SEQUENCE LISTING

<110> University of Bern

<120> Chimeric Opsin GPCR Proteins

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<170> BiSSAP 1.3.6

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aagagcgaga actcagagga cgccaagaag agcaggatca ccagcgaggg cgagtacatc 1320

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<223> PALMITATE

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Ser Ala His Gln Ala Ala Ala Trp Val Pro Phe Pro Thr Val Asp Val
    50                  55                  60
Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val Gly
65                  70                  75                  80
Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys Arg
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Asn Arg Gly Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu Ala
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Thr Ile Gly Arg Gly Ser Lys Arg Arg Thr Ala Leu Val Leu Leu Gly
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Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp
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Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr
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Met Thr Phe Thr Pro Gln Val Arg Ala Tyr Thr Met Leu Leu Phe Cys
225                 230                 235                 240
Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Phe Cys Tyr Ile Phe
                245                 250                 255
Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Cys Glu Gly Cys Gly
            260                 265                 270
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Trp Lys Met Ala Lys Val Ala Leu Ile Val Ile Leu Leu Phe Val Leu
    290                 295                 300
Ser Trp Ala Pro Tyr Ser Thr Val Ala Leu Val Ala Phe Ala Gly Tyr
305                 310                 315                 320
Ser His Ile Leu Thr Pro Tyr Met Ser Ser Val Pro Ala Val Ile Ala
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Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile Thr His Pro
            340                 345                 350
Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly Val Leu
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Leu Gly Val Ser Gly Gln Arg Ser His Pro Ser Leu Ser Tyr Arg Ser
    370                 375                 380
Thr His Arg Ser Thr Leu Ser Ser Gln Ser Ser Asp Leu His Pro Glu
385                 390                 395                 400
Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr Met
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Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala Lys Lys Ser Arg
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<223> Mela(palm)-mGluR6 cDNA

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<223> PALMITATE

<400> 4

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Gln Asn Val Ser Val Arg Ala Gln Leu Leu Ser Val Ser Pro Thr Thr
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Ser Ala His Gln Ala Ala Ala Trp Val Pro Phe Pro Thr Val Asp Val
    50                  55                  60
Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val Gly
65                  70                  75                  80
Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys Arg
                85                  90                  95
Asn Arg Gly Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu Ala
            100                 105                 110
Val Ser Asp Phe Leu Met Ser Val Thr Gln Ala Pro Val Phe Phe Ala
        115                 120                 125
Ser Ser Leu Tyr Lys Lys Trp Leu Phe Gly Glu Thr Gly Cys Glu Phe
    130                 135                 140
Tyr Ala Phe Cys Gly Ala Val Phe Gly Ile Thr Ser Met Ile Thr Leu
145                 150                 155                 160
Thr Ala Ile Ala Met Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu Ala
                165                 170                 175
Thr Ile Gly Arg Gly Ser Lys Arg Arg Thr Ala Leu Val Leu Leu Gly
            180                 185                 190
Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp
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Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr
    210                 215                 220
Met Thr Phe Thr Pro Gln Val Arg Ala Tyr Thr Met Leu Leu Phe Cys
225                 230                 235                 240
Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Phe Cys Tyr Ile Phe
                245                 250                 255
Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Cys Glu Gly Cys Gly
            260                 265                 270
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Trp Lys Met Ala Lys Val Ala Leu Ile Val Ile Leu Leu Phe Val Leu
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Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile Thr His Pro
            340                 345                 350
Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Phe His Pro
        355                 360                 365
Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr
    370                 375                 380
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385                 390                 395                 400
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acagtcgatg tcccagacca tgctcactat accctaggca cggtgatcct gctggtggga     240

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gccctggcct ggagtctgcc acctttcttt ggttggagtg cctacgtgcc cgaggggctg     660
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Ser Ala His Gln Ala Ala Ala Trp Val Pro Phe Pro Thr Val Asp Val
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Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Met Arg
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His Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Phe Ile
            100                 105                 110
Ile Asn Leu Ala Val Ser Asp Phe Leu Met Ser Val Thr Gln Ala Pro
        115                 120                 125
Val Phe Phe Ala Ser Ser Leu Tyr Lys Lys Trp Leu Phe Gly Glu Thr
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Gly Cys Glu Phe Tyr Ala Phe Cys Gly Ala Val Phe Gly Ile Thr Ser
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Met Ile Thr Leu Thr Ala Ile Ala Met Asp Arg Tyr Leu Val Ile Thr
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Val Leu Leu Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro
        195                 200                 205
Phe Phe Gly Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys
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Ser Trp Asp Tyr Met Thr Phe Thr Pro Gln Val Arg Ala Tyr Thr Met
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Leu Leu Phe Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Phe
                245                 250                 255
Cys Tyr Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Cys
            260                 265                 270
Glu Gly Cys Gly Glu Ser Pro Leu Arg Gln Arg Arg Gln Trp Gln Arg
        275                 280                 285
Leu Gln Ser Glu Trp Lys Met Ala Lys Val Ala Leu Ile Val Ile Leu
    290                 295                 300
Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Thr Val Ala Leu Val Ala
305                 310                 315                 320
Phe Ala Gly Tyr Ser His Ile Leu Thr Pro Tyr Met Ser Ser Val Pro
                325                 330                 335
Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala
            340                 345                 350
Ile Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys
        355                 360                 365
Leu Gly Val Leu Leu Gly Val Ser Gly Gln Arg Ser His Pro Ser Leu
    370                 375                 380
Ser Tyr Arg Ser Thr His Arg Ser Thr Leu Ser Ser Gln Ser Ser Asp
385                 390                 395                 400
Leu His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys
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Thr Ser Thr Met Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala
            420                 425                 430
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Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val Gly
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85 90 95
His Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Phe Ile
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Ile Asn Leu Ala Val Ser Asp Phe Leu Met Ser Val Thr Gln Ala Pro
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145 150 155 160
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165 170 175
Arg Pro Leu Ala Thr Ile Gly Arg Gly Ser Lys Arg Arg Thr Ala Leu
180 185 190
Val Leu Leu Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro
195 200 205
Phe Phe Gly Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys
210 215 220
Ser Trp Asp Tyr Met Thr Phe Thr Pro Gln Val Arg Ala Tyr Thr Met

225 230 235 240
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Cys Tyr Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Cys
260 265 270
Glu Gly Cys Gly Glu Ser Pro Leu Arg Gln Arg Arg Gln Trp Gln Arg
275 280 285
Leu Gln Ser Glu Trp Lys Met Ala Lys Val Ala Leu Ile Val Ile Leu
290 295 300
Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Thr Val Ala Leu Val Ala
305 310 315 320
Phe Ala Gly Tyr Ser His Ile Leu Thr Pro Tyr Met Ser Ser Val Pro
325 330 335
Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala
340 345 350
Ile Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys
355 360 365
Leu Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys
370 375 380
Lys Thr Ser Thr Met Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp
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<221> LIPID
<222> 365
<223> PALMITATE

<400> 10
Met Asp Ser Pro Ser Gly Pro Arg Val Leu Ser Ser Leu Thr Gln Asp
1 5 10 15

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Pro Ser Phe Thr Thr Ser Pro Ala Leu Gln Gly Ile Trp Asn Gly Thr
            20                  25                  30
Gln Asn Val Ser Val Arg Ala Gln Leu Leu Ser Val Ser Pro Thr Thr
        35                  40                  45
Ser Ala His Gln Ala Ala Ala Trp Val Pro Phe Pro Thr Val Asp Val
    50                  55                  60
Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val Gly
65                  70                  75                  80
Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys Arg
                85                  90                  95
Asn Arg Gly Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu Ala
            100                 105                 110
Val Ser Asp Phe Leu Met Ser Val Thr Gln Ala Pro Val Phe Phe Ala
        115                 120                 125
Ser Ser Leu Tyr Lys Lys Trp Leu Phe Gly Glu Thr Gly Cys Glu Phe
    130                 135                 140
Tyr Ala Phe Cys Gly Ala Val Phe Gly Ile Thr Ser Met Ile Thr Leu
145                 150                 155                 160
Thr Ala Ile Ala Met Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu Ala
                165                 170                 175
Thr Ile Gly Arg Gly Ser Lys Arg Arg Thr Ala Leu Val Leu Leu Gly
            180                 185                 190
Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp
        195                 200                 205
Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr
    210                 215                 220
Met Thr Phe Thr Pro Gln Val Arg Ala Tyr Thr Met Leu Leu Phe Cys
225                 230                 235                 240
Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Phe Cys Tyr Ile Phe
                245                 250                 255
Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Gly Val Pro Glu Thr Phe
            260                 265                 270
Asn Glu Ala Pro Leu Arg Gln Arg Arg Gln Trp Gln Arg Leu Gln Ser
        275                 280                 285
Glu Trp Lys Met Ala Lys Val Ala Leu Ile Val Ile Leu Leu Phe Val
    290                 295                 300
Leu Ser Trp Ala Pro Tyr Ser Thr Val Ala Leu Val Ala Phe Ala Gly
305                 310                 315                 320
Tyr Ser His Ile Leu Thr Pro Tyr Met Ser Ser Val Pro Ala Val Ile
                325                 330                 335
Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile Thr His
            340                 345                 350
Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly Val
        355                 360                 365
Leu Leu Gly Val Ser Gly Gln Arg Ser His Pro Ser Leu Ser Tyr Arg
    370                 375                 380
Ser Thr His Arg Ser Thr Leu Ser Ser Gln Ser Ser Asp Leu His Pro
385                 390                 395                 400
Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr
                405                 410                 415
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Met Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala Lys Lys Ser
420 425 430
Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile
435 440 445
Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
450 455

<210> 11
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm)-OPN1MW(IL1, IL2, IL3, CT) cDNA

<400> 11
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accagtcctg ccctgcaagg catttggaac ggcactcaga acgtctccgt aagagcccag 120

cttctctctg ttagccccac gacatctgca catcaggctg ctgcctgggt ccccttcccc 180

acagtcgatg tcccagacca tgctcactat accctaggca cggtgatcct gctggtggga 240

ctcacaggga tgctgggcaa tctgacggtc atctacgcca ccatgagatt caagaagctg 300

cgccatccag caaacatgtt catcatcaac ctcgcagtca gcgacttcct catgtcagtc 360

actcaggccc cggtcttctt tgccagcagc ctctacaaga agtggctctt tggggagaca 420

ggttgcgagt tctatgcctt ctgcggggct gtctttggca tcacttccat gatcaccctg 480

acagccatag ccatggaccg ctatctggtg atctgcaagc cctttggcaa tgtgagattt 540

gatgctaagc tgacggcact cgtcctgcta ggcgtctggc tttatgccct ggcctggagt 600

ctgccacctt tctttggttg gagtgcctac gtgcccgagg ggctgctgac atcctgctcc 660

tgggactaca tgaccttcac accccaggtg cgtgcctaca ccatgctgct cttctgcttt 720

gtcttcttcc tccccctgct catcatcatc ttctgctaca tccaagtgtg gctggccatc 780

cgagcagtgg caaagcaaca gaaagaatct gagtccactc agaaggccga gaaggaggtg 840

acaaaggtcg cactgattgt cattcttctc ttcgtgctgt cctgggctcc ctactccact 900

gtggctctgg tggcctttgc tggatactcg cacatcctga cgccctacat gagctcggtg 960

ccagccgtca tcgccaaggc ttctgccatc cacaatccca ttatctacgc catcactcac 1020

cccaagtaca gggtggccat tgcccagcac ctgccttgca actgcatctt acatctcttt 1080

ggaaagaagg ttgatgatag ctctgaactt tccagcacct ccaagacaga agtctcatct 1140

gtctcttcag tgtcacctgc ataa 1164

<210> 12
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-OPN1MW(IL1, IL2, IL3, CT) protein

<220>
<221> LIPID
<222> 353
<223> PALMITATE

<400> 12
Met Asp Ser Pro Ser Gly Pro Arg Val Leu Ser Ser Leu Thr Gln Asp
1 5 10 15
Pro Ser Phe Thr Thr Ser Pro Ala Leu Gln Gly Ile Trp Asn Gly Thr
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Gln Asn Val Ser Val Arg Ala Gln Leu Leu Ser Val Ser Pro Thr Thr
35 40 45
Ser Ala His Gln Ala Ala Ala Trp Val Pro Phe Pro Thr Val Asp Val
50 55 60
Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val Gly
65 70 75 80
Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Ala Thr Met Arg
85 90 95
Phe Lys Lys Leu Arg His Pro Ala Asn Met Phe Ile Ile Asn Leu Ala
100 105 110
Val Ser Asp Phe Leu Met Ser Val Thr Gln Ala Pro Val Phe Phe Ala
115 120 125
Ser Ser Leu Tyr Lys Lys Trp Leu Phe Gly Glu Thr Gly Cys Glu Phe
130 135 140
Tyr Ala Phe Cys Gly Ala Val Phe Gly Ile Thr Ser Met Ile Thr Leu
145 150 155 160
Thr Ala Ile Ala Met Asp Arg Tyr Leu Val Ile Cys Lys Pro Phe Gly
165 170 175
Asn Val Arg Phe Asp Ala Lys Leu Thr Ala Leu Val Leu Leu Gly Val
180 185 190
Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp Ser
195 200 205
Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr Met

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    210                 215                 220
Thr Phe Thr Pro Gln Val Arg Ala Tyr Thr Met Leu Leu Phe Cys Phe
225                 230                 235                 240
Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Phe Cys Tyr Ile Gln Val
                245                 250                 255
Trp Leu Ala Ile Arg Ala Val Ala Lys Gln Gln Lys Glu Ser Glu Ser
            260                 265                 270
Thr Gln Lys Ala Glu Lys Glu Val Thr Lys Val Ala Leu Ile Val Ile
        275                 280                 285
Leu Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Thr Val Ala Leu Val
    290                 295                 300
Ala Phe Ala Gly Tyr Ser His Ile Leu Thr Pro Tyr Met Ser Ser Val
305                 310                 315                 320
Pro Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr
                325                 330                 335
Ala Ile Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro
            340                 345                 350
Cys Asn Cys Ile Leu His Leu Phe Gly Lys Lys Val Asp Asp Ser Ser
        355                 360                 365
Glu Leu Ser Ser Thr Ser Lys Thr Glu Val Ser Ser Val Ser Ser Val
    370                 375                 380
Ser Pro Ala
385
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<210> 13
<211> 1092
<212> DNA
<213> Artificial Sequence

<220>
<223> OPN1MW(palm)-mGluR6 cDNA

<400> 13

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atggcccaaa ggcttacagg tgaacagaca ctggaccact atgaggatag cacccatgca      60

agcatcttca cctataccaa cagcaacagc accaaaggtc cctttgaagg ccccaattat     120

cacattgctc ccaggtgggt gtaccacctc accagcacct ggatgattct tgtggtcgtt     180

gcatctgtct tcactaatgg acttgtgctg gcagccacca tgagattcaa gaagctgcgc     240

catccactga actggattct ggtgaacttg gcagttgctg acctagcaga gaccattatt     300

gccagcacta tcagtgttgt gaaccaaatc tatggctact tcgttctggg acaccctctg     360

tgtgtcattg aaggctacat tgtctcattg tgtggaatca caggcctctg gtccctggcc     420

atcatttcct gggagagatg gctggtggtc tgcaagccct ttggcaatgt gagatttgat     480
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gctaagctgg ccactgtggg aatcgtcttc tcctgggtct gggctgctat atggacggcc 540

ccaccaatct ttggttggag caggtactgg ccttatggcc tgaagacatc ctgtggccca 600

gacgtgttca gcggtacctc gtaccccggg gttcagtctt atatgatggt cctcatggtc 660

acgtgctgca tcttcccact cagcatcatc gtgctctgct acctccaagt gtggctggcc 720

atccgagcag tggcaaagca acagaaagaa tctgagtcca ctcagaaggc cgagaaggag 780

gtgacacgca tggtggtggt gatggtcttc gcatactgcc tctgctgggg accctatact 840

ttctttgcat gctttgctac tgcccaccct ggctatgcct tccaccctct tgtggcctcc 900

ctaccatcct actttgccaa aagtgccact atctacaacc ccattatcta tgtctttatg 960

aaccggcagt ttcgaaactg catcttacat ctctttcatc cagagcagaa cgtgcagaag 1020

cggaagcgca gcctcaagaa gacctccacg atggcggccc cgcccaagag cgagaactca 1080

gaggacgcca ag 1092

<210> 14
<211> 393
<212> PRT
<213> Artificial Sequence

<220>
<223> OPN1MW(palm)-mGluR6 protein

<400> 14

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1               5                  10                  15
Ser Thr His Ala Ser Ile Phe Thr Tyr Thr Asn Ser Asn Ser Thr Lys
            20                  25                  30
Gly Pro Phe Glu Gly Pro Asn Tyr His Ile Ala Pro Arg Trp Val Tyr
        35                  40                  45
His Leu Thr Ser Thr Trp Met Ile Leu Val Val Val Ala Ser Val Phe
    50                  55                  60
Thr Asn Gly Leu Val Leu Ala Ala Thr Met Arg Phe Lys Lys Leu Arg
65                  70                  75                  80
His Pro Leu Asn Trp Ile Leu Val Asn Leu Ala Val Ala Asp Leu Ala
                85                  90                  95
Glu Thr Ile Ile Ala Ser Thr Ile Ser Val Val Asn Gln Ile Tyr Gly
            100                 105                 110
Tyr Phe Val Leu Gly His Pro Leu Cys Val Ile Glu Gly Tyr Ile Val
        115                 120                 125
Ser Leu Cys Gly Ile Thr Gly Leu Trp Ser Leu Ala Ile Ile Ser Trp
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    130                 135                 140
Glu Arg Trp Leu Val Val Cys Lys Pro Phe Gly Asn Val Arg Phe Asp
145                 150                 155                 160
Ala Lys Leu Ala Thr Val Gly Ile Val Phe Ser Trp Val Trp Ala Ala
                165                 170                 175
Ile Trp Thr Ala Pro Pro Ile Phe Gly Trp Ser Arg Tyr Trp Pro Tyr
            180                 185                 190
Gly Leu Lys Thr Ser Cys Gly Pro Asp Val Phe Ser Gly Thr Ser Tyr
        195                 200                 205
Pro Gly Val Gln Ser Tyr Met Met Val Leu Met Val Thr Cys Cys Ile
    210                 215                 220
Phe Pro Leu Ser Ile Ile Val Leu Cys Tyr Leu Gln Val Trp Leu Ala
225                 230                 235                 240
Ile Arg Ala Val Ala Lys Gln Gln Lys Glu Ser Glu Ser Thr Gln Lys
                245                 250                 255
Ala Glu Lys Glu Val Thr Arg Met Val Val Val Met Val Phe Ala Tyr
            260                 265                 270
Cys Leu Cys Trp Gly Pro Tyr Thr Phe Phe Ala Cys Phe Ala Thr Ala
        275                 280                 285
His Pro Gly Tyr Ala Phe His Pro Leu Val Ala Ser Leu Pro Ser Tyr
    290                 295                 300
Phe Ala Lys Ser Ala Thr Ile Tyr Asn Pro Ile Ile Tyr Val Phe Met
305                 310                 315                 320
Asn Arg Gln Phe Arg Asn Cys Ile Leu His Leu Phe His Pro Glu Gln
                325                 330                 335
Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr Met Ala
            340                 345                 350
Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala Lys Lys Ser Arg Ile
        355                 360                 365
Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile Asn Val
    370                 375                 380
Thr Glu Thr Ser Gln Val Ala Pro Ala
385                 390
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<210> 15
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm+33AA)-mGluR6 cDNA

<400> 15
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gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc 300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc 360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag 420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc 480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt 540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc cacccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgggggtg ctgctgggtg tatcacgccg gcacagtcgc 1140

ccctacccca gctaccgctc cacccaccgc tccacgctga ccagccacac ctccaacctc 1200

catccagagc agaatgtgca gaagcgaaag cggagcctca aggccacctc cacggtggca 1260

gccccaccca agggcgagga tgcagaggcc cacaagaaga gcaggatcac cagcgagggc 1320

gagtacatcc ccctggacca gatcgacatc aacgtgacag agaccagcca agtggcgcct 1380

gcctaa 1386

<210> 16
<211> 461
<212> PRT
<213> Artificial Sequence

<220>

<223> Mela(palm+33AA)-mGluR6 protein

<220>
<221> LIPID
<222> 367
<223> PALMITATE

<400> 16

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1               5                  10                  15
Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
            20                  25                  30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
        35                  40                  45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
    50                  55                  60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65                  70                  75                  80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
                85                  90                  95
Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
                325                 330                 335
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Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
            340                 345                 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
        355                 360                 365
Gly Val Leu Leu Gly Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser
    370                 375                 380
Tyr Arg Ser Thr His Arg Ser Thr Leu Thr Ser His Thr Ser Asn Leu
385                 390                 395                 400
His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala Thr
                405                 410                 415
Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His Lys
            420                 425                 430
Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile
        435                 440                 445
Asp Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
    450                 455                 460
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<210> 17
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 L isoform of h melanopsin comprising a Golgi export signal and a 1D4 tag cDNA

<400> 17

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gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc     120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc     180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg     240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc     300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc     360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag     420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc     480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt     540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc     600

tggagtctgc caccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc     660
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tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgttccat ccagagcaga atgtgcagaa gcgaaagcgg 1140

agcctcaagg ccacctccac ggtggcagcc ccacccaagg gcgaggatgc agaggcccac 1200

aagaagagca ggatcaccag cgagggcgag tacatccccc tggaccagat cgacatcaac 1260

gtgacagaga ccagccaagt ggcgcctgcc taa 1293

<210> 18
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 L isoform of h melanopsin comprising a Golgi export signal and a 1D4 tag protein

<220>
<221> LIPID
<222> 367
<223> PALMITATE

<400> 18
Met Asn Pro Pro Ser Gly Pro Arg Val Leu Pro Ser Pro Thr Gln Glu
1 5 10 15
Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
20 25 30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
35 40 45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
50 55 60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65 70 75 80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys

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                85                  90                  95
Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
                325                 330                 335
Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
            340                 345                 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
        355                 360                 365
Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
    370                 375                 380
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
385                 390                 395                 400
Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
                405                 410                 415
Ile Asp Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
            420                 425                 430
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<210> 19
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 P isoform of h melanopsin comprising a Golgi export signal and a 1D4 tag cDNA

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gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc 300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc 360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag 420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc 480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt 540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc cacccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgttccat ccagagcaga atgtgcagaa gcgaaagcgg 1140

agcctcaagg ccacctccac ggtggcagcc ccacccaagg gcgaggatgc agaggcccac 1200

aagaagagca ggatcaccag cgagggcgag tacatccccc tggaccagat cgacatcaac 1260

gtgacagaga ccagccaagt ggcgcctgcc taa 1293

<210> 20
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 P isoform of h melanopsin comprising a Golgi export signal and a 1D4 tag cDNAprotein

<220>
<221> LIPID
<222> 367
<223> PALMITATE

<400> 20

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Met Asn Pro Pro Ser Gly Pro Arg Val Pro Pro Ser Pro Thr Gln Glu
1               5                  10                  15
Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
            20                  25                  30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
        35                  40                  45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
    50                  55                  60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65                  70                  75                  80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
                85                  90                  95
Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
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```
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
                325                 330                 335
Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
            340                 345                 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
        355                 360                 365
Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
    370                 375                 380
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
385                 390                 395                 400
Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
                405                 410                 415
Ile Asp Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
            420                 425                 430
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<210> 21
<211> 1266
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 L isoform of h melanopsin comprising a Golgi export signal cDNA

<400> 21

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atgaaccctc cttcggggcc aagagtcctg cccagcccaa cccaagagcc cagctgcatg      60

gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc     120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc     180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg     240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc     300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc     360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag     420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc     480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt     540
```

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc cacccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgttccat ccagagcaga atgtgcagaa gcgaaagcgg 1140

agcctcaagg ccacctccac ggtggcagcc ccacccaagg gcgaggatgc agaggcccac 1200

aagaagagca ggatcaccag cgagggcgag tacatccccc tggaccagat cgacatcaac 1260

gtgtaa 1266

<210> 22
<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 L isoform of h melanopsin comprising a Golgi export signal protein

<400> 22

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Met Asn Pro Pro Ser Gly Pro Arg Val Leu Pro Ser Pro Thr Gln Glu
1               5                  10                  15
Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
            20                  25                  30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
        35                  40                  45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
    50                  55                  60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65                  70                  75                  80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
                85                  90                  95
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Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
                325                 330                 335
Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
            340                 345                 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
        355                 360                 365
Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
    370                 375                 380
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
385                 390                 395                 400
Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
                405                 410                 415
Ile Asp Ile Asn Val
            420
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<210> 23
<211> 1266
<212> DNA
<213> Artificial Sequence

<220>

<223> Mela(palm)-mGlur6 P isoform of h melanopsin comprising a Golgi export signal cDNA

<400> 23

atgaaccctc cttcggggcc aagagtcccg cccagcccaa cccaagagcc cagctgcatg 60

gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc 300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc 360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag 420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc 480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt 540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc caccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgttccat ccagagcaga atgtgcagaa gcgaaagcgg 1140

agcctcaagg ccacctccac ggtggcagcc ccacccaagg gcgaggatgc agaggcccac 1200

aagaagagca ggatcaccag cgagggcgag tacatccccc tggaccagat cgacatcaac 1260

gtgtaa 1266

<210> 24

<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGlur6 P isoform of h melanopsin comprising a Golgi export signal protein

<400> 24

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Met Asn Pro Pro Ser Gly Pro Arg Val Pro Pro Ser Pro Thr Gln Glu
1               5                  10                  15
Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
            20                  25                  30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
        35                  40                  45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
    50                  55                  60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65                  70                  75                  80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
                85                  90                  95
Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
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Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
325 330 335
Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
340 345 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
355 360 365
Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
370 375 380
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
385 390 395 400
Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
405 410 415
Ile Asp Ile Asn Val
420

<210> 25
<211> 1206
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 L isoform of h melanopsin without optional C-terminally added sequences cDNA

<400> 25
atgaaccctc cttcggggcc aagagtcctg cccagcccaa cccaagagcc cagctgcatg 60

gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc 300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc 360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag 420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc 480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt 540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc caccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgttccat ccagagcaga atgtgcagaa gcgaaagcgg 1140

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aagtaa 1206

<210> 26
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 L isoform of h melanopsin without optional C-terminally added sequences protein

<400> 26

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

```
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
                325                 330                 335
Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
            340                 345                 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
        355                 360                 365
Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
    370                 375                 380
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
385                 390                 395                 400
Lys
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<210> 27
<211> 1206
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 P isoform of h melanopsin without optional
C-terminally added sequences cDNA

<400> 27
atgaaccctc cttcggggcc aagagtcccg cccagcccaa cccaagagcc cagctgcatg 60

gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc 300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc 360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag 420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc 480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt 540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc caccttcttt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg ggctctccag accttcgggg cctgcaaggg caatggcgag 840

tccctgtggc agcggcagcg gctgcagagc gagtgcaaga tggccaagat catgctgctg 900

gtcatcctcc tcttcgtgct ctcctgggct ccctattccg ctgtggccct ggtggccttt 960

gctgggtacg cacacgtcct gacaccctac atgagctcgg tgccagccgt catcgccaag 1020

gcctctgcaa tccacaaccc catcatttac gccatcaccc accccaagta cagggtggcc 1080

attgcccagc acctgccctg cctgttccat ccagagcaga atgtgcagaa gcgaaagcgg 1140

agcctcaagg ccacctccac ggtggcagcc ccacccaagg gcgaggatgc agaggcccac 1200

aagtaa 1206

<210> 28
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm)-mGluR6 P isoform of h melanopsin without optional
C-terminally added sequences protein

<400> 28
Met Asn Pro Pro Ser Gly Pro Arg Val Pro Pro Ser Pro Thr Gln Glu
1 5 10 15

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Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
            20                  25                  30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
        35                  40                  45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
    50                  55                  60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65                  70                  75                  80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
                85                  90                  95
Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
            260                 265                 270
Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
        275                 280                 285
Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
    290                 295                 300
Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
305                 310                 315                 320
Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
                325                 330                 335
Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
            340                 345                 350
Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
        355                 360                 365
Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
    370                 375                 380
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
385                 390                 395                 400
Lys
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<210> 29
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm+33A)+mGluR6 (IL1, CT) cDNA

<400> 29
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gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttccggta caacaacacg 300

cccatcgtcc gggcctcggg ccgagagctc ttcattatca acctcgcggt cagcgacttc 360

ctcatgtcct tcacccaggc ccctgtcttc ttcaccagta gcctctataa gcagtggctc 420

tttggggaga caggctgcga gttctatgcc ttctgtggag ctctctttgg catttcctcc 480

atgatcaccc tgacggccat cgccctggac cgctacctgg taatcacacg cccgctggcc 540

acctttggtg tggcgtccaa gaggcgtgcg gcatttgtcc tgctgggcgt ttggctctat 600

gccctggcct ggagtctgcc acccttcttc ggctggagcg cctacgtgcc cgaggggttg 660

ctgacatcct gctcctggga ctacatgagc ttcacgccgg ccgtgcgtgc ctacaccatg 720

cttctctgct gcttcgtgtt cttcctccct ctgcttatca tcatctactg ctacatcttc 780

atcttcaggg ccatccggga gacaggacgg gctctccaga ccttcggggc ctgcaagggc 840

aatggcgagt ccctgtggca gcggcagcgg ctgcagagcg agtgcaagat ggccaagatc 900

atgctgctgg tcatcctcct cttcgtgctc tcctgggctc cctattccgc tgtggccctg 960

gtggcctttg ctgggtacgc acacgtcctg acaccctaca tgagctcggt gccagccgtc 1020

atcgccaagg cctctgcaat ccacaacccc atcatttacg ccatcaccca ccccaagtac 1080

agggtggcca ttgcccagca cctgccctgc ctgggggtgc tgctgggtgt atcacgccgg 1140

cacagtcgcc cctaccccag ctaccgctcc acccaccgct ccacgctgac cagccacacc 1200

tccaacctcc atccagagca gaatgtgcag aagcgaaagc ggagcctcaa ggccacctcc 1260

acggtggcag ccccacccaa gggcgaggat gcagaggccc acaagaagag caggatcacc 1320

agcgagggcg agtacatccc cctggaccag atcgacatca acgtgacaga gaccagccaa 1380

gtggcgcctg cctaa 1395

<210> 30
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm+33A)+mGluR6 (IL1, CT) protein

<220>
<221> LIPID
<222> 370
<223> PALMITATE

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Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
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Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
35 40 45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
50 55 60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65 70 75 80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Arg
85 90 95
Tyr Asn Asn Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Phe Ile
100 105 110
Ile Asn Leu Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro
115 120 125
Val Phe Phe Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr
130 135 140
Gly Cys Glu Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser
145 150 155 160
Met Ile Thr Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr
165 170 175
Arg Pro Leu Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe
180 185 190
Val Leu Leu Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro

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        195                 200                 205
Phe Phe Gly Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys
    210                 215                 220
Ser Trp Asp Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met
225                 230                 235                 240
Leu Leu Cys Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr
                245                 250                 255
Cys Tyr Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu
            260                 265                 270
Gln Thr Phe Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg
        275                 280                 285
Gln Arg Leu Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val
    290                 295                 300
Ile Leu Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu
305                 310                 315                 320
Val Ala Phe Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser
                325                 330                 335
Val Pro Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile
            340                 345                 350
Tyr Ala Ile Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu
        355                 360                 365
Pro Cys Leu Gly Val Leu Leu Gly Val Ser Arg Arg His Ser Arg Pro
    370                 375                 380
Tyr Pro Ser Tyr Arg Ser Thr His Arg Ser Thr Leu Thr Ser His Thr
385                 390                 395                 400
Ser Asn Leu His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu
                405                 410                 415
Lys Ala Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu
            420                 425                 430
Ala His Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu
        435                 440                 445
Asp Gln Ile Asp Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
    450                 455                 460
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<210> 31
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> Mela(palm+33A)+mGluR6 (IL3, CT) cDNA

<400> 31
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gccaccccag caccacccag ctggtgggac agctcccaga gcagcatctc cagcctgggc 120

cggcttccat ccatcagtcc cacagcacct gggacttggg ctgctgcctg ggtccccctc 180

cccacggttg atgttccaga ccatgcccac tataccctgg gcacagtgat cttgctggtg 240

ggactcacgg ggatgctggg caacctgacg gtcatctata ccttctgcag gagcagaagc 300

ctccggacac ctgccaacat gttcattatc aacctcgcgg tcagcgactt cctcatgtcc 360

ttcacccagg cccctgtctt cttcaccagt agcctctata agcagtggct ctttggggag 420

acaggctgcg agttctatgc cttctgtgga gctctctttg gcatttcctc catgatcacc 480

ctgacggcca tcgccctgga ccgctacctg gtaatcacac gcccgctggc cacctttggt 540

gtggcgtcca agaggcgtgc ggcatttgtc ctgctgggcg tttggctcta tgccctggcc 600

tggagtctgc cacccttctt cggctggagc gcctacgtgc ccgaggggtt gctgacatcc 660

tgctcctggg actacatgag cttcacgccg gccgtgcgtg cctacaccat gcttctctgc 720

tgcttcgtgt tcttcctccc tctgcttatc atcatctact gctacatctt catcttcagg 780

gccatccggg agacaggacg gggcgtgccc gagaccttca acgaggccaa gggcaatggc 840

gagtccctgt ggcagcggca gcggctgcag agcgagtgca agatggccaa gatcatgctg 900

ctggtcatcc tcctcttcgt gctctcctgg gctccctatt ccgctgtggc cctggtggcc 960

tttgctgggt acgcacacgt cctgacaccc tacatgagct cggtgccagc cgtcatcgcc 1020

aaggcctctg caatccacaa ccccatcatt tacgccatca cccaccccaa gtacagggtg 1080

gccattgccc agcacctgcc ctgcctgggg gtgctgctgg gtgtatcacg ccggcacagt 1140

cgcccctacc ccagctaccg ctccacccac cgctccacgc tgaccagcca cacctccaac 1200

ctccatccag agcagaatgt gcagaagcga aagcggagcc tcaaggccac ctccacggtg 1260

gcagccccac ccaagggcga ggatgcagag gcccacaaga agagcaggat caccagcgag 1320

ggcgagtaca tccccctgga ccagatcgac atcaacgtga cagagaccag ccaagtggcg 1380

cctgcctaa 1389

<210> 32
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Mela(palm+33A)+mGluR6 (IL3, CT) protein

<220>
<221> LIPID
<222> 368
<223> PALMITATE

<400> 32

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Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
            20                  25                  30
Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
        35                  40                  45
Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
    50                  55                  60
Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
65                  70                  75                  80
Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
                85                  90                  95
Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
            100                 105                 110
Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
        115                 120                 125
Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
    130                 135                 140
Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
145                 150                 155                 160
Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
                165                 170                 175
Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
            180                 185                 190
Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
        195                 200                 205
Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
    210                 215                 220
Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
225                 230                 235                 240
Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
                245                 250                 255
Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Gly Val Pro Glu Thr
            260                 265                 270
Phe Asn Glu Ala Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg
        275                 280                 285
Leu Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu
    290                 295                 300
Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala
305                 310                 315                 320
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Phe Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro
325 330 335
Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala
340 345 350
Ile Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys
355 360 365
Leu Gly Val Leu Leu Gly Val Ser Arg Arg His Ser Arg Pro Tyr Pro
370 375 380
Ser Tyr Arg Ser Thr His Arg Ser Thr Leu Thr Ser His Thr Ser Asn
385 390 395 400
Leu His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Ala
405 410 415
Thr Ser Thr Val Ala Ala Pro Pro Lys Gly Glu Asp Ala Glu Ala His
420 425 430
Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
435 440 445
Ile Asp Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
450 455 460

<210> 33
<211> 1095
<212> DNA
<213> Artificial Sequence

<220>
<223> JellyOP(palm)-mGluR6 cDNA

<400> 33
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ataagcttga atatgatagt tctaattaca ttttaccgct tacgacataa attggctttt 120

aaagatgctc tcatggctag tatggcgttc agtgatgttg tacaagctat cgtaggatat 180

cctttagagg tattcactgt agtagacgga aaatggacat tcggaatgga attatgtcaa 240

gttgcaggat ttttcattac tgcccttggt caagtttcca tcgctcatct cactgctctc 300

gccttagatc gatacttcac agtgtgcaga cctttcgtgg caactgcgat tcacggatca 360

atgagaaatg caggtatggt catatttgtt tgctggttct acgcgtcctt ctgggcagtc 420

ctacccttag ttggatggtc aaattatgac gtggagggtg acggtatgcg atgctccatc 480

aactgggcag acgacagtcc taaaagctac tcatacaggg tttgtttatt cgtattcatc 540

tacctgattc ctgttctttt gatggtggct acttacgtgt tggttcaagg agagatgaag 600

aatatgcgag gtcgtgcagc acagttgttt ggttcagaat ccgaggctgc actaaagaat 660

atcaaggccg aaaagcgaca cacaaggctg gttttcgtca tgatcctttc tttcatcgta 720

gcttggaccc catatacctt cgtcgccatg tgggtttcct ttttcacgaa acaacttggg 780

ccaatacctt tatacgttga tactttggca gctatgcttg caaagtcgtc ggctatgttc 840

aaccccatca tttactgctt cctccacaag caattcagaa gagctgtatt acgtggtgtt 900

tgtctgttcc atccagagca gaacgtgcag aagcggaagc gcagcctcaa gaagacctcc 960

acgatggcgg ccccgcccaa gagcgagaac tcagaggacg ccaagacaga gaccagccaa 1020

gtggcgcctg ccaagagcag gatcaccagc gagggcgagt acatcccccc ggaccagatc 1080

gacatcaacg tgtaa 1095

<210> 34
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> JellyOP(palm)-mGluR6 protein

<220>
<221> LIPID
<222> 301
<223> PALMITATE

<400> 34
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Val Phe Leu Ser Ile Ser Leu Asn Met Ile Val Leu Ile Thr Phe Tyr
20 25 30
Arg Leu Arg His Lys Leu Ala Phe Lys Asp Ala Leu Met Ala Ser Met
35 40 45
Ala Phe Ser Asp Val Val Gln Ala Ile Val Gly Tyr Pro Leu Glu Val
50 55 60
Phe Thr Val Val Asp Gly Lys Trp Thr Phe Gly Met Glu Leu Cys Gln
65 70 75 80
Val Ala Gly Phe Phe Ile Thr Ala Leu Gly Gln Val Ser Ile Ala His
85 90 95
Leu Thr Ala Leu Ala Leu Asp Arg Tyr Phe Thr Val Cys Arg Pro Phe
100 105 110
Val Ala Thr Ala Ile His Gly Ser Met Arg Asn Ala Gly Met Val Ile
115 120 125
Phe Val Cys Trp Phe Tyr Ala Ser Phe Trp Ala Val Leu Pro Leu Val

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    130                 135                 140
Gly Trp Ser Asn Tyr Asp Val Glu Gly Asp Gly Met Arg Cys Ser Ile
145                 150                 155                 160
Asn Trp Ala Asp Asp Ser Pro Lys Ser Tyr Ser Tyr Arg Val Cys Leu
                165                 170                 175
Phe Val Phe Ile Tyr Leu Ile Pro Val Leu Leu Met Val Ala Thr Tyr
            180                 185                 190
Val Leu Val Gln Gly Glu Met Lys Asn Met Arg Gly Arg Ala Ala Gln
        195                 200                 205
Leu Phe Gly Ser Glu Ser Glu Ala Ala Leu Lys Asn Ile Lys Ala Glu
    210                 215                 220
Lys Arg His Thr Arg Leu Val Phe Val Met Ile Leu Ser Phe Ile Val
225                 230                 235                 240
Ala Trp Thr Pro Tyr Thr Phe Val Ala Met Trp Val Ser Phe Phe Thr
                245                 250                 255
Lys Gln Leu Gly Pro Ile Pro Leu Tyr Val Asp Thr Leu Ala Ala Met
            260                 265                 270
Leu Ala Lys Ser Ser Ala Met Phe Asn Pro Ile Ile Tyr Cys Phe Leu
        275                 280                 285
His Lys Gln Phe Arg Arg Ala Val Leu Arg Gly Val Cys Leu Phe His
    290                 295                 300
Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser
305                 310                 315                 320
Thr Met Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala Lys Lys
                325                 330                 335
Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp
            340                 345                 350
Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
        355                 360
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<210> 35
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> JellyOP(palm)-5HT7 cDNA

<400> 35

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ataagcttga atatgatagt tctaattaca ttttaccgct tacgacataa attggctttt     120

aaagatgctc tcatggctag tatggcgttc agtgatgttg tacaagctat cgtaggatat     180

cctttagagg tattcactgt agtagacgga aaatggacat tcggaatgga attatgtcaa     240

gttgcaggat ttttcattac tgcccttggt caagtttcca tcgctcatct cactgctctc     300
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gccttagatc gatacttcac agtgtgcaga cctttcgtgg caactgcgat tcacggatca 360

atgagaaatg caggtatggt catatttgtt tgctggttct acgcgtcctt ctgggcagtc 420

ctacccttag ttggatggtc aaattatgac gtggagggtg acggtatgcg atgctccatc 480

aactgggcag acgacagtcc taaaagctac tcatacaggg tttgtttatt cgtattcatc 540

tacctgattc ctgttctttt gatggtggct acttacgtgt tggttcaagg agagatgaag 600

aatatgcgag gtcgtgcagc acagttgttt ggttcagaat ccgaggctgc actaaagaat 660

atcaaggccg aaaagcgaca cacaaggctg gttttcgtca tgatcctttc tttcatcgta 720

gcttggaccc catatacctt cgtcgccatg tgggtttcct ttttcacgaa acaacttggg 780

ccaatacctt tatacgttga tactttggca gctatgcttg caaagtcgtc ggctatgttc 840

aaccccatca tttactgctt cctccacaag caattcagaa gagctgtatt acgtggtgtt 900

tgtcagtacc ggaatatcaa ccggaagctc tctgctgcag gcatgcacga agccctgaaa 960

cttgctgaga ggcctgagag aagcgagttt gtgctacaaa actgtgacca ctgtgggaaa 1020

aaaggtcatg atacatgaaa gagcaggatc accagcgagg gcgagtacat ccccctggac 1080

cagatcgaca tcaacgtgac agagaccagc caagtggcgc ctgcctaa 1128

<210> 36
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> JellyOP(palm)-5HT7 protein

<220>
<221> LIPID
<222> 301
<223> PALMITATE

<400> 36
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1 5 10 15
Val Phe Leu Ser Ile Ser Leu Asn Met Ile Val Leu Ile Thr Phe Tyr
20 25 30
Arg Leu Arg His Lys Leu Ala Phe Lys Asp Ala Leu Met Ala Ser Met
35 40 45

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Ala Phe Ser Asp Val Val Gln Ala Ile Val Gly Tyr Pro Leu Glu Val
    50                  55                  60
Phe Thr Val Val Asp Gly Lys Trp Thr Phe Gly Met Glu Leu Cys Gln
65                  70                  75                  80
Val Ala Gly Phe Phe Ile Thr Ala Leu Gly Gln Val Ser Ile Ala His
                85                  90                  95
Leu Thr Ala Leu Ala Leu Asp Arg Tyr Phe Thr Val Cys Arg Pro Phe
            100                 105                 110
Val Ala Thr Ala Ile His Gly Ser Met Arg Asn Ala Gly Met Val Ile
        115                 120                 125
Phe Val Cys Trp Phe Tyr Ala Ser Phe Trp Ala Val Leu Pro Leu Val
    130                 135                 140
Gly Trp Ser Asn Tyr Asp Val Glu Gly Asp Gly Met Arg Cys Ser Ile
145                 150                 155                 160
Asn Trp Ala Asp Asp Ser Pro Lys Ser Tyr Ser Tyr Arg Val Cys Leu
                165                 170                 175
Phe Val Phe Ile Tyr Leu Ile Pro Val Leu Leu Met Val Ala Thr Tyr
            180                 185                 190
Val Leu Val Gln Gly Glu Met Lys Asn Met Arg Gly Arg Ala Ala Gln
        195                 200                 205
Leu Phe Gly Ser Glu Ser Glu Ala Ala Leu Lys Asn Ile Lys Ala Glu
    210                 215                 220
Lys Arg His Thr Arg Leu Val Phe Val Met Ile Leu Ser Phe Ile Val
225                 230                 235                 240
Ala Trp Thr Pro Tyr Thr Phe Val Ala Met Trp Val Ser Phe Phe Thr
                245                 250                 255
Lys Gln Leu Gly Pro Ile Pro Leu Tyr Val Asp Thr Leu Ala Ala Met
            260                 265                 270
Leu Ala Lys Ser Ser Ala Met Phe Asn Pro Ile Ile Tyr Cys Phe Leu
        275                 280                 285
His Lys Gln Phe Arg Arg Ala Val Leu Arg Gly Val Cys Gln Tyr Arg
    290                 295                 300
Asn Ile Asn Arg Lys Leu Ser Ala Ala Gly Met His Glu Ala Leu Lys
305                 310                 315                 320
Leu Ala Glu Arg Pro Glu Arg Ser Glu Phe Val Leu Gln Asn Cys Asp
                325                 330                 335
His Cys Gly Lys Lys Gly His Asp Thr Lys Ser Arg Ile Thr Ser Glu
            340                 345                 350
Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile Asn Val Thr Glu Thr
        355                 360                 365
Ser Gln Val Ala Pro Ala
    370
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<210> 37
<211> 1118
<212> DNA
<213> Artificial Sequence

<220>

<223> PPO(palm)-mGluR6 cDNA

<400> 37
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gctacggctt caccatcctc gccgtgatca tggccgtgtt caccatcgcc tcgctcgtgc 120

tcaacagcac cgtcgtcatc gtcaccctgc gccaccgcca gctacgccac ccgctcaact 180

tctcgctcgt caacctcgcc gtggcggacc tgggcgtcac ggtgttcggc gccagcctcg 240

tcgtggagac caacgccgtc gggtacttca acctcggccg cgtcggctgc gtcatcgaag 300

ggttcgccgt cgctttcttc ggcatcgccg ctctgtgcac gatcgccgtg atcgccgtcg 360

atcgcttcgt ggtggtgtgc aagccgctgg gcacgctgat gttcacgcgg cgccacgcgc 420

tgctgggcat cgcctgggcc tggctctggt cgttcgtgtg gaacacgccg ccgctcttcg 480

gctggggcag ctacgagctg gagggcgtgc ggacgtcgtg cgcgcccgac tggtacagcc 540

gcgaccccgc caacgtgtcg tacattacga gctacttcgc cttctgcttc gccatcccct 600

tcctcgtcat cgtggtggcg tacggccgcc tcatgtggac cctccaccag gtggccaagc 660

tggggatggg cgagagcggc agcaccgcca aggcggaggc gcaggtgtcg cgcatggtgg 720

tggtcatggt ggtggccttc ctcgtctgct ggctgcccta cgcgctcttc gccatgatcg 780

tggtgaccaa gcccgacgtg tacatcgacc cggtcatcgc cacactgccc atgtacctga 840

ccaagacgag cacggtctac aaccccatca tctacatctt catgaaccgc cagttccggg 900

actgcgccgt gcccttcctg ctctgcctgt tccatccaga gcagaacgtg cagaagcgga 960

agcgcagcct caagaagacc tccacgatgg cggccccgcc caagagcgag aactcagagg 1020

acgccaagac agagaccagc caagtggcgc ctgccaagag caggatcacc agcgagggcg 1080

agtacatccc cctggaccag atcgacatca acgtgtaa 1118

<210> 38
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> PPO(palm)-mGluR6 protein

<220>
<221> LIPID
<222> 308
<223> PALMITATE

<400> 38
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Leu Met Pro Arg Tyr Gly Phe Thr Ile Leu Ala Val Ile Met Ala Val
            20   25   30
Phe Thr Ile Ala Ser Leu Val Leu Asn Ser Thr Val Val Ile Val Thr
        35   40   45
Leu Arg His Arg Gln Leu Arg His Pro Leu Asn Phe Ser Leu Val Asn
    50   55   60
Leu Ala Val Ala Asp Leu Gly Val Thr Val Phe Gly Ala Ser Leu Val
65   70   75   80
Val Glu Thr Asn Ala Val Gly Tyr Phe Asn Leu Gly Arg Val Gly Cys
                85   90   95
Val Ile Glu Gly Phe Ala Val Ala Phe Phe Gly Ile Ala Ala Leu Cys
            100   105   110
Thr Ile Ala Val Ile Ala Val Asp Arg Phe Val Val Val Cys Lys Pro
        115   120   125
Leu Gly Thr Leu Met Phe Thr Arg Arg His Ala Leu Leu Gly Ile Ala
    130   135   140
Trp Ala Trp Leu Trp Ser Phe Val Trp Asn Thr Pro Pro Leu Phe Gly
145   150   155   160
Trp Gly Ser Tyr Glu Leu Glu Gly Val Arg Thr Ser Cys Ala Pro Asp
                165   170   175
Trp Tyr Ser Arg Asp Pro Ala Asn Val Ser Tyr Ile Thr Ser Tyr Phe
            180   185   190
Ala Phe Cys Phe Ala Ile Pro Phe Leu Val Ile Val Val Ala Tyr Gly
        195   200   205
Arg Leu Met Trp Thr Leu His Gln Val Ala Lys Leu Gly Met Gly Glu
    210   215   220
Ser Gly Ser Thr Ala Lys Ala Glu Ala Gln Val Ser Arg Met Val Val
225   230   235   240
Val Met Val Val Ala Phe Leu Val Cys Trp Leu Pro Tyr Ala Leu Phe
                245   250   255
Ala Met Ile Val Val Thr Lys Pro Asp Val Tyr Ile Asp Pro Val Ile
            260   265   270
Ala Thr Leu Pro Met Tyr Leu Thr Lys Thr Ser Thr Val Tyr Asn Pro
        275   280   285
Ile Ile Tyr Ile Phe Met Asn Arg Gln Phe Arg Asp Cys Ala Val Pro
    290   295   300
Phe Leu Leu Cys Leu Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys
305   310   315   320
Arg Ser Leu Lys Lys Thr Ser Thr Met Ala Ala Pro Pro Lys Ser Glu
                325   330   335
Asn Ser Glu Asp Ala Lys Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr

340 345 350
Ile Pro Leu Asp Gln Ile Asp Ile Asn Val Thr Glu Thr Ser Gln Val
355 360 365
Ala Pro Ala
370

<210> 39
<211> 1238
<212> DNA
<213> Artificial Sequence

<220>
<223> JSR1(palm)-mGluR6 cDNA

<400> 39
atgttaccac atgcagcaaa aatggcggcc agggtggctg gcgatcacga tggaagaaac 60

atttcaattg ttgatcttct gccagaagac atgctaccga tgattcacga acattggtat 120

aagttccccc cgatggaaac ttccatgcat tatatcctcg gaatgcttat tatagttata 180

ggaatcatca gtgtatcagg taatggagtt gtcatgtact taatgatgac agtgaagaac 240

ctccgaactc ccggtaattt tctggtattg aatcttgccc tatctgattt tggtatgctg 300

ttttttatga tgccgacgat gtccataaat tgcttcgccg aaacgtgggt tataggacct 360

ttcatgtgtg agctctatgg aatgatcggc tcattatttg gaagtgcatc tatctggagt 420

ctggtaatga taacactcga ccgatacaat gtcatcgtga aaggaatggc tggaaaacct 480

ctaacgaaag ttggagcact gttaagaatg cttttcgtct ggatttggtc attaggctgg 540

accattgcac cgatgtacgg atggagcagg tatgttcctg aaggctcgat gacatcatgc 600

actattgact acatagatac agctattaat ccaatgtctt accttatcgc ctacgctatt 660

tttgtatact tcgtaccact ctttatcatt atttactgct acgctttcat cgtaatgcaa 720

gtagcagccc acgagaaatc cctacgagaa caagctaaaa agatgaacat caaatccctc 780

agatcaaatg aagataacaa gaaagcaagt gcagaattca gactggctaa ggtggctttt 840

atgaccatct gctgctggtt catggcgtgg actccttatc taaccctgtc cttccttgga 900

atcttctccg acaggacctg gctaacacct atgacatccg tttggggagc catatttgca 960

aaagctagtg cctgctacaa tcctattgtt tatggaataa gtcatcctaa gtatcgtgcc 1020

gctttacatg ataagttccc atgcctctgt tccatccaga gcagaacgtg cagaagcgga 1080

agcgcagcct caagaagacc tccacgatgg cggccccgcc caagagcgag aactcagagg 1140

acgccaagac agagaccagc caagtggcgc ctgccaagag caggatcacc agcgagggcg 1200

agtacatccc cctggaccag atcgacatca acgtgtaa 1238

<210> 40
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> JSR1(palm)-mGluR6 protein

<220>
<221> LIPID
<222> 348
<223> PALMITATE

<400> 40

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Met Leu Pro His Ala Ala Lys Met Ala Ala Arg Val Ala Gly Asp His
1               5                  10                  15
Asp Gly Arg Asn Ile Ser Ile Val Asp Leu Leu Pro Glu Asp Met Leu
            20                  25                  30
Pro Met Ile His Glu His Trp Tyr Lys Phe Pro Pro Met Glu Thr Ser
        35                  40                  45
Met His Tyr Ile Leu Gly Met Leu Ile Ile Val Ile Gly Ile Ile Ser
    50                  55                  60
Val Ser Gly Asn Gly Val Val Met Tyr Leu Met Met Thr Val Lys Asn
65                  70                  75                  80
Leu Arg Thr Pro Gly Asn Phe Leu Val Leu Asn Leu Ala Leu Ser Asp
                85                  90                  95
Phe Gly Met Leu Phe Phe Met Met Pro Thr Met Ser Ile Asn Cys Phe
            100                 105                 110
Ala Glu Thr Trp Val Ile Gly Pro Phe Met Cys Glu Leu Tyr Gly Met
        115                 120                 125
Ile Gly Ser Leu Phe Gly Ser Ala Ser Ile Trp Ser Leu Val Met Ile
    130                 135                 140
Thr Leu Asp Arg Tyr Asn Val Ile Val Lys Gly Met Ala Gly Lys Pro
145                 150                 155                 160
Leu Thr Lys Val Gly Ala Leu Leu Arg Met Leu Phe Val Trp Ile Trp
                165                 170                 175
Ser Leu Gly Trp Thr Ile Ala Pro Met Tyr Gly Trp Ser Arg Tyr Val
            180                 185                 190
Pro Glu Gly Ser Met Thr Ser Cys Thr Ile Asp Tyr Ile Asp Thr Ala
        195                 200                 205
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Ile Asn Pro Met Ser Tyr Leu Ile Ala Tyr Ala Ile Phe Val Tyr Phe
210 215 220
Val Pro Leu Phe Ile Ile Ile Tyr Cys Tyr Ala Phe Ile Val Met Gln
225 230 235 240
Val Ala Ala His Glu Lys Ser Leu Arg Glu Gln Ala Lys Lys Met Asn
245 250 255
Ile Lys Ser Leu Arg Ser Asn Glu Asp Asn Lys Lys Ala Ser Ala Glu
260 265 270
Phe Arg Leu Ala Lys Val Ala Phe Met Thr Ile Cys Cys Trp Phe Met
275 280 285
Ala Trp Thr Pro Tyr Leu Thr Leu Ser Phe Leu Gly Ile Phe Ser Asp
290 295 300
Arg Thr Trp Leu Thr Pro Met Thr Ser Val Trp Gly Ala Ile Phe Ala
305 310 315 320
Lys Ala Ser Ala Cys Tyr Asn Pro Ile Val Tyr Gly Ile Ser His Pro
325 330 335
Lys Tyr Arg Ala Ala Leu His Asp Lys Phe Pro Cys Leu Phe His Pro
340 345 350
Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr
355 360 365
Met Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala Lys Lys Ser
370 375 380
Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile
385 390 395 400
Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
405 410

<210> 41
<211> 1722
<212> DNA
<213> Artificial Sequence

<220>
<223> hJSR(S186F)palm-GABAB2-TS-1D4 cDNA

<400> 41
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atctctatcg tggacctgct gcctgaagat atgcttccaa tgattcacga gcactggtac 120

aagtttcccc ccatggaaac cagcatgcac tacatcctgg gcatgctgat catcgtgatc 180

ggaatcattt ctgtgtccgg caatggcgtg gtgatgtacc tgatgatgac cgttaagaac 240

ctgcggacac ctggaaattt cctggtgctg aacctggctc tgagcgactt cggcatgctg 300

ttcttcatga tgcccaccat gagcatcaac tgtttcgccg agacatgggt catcggtcct 360

ttcatgtgcg agctgtacgg catgatcggc tctctgtttg gcagcgccag catctggtct 420

cttgtgatga tcaccctgga ccggtataat gtcatcgtta agggaatggc cggaaagcct 480

ctgaccaagg tgggcgctct gctgagaatg ctcttcgtgt ggatctggtc cctgggctgg 540

accattgccc ctatgtacgg ctggagcaga tatgtgccag agggctctat gaccttctgc 600

accatcgatt acatcgacac cgccattaac cccatgagct acctgatcgc ctacgccatc 660

ttcgtgtact tcgtgccccc gttcatcatc atctactgct acgcctttat cgtgatgcag 720

gtggctgccc atgagaagag cctgcgggaa caggccaaga aaatgaacat caagagcctg 780

cgctccaacg aggacaacaa gaaggcctct gccgagttca gactggccaa agtggccttc 840

atgaccatct gctgttggtt catggcttgg acccccttacc tgacactgag cttcctgggc 900

atcttcagcg acagaacatg gctgacccct atgacaagcg tgtggggcgc catctttgcc 960

aaggccagcg cctgttacaa ccctatcgtg tacggcatca gccaccccaa gtacagagcc 1020

gccctgcacg ataagtttcc ttgcactctg aggacaaacc ctgacgcagc cactcagaac 1080

aggcgattcc agttcacaca gaaccagaag aaagaagatt cgaagacctc cacctcagtc 1140

accagcgtga accaggcgag cacgtcacgc ctggagggac tgcagtcaga aaaccaccgc 1200

ctacgaatga agatcacaga gctggacaaa gacttggaag aagtcaccat gcagctacaa 1260

gacacaccag agaagaccac atacatcaaa cagaatcact accaagagct caacgacatc 1320

ctcagcttgg gcaacttcac agagagcaca gatggaggaa aggccattct aaaaaatcac 1380

ctcgatcaaa accctcagct ccagtggaac acgaccgagc cctcaagaac atgcaaagac 1440

cccatagagg acatcaactc cccagagcac atccagcgcc ggctgtccct ccagctcccc 1500

atcctccacc acgcctacct cccgtccatt ggaggcgtgg acgccagctg cgtcagcccc 1560

tgtgtcagcc ctacagccag ccctcgccac agacacgtac caccctcctt ccgagtcatg 1620

gtctcgggcc tgaagagcag gatcaccagc gagggcgagt acatcccccct ggaccagatc 1680

gacatcaacg tgacagagac cagccaagtg gcgcctgcct aa 1722

<210> 42
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> hJSR(S186F)palm-GABAB2-TS-1D4 protein

<400> 42
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Met Leu Pro His Ala Ala Lys Met Ala Ala Arg Val Ala Gly Asp His
1               5                  10                  15
Asp Gly Arg Asn Ile Ser Ile Val Asp Leu Leu Pro Glu Asp Met Leu
            20                  25                  30
Pro Met Ile His Glu His Trp Tyr Lys Phe Pro Pro Met Glu Thr Ser
        35                  40                  45
Met His Tyr Ile Leu Gly Met Leu Ile Ile Val Ile Gly Ile Ile Ser
    50                  55                  60
Val Ser Gly Asn Gly Val Val Met Tyr Leu Met Met Thr Val Lys Asn
65                  70                  75                  80
Leu Arg Thr Pro Gly Asn Phe Leu Val Leu Asn Leu Ala Leu Ser Asp
                85                  90                  95
Phe Gly Met Leu Phe Phe Met Met Pro Thr Met Ser Ile Asn Cys Phe
            100                 105                 110
Ala Glu Thr Trp Val Ile Gly Pro Phe Met Cys Glu Leu Tyr Gly Met
        115                 120                 125
Ile Gly Ser Leu Phe Gly Ser Ala Ser Ile Trp Ser Leu Val Met Ile
    130                 135                 140
Thr Leu Asp Arg Tyr Asn Val Ile Val Lys Gly Met Ala Gly Lys Pro
145                 150                 155                 160
Leu Thr Lys Val Gly Ala Leu Leu Arg Met Leu Phe Val Trp Ile Trp
                165                 170                 175
Ser Leu Gly Trp Thr Ile Ala Pro Met Tyr Gly Trp Ser Arg Tyr Val
            180                 185                 190
Pro Glu Gly Ser Met Thr Phe Cys Thr Ile Asp Tyr Ile Asp Thr Ala
        195                 200                 205
Ile Asn Pro Met Ser Tyr Leu Ile Ala Tyr Ala Ile Phe Val Tyr Phe
    210                 215                 220
Val Pro Leu Phe Ile Ile Ile Tyr Cys Tyr Ala Phe Ile Val Met Gln
225                 230                 235                 240
Val Ala Ala His Glu Lys Ser Leu Arg Glu Gln Ala Lys Lys Met Asn
                245                 250                 255
Ile Lys Ser Leu Arg Ser Asn Glu Asp Asn Lys Lys Ala Ser Ala Glu
            260                 265                 270
Phe Arg Leu Ala Lys Val Ala Phe Met Thr Ile Cys Cys Trp Phe Met
        275                 280                 285
Ala Trp Thr Pro Tyr Leu Thr Leu Ser Phe Leu Gly Ile Phe Ser Asp
    290                 295                 300
Arg Thr Trp Leu Thr Pro Met Thr Ser Val Trp Gly Ala Ile Phe Ala
305                 310                 315                 320
Lys Ala Ser Ala Cys Tyr Asn Pro Ile Val Tyr Gly Ile Ser His Pro
                325                 330                 335
Lys Tyr Arg Ala Ala Leu His Asp Lys Phe Pro Cys Thr Leu Arg Thr
            340                 345                 350
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Asn Pro Asp Ala Ala Thr Gln Asn Arg Arg Phe Gln Phe Thr Gln Asn
        355                 360                 365
Gln Lys Lys Glu Asp Ser Lys Thr Ser Thr Ser Val Thr Ser Val Asn
    370                 375                 380
Gln Ala Ser Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn His Arg
385                 390                 395                 400
Leu Arg Met Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu Val Thr
                405                 410                 415
Met Gln Leu Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys Gln Asn
            420                 425                 430
His Tyr Gln Glu Leu Asn Asp Ile Leu Ser Leu Gly Asn Phe Thr Glu
        435                 440                 445
Ser Thr Asp Gly Gly Lys Ala Ile Leu Lys Asn His Leu Asp Gln Asn
    450                 455                 460
Pro Gln Leu Gln Trp Asn Thr Thr Glu Pro Ser Arg Thr Cys Lys Asp
465                 470                 475                 480
Pro Ile Glu Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg Leu Ser
                485                 490                 495
Leu Gln Leu Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile Gly Gly
            500                 505                 510
Val Asp Ala Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala Ser Pro
        515                 520                 525
Arg His Arg His Val Pro Pro Ser Phe Arg Val Met Val Ser Gly Leu
    530                 535                 540
Lys Ser Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile
545                 550                 555                 560
Asp Ile Asn Val Thr Glu Thr Ser Gln Val Ala Pro Ala
                565                 570
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<210> 43
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> JSR(S186F)palm-beta2AR cDNA

<400> 43

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atgctgcctc acgccgctaa aatggccgca agagtggccg gagatcacga cggcagaaac      60

atctctatcg tggacctgct gcctgaagat atgcttccaa tgattcacga gcactggtac     120

aagtttcccc ccatggaaac cagcatgcac tacatcctgg gcatgctgat catcgtgatc     180

ggaatcattt ctgtgtccgg caatggcgtg gtgatgtacc tgatgatgac cgttaagaac     240

ctgcggacac ctggaaattt cctggtgctg aacctggctc tgagcgactt cggcatgctg     300

ttcttcatga tgcccaccat gagcatcaac tgtttcgccg agacatgggt catcggtcct     360
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ttcatgtgcg agctgtacgg catgatcggc tctctgtttg gcagcgccag catctggtct 420

cttgtgatga tcaccctgga ccggtataat gtcatcgtta agggaatggc cggaaagcct 480

ctgaccaagg tgggcgctct gctgagaatg ctcttcgtgt ggatctggtc cctgggctgg 540

accattgccc ctatgtacgg ctggagcaga tatgtgccag agggctctat gaccttctgc 600

accatcgatt acatcgacac cgccattaac cccatgagct acctgatcgc ctacgccatc 660

ttcgtgtact tcgtgccccc gttcatcatc atctactgct acgcctttat cgtgatgcag 720

gtggctgccc atgagaagag cctgcgggaa caggccaaga aaatgaacat caagagcctg 780

cgctccaacg aggacaacaa gaaggcctct gccgagttca gactggccaa agtggccttc 840

atgaccatct gctgttggtt catggcttgg acccccttacc tgacactgag cttcctgggc 900

atcttcagcg acagaacatg gctgacccct atgacaagcg tgtggggcgc catctttgcc 960

aaggccagcg cctgttacaa ccctatcgtg tacggcatca gccaccccaa gtacagagcc 1020

gccctgcacg ataagtttcc ttgcattgcc ttccaggagc ttctgtgcct gcgcaggtct 1080

tctttgaagg cctatgggaa tggctactcc agcaacggca acacagggga gcagagtgga 1140

tatcacgtgg aacaggagaa agaaaataaa ctgctgtgtg aagacctccc aggcacggaa 1200

gactttgtgg gccatcaagg tactgtgcct agcgataaca ttgattcaca agggaggaat 1260

tgtagtacaa atgactcact gctgaagagc aggatcacca gcgagggcga gtacatcccc 1320

ctggaccaga tcgacatcaa cgtgacagag accagccaag tggcgcctgc ctaa 1374

<210> 44
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> JSR(S186F)palm-beta2AR protein

<400> 44
Met Leu Pro His Ala Ala Lys Met Ala Ala Arg Val Ala Gly Asp His
1 5 10 15
Asp Gly Arg Asn Ile Ser Ile Val Asp Leu Leu Pro Glu Asp Met Leu
20 25 30

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Pro Met Ile His Glu His Trp Tyr Lys Phe Pro Pro Met Glu Thr Ser
        35                  40                  45
Met His Tyr Ile Leu Gly Met Leu Ile Ile Val Ile Gly Ile Ile Ser
    50                  55                  60
Val Ser Gly Asn Gly Val Val Met Tyr Leu Met Met Thr Val Lys Asn
65                  70                  75                  80
Leu Arg Thr Pro Gly Asn Phe Leu Val Leu Asn Leu Ala Leu Ser Asp
                85                  90                  95
Phe Gly Met Leu Phe Phe Met Met Pro Thr Met Ser Ile Asn Cys Phe
            100                 105                 110
Ala Glu Thr Trp Val Ile Gly Pro Phe Met Cys Glu Leu Tyr Gly Met
        115                 120                 125
Ile Gly Ser Leu Phe Gly Ser Ala Ser Ile Trp Ser Leu Val Met Ile
    130                 135                 140
Thr Leu Asp Arg Tyr Asn Val Ile Val Lys Gly Met Ala Gly Lys Pro
145                 150                 155                 160
Leu Thr Lys Val Gly Ala Leu Leu Arg Met Leu Phe Val Trp Ile Trp
                165                 170                 175
Ser Leu Gly Trp Thr Ile Ala Pro Met Tyr Gly Trp Ser Arg Tyr Val
            180                 185                 190
Pro Glu Gly Ser Met Thr Phe Cys Thr Ile Asp Tyr Ile Asp Thr Ala
        195                 200                 205
Ile Asn Pro Met Ser Tyr Leu Ile Ala Tyr Ala Ile Phe Val Tyr Phe
    210                 215                 220
Val Pro Leu Phe Ile Ile Ile Tyr Cys Tyr Ala Phe Ile Val Met Gln
225                 230                 235                 240
Val Ala Ala His Glu Lys Ser Leu Arg Glu Gln Ala Lys Lys Met Asn
                245                 250                 255
Ile Lys Ser Leu Arg Ser Asn Glu Asp Asn Lys Lys Ala Ser Ala Glu
            260                 265                 270
Phe Arg Leu Ala Lys Val Ala Phe Met Thr Ile Cys Cys Trp Phe Met
        275                 280                 285
Ala Trp Thr Pro Tyr Leu Thr Leu Ser Phe Leu Gly Ile Phe Ser Asp
    290                 295                 300
Arg Thr Trp Leu Thr Pro Met Thr Ser Val Trp Gly Ala Ile Phe Ala
305                 310                 315                 320
Lys Ala Ser Ala Cys Tyr Asn Pro Ile Val Tyr Gly Ile Ser His Pro
                325                 330                 335
Lys Tyr Arg Ala Ala Leu His Asp Lys Phe Pro Cys Ile Ala Phe Gln
            340                 345                 350
Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly
        355                 360                 365
Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu
    370                 375                 380
Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu
385                 390                 395                 400
Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser
                405                 410                 415
Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu Lys Ser Arg Ile
            420                 425                 430
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Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile Asn Val
435 440 445
Thr Glu Thr Ser Gln Val Ala Pro Ala
450 455

<210> 45
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site palm Mela hOPN4 trunc CT mGlur6 CT

<400> 45
Asn Pro Ile Ile Tyr Ala Ile Thr His Pro Lys Tyr Arg Val Ala Ile
1 5 10 15
Ala Gln His Leu Pro Cys Leu Phe His Pro Glu Gln Asn Val Gln Lys
20 25 30
Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr Met Ala Ala Pro Pro Lys
35 40 45
Ser Glu Asn Ser Glu Asp Ala Lys
50 55

<210> 46
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site palm+33 Mela hOPN4 trunc CT mGlur6 CT

<400> 46
His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly
1 5 10 15
Val Leu Leu Gly Val Ser Gly Gln Arg Ser His Pro Ser Leu Ser Tyr
20 25 30
Arg Ser Thr His Arg Ser Thr Leu Ser Ser Gln Ser Ser Asp Leu His
35 40 45
Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Leu Lys Lys Thr Ser
50 55 60
Thr Met Ala Ala Pro Pro Lys Ser Glu Asn Ser Glu Asp Ala Lys
65 70 75

<210> 47
<211> 40
<212> PRT

<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site Jct a Jct b Mela hOPN4 TM1 TM2 mGlur6 IL1

<400> 47
Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Met Arg His Asn
1 5 10 15
Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Phe Ile Ile Asn
20 25 30
Leu Ala Val Ser Asp Phe Leu Met
35 40

<210> 48
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site variable region Mela hOPN4 proxim IL3 region distal IL3 region mGlur6 IL3

<400> 48
Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Gly Val Pro Glu
1 5 10 15
Thr Phe Asn Glu Ala Pro Leu Arg Gln Arg Arg Gln Trp Gln Arg Leu
20 25 30
Gln Ser Glu Trp Lys Met Ala Lys Val Ala Leu Ile Val Ile Leu
35 40 45

<210> 49
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site palm Jellyopsin Cubop trunc CT m5HT7 CT

<400> 49
Phe Asn Pro Ile Ile Tyr Cys Phe Leu His Lys Gln Phe Arg Arg Ala
1 5 10 15
Val Leu Arg Gly Val Cys Gln Tyr Arg Asn Ile Asn Arg Lys Leu Ser
20 25 30
Ala Ala Gly Met His Glu Ala Leu Lys Leu Ala Glu Arg Pro Glu Arg
35 40 45

Ser Glu Phe Val Leu Gln Asn Cys Asp His Cys Gly Lys Lys Gly His
50 55 60
Asp Thr
65

<210> 50
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site palm JellyOP cubop trunc CT mGlur6 CT

<400> 50
Phe Asn Pro Ile Ile Tyr Cys Phe Leu His Lys Gln Phe Arg Arg Ala
1 5 10 15
Val Leu Arg Gly Val Cys Leu Phe His Pro Glu Gln Asn Val Gln Lys
20 25 30
Arg Lys Arg Ser Leu Lys Lys Thr Ser Thr Met Ala Ala Pro Pro Lys
35 40 45
Ser Glu Asn Ser Glu Asp Ala Lys
50 55

<210> 51
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site palm Cone opsin hOPN1MW trunc CT mGlur6 CT

<400> 51
Tyr Asn Pro Ile Ile Tyr Val Phe Met Asn Arg Gln Phe Arg Asn Cys
1 5 10 15
Ile Leu His Leu Phe His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg
20 25 30
Ser Leu Lys Lys Thr Ser Thr Met Ala Ala Pro Pro Lys Ser Glu Asn
35 40 45
Ser Glu Asp Ala Lys
50

<210> 52
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site palm Mela hOPN4 trunc CT
Cone opsin OPN1MW CT

<400> 52
Asn Pro Ile Ile Tyr Ala Ile Thr His Pro Lys Tyr Arg Val Ala Ile
1 5 10 15
Ala Gln His Leu Pro Cys Gly Lys Lys Val Asp Asp Ser Ser Glu Leu
20 25 30
Ser Ser Thr Ser Lys Thr Glu Val Ser Ser Val Ser Ser Val Ser Pro
35 40 45
Ala

<210> 53
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D4 tag

<400> 53
Glu Thr Ser Gln Val Ala Pro Ala
1 5

<210> 54
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site Jct a Jct b Mela hOPN4 TM1
TM2 Cone opsin OPN1MW IL1

<400> 54
Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Ala Thr Met Lys Phe
1 5 10 15
Lys Lys Leu Arg His Pro Ala Asn Met Phe Ile Ile Asn Leu Ala Val
20 25 30
Ser Asp Phe Leu
35

<210> 55
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site Jct c Jct d Mela hOPN4 TM3
TM4 Cone opsin OPN1MW IL2

<400> 55
Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Cys Lys Pro Phe Gly
1 5 10 15
Asn Val Arg Phe Asp Ala Lys Leu Thr Ala Leu Val Leu Leu Gly Val
20 25 30
Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe
35 40

<210> 56
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence at Splicing Site Jct e Jct f Mela hOPN4 TM5
TM6 Cone opsin OPN1MW IL3

<400> 56
Leu Ile Ile Ile Phe Cys Tyr Ile Gln Val Trp Leu Ala Ile Arg Ala
1 5 10 15
Val Ala Lys Gln Gln Lys Glu Ser Glu Ser Thr Gln Lys Ala Glu Lys
20 25 30
Glu Val Thr Lys Val Ala Leu Ile Val Ile Leu Leu Phe Val Leu
35 40 45

<210> 57
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence section human melanopsin gene (OPN4) C-terminal
melanopsin fragment

<400> 57
His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly
1 5 10 15
Val Leu Leu Gly Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser Tyr
20 25 30
Arg Ser Thr His Arg Ser Thr Leu Thr Ser His Thr Ser Asn Leu Ser
35 40 45
Trp Ile Ser Ile Arg Arg Arg Gln Glu Ser Leu Gly Ser Glu Ser Glu

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

<210> 58
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence section murine melanopsin gene (OPN4) C-terminal melanopsin fragment

<400> 58
His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly
1 5 10 15
Val Leu Leu Gly Val Ser Gly Gln Arg Ser His Pro Ser Leu Ser Tyr
20 25 30
Arg Ser Thr His Arg Ser Thr Leu Ser Ser Gln Ser Ser Asp Leu Ser
35 40 45
Trp Ile Ser Gly Arg Lys Arg Gln Glu Ser Leu Gly Ser Glu Ser Glu
50 55 60
Val Gly Trp Thr Asp Thr Glu Thr Thr Ala Ala Trp Gly Ala Ala Gln
65 70 75 80
Gln Ala Ser Gly Gln Ser Phe Cys Ser Gln Asn Leu Glu Asp Gly Glu
85 90 95
Leu Lys Ala Ser Ser Ser Pro Gln Thr Lys Gly His Leu Pro Ser Leu
100 105 110
Asp Leu Gly Met
115

<210> 59
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> wild type capsid AAV2 sequence

<400> 59
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
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Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
Asn Ser Glu Phe Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 60
<211> 7
<212> PRT
<213> Artificial Sequence


<220>
<223> peptide insert SASEAST
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<400> 60
Ser Ala Ser Glu Ala Ser Thr
1 5

<210> 61
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert TPPSITA

<400> 61
Thr Pro Pro Ser Ile Thr Ala
1 5

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert PRTPHTA

<400> 62
Pro Arg Thr Pro His Thr Ala
1 5

<210> 63
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert NHAPNHC

<400> 63
Asn His Ala Pro Asn His Cys
1 5

<210> 64
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> peptide insert AAASASEASTAA

<400> 64
Ala Ala Ala Ser Ala Ser Glu Ala Ser Thr Ala Ala
1 5 10

<210> 65
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert AAATPPSITAAA

<400> 65
Ala Ala Ala Thr Pro Pro Ser Ile Thr Ala Ala Ala
1 5 10

<210> 66
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert AAAPRTPHTAAA

<400> 66
Ala Ala Ala Pro Arg Thr Pro His Thr Ala Ala Ala
1 5 10

<210> 67
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert NLANHAPNHCAR

<400> 67
Asn Leu Ala Asn His Ala Pro Asn His Cys Ala Arg
1 5 10

<210> 68
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert NLAPRTPHTAAR

<400> 68
Asn Leu Ala Pro Arg Thr Pro His Thr Ala Ala Arg
1   5   10

<210> 69
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert SASEAST with linker

<400> 69
Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Ser Ala Ser Glu
1   5   10   15
Ala Ser Thr Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
            20   25   30
Gly Val Leu Pro Gly
        35

<210> 70
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert TPPSITA with linker

<400> 70
Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Thr Pro Pro Ser
1   5   10   15
Ile Thr Ala Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
            20   25   30
Gly Val Leu Pro Gly
        35

<210> 71
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert PRTPHTA with linker

<400> 71
Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Pro Arg Thr Pro
1 5 10 15
His Thr Ala Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
20 25 30
Gly Val Leu Pro Gly
35

<210> 72
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert NHAPNHC with linker

<400> 72
Val Ser Thr Asn Leu Gln Arg Gly Asn Asn Leu Ala Asn His Ala Pro
1 5 10 15
Asn His Cys Ala Arg Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
20 25 30
Gly Val Leu Pro Gly
35

<210> 73
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide insert PRTPHTA-AR with linker

<400> 73
Val Ser Thr Asn Leu Gln Arg Gly Asn Asn Leu Ala Pro Arg Thr Pro
1 5 10 15
His Thr Ala Ala Arg Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
20 25 30
Gly Val Leu Pro Gly
35

<210> 74
<211> 747
<212> PRT
<213> Artificial Sequence

<220>

<223> AAV capsid with NLAPRTPHTAAR insertion

<400> 74
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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Phe Asn Asn His Leu
                245                 250                 255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Phe
            260                 265                 270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
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    370                 375                 380
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Phe Leu Ser Arg Thr
        435                 440                 445
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
Asn Ser Glu Phe Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Asn Leu Ala Pro Arg
            580                 585                 590
Thr Pro His Thr Ala Ala Arg Arg Gln Ala Ala Thr Ala Asp Val Asn
        595                 600                 605
Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
    610                 615                 620
Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
625                 630                 635                 640
His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
                645                 650                 655
Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
            660                 665                 670
Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
        675                 680                 685
Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
    690                 695                 700
Arg Trp Asn Pro Glu Ile Gln Phe Thr Ser Asn Tyr Asn Lys Ser Val
705                 710                 715                 720
Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
                725                 730                 735
Pro Ile Gly Thr Arg Phe Leu Thr Arg Asn Leu
            740                 745
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<210> 75
<211> 1354

<212> DNA
<213> Artificial Sequence

<220>
<223> ON-Bipolar cell specific promoter 770En_566P(hGRM6)

<400> 75
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caattccttc taataaatct gtataatata tctgtctata taataaatat gtacttacat 120

aactctgtat gttacatcta tctattctat ctatctatct atctatctat ctatctatct 180

atctatcatc tatctatcta tttatctatt ctctgtgtct ttggagaacc ctgacatagt 240

aagcaatcat atcacctgca aatgatgaaa gctgtgtatt ttccaaatca gtcgttttat 300

gtctttttt cttgcactga ctagtgcccc ctagagggaa tgataattgg aattattgtc 360

ttgctctgat tttaaaggaa gtagatactt caaataattc atcatggagt gcaatatttt 420

ctgtaggctt ttagtagata acttcatcag tttaaagaag atccttagat tatgaaacat 480

ttacaattat gaatgaatat tagatgttat caaatgcttt ttctgcatcc atttagataa 540

tcatgttttt cctttaatct gttaatgcgg tgaattacat taatagattt cctaagtcat 600

taatctgcta aagtgcattt ctgggacaaa ccagacttgg ttatgacatt gtatgtattt 660

cagtttgcaa atattggact aggatttttg tatctatatt ccttagtttg acctgtaaat 720

tttatttctt gtactaagta ttagcctcac gaaaggcatt gtcaaatgtt caattgatat 780

aatgctagcc aagaagagga cagaggcaga aagccaggga cagagactga gaaacagaga 840

cctagaggca gaagaagact gagatagaga tggacagaga ttgtgtcaga cacagcccca 900

gagacagcca gacagtctga gtcagacgca aaccaaagac aagaaaacag gaaaacagac 960

ccagagattg ggagagggag gggaaggaga tgcggggaga gccagcaccg ccacccccca 1020

cactcaggag gggtctccac cctcggagcg gtctctcatc cctccctaga atccttaaat 1080

cctctctcgc tcagggcctc ggccgcatct gtcacagact tgtcctgaac cgacagcggc 1140

tggcgcaggt gactggcttg gggcgggagc ctgggtgtgc gctggggatg gaccccgagg 1200

aagaggggcc aagctgtcgg gaagcggcag ggctggaggg gtggaggcag tggtcgggcg 1260

ggaccccggg cgacagggtt cggcgcttgt aagagcgaga cggaggcccg ggcaggccgg 1320

ctgagctaac tccccagagc cgaagtggaa ggcg 1354

<210> 76
<211> 917
<212> DNA
<213> Artificial Sequence

<220>
<223> ON-Bipolar cell specific promoter 444En_454P(hGRM6)

<400> 76
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gatgaaagct gtgtattttc caaatcagtc gttttatgtc ttttttttctt gcactgacta 120

gtgcccccta gagggaatga taattggaat tattgtcttg ctctgatttt aaaggaagta 180

gatacttcaa ataattcatc atggagtgca atattttctg taggctttta gtagataact 240

tcatcagttt aaagaagatc cttagattat gaaacattta caattatgaa tgaatattag 300

atgttatcaa atgctttttc tgcatccatt tagataatca tgtttttcct ttaatctgtt 360

aatgcggtga attacattaa tagatttcct aagtcattaa tctgctaaag tgcatttctg 420

ggacaaacca gacttggtta tgaccaattg atataatgct agcggagggg tctccaccct 480

cggagcggtc tctcatccct ccctagaatc cttaaatcct ctctcgctca gggcctcggc 540

cgcatctgtc acagacttgt cctgaaccga cagcggctgg cgcaggtgac tggcttgggg 600

cgggagcctg ggtgtgcgct ggggatggac cccgaggaag aggggccaag ctgtcgggaa 660

gcggcagggc tggaggggtg gaggcagtgg tcgggcggga ccccgggcga cagggttcgg 720

cgcttgtaag agcgagacgg aggcccgggc aggccggctg agctaactcc ccagagccga 780

agtggaaggc gcgccccgag cgccttctcc ccaggacccc ggtgtccctc cccgcgcccc 840

gagcccgcgc tctccttccc ccgccctcag agcgctcccc gcccctctgt ctccccgcag 900

cccgctagac gagccga 917

<210> 77
<211> 13

<212> RNA
<213> Artificial Sequence

<220>
<223> KOZAK consensus sequence 1

<400> 77
gccgccacca ugg 13

<210> 78
<211> 13
<212> RNA
<213> Artificial Sequence

<220>
<223> KOZAK consensus sequence 2

<400> 78
gccgccgcca ugg 13

<210> 79
<211> 6020
<212> DNA
<213> Artificial Sequence

<220>
<223> rAAV vector OPN4-mGluR6-TS-1D4

<400> 79
ccttaattag gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccgggcgtc 60

gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgcagagag ggagtggcca 120

actccatcac taggggttcc ttgtagttaa tgattaaccc gccatgctac ttatctacgt 180

agccatgctc taggaagatc ggaattcgcc cttaagtcta gagggtctcc aacttgccaa 240

ctgtagatct tggaaccttt catccttcat aactgcataa gccaattcct tctaataaat 300

ctgtataata tatctgtcta tataataaat atgtacttac ataactctgt atgttacatc 360

tatctattct atctatctat ctatctatct atctatctat ctatctatca tctatctatc 420

tatttatcta ttctctgtgt ctttggagaa ccctgacata gtaagcaatc atatcacctg 480

caaatgatga aagctgtgta ttttccaaat cagtcgtttt atgtcttttt ttcttgcact 540

gactagtgcc ccctagaggg aatgataatt ggaattattg tcttgctctg attttaaagg 600

aagtagatac ttcaaataat tcatcatgga gtgcaatatt ttctgtaggc ttttagtaga 660

taacttcatc agtttaaaga agatccttag attatgaaac atttacaatt atgaatgaat 720

attagatgtt atcaaatgct ttttctgcat ccatttagat aatcatgttt ttcctttaat 780

ctgttaatgc ggtgaattac attaatagat ttcctaagtc attaatctgc taaagtgcat 840

ttctgggaca aaccagactt ggttatgaca ttgtatgtat ttcagtttgc aaatattgga 900

ctaggatttt tgtatctata ttccttagtt tgacctgtaa attttatttc ttgtactaag 960

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gcctcggccg catctgtcac agacttgtcc tgaaccgaca gcggctggcg caggtgactg 1140

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gagggcgagt acatcccccc ggaccagatc gacatcaacg tgacagagac cagccaagtg 2760

gcgcctgcct aaggatctgc ctcgactgtg ccttctagtt gccagccatc tgttgtttgc 2820

ccctcccccg tgccttcctt gaccctggaa ggtgccactc ccactgtcct ttcctaataa 2880

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ggcggcctca gtgagcgagc gagcgcgcag ccttaattaa cctaattcac tggccgtcgt 3240

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tccccctttc gccagctggc gtaatagcga agaggcccgc accgatcgcc cttcccaaca 3360

gttgcgcagc ctgaatggcg aatgggacgc gccctgtagc ggcgcattaa gcgcggcggg 3420

tgtggtggtt acgcgcagcg tgaccgctac acttgccagc gccctagcgc ccgctccttt 3480

cgctttcttc ccttcctttc tcgccacgtt cgccggcttt ccccgtcaag ctctaaatcg 3540

ggggctccct ttagggttcc gatttagtgc tttacggcac ctcgacccca aaaaacttga 3600

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