCG TGC CAC ATG AAA ACG TTT    555
Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr Ser Cys His Met Lys Thr Phe
        170                 175                 180

TAC AGA TCC AAA GGT GGA GTG AAA GAA TTC CCG GAA TAT CAC TTT ATC    603
Tyr Arg Ser Lys Gly Gly Val Lys Glu Phe Pro Glu Tyr His Phe Ile
    185                 190                 195

CAT CAT CGT CTG GAG AAA ACC TAC GTG GAA GAA GGA AGC TTC GTG GAA    651
His His Arg Leu Glu Lys Thr Tyr Val Glu Glu Gly Ser Phe Val Glu
200                 205                 210                 215

CAA CAC GAG ACG GCC ATT GCA CAA CTG ACC ACA ATT GGA AAA CCT CTG    699
Gln His Glu Thr Ala Ile Ala Gln Leu Thr Thr Ile Gly Lys Pro Leu
                220                 225                 230

GGC TCC CTT CAT GAA TGG GTG TAG AAAATGACCA ATATACTGGG GAAAATCACC   753
Gly Ser Leu His Glu Trp Val

AATATACTGG GGAAAATGAC CAATTTACTG GGGAAAATGA CCAATATACT GTAGAAAATC  813
ACCAATATAC TGGGGAAAAT GACCAATTTA CTGGGGAAAT GACCAATTTA CTGTAGAAAA  873
TCACCAATAT ACTGTGGAAA ATGACCAAAA TACTGTAGAA ATGTTCACAC TGGGTTGATA  933
ACCGTTTCGA TAACCGTTTG GAAGCTTGTG TATACAAGTT ATTTGGGGTC ATTTTGTAAT  993
GTGTATGTGT GTTGTATGAT CTATAGACGT CGTCATTCAT AGCTTGAATC CTTCAGCAAA 1053
AGAAACCTCG AAGCATATTG AAACCTCGAC GGAGAGCATA AAGAGACCGC ACGTACACAA 1113
ATTATAATAC CAGCAGTTGG AATCTTTAAA CCGATCAAAA CTATTAATAT ATATATACAC 1173
CCTGTATAAC ATATATATAT ATATATATCT ACATAGTTTG ATATTGATTA AATCTGTTCT 1233
TGATCACTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA               1279
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 amino acids

(B) TYPE: polypeptide
(C) STRANDEDNESS: N/A
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: Protein

(A) NAME/KEY: Ptilosarcus gurneyi Green Fluorescent Protein (GFP)
(B) LOCATION:
(D) OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP)

(vi) ORIGINAL SOURCE: Ptilosarcus gurneyi

(x) PUBLICATION INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile Met Ser
1 5 10 15

Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
20 25 30

Glu Gly Phe Gly Lys Gly Asn Asn Val Leu Phe Gly Asn Gln Leu Met Gln
35 40 45

Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
50 55 60

Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
65 70 75 80

Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
85 90 95

Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
100 105 110

Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
115 120 125

Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
130 135 140

Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
145 150 155 160

Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
165 170 175

Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
180 185 190

Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr Tyr Val
195 200 205

Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
210 215 220

Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225 230