

33031-US-3-PRO_ST25
SEQUENCE LISTING

<110> Hitko, Carolyn W.
Kirkland, Thomas
Machleidt, Thomas
Ohana, Rachel Friedman
Roberts, Matt
Wood, Keith

<120> Recognition of Cellular Target Binding by a Bioactive Agent Using
Intracellular Bioluminescence Resonance Energy Transfer

<130> PRMG-33031/US-3/PRO

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<170> PatentIn version 3.5

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ggggatgagg	gtgccagcag	ccagatcggc	cgggctgcgg	gcacaggctt	caccgtcaac	2640
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gtgcttccca	ttgcctacga	gtttaaccca	gaactgggtg	tggtctcagc	tggctttgat	2760
gctgcacggg	gggatccgct	ggggggctgc	cagggtgtcac	ctgagggtta	tgcccacctc	2820
accacactgc	tgatgggcct	tgccagtggc	cgcattatcc	ttatcctaga	gggtggctat	2880
aacctgacat	ccatctcaga	gtccatggct	gcctgcactc	gctccctcct	tggagaccca	2940
ccacccctgc	tgaccctgcc	acggcccca	ctatcagggg	ccctggcctc	aatcactgag	3000
accatccaag	tccatcgag	atactggcg	agcttacggg	tcatgaagg	agaagacaga	3060
gaaggaccct	ccagttctaa	gttggtcacc	aagaaggcac	cccaaccagc	caaacctagg	3120
ttagctgagc	ggatgaccac	acgagaaaag	aaggttctgg	aagcaggcat	ggggaaagtc	3180

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acctcggcat catttgggga agagtccact ccaggccaga ctaactcaga gacagctgtg 3240
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 ctgacctga gcacagacca ccagaccccc ccaacctcac ctgtgcaggg aactacaccc 3660
 cagatatctc ccagtacact gattgggagt ctcaggacct tggagctagg cagcgaatct 3720
 cagggggcct cagaatctca ggccccagga gaggagaacc tactaggaga ggcagctgga 3780
 ggtcaggaca tggctgattc gatgctgatg cagggatcta ggggcctcac tgatcaggcc 3840
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 cctgcagcag gcctagacgt gacccaacct tgtggggact gtggaacaat ccaagagaat 3960
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 caacaccatg gaaattctgg acaccgctg gtcctcagct acatcgacct gtcagcctgg 4080
 tgttactact gtcaggccta tgtccaccac caggctctcc tagatgtgaa gaacatcgcc 4140
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 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 5

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

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
 35 40 45

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

Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
 65 70 75 80

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Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
 85 90 95
 Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
 100 105 110
 Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
 115 120 125
 Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
 130 135 140
 Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Gly Val
 145 150 155 160
 Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala Gly Ser Ser Gly Ala
 165 170 175
 Ile Ala Met Thr Ser Thr Gly Gln Asp Ser Thr Thr Thr Arg Gln Arg
 180 185 190
 Arg Ser Arg Gln Asn Pro Gln Ser Pro Pro Gln Asp Ser Ser Val Thr
 195 200 205
 Ser Lys Arg Asn Ile Lys Lys Gly Ala Val Pro Arg Ser Ile Pro Asn
 210 215 220
 Leu Ala Glu Val Lys Lys Lys Gly Lys Met Lys Lys Leu Gly Gln Ala
 225 230 235 240
 Met Glu Glu Asp Leu Ile Val Gly Leu Gln Gly Met Asp Leu Asn Leu
 245 250 255
 Glu Ala Glu Ala Leu Ala Gly Thr Gly Leu Val Leu Asp Glu Gln Leu
 260 265 270
 Asn Glu Phe His Cys Leu Trp Asp Asp Ser Phe Pro Glu Gly Pro Glu
 275 280 285
 Arg Leu His Ala Ile Lys Glu Gln Leu Ile Gln Glu Gly Leu Leu Asp
 290 295 300
 Arg Cys Val Ser Phe Gln Ala Arg Phe Ala Glu Lys Glu Glu Leu Met
 305 310 315 320
 Leu Val His Ser Leu Glu Tyr Ile Asp Leu Met Glu Thr Thr Gln Tyr

Met Asn Glu Gly Glu Leu Arg Val Leu Ala Asp Thr Tyr Asp Ser Val
 340 345 350
 Tyr Leu His Pro Asn Ser Tyr Ser Cys Ala Cys Leu Ala Ser Gly Ser
 355 360 365
 Val Leu Arg Leu Val Asp Ala Val Leu Gly Ala Glu Ile Arg Asn Gly
 370 375 380
 Met Ala Ile Ile Arg Pro Pro Gly His His Ala Gln His Ser Leu Met
 385 390 395 400
 Asp Gly Tyr Cys Met Phe Asn His Val Ala Val Ala Ala Arg Tyr Ala
 405 410 415
 Gln Gln Lys His Arg Ile Arg Arg Val Leu Ile Val Asp Trp Asp Val
 420 425 430
 His His Gly Gln Gly Thr Gln Phe Thr Phe Asp Gln Asp Pro Ser Val
 435 440 445
 Leu Tyr Phe Ser Ile His Arg Tyr Glu Gln Gly Arg Phe Trp Pro His
 450 455 460
 Leu Lys Ala Ser Asn Trp Ser Thr Thr Gly Phe Gly Gln Gly Gln Gly
 465 470 475 480
 Tyr Thr Ile Asn Val Pro Trp Asn Gln Val Gly Met Arg Asp Ala Asp
 485 490 495
 Tyr Ile Ala Ala Phe Leu His Val Leu Leu Pro Val Ala Leu Glu Phe
 500 505 510
 Gln Pro Gln Leu Val Leu Val Ala Ala Gly Phe Asp Ala Leu Gln Gly
 515 520 525
 Asp Pro Lys Gly Glu Met Ala Ala Thr Pro Ala Gly Phe Ala Gln Leu
 530 535 540
 Thr His Leu Leu Met Gly Leu Ala Gly Gly Lys Leu Ile Leu Ser Leu
 545 550 555 560
 Glu Gly Gly Tyr Asn Leu Arg Ala Leu Ala Glu Gly Val Ser Ala Ser
 565 570 575

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

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Gly Thr Gln His Met Phe Glu Asp Asp Pro Ser Val Leu Tyr Val Ser
835 840 845

Leu His Arg Tyr Asp His Gly Thr Phe Phe Pro Met Gly Asp Glu Gly
850 855 860

Ala Ser Ser Gln Ile Gly Arg Ala Ala Gly Thr Gly Phe Thr Val Asn
865 870 875 880

Val Ala Trp Asn Gly Pro Arg Met Gly Asp Ala Asp Tyr Leu Ala Ala
885 890 895

Trp His Arg Leu Val Leu Pro Ile Ala Tyr Glu Phe Asn Pro Glu Leu
900 905 910

Val Leu Val Ser Ala Gly Phe Asp Ala Ala Arg Gly Asp Pro Leu Gly
915 920 925

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

Met Gly Leu Ala Ser Gly Arg Ile Ile Leu Ile Leu Glu Gly Gly Tyr
945 950 955 960

Asn Leu Thr Ser Ile Ser Glu Ser Met Ala Ala Cys Thr Arg Ser Leu
965 970 975

Leu Gly Asp Pro Pro Pro Leu Leu Thr Leu Pro Arg Pro Pro Leu Ser
980 985 990

Gly Ala Leu Ala Ser Ile Thr Glu Thr Ile Gln Val His Arg Arg Tyr
995 1000 1005

Trp Arg Ser Leu Arg Val Met Lys Val Glu Asp Arg Glu Gly Pro
1010 1015 1020

Ser Ser Ser Lys Leu Val Thr Lys Lys Ala Pro Gln Pro Ala Lys
1025 1030 1035

Pro Arg Leu Ala Glu Arg Met Thr Thr Arg Glu Lys Lys Val Leu
1040 1045 1050

Glu Ala Gly Met Gly Lys Val Thr Ser Ala Ser Phe Gly Glu Glu
1055 1060 1065

Ser Thr Pro Gly Gln Thr Asn Ser Glu Thr Ala Val Val Ala Leu
1070 1075 1080

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Thr Gln Asp Gln Pro Ser Glu Ala Ala Thr Gly Gly Ala Thr Leu
 1085 1090 1095
 Ala Gln Thr Ile Ser Glu Ala Ala Ile Gly Gly Ala Met Leu Gly
 1100 1105 1110
 Gln Thr Thr Ser Glu Glu Ala Val Gly Gly Ala Thr Pro Asp Gln
 1115 1120 1125
 Thr Thr Ser Glu Glu Thr Val Gly Gly Ala Ile Leu Asp Gln Thr
 1130 1135 1140
 Thr Ser Glu Asp Ala Val Gly Gly Ala Thr Leu Gly Gln Thr Thr
 1145 1150 1155
 Ser Glu Glu Ala Val Gly Gly Ala Thr Leu Ala Gln Thr Thr Ser
 1160 1165 1170
 Glu Ala Ala Met Glu Gly Ala Thr Leu Asp Gln Thr Thr Ser Glu
 1175 1180 1185
 Glu Ala Pro Gly Gly Thr Glu Leu Ile Gln Thr Pro Leu Ala Ser
 1190 1195 1200
 Ser Thr Asp His Gln Thr Pro Pro Thr Ser Pro Val Gln Gly Thr
 1205 1210 1215
 Thr Pro Gln Ile Ser Pro Ser Thr Leu Ile Gly Ser Leu Arg Thr
 1220 1225 1230
 Leu Glu Leu Gly Ser Glu Ser Gln Gly Ala Ser Glu Ser Gln Ala
 1235 1240 1245
 Pro Gly Glu Glu Asn Leu Leu Gly Glu Ala Ala Gly Gly Gln Asp
 1250 1255 1260
 Met Ala Asp Ser Met Leu Met Gln Gly Ser Arg Gly Leu Thr Asp
 1265 1270 1275
 Gln Ala Ile Phe Tyr Ala Val Thr Pro Leu Pro Trp Cys Pro His
 1280 1285 1290
 Leu Val Ala Val Cys Pro Ile Pro Ala Ala Gly Leu Asp Val Thr
 1295 1300 1305
 Gln Pro Cys Gly Asp Cys Gly Thr Ile Gln Glu Asn Trp Val Cys

1310

1315

1320

Leu Ser Cys Tyr Gln Val Tyr Cys Gly Arg Tyr Ile Asn Gly His
 1325 1330 1335

Met Leu Gln His His Gly Asn Ser Gly His Pro Leu Val Leu Ser
 1340 1345 1350

Tyr Ile Asp Leu Ser Ala Trp Cys Tyr Tyr Cys Gln Ala Tyr Val
 1355 1360 1365

His His Gln Ala Leu Leu Asp Val Lys Asn Ile Ala His Gln Asn
 1370 1375 1380

Lys Phe Gly Glu Asp Met Pro His Pro His Val
 1385 1390

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 6

Met Gly Val Thr Gly Trp Arg Leu Cys Glu Arg Ile Leu Ala
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<210> 7
 <211> 159
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 7

Met Val Phe Thr Leu Glu Asp Phe Val Gly Asp Trp Arg Gln Thr Ala
 1 5 10 15

Gly Tyr Asn Leu Asp Gln Val Leu Glu Gln Gly Gly Val Ser Ser Leu
 20 25 30

Phe Gln Asn Leu Gly Val Ser Val Thr Pro Ile Gln Arg Ile Val Leu
 35 40 45

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

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Glu Gly Leu Ser Gly Asp Gln Met Gly Gln Ile Glu Lys Ile Phe Lys
65 70 75 80

Val Val Tyr Pro Val Asp Asp His His Phe Lys Val Ile Leu His Tyr
85 90 95

Gly Thr Leu Val Ile Asp Gly Val Thr Pro Asn Met Ile Asp Tyr Phe
100 105 110

Gly Arg Pro Tyr Glu Gly Ile Ala Val Phe Asp Gly Lys Lys Ile Thr
115 120 125

Val Thr Gly Thr Leu Trp Asn Gly Asn Lys Ile Ile Asp Glu Arg Leu
130 135 140

Ile Asn Pro Asp Gly Ser Leu Leu Phe Arg Val Thr Ile Asn Val
145 150 155

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<211> 477
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

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gaccaagtcc ttgaacaggg aggtgtgtcc agtttgtttc agaatctcgc cgtgtccgta 120
actccgatcc aaaggattgt cctgagcggg gaaaatgggc tgaagatcga catccatgtc 180
atcatcccgt atgaagggtc gagcgccgac caaatggccc agatcgaaaa aatttttaag 240
gtggtgtacc ctgtggatga tcatcacttt aagggtgatcc tgcactatgg cacactggta 300
atcgacgggg ttacgccgaa catgatcgac tatttcggac ggccgtatga aggcacgcgc 360
gtgttcgacg gcaaaaagat cactgtaaca gggaccctgt ggaacggcaa caaaattatc 420
gacgagcgcc tgatcaaccc cgacgggtcc ctgctgttcc gagtaaccat caacggtt 477