

pctau2013000378-seq1
SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research Organisation

<120> Methods and systems for detecting an analyte or classifying a sample

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<150> US 61/624,899

<151> 2012-04-16

<150> AU 2013204332

<151> 2013-04-12

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<170> PatentIn version 3.5

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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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 Gln Gly Gly Thr Gly Gly Gly Met Lys Ile Glu Glu Gly Lys Leu Val
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accttcctgg	ttgacctgat	taaaaacaaa	cacatgaatg	cagacaccga	ttactccatc	1380
gcagaagctg	cctttaataa	aggcgaaaca	gcgatgacca	tcaacggccc	gtgggcatgg	1440
tccaacatcg	acaccagcaa	agtgaattat	gggtgaacgg	tactgccgac	cttcaagggg	1500
caaccatcca	aaccgttcgt	tggcgtgctg	agcgcaggta	ttaacgccgc	cagtccgaac	1560
aaagagctgg	caaaagagtt	cctcgaaaac	tatctgctga	ctgatgaagg	tctggaagcg	1620
gttaataaaag	acaaaccgct	gggtgccgta	gcgctgaagt	cttacgagga	agagttgggtg	1680
aaagatccgc	gtattgccgc	cactatggaa	aacgcccaga	aaggtgaaat	catgccgaac	1740
atcccgcaga	tgtccgcttt	cgcgatgcc	gtgcgtactg	cggtgatcaa	cgccgccagc	1800
ggtcgtcaga	ctgtcgatga	agccctgaaa	gacgcgcaga	ctgccctgaa	agacgcgcag	1860
actggcggcg	gtaccggtgg	attcgaaatg	gcttccaagg	tgtacgacct	cgagcaacgc	1920
aaacgcatga	tactggggcc	tcagtgggtg	gctcgctgca	agcaaatgaa	cgtgctggac	1980
tccttcatca	actactatga	ttccgagaag	cacgccgaga	acgccgtgat	ttttctgcat	2040
ggtaacgctg	cctccagcta	cctgtggagg	cacgtcgtgc	ctcacatcga	gcccgtggct	2100
agatgcatca	tccctgatct	gatcggaatg	ggtaagtccg	gcaagagcgg	gaatggctca	2160
tatcgcttcc	tggatcacta	caagtacctc	accgcttggg	tcgagctgct	gaaccttcca	2220
aagaaaatca	tctttgtggg	ccacgactgg	ggggctgctc	tggcctttca	ctactcctac	2280
gagcaccaag	acaagatcaa	ggccatcgtc	catgctgaga	gtgtcgtgga	cgtgatcgag	2340
tcctggggacg	agtggcctga	catcgaggag	gatatcgccc	tgatcaagag	cgaagagggc	2400
gagaaaatgg	tgcttgagaa	taacttcttc	gtcgagaccg	tgctcccaag	caagatcatg	2460
cggaaaactgg	agcctgagga	gttcgctgcc	tacctggagc	cattcaagga	gaagggcgag	2520
gttagacggc	ctaccctctc	ctggcctcgc	gagatccctc	tcgttaaggg	aggcaagccc	2580
gacgtcgtcc	agattgtccg	caactacaac	gcctaccttc	gggccagcga	cgatctgcct	2640
aagatgttca	tcgagtccga	ccctgggttc	ttttccaacg	ctattgtcga	gggagctaag	2700
aagttcccta	acaccgagtt	cgtgaagggtg	aagggcctcc	acttcagcca	ggaggacgct	2760
ccagatgaaa	tgggtaagta	catcaagagc	ttcgtggagc	gcgtgctgaa	gaacgagcag	2820
taa						2823

<210> 6
 <211> 940
 <212> PRT
 <213> Artificial Sequence

pctau2013000378-seq1

<220>

<223> GFP2-MBP-RLuc2 W140A fusion protein

<400> 6

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Gly Gly Thr Gly Gly Gly Met Lys Ile Glu Glu Gly Lys Leu Val
245    250    255

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Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly
260                265                270

Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu His Pro
275                280                285

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

Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr Ala Gln
305                310                315                320

Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys
325                330                335

Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile
340                345                350

Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp
355                360                365

Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp
370                375                380

Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn Leu Gln
385                390                395                400

Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala
405                410                415

Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val Asp
420                425                430

Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu Ile Lys
435                440                445

Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala
450                455                460

Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp
465                470                475                480

Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro
485                490                495

Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala
500                505                510

Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu
515                520                525

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Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp
530 535 540
Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Val
545 550 555 560
Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu
565 570 575
Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Ala Tyr Ala Val Arg
580 585 590
Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala
595 600 605
Leu Lys Asp Ala Gln Thr Ala Leu Lys Asp Ala Gln Thr Gly Gly Gly
610 615 620
Thr Gly Gly Phe Glu Met Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg
625 630 635 640
Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met
645 650 655
Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala
660 665 670
Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu
675 680 685
Trp Arg His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile
690 695 700
Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser
705 710 715 720
Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu
725 730 735
Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala
740 745 750
Ala Leu Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala
755 760 765
Ile Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu
770 775 780
Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly
785 790 795 800

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Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Val Leu Pro
805 810 815

Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu
820 825 830

Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp
835 840 845

Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln
850 855 860

Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro
865 870 875 880

Lys Met Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val
885 890 895

Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly
900 905 910

Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile
915 920 925

Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln
930 935 940

<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
cacgactggg gcgccgccct ggccttccac tac

33

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
gtagtgaag gccaggcg cgccccagtc gtg

33

<210> 9
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 9

cttcttcgtg gagaccgtgc tgcccagcaa gatc

34

<210> 10

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 10

gatcttgctg ggcagcacgg tctccacgaa gaag

34

<210> 11

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 11

cagatgtccg ctttcgcgta tgccgtgcgt ac

32

<210> 12

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

gtacgcacgg catacgcgaa agcggacatc tg

32

<210> 13

<211> 896

<212> PRT

<213> Artificial Sequence

<220>

<223> GFP2-str-112 SGSR-RLuc fusion protein

<400> 13

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe
770 775 780

Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg Pro
785 790 795 800

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

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

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

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

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

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

<210> 14
<211> 897
<212> PRT
<213> Artificial Sequence

<220>
<223> GFP2-str-113 SGSR-RLuc fusion protein

<400> 14

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

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

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

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

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

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

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

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

Ala Ser Trp Gly Phe Ala Ala Phe Ile Leu Tyr Pro Glu Thr Glu Arg
145 150 155 160

Thr Arg Thr Ala Leu Ile His Val Ile Gln Thr Ser Tyr Glu Leu Asp
165 170 175

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

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

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

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Asn Thr Tyr Lys Thr Leu Asn Gly Ser Leu Gly Val Ser Glu Lys Thr
225 230 235 240
Ser Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
245 250 255
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
260 265 270
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
275 280 285
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
290 295 300
Thr Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
305 310 315 320
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
325 330 335
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
340 345 350
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
355 360 365
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
370 375 380
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
385 390 395 400
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
405 410 415
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
420 425 430
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
435 440 445
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
450 455 460
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
465 470 475 480
Lys Val Asp Lys Glu Met His Thr Gln Leu Phe Lys Ala Leu Val Leu
485 490 495

pctau2013000378-seq1

Gln Thr Ile Ile Pro Thr Thr Leu Met Tyr Ile Pro Thr Thr Met Leu
500 505 510
Phe Val Thr Pro Phe Val Gly Leu Asn Ile Gly Cys Tyr Gly Asn Ile
515 520 525
Thr Thr Ala Thr Val His Leu Tyr Pro Gly Ile Asp Pro Val Val Leu
530 535 540
Ile Phe Ile Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe Arg
545 550 555 560
Cys Phe Tyr Arg Ser Asn Ser Val Glu Asn Thr Ala Thr Ile Arg Gln
565 570 575
Tyr Gln Gln Ser Ser Ser Lys Gly Ser Arg Met Thr Ser Lys Val Tyr
580 585 590
Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala
595 600 605
Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn Tyr Tyr Asp
610 615 620
Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala
625 630 635 640
Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile Glu Pro Val
645 650 655
Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys
660 665 670
Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr
675 680 685
Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly
690 695 700
His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr Ser Tyr Glu His Gln
705 710 715 720
Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser Val Val Asp Val Ile
725 730 735
Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile
740 745 750
Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val
755 760 765

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Glu Thr Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu
770 775 780

Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg
785 790 795 800

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

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

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

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

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

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

Gln

<210> 15
<211> 904
<212> PRT
<213> Artificial Sequence

<220>
<223> GFP2-str-114 SGSR-RLuc fusion protein
<400> 15

Met Ser Asp Ile Tyr Trp Ile Gln Ile Thr Glu Val Cys Ser Phe Val
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Gly Phe Met Leu Ser Val Leu Gly Asn Ser Thr Leu Leu Val Leu Leu
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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Ala Glu Val₃₅₅ Lys Phe Glu Gly Asp₃₆₀ Thr Leu Val Asn Arg₃₆₅ Ile Glu Leu

Lys Gly₃₇₀ Ile Asp Phe Lys Glu₃₇₅ Asp Gly Asn Ile Leu₃₈₀ Gly His Lys Leu

Glu₃₈₅ Tyr Asn Tyr Asn Ser₃₉₀ His Asn Val Tyr Ile₃₉₅ Met Ala Asp Lys Gln₄₀₀

Lys Asn Gly Ile Lys₄₀₅ Val Asn Phe Lys Ile₄₁₀ Arg His Asn Ile Glu₄₁₅ Asp

Gly Ser Val Gln₄₂₀ Leu Ala Asp His Tyr₄₂₅ Gln Gln Asn Thr Pro₄₃₀ Ile Gly

Asp Gly Pro₄₃₅ Val Leu Leu Pro Asp₄₄₀ Asn His Tyr Leu Ser₄₄₅ Thr Gln Ser

Ala Leu₄₅₀ Ser Lys Asp Pro Asn₄₅₅ Glu Lys Arg Asp His₄₆₀ Met Val Leu Leu

Glu₄₆₅ Phe Val Thr Ala Ala₄₇₀ Gly Ile Thr Leu Gly₄₇₅ Met Asp Glu Leu Tyr₄₈₀

Lys Val Asp Lys Asp₄₈₅ Leu Gln Asn Gln Phe₄₉₀ Phe Thr Ala Leu Val₄₉₅ Ala

Gln Thr Val Val₅₀₀ Pro Leu Ile Phe Met₅₀₅ Phe Ile Pro Asn Met₅₁₀ Val Leu

Thr Thr Ala₅₁₅ Ala Leu Ile Asp Gly₅₂₀ Thr Phe Gly Ser Trp₅₂₅ Ala Asn Ile

Thr Val₅₃₀ Val Met Asn His Leu₅₃₅ Tyr Pro Ala Ala Asp₅₄₀ Pro Phe Val Ile

Leu₅₄₅ Phe Ile Ile Lys Gly₅₅₀ Phe Arg Asn Ser Ile₅₅₅ Arg Asn Val Ile Tyr₅₆₀

Arg Cys Thr Lys Thr₅₆₅ Lys Lys Ala Ser Val₅₇₀ Ser Ser Val Val Arg₅₇₅ Gly

Ile Glu Ala Gln₅₈₀ Ser Lys Lys Gln Ser₅₈₅ Phe Ser Arg Val Asp₅₉₀ Ile Ser

Arg Met Thr₅₉₅ Ser Lys Val Tyr Asp₆₀₀ Pro Glu Gln Arg Lys₆₀₅ Arg Met Ile

Thr Gly₆₁₀ Pro Gln Trp Trp Ala₆₁₅ Arg Cys Lys Gln Met₆₂₀ Asn Val Leu Asp

pctau2013000378-seq1

Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val
625 630 635 640

Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val
645 650 655

Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile
660 665 670

Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu
675 680 685

Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro
690 695 700

Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe
705 710 715 720

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

Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile
740 745 750

Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val
755 760 765

Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met
770 775 780

Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys
785 790 795 800

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

Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn
820 825 830

Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile
835 840 845

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

Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser
865 870 875 880

Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val
885 890 895

pctau2013000378-seq1
 Glu Arg Val Leu Lys Asn Glu Gln
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<210> 16
 <211> 890
 <212> PRT
 <213> Artificial Sequence

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 <223> GFP2-str-115 SGSR-RLuc fusion protein

<400> 16

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

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

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

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

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

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

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

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

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

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

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

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

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

pctau2013000378-seq1

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

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

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

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
      275      280      285

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

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

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

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

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

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

Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
385      390      395

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

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

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

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

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

Tyr Lys Val Asp Arg Cys Ile Gln Leu Gln Leu Phe Arg Ala Leu Val
      485      490      495

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Ala Gln Thr Ile Leu Pro Met Phe Met Met Tyr Ile Pro Val Gly Phe
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Met Phe Ala Cys Pro Tyr Phe Asp Leu Gln Leu Gly Ala Tyr Thr Asn
515 520 525
Tyr Gln Thr Val Met Ala Gln Leu Tyr Pro Gly Ile Asp Pro Phe Val
530 535 540
Met Leu Phe Leu Ile Asp Ser Tyr Arg Ile Thr Ile Phe Gly Trp Leu
545 550 555 560
Cys Pro Arg Phe Val Tyr Val Lys Pro Met His Ser Thr Tyr Thr Leu
565 570 575
Thr Ser Arg Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
580 585 590
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
595 600 605
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
610 615 620
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
625 630 635 640
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
645 650 655
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
660 665 670
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn
675 680 685
Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu
690 695 700
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
705 710 715 720
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
725 730 735
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
740 745 750
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
755 760 765

pctau2013000378-seq1

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

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

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

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

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

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

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

Phe Val Glu Arg Val Leu Lys Asn Glu Gln
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Gly Phe Thr Met Ser Ile Phe Ser Asn Ser Val Leu Leu Ser Leu Ile
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Phe Ser Ser Ser Ser Pro Ile Lys Gly Ala Tyr Lys Asn Met Leu Ile
35 40 45

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

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

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

pctau2013000378-seq1

Tyr Cys Trp Cys₁₀₀ Tyr Ala Met Ser Phe₁₀₅ Ser Leu Phe Ala Leu₁₁₀ Gln Phe
 Leu Tyr Arg₁₁₅ Tyr Val Ala Val Cys₁₂₀ Lys Pro His Leu Val₁₂₅ Val Phe Phe
 Thr Gly₁₃₀ Cys Tyr Phe Tyr Tyr₁₃₅ Trp Leu Ala Leu Ile₁₄₀ Leu Ser Leu Ala
 Thr₁₄₅ Ser Trp Gly Leu Thr₁₅₀ Ala Ala Phe Met Phe₁₅₅ Pro Gln Thr Asn Arg₁₆₀
 Thr Thr Glu Ser Phe₁₆₅ Asn Tyr Val Ile Lys₁₇₀ Thr Ser Tyr Asp Leu₁₇₅ Asp
 Pro Tyr Trp Thr₁₈₀ Asp Tyr Val Ala Tyr₁₈₅ Lys Tyr Phe Asp Thr₁₉₀ Asp Glu
 Asn His Val₁₉₅ Arg Trp Val Asn Val₂₀₀ Leu Ser Leu Phe Gly₂₀₅ Val Leu Gln
 His Gly₂₁₀ Leu Val Ile Thr Leu₂₁₅ Ser Phe Gly Thr Leu₂₂₀ Phe Tyr Cys Gly
 Ile₂₂₅ Lys Thr Tyr Leu Ser₂₃₀ Ile Thr Glu His Val₂₃₅ Gly Met Ser Ser Lys₂₄₀
 Thr Ser Gly Met Val₂₄₅ Ser Lys Gly Glu Glu₂₅₀ Leu Phe Thr Gly Val₂₅₅ Val
 Pro Ile Leu Val₂₆₀ Glu Leu Asp Gly Asp₂₆₅ Val Asn Gly His Lys₂₇₀ Phe Ser
 Val Ser Gly₂₇₅ Glu Gly Glu Gly Asp₂₈₀ Ala Thr Tyr Gly Lys₂₈₅ Leu Thr Leu
 Lys Phe₂₉₀ Ile Cys Thr Thr Gly₂₉₅ Lys Leu Pro Val Pro₃₀₀ Trp Pro Thr Leu
 Val₃₀₅ Thr Thr Leu Ser Tyr₃₁₀ Gly Val Gln Cys Phe₃₁₅ Ser Arg Tyr Pro Asp₃₂₀
 His Met Lys Gln His₃₂₅ Asp Phe Phe Lys Ser₃₃₀ Ala Met Pro Glu Gly₃₃₅ Tyr
 Val Gln Glu Arg₃₄₀ Thr Ile Phe Phe Lys₃₄₅ Asp Asp Gly Asn Tyr₃₅₀ Lys Thr
 Arg Ala Glu₃₅₅ Val Lys Phe Glu Gly₃₆₀ Asp Thr Leu Val Asn₃₆₅ Arg Ile Glu

pctau2013000378-seq1

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

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

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

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

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

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

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

Tyr Lys Val Asp Arg Ser Leu Gln Leu Gln Leu Phe Arg Ala Leu Val
485 490 495

Ala Gln Thr Cys Leu Pro Met Leu Met Met Tyr Met Pro Ile Gly Phe
500 505 510

Met Phe Ser Cys Pro Tyr Phe Asp Leu Gln Leu Gly Ala Val Thr Asn
515 520 525

Tyr Gln Thr Val Met Ala Gln Leu Tyr Pro Gly Ile Asp Pro Phe Met
530 535 540

Leu Leu Phe Leu Ile Asn Ala Tyr Arg Lys Thr Val Leu Ser Leu Ile
545 550 555 560

Cys Pro Asn Phe Ile Gln Lys Lys Tyr Val Gln Thr Ala Thr Thr Arg
565 570 575

Asp Gly Thr Asp Ala Ser Ala Thr Met Asn Ser Val Lys Ser Thr Gln
580 585 590

Leu Ser Arg Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
595 600 605

Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
610 615 620

Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
625 630 635 640

pctau2013000378-seq1

Ala Val Ile Phe Leu₆₄₅ His Gly Asn Ala Ala₆₅₀ Ser Ser Tyr Leu Trp₆₅₅ Arg

His Val Val Pro₆₆₀ His Ile Glu Pro Val₆₆₅ Ala Arg Cys Ile Ile₆₇₀ Pro Asp

Leu Ile Gly₆₇₅ Met Gly Lys Ser Gly₆₈₀ Lys Ser Gly Asn Gly₆₈₅ Ser Tyr Arg

Leu Leu₆₉₀ Asp His Tyr Lys Tyr₆₉₅ Leu Thr Ala Trp Phe₇₀₀ Glu Leu Leu Asn

Leu₇₀₅ Pro Lys Lys Ile Ile₇₁₀ Phe Val Gly His Asp₇₁₅ Trp Gly Ala Cys Leu₇₂₀

Ala Phe His Tyr Ser₇₂₅ Tyr Glu His Gln Asp₇₃₀ Lys Ile Lys Ala Ile₇₃₅ Val

His Ala Glu Ser₇₄₀ Val Val Asp Val Ile₇₄₅ Glu Ser Trp Asp Glu₇₅₀ Trp Pro

Asp Ile Glu₇₅₅ Glu Asp Ile Ala Leu₇₆₀ Ile Lys Ser Glu Glu₇₆₅ Gly Glu Lys

Met Val₇₇₀ Leu Glu Asn Asn Phe₇₇₅ Phe Val Glu Thr Met₇₈₀ Leu Pro Ser Lys

Ile₇₈₅ Met Arg Lys Leu Glu₇₉₀ Pro Glu Glu Phe Ala₇₉₅ Ala Tyr Leu Glu Pro₈₀₀

Phe Lys Glu Lys Gly₈₀₅ Glu Val Arg Arg Pro₈₁₀ Thr Leu Ser Trp Pro₈₁₅ Arg

Glu Ile Pro Leu₈₂₀ Val Lys Gly Gly Lys₈₂₅ Pro Asp Val Val Gln Ile Val

Arg Asn Tyr₈₃₅ Asn Ala Tyr Leu Arg₈₄₀ Ala Ser Asp Asp Leu₈₄₅ Pro Lys Met

Phe Ile₈₅₀ Glu Ser Asp Pro Gly₈₅₅ Phe Phe Ser Asn Ala₈₆₀ Ile Val Glu Gly

Ala Lys Lys Phe Pro Asn₈₇₀ Thr Glu Phe Val Lys₈₇₅ Val Lys Gly Leu His₈₈₀

Phe Ser Gln Glu Asp₈₈₅ Ala Pro Asp Glu Met₈₉₀ Gly Lys Tyr Ile Lys₈₉₅ Ser

Phe Val Glu Arg₉₀₀ Val Leu Lys Asn Glu₉₀₅ Gln

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<400> 18

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Val Asp Lys Glu Met His Thr Gln Leu Phe Lys Ala Leu Val Leu
485 490 495

Gln Thr Ile Ile Pro Thr Thr Leu Met Tyr Ile Pro Thr Thr Met Leu
500 505 510

pctau2013000378-seq1

Phe Val Thr Pro Phe Val Gly Leu Asn Ile Gly Cys Tyr Gly Asn Ile
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Thr Thr Ala Thr Val His Leu Tyr Pro Gly Ile Asp Pro Val Val Leu
530 535 540
Ile Phe Ile Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe Arg
545 550 555 560
Cys Phe Tyr Arg Ser Asn Ser Val Glu Asn Thr Ala Thr Ile Arg Gln
565 570 575
Tyr Gln Gln Ser Ser Ser Lys Gly Ser Arg Glu Phe Gly Thr Met Ala
580 585 590
Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro
595 600 605
Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile
610 615 620
Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu
625 630 635 640
His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His
645 650 655
Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly
660 665 670
Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr
675 680 685
Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile
690 695 700
Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His Tyr Ser
705 710 715 720
Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser Val
725 730 735
Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp
740 745 750
Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn
755 760 765
Asn Phe Phe Val Glu Thr Val Leu Pro Ser Lys Ile Met Arg Lys Leu
770 775 780

pctau2013000378-seq1

Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly
785 790 795 800

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

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

Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp
835 840 845

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

Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp
865 870 875 880

Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val
885 890 895

Leu Lys Asn Glu Gln
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<212> DNA
<213> Artificial Sequence

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aaaaacttat tgggttggtt cgttcattac ttcgttatgt ctatgacatt cgttgttgtt 660
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pctau2013000378-seq1

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cattacttat caactcaatc cgctttgagt aaggatccaa acgaaaagag agatcatatg	1380
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gaatggccag atatcgaaga agatatcgct ttaattaagt ccgaagaagg tgaaaagatg	2280
gttttggaac acaacttttt cgttgaaact atgttgcccta gtaagatcat gagaaagttg	2340
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cctacattat ctgggcctag agaaattcca ttggttaaag gtggtaaacc agatgttggt	2460
caaatcgtta gaaactacaa cgcttactta agagcatctg atgatttgcc aaagatgttc	2520
atcgaatctg atcctggttt cttttcta atgctattgtg aagggtgctaa gaaattccct	2580
aacacagaat tcgttaaggt taagggtttg catttctctc aagaagatgc tccagatgaa	2640
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<211> 2694

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-113 SGSR-RLuc fusion protein

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<210> 21

<211> 2715

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-114 SGSR-RLuc fusion protein

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<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-115 SGSR-RLuc fusion protein

<400> 22

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gaagtcatgc ttcagccact aatccatatt tacgacgaca ctttattttt gattcatcga	240
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<210> 23

<211> 2721

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-116 SGSR-RLuc fusion protein

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<211> 2706

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-113/114 SGsR-RLuc fusion protein

<400> 24

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gactccttca tcaactacta tgattccgag aagcacgccg agaacgccgt gattttttctg 1920
catggtaacg ctgcctccag ctacctgtgg aggcacgtcg tgcctcacat cgagcccgtg 1980
gctagatgca tcatccctga tctgatcgga atgggtaagt ccggcaagag cgggaatggc 2040
tcatatcgcc tcctggatca ctacaagtac ctcaccgctt ggttcgagct gctgaacctt 2100
ccaaagaaaa tcatctttgt gggccacgac tggggggctg ctctggcctt tcactactcc 2160
tacgagcacc aagacaagat caaggccatc gtccatgctg agagtgtcgt ggacgtgatc 2220
gagtcctggg acgagtggcc tgacatcgag gaggatatcg ccctgatcaa gagcgaagag 2280
ggcgagaaaa tggtgcttga gaataacttc ttcgtcgaga ccgtgctccc aagcaagatc 2340
atgcggaaac tggagcctga ggagttcgct gcctacctgg agccattcaa ggagaagggc 2400
gaggttagac ggcctaccct ctctggcct cgcgagatcc ctctcgtaa gggaggcaag 2460
cccgacgtcg tccagattgt ccgcaactac aacgcctacc ttcggggccag cgacgatctg 2520
cctaagatgt tcatcgagtc cgaccctggg ttcttttcca acgctattgt cgagggagct 2580
aagaagttcc ctaacaccga gttcgtgaag gtgaagggcc tccacttcag ccaggaggac 2640
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cagtaa 2706

<210> 25
<211> 889
<212> PRT
<213> Artificial Sequence

<220>
<223> GFP2-OGOR-RLuc2 protein

<400> 25

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

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

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

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

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

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

pctau2013000378-seq1

Cys Ala Cys Phe₁₀₀ Ala Thr Ser Phe Val₁₀₅ Val Ser Gly Val His₁₁₀ Phe Val
Tyr Arg Tyr₁₁₅ Phe Ala Thr Cys Lys₁₂₀ Pro Asn Leu Leu Arg₁₂₅ Leu Phe Asn
Leu Pro₁₃₀ Thr Leu Leu Leu Trp₁₃₅ Pro Leu Gly Cys Ser₁₄₀ Val Pro Val Thr
Met Trp Ala Ser Val₁₅₀ Ser Tyr Phe Leu Tyr Pro₁₅₅ Asp Thr Glu Tyr Thr₁₆₀
Glu Ala Ala Val Thr₁₆₅ Asn Val Leu Asn Asn₁₇₀ His Tyr Asn Trp Ile₁₇₅ Lys
Lys Glu Asn Val₁₈₀ Ser Tyr Ile Ala Tyr₁₈₅ Val Tyr Tyr Gln Tyr₁₉₀ Glu Asn
Gly Val Arg₁₉₅ His Ile Tyr Leu Lys₂₀₀ Asn Leu Leu Gly Cys₂₀₅ Phe Val His
Tyr Phe Val₂₁₀ Met Ser Met Thr₂₁₅ Phe Val Val Met Phe₂₂₀ Tyr Cys Gly Tyr
Ala Thr Trp Lys Thr Met₂₃₀ Asn Glu His Lys Asp₂₃₅ Val Ser Asp Arg Thr₂₄₀
Met Val Ser Lys Gly₂₄₅ Glu Glu Leu Phe Thr₂₅₀ Gly Val Val Pro Ile₂₅₅ Leu
Val Glu Leu Asp₂₆₀ Gly Asp Val Asn Gly₂₆₅ His Lys Phe Ser Val₂₇₀ Ser Gly
Glu Gly Glu₂₇₅ Gly Asp Ala Thr Tyr₂₈₀ Gly Lys Leu Thr Leu₂₈₅ Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro₂₉₅ Val Pro Trp Pro Thr₃₀₀ Leu Val Thr Thr
Leu Ser Tyr Gly Val Gln₃₁₀ Cys Phe Ser Arg Tyr₃₁₅ Pro Asp His Met Lys₃₂₀
Gln His Asp Phe Phe₃₂₅ Lys Ser Ala Met Pro Glu Gly Tyr Val Gln₃₃₅ Glu
Arg Thr Ile Phe₃₄₀ Phe Lys Asp Asp Gly₃₄₅ Asn Tyr Lys Thr Arg₃₅₀ Ala Glu
Val Lys Phe₃₅₅ Glu Gly Asp Thr Leu₃₆₀ Val Asn Arg Ile Glu₃₆₅ Leu Lys Gly

pctau2013000378-seq1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

pctau2013000378-seq1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Glu Arg Val Leu Lys Asn Glu Gln
885

<210> 26
<211> 889
<212> PRT
<213> Artificial sequence

pctau2013000378-seq1

<220>

<223> GFP2-OGOR-RLuc2 mutant protein

<400> 26

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

pctau2013000378-seq1

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
260 265 270
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
275 280 285
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
290 295 300
Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
305 310 315 320
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
325 330 335
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
340 345 350
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
355 360 365
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
370 375 380
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
385 390 395 400
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
405 410 415
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
420 425 430
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
435 440 445
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
450 455 460
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg
465 470 475 480
Ala Leu Gln Lys Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Leu Ile
485 490 495
Pro Thr Ile Phe Met Tyr Ala Pro Thr Gly Val Met Phe Ile Ala Pro
500 505 510
Phe Phe Asp Val Asn Leu Asn Ala Asn Ala Asn Phe Ile Val Phe Cys
515 520 525

pctau2013000378-seq1

Ser Phe Leu Tyr Pro Gly Leu Asp Pro Leu Ile Leu Ile Leu Ile Ile
530 535 540
Arg Asp Phe Arg Arg Thr Ile Phe Asn Phe Leu Cys Gly Lys Lys Asn
545 550 555 560
Ser Val Asp Glu Ser Arg Ser Thr Thr Arg Ala Asn Leu Ser Gln Val
565 570 575
Pro Thr Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met
580 585 590
Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu
595 600 605
Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala
610 615 620
Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His
625 630 635 640
Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu
645 650 655
Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu
660 665 670
Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu
675 680 685
Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala
690 695 700
Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His
705 710 715 720
Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp
725 730 735
Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met
740 745 750
Val Leu Glu Asn Asn Phe Phe Val Glu Thr Val Leu Pro Ser Lys Ile
755 760 765
Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe
770 775 780
Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu
785 790 795 800

pctau2013000378-seq1

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

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

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

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

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

Val Glu Arg Val Leu Lys Asn Glu Gln
885

<210> 27

<211> 897

<212> PRT

<213> Artificial Sequence

<220>

<223> GFP2-str-112 SGSR-RLuc2 mutant protein

<400> 27

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

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

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

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

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

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

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

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

pctau2013000378-seq1

Asn Leu Pro His Leu Leu Leu Trp Pro Leu Met Cys Ser Ile Pro Val
 130 135 140
 Thr Ala Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr
 145 150 155 160
 Thr Glu Ala Ala Val Thr Tyr Val Leu Lys Thr His Tyr Glu Val Ile
 165 170 175
 Lys Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu
 180 185 190
 Asn Gly Glu Arg His Ile Tyr Ile Lys Asn Leu Leu Gly Cys Phe Val
 195 200 205
 His Tyr Phe Val Met Ser Met Thr Phe Val Val Val Phe Tyr Cys Gly
 210 215 220
 Phe Ser Thr Trp Trp Thr Ile Arg Glu His Arg Gly Ala Ser Asp Arg
 225 230 235 240
 Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 245 250 255
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 260 265 270
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 275 280 285
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 290 295 300
 Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 305 310 315 320
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 325 330 335
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 340 345 350
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 355 360 365
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 370 375 380
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 385 390 395 400

pctau2013000378-seq1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

pctau2013000378-seq1

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

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

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

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

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

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

Glu Thr Val Leu Pro Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu
770 775 780

Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu Val Arg Arg
785 790 795 800

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

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

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

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

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

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

Gln

<210> 28
<211> 901
<212> PRT
<213> Artificial Sequence

<220>
<223> SFP2-str-113 SGSR-RLuc2 mutant protein

pctau2013000378-seq1

<400> 28

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

pctau2013000378-seq1

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
275 280 285
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
290 295 300
Thr Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
305 310 315 320
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
325 330 335
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
340 345 350
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
355 360 365
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
370 375 380
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
385 390 395 400
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
405 410 415
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
420 425 430
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
435 440 445
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
450 455 460
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
465 470 475 480
Lys Val Asp Lys Glu Met His Thr Gln Leu Phe Lys Ala Leu Val Leu
485 490 495
Gln Thr Ile Ile Pro Thr Thr Leu Met Tyr Ile Pro Thr Thr Met Leu
500 505 510
Phe Val Thr Pro Phe Val Gly Leu Asn Ile Gly Cys Tyr Gly Asn Ile
515 520 525
Thr Thr Ala Thr Val His Leu Tyr Pro Gly Ile Asp Pro Val Val Leu
530 535 540

pctau2013000378-seq1

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Ile Phe Ile Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe Arg
545          550          555          560

Cys Phe Tyr Arg Ser Asn Ser Val Glu Asn Thr Ala Thr Ile Arg Gln
          565          570          575

Tyr Gln Gln Ser Ser Ser Lys Gly Ser Arg Glu Phe Gly Thr Met Thr
          580          585          590

Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro
          595          600          605

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

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

His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His
          645          650          655

Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly
          660          665          670

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

Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile
690          695          700

Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His Tyr Ser
705          710          715          720

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

Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp
          740          745          750

Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn
755          760          765

Asn Phe Phe Val Glu Thr Val Leu Pro Ser Lys Ile Met Arg Lys Leu
770          775          780

Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly
785          790          795          800

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

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pctau2013000378-seq1

Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr Asn Ala
820 825 830
Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp
835 840 845
Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro
850 855 860
Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp
865 870 875 880
Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val
885 890 895
Leu Lys Asn Glu Gln
900

<210> 29
<211> 908
<212> PRT
<213> Artificial Sequence

<220>
<223> GFP2-str-114 SGSR-RLuc2 mutant protein
<400> 29

Met Ser Asp Ile Tyr Trp Ile Gln Ile Thr Glu Val Cys Ser Phe Val
1 5 10 15
Gly Phe Met Leu Ser Val Leu Gly Asn Ser Thr Leu Leu Val Leu Leu
20 25 30
Ser Gly Lys Ser Ile Asp Gly Ile Gly Thr Tyr Arg Tyr Leu Met Ile
35 40 45
Thr Phe Cys Val Phe Ser Leu Leu Phe Thr Ile Leu Glu Asp Phe Ile
50 55 60
Arg Pro Leu Met His His Tyr Asn Asn Thr Ile Ile Val Leu Gln Arg
65 70 75 80
Lys Arg Phe Gln Phe Ser Asp Ser Thr Ala Arg Ile Leu Thr Val Ser
85 90 95
Tyr Cys Gly Cys Phe Ala Met Cys Phe Val Met Phe Ala Val His Phe
100 105 110
Ile Tyr Arg Tyr Leu Val Ala Cys His Pro Thr Lys Leu His Tyr Phe
115 120 125

pctau2013000378-seq1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Val Asp Lys Asp Leu Gln Asn Gln Phe Phe Thr Ala Leu Val Ala
485 490 495

Gln Thr Val Val Pro Leu Ile Phe Met Phe Ile Pro Asn Met Val Leu
500 505 510

Thr Thr Ala Ala Leu Ile Asp Gly Thr Phe Gly Ser Trp Ala Asn Ile
515 520 525

Thr Val Val Met Asn His Leu Tyr Pro Ala Ala Asp Pro Phe Val Ile
530 535 540

Leu Phe Ile Ile Lys Gly Phe Arg Asn Ser Ile Arg Asn Val Ile Tyr
545 550 555 560

Arg Cys Thr Lys Thr Lys Lys Ala Ser Val Ser Ser Val Val Arg Gly
565 570 575

Ile Glu Ala Gln Ser Lys Lys Gln Ser Phe Ser Arg Val Asp Ile Ser
580 585 590

Arg Glu Phe Gly Thr Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg
595 600 605

Lys Arg Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met
610 615 620

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

Glu Asn Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu
645 650 655

Trp Arg His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile
660 665 670

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Pro Asp Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser
675 680 685

Tyr Arg Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu
690 695 700

Leu Asn Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala
705 710 715 720

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

Ile Val His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu
740 745 750

Trp Pro Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly
755 760 765

Glu Lys Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Val Leu Pro
770 775 780

Ser Lys Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu
785 790 795 800

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

Pro Arg Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln
820 825 830

Ile Val Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro
835 840 845

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

Glu Gly Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly
865 870 875 880

Leu His Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile
885 890 895

Lys Ser Phe Val Glu Arg Val Leu Lys Asn Glu Gln
900 905

<210> 30
<211> 901
<212> PRT
<213> Artificial Sequence

<220>
<223> GFP2-str-113/114 SGSR-RLuc2 mutant protein

pctau2013000378-seq1

<400> 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Val Asp Lys Glu Met His Thr Gln Leu Phe Lys Ala Leu Val Leu
485 490 495

Gln Thr Ile Ile Pro Thr Thr Leu Met Tyr Ile Pro Thr Thr Met Leu
500 505 510

Phe Val Thr Pro Phe Val Gly Leu Asn Ile Gly Cys Tyr Gly Asn Ile
515 520 525

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

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Ile Phe Ile Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe Arg
545 550 555 560

Cys Phe Tyr Arg Ser Asn Ser Val Glu Asn Thr Ala Thr Ile Arg Gln
565 570 575

Tyr Gln Gln Ser Ser Ser Lys Gly Ser Arg Glu Phe Gly Thr Met Thr
580 585 590

Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro
595 600 605

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

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

His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His
645 650 655

Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly
660 665 670

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

Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile
690 695 700

Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His Tyr Ser
705 710 715 720

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

Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp
740 745 750

Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn
755 760 765

Asn Phe Phe Val Glu Thr Val Leu Pro Ser Lys Ile Met Arg Lys Leu
770 775 780

Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly
785 790 795 800

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

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Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr Asn Ala
820 825 830
Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp
835 840 845
Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro
850 855 860
Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp
865 870 875 880
Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val
885 890 895
Leu Lys Asn Glu Gln
900

<210> 31
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> GFP2-str-115 SGSR-RLuc2 mutant protein
<400> 31

Met Thr Asp Gln His Trp Val Ile Ile Thr Asp Ile Ala Gly Pro Ile
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Gly Phe Ser Met Ser Ile Phe Ser Asn Ser Ile Leu Leu Phe Leu Ile
20 25 30
Phe Ser His Ser Ser Pro Ile Lys Gly Pro Tyr Lys Arg Met Leu Ile
35 40 45
Val Phe Cys Ile Phe Thr Val Phe Tyr Ser Phe Val Glu Val Met Leu
50 55 60
Gln Pro Leu Ile His Ile Tyr Asp Asp Thr Leu Phe Leu Ile His Arg
65 70 75 80
Lys Arg Ile Asp Leu Pro Lys Trp Leu Thr Arg Leu Val Pro Thr Thr
85 90 95
Tyr Cys Trp Cys Tyr Ala Met Ser Phe Ser Leu Phe Ala Leu Gln Phe
100 105 110
Leu Tyr Arg Tyr Val Ala Val Cys Lys Pro Gln Tyr Val Asp Leu Phe
115 120 125

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Val	Gly	Cys	His	Phe	Tyr	Ala	Trp	Val	Val	Leu	Ile	Leu	Ser	Leu	Ala
	130					135					140				
Thr	Ser	Trp	Gly	Leu	Thr	Ala	Ala	Phe	Met	Phe	Pro	Gln	Thr	Asp	Arg
145					150					155					160
Thr	Thr	Glu	Ile	Phe	Leu	His	Ile	Ile	Tyr	Ser	Ser	Tyr	Asp	Leu	Glu
				165					170					175	
Pro	Tyr	Trp	Thr	Asp	Tyr	Val	Ala	Tyr	Lys	Tyr	Phe	Asp	Thr	Asp	Glu
			180					185					190		
Asn	Asn	Val	Arg	Trp	Val	Asn	Val	Leu	Ser	Phe	Phe	Gly	Val	Leu	Gln
		195					200					205			
His	Gly	Ile	Val	Ile	Thr	Leu	Ser	Phe	Gly	Thr	Leu	Tyr	Tyr	Cys	Gly
	210					215					220				
Ile	Asn	Thr	Tyr	Leu	Lys	Ile	Lys	Lys	His	Thr	Gly	Thr	Ser	Asn	Arg
225					230					235					240
Thr	Ser	Gly	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val
				245					250					255	
Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser
			260					265					270		
Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu
		275					280					285			
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu
	290					295					300				
Val	Thr	Thr	Leu	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp
305					310					315					320
His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr
				325					330					335	
Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr
			340					345					350		
Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu
		355					360					365			
Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys
	370					375					380				
Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys
385					390					395					400

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

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

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

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

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

Tyr Lys Val Asp Arg Cys Ile Gln Leu Gln Leu Phe Arg Ala Leu Val
485 490 495

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

Met Phe Ala Cys Pro Tyr Phe Asp Leu Gln Leu Gly Ala Tyr Thr Asn
515 520 525

Tyr Gln Thr Val Met Ala Gln Leu Tyr Pro Gly Ile Asp Pro Phe Val
530 535 540

Met Leu Phe Leu Ile Asp Ser Tyr Arg Ile Thr Ile Phe Gly Trp Leu
545 550 555 560

Cys Pro Arg Phe Val Tyr Val Lys Pro Met His Ser Thr Tyr Thr Leu
565 570 575

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Val Glu Arg Val Leu Lys Asn Glu Gln
885 890

<210> 32

<211> 906

<212> PRT

<213> Artificial Sequence

<220>

<223> GFP2-str-116 SGSR-RLuc2 mutant protein

<400> 32

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

pctau2013000378-seq1

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
290 295 300
Val Thr Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
305 310 315 320
His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
325 330 335
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
340 345 350
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
355 360 365
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
370 375 380
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
385 390 395 400
Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
405 410 415
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
420 425 430
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
435 440 445
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
450 455 460
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
465 470 475 480
Tyr Lys Val Asp Arg Ser Leu Gln Leu Gln Leu Phe Arg Ala Leu Val
485 490 495
Ala Gln Thr Cys Leu Pro Met Leu Met Met Tyr Met Pro Ile Gly Phe
500 505 510
Met Phe Ser Cys Pro Tyr Phe Asp Leu Gln Leu Gly Ala Val Thr Asn
515 520 525
Tyr Gln Thr Val Met Ala Gln Leu Tyr Pro Gly Ile Asp Pro Phe Met
530 535 540
Leu Leu Phe Leu Ile Asn Ala Tyr Arg Lys Thr Val Leu Ser Leu Ile
545 550 555 560

pctau2013000378-seq1

Cys Pro Asn Phe Ile Gln Lys Lys Tyr Val Gln Thr Ala Thr Thr Arg
 565 570 575
 Asp Gly Thr Asp Ala Ser Ala Thr Met Asn Ser Val Lys Ser Thr Gln
 580 585 590
 Leu Gly Thr Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
 595 600 605
 Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
 610 615 620
 Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
 625 630 635 640
 Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
 645 650 655
 His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
 660 665 670
 Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
 675 680 685
 Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn
 690 695 700
 Leu Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu
 705 710 715 720
 Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
 725 730 735
 His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
 740 745 750
 Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
 755 760 765
 Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Val Leu Pro Ser Lys
 770 775 780
 Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
 785 790 795 800
 Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
 805 810 815
 Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
 820 825 830

pctau2013000378-seq1

Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
835 840 845

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

Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
865 870 875 880

Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
885 890 895

Phe Val Glu Arg Val Leu Lys Asn Glu Gln
900 905

<210> 33
<211> 2670
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding GFP2-OGOR-Rluc2 fusion

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acttataaat atctcatggc gtttttctca gtattctcga ttttttacgc catcatcgag 180
ttcatattac gacctataat gcatattgag aacaccactt tctttttgat ctcaaggaaa 240
agattcaact actccaccaa acttggaaaa atcaactctg cgttttactg tgcttgtttt 300
gccaccagtt ttgttgcttc aggagttcac tttgtttatc gatattttgc aacttgcaaa 360
ccgaatctac ttcgtttggt caacttgcca actcttctac tttggccact tggttgcagt 420
gtacccgtga caatgtgggc tagtgtctca tattttttgt atccagatac cgagtacacg 480
gaagcggctg tcaccaatgt actaaataac cactataact ggatcaaaaa ggagaatgta 540
tcgtacattg catacgtcta ttaccaatac gaaaacggag taaggcatat ctacctcaaa 600
aacttgcttg gatgctttgt tcattacttt gtcattgtcga tgacgtttgt tgtgatgttc 660
tactgcggat atgccacgtg gaaaactatg aatgaacaca aggatgtatc tgatagaact 720
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggg cgagctggac 780
ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 840
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 900
ctcgtgacca ccctgagcta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 960
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ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg 1080
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 1140

pctau2013000378-seq1

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ggcatcaagg	tgaacttcaa	gatccgccac	aacatcgagg	acggcagcgt	gcagctcgcc	1260
gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgctgctgcc	cgacaaccac	1320
tacctgagca	cccagtccgc	cctgagcaaa	gaccccaacg	agaagcgcg	tcacatggtc	1380
ctgctggagt	tcgtgaccgc	cgccgggata	actctcggca	tggacgagct	gtacaagcga	1440
gcgctacaga	aacaactttt	caaagcttta	gttcttcaga	cactcatccc	aactatcttc	1500
atgtacgccc	caactggagt	catgttcata	gcaccgtttt	ttgacgtgaa	tttgaatgca	1560
aacgcccaatt	tcattgtgtt	ttgtcattt	ctgtaccggg	gactcgatcc	actcattctg	1620
attttgatca	ttcgtgattt	ccgaagaaca	atattcaatt	tcttggtgtg	aaagaaaaac	1680
agtgttgatg	aatcccgctc	gacaacaaga	gccaatattg	ctcaagttcc	gacgatgacc	1740
agcaaggtgt	acgacccgga	gcagaggaag	aggatgatca	ccggccccca	gtggtggggc	1800
aggtgcaagc	agatgaacgt	gctggacagc	ttcatcaact	actacgacag	cgagaagcac	1860
gccgagaacg	ccgtgatctt	cctgcacggc	aacgccgcta	gcagctacct	gtggaggcac	1920
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aagagcggca	agagcggcaa	cggcagctac	aggctgctgg	accactacaa	gtacctgacc	2040
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<210> 34

<211> 2670

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-OGOR-RLuc2 mutant protein

<400> 34

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acttataaat	atctcatggc	gtttttctca	gtattctcga	ttttttacgc	catcatcgag	180
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<210> 35

<211> 2714

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-112 SGSR-RLuc2 mutant protein

<400> 35

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<210> 36

<211> 2714

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-113 SGSR-RLuc2 mutant protein

<400> 36

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<210> 37

<211> 2714

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-114 SGSR-RLuc2 mutant protein

<400> 37

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<210> 38

<211> 2714

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding GFP2-str-113/114 SGSR-RLuc2 mutant protein

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

Arg Phe Asp Tyr Ser Thr Arg Leu Gly Lys Ile Asn Ser Ala Phe Tyr
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Cys Ala Cys Phe Ala Thr Ser Phe Val Leu Ser Ala Val His Phe Val
 100 105 110

Tyr Arg Tyr Phe Ala Ala Cys Lys Pro Asn Leu Leu Arg Leu Phe Asn
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Leu Pro His Leu Leu Leu Trp Pro Leu Met Cys Ser Ile Pro Val Thr
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Ala Trp Ala Ser Val Ser Tyr Phe Leu Tyr Pro Asp Thr Glu Tyr Thr
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Lys Glu Asn Val Ser Tyr Ile Ala Tyr Val Tyr Tyr Gln Tyr Glu Asn
180 185 190

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

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

Ser Thr Trp Trp Thr Ile Arg Glu His Arg Gly Ala Ser Asp Arg Thr
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Arg His Leu His Arg Gln Leu Phe Lys Ala Leu Val Phe Gln Thr Leu
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Val Pro Ser Ile Phe Met Tyr Ile Pro Thr Gly Val Met Phe Ile Ala
260 265 270

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

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

Ile Arg Glu Phe Arg Val Thr Ile Leu Asn Ile Ile Arg Gly Asn Glu
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Lys Arg Phe Gln Tyr Ser Glu Gly Thr Ala Arg Ala Ile Ser Ser Thr
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Val Tyr Arg Tyr Tyr Ala Ala Cys Lys Pro Asp Asn Leu Arg Tyr Phe
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Gln Gly Cys Tyr Phe Val Ala Trp Val Phe Gly Ala Met Ala Val Ala
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145 150 155 160

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165 170 175

Pro Glu Trp Val Gly Asn Val Pro Tyr Ser Tyr Trp Arg Thr Glu Asn
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195 200 205

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

Asn Thr Tyr Lys Thr Leu Asn Gly Ser Leu Gly Val Ser Glu Lys Thr
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Lys Glu Met His Thr Gln Leu Phe Lys Ala Leu Val Leu Gln Thr Ile
245 250 255

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

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

Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe Arg Cys Phe Tyr
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Ser Ser Ser Lys Gly
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Thr Phe Cys Val Phe Ser Leu Phe Tyr Thr Ser Ile Glu Thr Phe Leu
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Arg Pro Leu Ile His Ile Tyr Asp Asn Thr Ile Phe Val Ile Gln Arg
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Lys Arg Phe Gln Tyr Ser Glu Gly Thr Ala Arg Ala Ile Ser Ser Thr
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Tyr Cys Gly Cys Tyr Ala Met Ser Phe Thr Leu Phe Ala Val His Phe
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Val Tyr Arg Tyr Tyr Ala Ala Cys Lys Pro Asp Asn Leu Arg Tyr Phe
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Thr Arg Thr Ala Leu Ile His Val Ile Gln Thr Ser Tyr Glu Leu Asp
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Leu Gln Thr Ile Ile Pro Thr Thr Leu Met Tyr Ile Pro Thr Thr Met
260 265 270

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275 280 285

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

Leu Ile Phe Ile Ile Arg Asp Phe Arg Gln Thr Ile Leu Arg Pro Phe
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