SEQUENCE LISTING

<110> Howard Hughes Medical Institute

<120> MODIFIED LIGAND-GATED ION CHANNELS AND METHODS OF USE

<130> 30872-0024WO1

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<151> 2018-09-11

<160> 34

<170> PatentIn version 3.5

<210> 1
<211> 224
<212> PRT
<213> human

<400> 1

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Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1               5                  10                  15


Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30


Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45


Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60


Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80


Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95


Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
```

```
            100                 105                 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125

Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160

Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
    210                 215                 220
```

<210> 2
<211> 229
<212> PRT
<213> human

<400> 2

```
Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1               5                   10                  15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45
```

```
Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100                 105                 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125

Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160

Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
    210                 215                 220

Thr Met Arg Arg Arg
225
```

<210> 3
<211> 247

<212> PRT
<213> mouse

<400> 3

```
Ile Ile Arg Arg Arg Pro Leu Phe Tyr Ala Val Ser Leu Leu Leu Pro
1               5                  10                  15

Ser Ile Phe Leu Met Val Val Asp Ile Val Gly Phe Cys Leu Pro Pro
            20                  25                  30

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

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

Thr Pro Leu Ile Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu Val
65                  70                  75                  80

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

Asp Leu Gln Arg Pro Val Pro Asp Trp Leu Arg His Leu Val Leu Asp
            100                 105                 110

Arg Ile Ala Trp Ile Leu Cys Leu Gly Glu Gln Pro Met Ala His Arg
        115                 120                 125

Pro Pro Ala Thr Phe Gln Ala Asn Lys Thr Asp Asp Cys Ser Gly Ser
    130                 135                 140

Asp Leu Leu Pro Ala Met Gly Asn His Cys Ser His Val Gly Gly Pro
145                 150                 155                 160

Gln Asp Leu Glu Lys Thr Pro Arg Gly Arg Gly Ser Pro Leu Pro Pro
                165                 170                 175

Pro Arg Glu Ala Ser Leu Ala Val Arg Gly Leu Leu Gln Glu Leu Ser
```

```
            180                 185                 190

Ser Ile Arg His Phe Leu Glu Lys Arg Asp Glu Met Arg Glu Val Ala
        195                 200                 205

Arg Asp Trp Leu Arg Val Gly Tyr Val Leu Asp Arg Leu Leu Phe Arg
    210                 215                 220

Ile Tyr Leu Leu Ala Val Leu Ala Tyr Ser Ile Thr Leu Val Thr Leu
225                 230                 235                 240

Trp Ser Ile Trp His Tyr Ser
                245
```

<210> 4
<211> 242
<212> PRT
<213> human

<400> 4

```
Ile Ile Arg Arg Arg Pro Leu Phe Tyr Val Val Ser Leu Leu Leu Pro
1               5                   10                  15

Ser Ile Phe Leu Met Val Met Asp Ile Val Gly Phe Tyr Leu Pro Pro
            20                  25                  30

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

Ser Val Phe Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr Ala Ile
    50                  55                  60

Gly Thr Pro Leu Ile Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu
65                  70                  75                  80

Val Ile Ser Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val His Lys
                85                  90                  95
```

```
Gln Asp Leu Gln Gln Pro Val Pro Ala Trp Leu Arg His Leu Val Leu
            100                 105                 110

Glu Arg Ile Ala Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr Ser Gln
        115                 120                 125

Arg Pro Pro Ala Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys Ser Ala
    130                 135                 140

Met Gly Asn His Cys Ser His Met Gly Gly Pro Gln Asp Phe Glu Lys
145                 150                 155                 160

Ser Pro Arg Asp Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu Ala Ser
                165                 170                 175

Leu Ala Val Cys Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg Gln Phe
            180                 185                 190

Leu Glu Lys Arg Asp Glu Ile Arg Glu Val Ala Arg Asp Trp Leu Arg
        195                 200                 205

Val Gly Ser Val Leu Asp Lys Leu Leu Phe His Ile Tyr Leu Leu Ala
    210                 215                 220

Val Leu Ala Tyr Ser Ile Thr Leu Val Met Leu Trp Ser Ile Trp Gln
225                 230                 235                 240

Tyr Ala
```

<210> 5
<211> 202
<212> PRT
<213> human

<400> 5

```
Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val
1               5                   10                  15
```

```
Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala
            20                  25                  30

Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser
        35                  40                  45

Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile
    50                  55                  60

Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe Ser Ala Leu Leu
65                  70                  75                  80

Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln His Lys Glu Leu Leu
                85                  90                  95

Arg Phe Arg Arg Lys Arg Arg His His Lys Glu Asp Glu Ala Gly Glu
            100                 105                 110

Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln
        115                 120                 125

Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr
    130                 135                 140

Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys Leu
145                 150                 155                 160

Phe Ile Gln Arg Ala Lys Lys Ile Asp Lys Ile Ser Arg Ile Gly Phe
                165                 170                 175

Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr Lys
            180                 185                 190

Ile Val Arg Arg Glu Asp Val His Asn Gln
        195                 200
```

<210> 6

<211> 471
<212> PRT
<213> artificial

<220>
<223> alpha7-5HT3 chimeric receptor sequence

<400> 6

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1 5 10 15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
20 25 30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
35 40 45

Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
50 55 60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65 70 75 80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
85 90 95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
100 105 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
115 120 125

Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
130 135 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145 150 155 160

Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp

```
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
    210                 215                 220

Ile Ile Arg Arg Arg Pro Leu Phe Tyr Ala Val Ser Leu Leu Leu Pro
225                 230                 235                 240

Ser Ile Phe Leu Met Val Val Asp Ile Val Gly Phe Cys Leu Pro Pro
                245                 250                 255

Asp Ser Gly Glu Arg Val Ser Phe Lys Ile Thr Leu Leu Leu Gly Tyr
            260                 265                 270

Ser Val Phe Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr Ile Gly
        275                 280                 285

Thr Pro Leu Ile Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu Val
    290                 295                 300

Ile Ser Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val His Lys Gln
305                 310                 315                 320

Asp Leu Gln Arg Pro Val Pro Asp Trp Leu Arg His Leu Val Leu Asp
                325                 330                 335

Arg Ile Ala Trp Ile Leu Cys Leu Gly Glu Gln Pro Met Ala His Arg
            340                 345                 350

Pro Pro Ala Thr Phe Gln Ala Asn Lys Thr Asp Asp Cys Ser Gly Ser
        355                 360                 365
```

```
Asp Leu Leu Pro Ala Met Gly Asn His Cys Ser His Val Gly Gly Pro
    370                 375                 380

Gln Asp Leu Glu Lys Thr Pro Arg Gly Arg Gly Ser Pro Leu Pro Pro
385                 390                 395                 400

Pro Arg Glu Ala Ser Leu Ala Val Arg Gly Leu Leu Gln Glu Leu Ser
                405                 410                 415

Ser Ile Arg His Phe Leu Glu Lys Arg Asp Glu Met Arg Glu Val Ala
            420                 425                 430

Arg Asp Trp Leu Arg Val Gly Tyr Val Leu Asp Arg Leu Leu Phe Arg
        435                 440                 445

Ile Tyr Leu Leu Ala Val Leu Ala Tyr Ser Ile Thr Leu Val Thr Leu
    450                 455                 460

Trp Ser Ile Trp His Tyr Ser
465                 470
```

<210> 7
<211> 430
<212> PRT
<213> artificial

<220>
<223> alpha7-GlyR chimeric receptor sequence

<400> 7

```
Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1               5                   10                  15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45
```

```
Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95

Val Lys Thr Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile Leu
            100                 105                 110

Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr Asn
        115                 120                 125

Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly Ile
    130                 135                 140

Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp Val
145                 150                 155                 160

Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp Ser
                165                 170                 175

Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro Asn
            180                 185                 190

Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg Phe
        195                 200                 205

Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val Thr
    210                 215                 220

Met Arg Arg Arg Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser
225                 230                 235                 240

Leu Leu Ile Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met Asp
```

```
                245                 250                 255

Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met
            260                 265                 270

Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr
        275                 280                 285

Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe
    290                 295                 300

Ser Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln His
305                 310                 315                 320

Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Glu Asp
                325                 330                 335

Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro
            340                 345                 350

Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn
        355                 360                 365

Ser Asn Thr Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu
    370                 375                 380

Met Arg Lys Leu Phe Ile Gln Arg Ala Lys Lys Ile Asp Lys Ile Ser
385                 390                 395                 400

Arg Ile Gly Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp
                405                 410                 415

Ile Ile Tyr Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
            420                 425                 430
```

<210> 8
<211> 466
<212> PRT

<213> artificial

<220>
<223> alpha7-5HT3 chimeric receptor sequence

<400> 8

```
Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1               5                  10                  15


Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30


Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45


Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60


Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80


Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95


Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100                 105                 110


Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125


Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140


Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160


Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175
```

```
Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
    210                 215                 220

Ile Ile Arg Arg Arg Pro Leu Phe Tyr Val Val Ser Leu Leu Leu Pro
225                 230                 235                 240

Ser Ile Phe Leu Met Val Met Asp Ile Val Gly Phe Tyr Leu Pro Pro
                245                 250                 255

Asn Ser Gly Glu Arg Val Ser Phe Lys Ile Thr Leu Leu Leu Gly Tyr
            260                 265                 270

Ser Val Phe Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr Ala Ile
        275                 280                 285

Gly Thr Pro Leu Ile Gly Val Tyr Phe Val Val Cys Met Ala Leu Leu
    290                 295                 300

Val Ile Ser Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val His Lys
305                 310                 315                 320

Gln Asp Leu Gln Gln Pro Val Pro Ala Trp Leu Arg His Leu Val Leu
                325                 330                 335

Glu Arg Ile Ala Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr Ser Gln
            340                 345                 350

Arg Pro Pro Ala Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys Ser Ala
        355                 360                 365

Met Gly Asn His Cys Ser His Met Gly Gly Pro Gln Asp Phe Glu Lys
```

```
    370                 375                 380

Ser Pro Arg Asp Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu Ala Ser
385                 390                 395                 400

Leu Ala Val Cys Gly Leu Leu Gln Glu Leu Ser Ser Ile Arg Gln Phe
                405                 410                 415

Leu Glu Lys Arg Asp Glu Ile Arg Glu Val Ala Arg Asp Trp Leu Arg
            420                 425                 430

Val Gly Ser Val Leu Asp Lys Leu Leu Phe His Ile Tyr Leu Leu Ala
        435                 440                 445

Val Leu Ala Tyr Ser Ile Thr Leu Val Met Leu Trp Ser Ile Trp Gln
    450                 455                 460

Tyr Ala
465
```

<210> 9
<211> 195
<212> PRT
<213> human

<400> 9

```
Leu Leu Gln Thr Tyr Phe Pro Ala Thr Leu Met Val Met Leu Ser Trp
1               5                   10                  15

Val Ser Phe Trp Ile Asp Arg Arg Ala Val Pro Ala Arg Val Pro Leu
            20                  25                  30

Gly Ile Thr Thr Val Leu Thr Met Ser Thr Ile Ile Thr Gly Val Asn
        35                  40                  45

Ala Ser Met Pro Arg Val Ser Tyr Ile Lys Ala Val Asp Ile Tyr Leu
    50                  55                  60
```

```
Trp Val Ser Phe Val Phe Val Phe Leu Ser Val Leu Glu Tyr Ala Ala
65                  70                  75                  80


Val Asn Tyr Leu Thr Thr Val Gln Glu Arg Lys Glu Gln Lys Leu Arg
                85                  90                  95


Glu Lys Leu Pro Cys Thr Ser Gly Leu Pro Pro Pro Arg Thr Ala Met
            100                 105                 110


Leu Asp Gly Asn Tyr Ser Asp Gly Glu Val Asn Asp Leu Asp Asn Tyr
        115                 120                 125


Met Pro Glu Asn Gly Glu Lys Pro Asp Arg Met Met Val Gln Leu Thr
    130                 135                 140


Leu Ala Ser Glu Arg Ser Ser Pro Gln Arg Lys Ser Gln Arg Ser Ser
145                 150                 155                 160


Tyr Val Ser Met Arg Ile Asp Thr His Ala Ile Asp Lys Tyr Ser Arg
                165                 170                 175


Ile Ile Phe Pro Ala Ala Tyr Ile Leu Phe Asn Leu Ile Tyr Trp Ser
            180                 185                 190


Ile Phe Ser
        195


<210>  10
<211>  428
<212>  PRT
<213>  artificial

<220>
<223>  alpha7- GABAC chimeric receptor sequence

<400>  10

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1               5                   10                  15
```

```
Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45

Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100                 105                 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125

Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160

Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
    210                 215                 220
```

```
Thr Met Arg Arg Arg Thr Leu Tyr Tyr Leu Leu Gln Thr Tyr Phe Pro
225                 230                 235                 240

Ala Thr Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile Asp Arg
                245                 250                 255

Arg Ala Val Pro Ala Arg Val Pro Leu Gly Ile Thr Thr Val Leu Thr
            260                 265                 270

Met Ser Thr Ile Ile Thr Gly Val Asn Ala Ser Met Pro Arg Val Ser
        275                 280                 285

Tyr Ile Lys Ala Val Asp Ile Tyr Leu Trp Val Ser Phe Val Phe Val
    290                 295                 300

Phe Leu Ser Val Leu Glu Tyr Ala Ala Val Asn Tyr Leu Thr Thr Val
305                 310                 315                 320

Gln Glu Arg Lys Glu Gln Lys Leu Arg Glu Lys Leu Pro Cys Thr Ser
                325                 330                 335

Gly Leu Pro Pro Pro Arg Thr Ala Met Leu Asp Gly Asn Tyr Ser Asp
            340                 345                 350

Gly Glu Val Asn Asp Leu Asp Asn Tyr Met Pro Glu Asn Gly Glu Lys
        355                 360                 365

Pro Asp Arg Met Met Val Gln Leu Thr Leu Ala Ser Glu Arg Ser Ser
    370                 375                 380

Pro Gln Arg Lys Ser Gln Arg Ser Ser Tyr Val Ser Met Arg Ile Asp
385                 390                 395                 400

Thr His Ala Ile Asp Lys Tyr Ser Arg Ile Ile Phe Pro Ala Ala Tyr
                405                 410                 415
```

```
Ile Leu Phe Asn Leu Ile Tyr Trp Ser Ile Phe Ser
            420                 425


<210>  11
<211>  233
<212>  PRT
<213>  human

<400>  11

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1               5                   10                  15


Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30


Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45


Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60


Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80


Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95


Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100                 105                 110


Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125


Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140


Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160
```

```
Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175


Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190


Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205


Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
    210                 215                 220


Thr Met Arg Arg Arg Thr Leu Tyr Tyr
225                 230


<210>  12
<211>  502
<212>  PRT
<213>  rat

<400>  12

Met Gly Gly Gly Arg Gly Gly Ile Trp Leu Ala Leu Ala Ala Ala Leu
1               5                   10                  15


Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Arg Leu Tyr Lys Glu
            20                  25                  30


Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45


Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60


Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80


Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Met Ser Glu Tyr Pro Gly
                85                  90                  95
```

```
Val Lys Asn Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100                 105                 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125

Asn Val Leu Val Asn Ala Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160

Val Gln Gln Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Ser Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Met Gly Ile Pro Gly Lys Arg Asn Glu Lys
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Tyr Thr Val
    210                 215                 220

Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu Ile Pro
225                 230                 235                 240

Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu Pro Ala
                245                 250                 255

Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu Ser Leu
            260                 265                 270

Thr Val Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr Ser Asp
        275                 280                 285
```

```
Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile Ile Val
    290                 295                 300

Gly Leu Ser Val Val Val Thr Val Ile Val Leu Arg Tyr His His His
305                 310                 315                 320

Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Ile Ile Leu Leu
                325                 330                 335

Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu Asp Lys
            340                 345                 350

Val Arg Pro Ala Cys Gln His Lys Pro Arg Arg Cys Ser Leu Ala Ser
        355                 360                 365

Val Glu Leu Ser Ala Gly Ala Gly Pro Pro Thr Ser Asn Gly Asn Leu
    370                 375                 380

Leu Tyr Ile Gly Phe Arg Gly Leu Glu Gly Met His Cys Ala Pro Thr
385                 390                 395                 400

Pro Asp Ser Gly Val Val Cys Gly Arg Leu Ala Cys Ser Pro Thr His
                405                 410                 415

Asp Glu His Leu Met His Gly Ala His Pro Ser Asp Gly Asp Pro Asp
            420                 425                 430

Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg Asn Arg
        435                 440                 445

Cys Gln Asp Glu Ser Glu Val Ile Cys Ser Glu Trp Lys Phe Ala Ala
    450                 455                 460

Cys Val Val Asp Pro Leu Cys Leu Met Ala Phe Ser Val Phe Thr Ile
465                 470                 475                 480

Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val Glu Ala
                485                 490                 495
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Val Ser Lys Asp Phe Ala
            500

<210> 13
<211> 438
<212> PRT
<213> artificial

<220>
<223> PSAM4-GlyR-KirM3M4 sequence

<400> 13

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1   5   10   15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20   25   30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35   40   45

Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50   55   60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65   70   75   80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85   90   95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100   105   110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115   120   125

Asn Val Gly Val Asn Ser Ser Gly His Cys Leu Tyr Leu Pro Pro Gly
    130   135   140

```
Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160

Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Phe Pro Asp Val Thr Phe Thr Val
    210                 215                 220

Thr Met Arg Arg Arg Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro
225                 230                 235                 240

Ser Leu Leu Ile Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met
                245                 250                 255

Asp Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr
            260                 265                 270

Met Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser
        275                 280                 285

Tyr Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val
    290                 295                 300

Phe Ser Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln
305                 310                 315                 320

His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Glu
                325                 330                 335
```

```
Asp Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly
            340                 345                 350

Pro Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn
        355                 360                 365

Asn Ser Asn Phe Cys Tyr Glu Asn Glu Val Thr Thr Asn Pro Pro Pro
    370                 375                 380

Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys Leu Phe Ile Gln Arg
385                 390                 395                 400

Ala Lys Lys Ile Asp Lys Ile Ser Arg Ile Gly Phe Pro Met Ala Phe
                405                 410                 415

Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr Lys Ile Val Arg Arg
            420                 425                 430

Glu Asp Val His Asn Gln
        435
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<210> 14
<211> 437
<212> PRT
<213> artificial

<220>
<223> PSAM4-GlyR-B4sig sequence

<400> 14

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Met Arg Arg Ala Pro Ser Leu Val Leu Phe Phe Leu Val Ala Leu Cys
1               5                   10                  15

Gly Arg Gly Asn Cys Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu Leu
            20                  25                  30

Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser Gln
        35                  40                  45
```

```
Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp Val
    50                  55                  60

Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met Ser
65                  70                  75                  80

Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly Val
                85                  90                  95

Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile Leu
            100                 105                 110

Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr Asn
        115                 120                 125

Val Gly Val Asn Ser Ser Gly His Cys Leu Tyr Leu Pro Pro Gly Ile
    130                 135                 140

Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp Val
145                 150                 155                 160

Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp Ser
                165                 170                 175

Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro Asn
            180                 185                 190

Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg Phe
        195                 200                 205

Tyr Glu Cys Cys Lys Glu Pro Phe Pro Asp Val Thr Phe Thr Val Thr
    210                 215                 220

Met Arg Arg Arg Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser
225                 230                 235                 240

Leu Leu Ile Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met Asp
                245                 250                 255
```

```
Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met
            260                 265                 270

Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr
        275                 280                 285

Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe
    290                 295                 300

Ser Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln His
305                 310                 315                 320

Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Glu Asp
                325                 330                 335

Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro
            340                 345                 350

Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn
        355                 360                 365

Ser Asn Phe Cys Tyr Glu Asn Glu Val Thr Thr Asn Pro Pro Pro Ala
    370                 375                 380

Pro Ser Lys Ser Pro Glu Glu Met Arg Lys Leu Phe Ile Gln Arg Ala
385                 390                 395                 400

Lys Lys Ile Asp Lys Ile Ser Arg Ile Gly Phe Pro Met Ala Phe Leu
                405                 410                 415

Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr Lys Ile Val Arg Arg Glu
            420                 425                 430

Asp Val His Asn Gln
        435
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<210> 15
<211> 496
<212> PRT
<213> artificial

<220>
<223> PSAM4-GlyR-Kv2M3M4-soma sequence

<400> 15

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
1 5 10 15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
20 25 30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
35 40 45

Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
50 55 60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65 70 75 80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
85 90 95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
100 105 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
115 120 125

Asn Val Gly Val Asn Ser Ser Gly His Cys Leu Tyr Leu Pro Pro Gly
130 135 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145 150 155 160

```
Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
                165                 170                 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
            180                 185                 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
        195                 200                 205

Phe Tyr Glu Cys Cys Lys Glu Pro Phe Pro Asp Val Thr Phe Thr Val
    210                 215                 220

Thr Met Arg Arg Arg Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro
225                 230                 235                 240

Ser Leu Leu Ile Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met
                245                 250                 255

Asp Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr
            260                 265                 270

Met Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser
        275                 280                 285

Tyr Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val
    290                 295                 300

Phe Ser Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln
305                 310                 315                 320

His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Glu
                325                 330                 335

Asp Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly
            340                 345                 350

Pro Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn
        355                 360                 365
```

```
Asn Ser Asn Gln Ser Gln Pro Ile Leu Asn Thr Lys Glu Met Ala Pro
    370                 375                 380

Gln Ser Lys Pro Pro Glu Glu Leu Glu Met Ser Ser Met Pro Ser Pro
385                 390                 395                 400

Val Ala Pro Leu Pro Ala Arg Thr Glu Gly Val Ile Asp Met Arg Ser
                405                 410                 415

Met Ser Ser Ile Asp Ser Phe Ile Ser Cys Ala Thr Asp Phe Pro Glu
            420                 425                 430

Ala Thr Arg Phe Thr Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro
        435                 440                 445

Glu Glu Met Arg Lys Leu Phe Ile Gln Arg Ala Lys Lys Ile Asp Lys
    450                 455                 460

Ile Ser Arg Ile Gly Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe
465                 470                 475                 480

Tyr Trp Ile Ile Tyr Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
                485                 490                 495
```

<210> 16
<211> 7
<212> PRT
<213> artificial

<220>
<223> endoplasmic reticulum export sequence

<400> 16

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Phe Cys Tyr Glu Asn Glu Val
1               5
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<210> 17
<211> 21

<212> PRT
<213> artificial

<220>
<223> CHRNB4 signal sequence

<400> 17

Met Arg Arg Ala Pro Ser Leu Val Leu Phe Phe Leu Val Ala Leu Cys
1 5 10 15

Gly Arg Gly Asn Cys
20

<210> 18
<211> 65
<212> PRT
<213> artificial

<220>
<223> KCNB1 somatic targeting sequence

<400> 18

Gln Ser Gln Pro Ile Leu Asn Thr Lys Glu Met Ala Pro Gln Ser Lys
1 5 10 15

Pro Pro Glu Glu Leu Glu Met Ser Ser Met Pro Ser Pro Val Ala Pro
20 25 30

Leu Pro Ala Arg Thr Glu Gly Val Ile Asp Met Arg Ser Met Ser Ser
35 40 45

Ile Asp Ser Phe Ile Ser Cys Ala Thr Asp Phe Pro Glu Ala Thr Arg
50 55 60

Phe
65

<210> 19
<211> 1509
<212> DNA
<213> rat

<400> 19
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ctgcaaggcg agttccagag gaggctgtac aaggagctgg tcaagaacta caacccgctg 120

gagaggccgg tggccaacga ctcgcagccg ctcaccgtgt acttctccct gagtctcctg 180

cagatcatgg atgtggatga gaagaaccaa gttttaacca ccaacatttg gctacaaatg 240

tcttggacag atcactattt gcagtggaac atgtctgagt accccggagt gaagaatgtt 300

cgttttccag atggccagat ttggaaacca gacattctcc tctataacag tgctgatgag 360

cgctttgatg ccacgttcca caccaatgtt ttggtgaatg catctgggca ttgccagtat 420

ctccctccag gcatattcaa gagctcctgc tacattgacg ttcgctggtt ccctttttgat 480

gtgcagcagt gcaaactgaa gtttgggtcc tggtcctatg gagggtggtc actggacctg 540

caaatgcaag aggcagatat cagcagctat atccccaacg gagaatggga tctcatggga 600

atccctggca aaaggaatga gaagttctat gagtgctgca aagagccata cccagatgtc 660

acctacacag taaccatgcg ccgtaggaca ctctactatg gcctcaatct gctcatccct 720

tgtgtactca tttcagccct ggctctgctg gtattcttgc tgcctgcaga ctctggagag 780

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atgatcatcg tgggcctctc tgtagtggtg acagtgattg tgctgagata tcaccaccat 960

gaccctgatg gtggcaaaat gcctaagtgg accagaatca ttctcctgaa ctggtgtgca 1020

tggtttctgc gcatgaagag gcccggagag gacaaggtgc ggccagcttg tcagcacaag 1080

cctcggcgct gcagcctggc cagtgtggag ctgagtgcag gtgctgggcc acccaccagc 1140

aatggcaacc tgctctacat tggcttccga ggcctggagg gcatgcactg tgccccaact 1200

ccagactctg gggtcgtatg tggccgtttg gcctgctccc caacacatga tgagcacctc 1260

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cgctacatcg ccaaccgcaa ccgctgccag gacgagagtg aggtgatctg cagtgaatgg 1380

aagtttgcag cctgcgtggt ggacccgctt tgcctcatgg ccttttcggt ctttaccatc 1440

atctgtacca tcggcatcct catgtcagct ccaaactttg tggaggctgt gtccaaagac 1500

tttgcttaa 1509

<210> 20
<211> 672
<212> DNA
<213> human

<400> 20
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ctgcagggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taacccccctg 120

gagcggccgg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg 180

cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatttg gttgcagatg 240

tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta 300

agattccctg acggccaaat ctggaaacca gatatcctgc tgtacaacag cgcagacgaa 360

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atccccggta aaagaagcga gcgattttat gaatgctgca aggaacccta ccctgacgta 660

acattcacag tt 672

<210> 21
<211> 687
<212> DNA
<213> human

<400> 21
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ctgcagggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taacccccctg 120

gagcggccgg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg 180

cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatttg gttgcagatg 240

tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta 300

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caaatgcagg aggctgacat ctctggttac atcccgaatg gggagtggga ccttgtggga 600

atccccggta aaagaagcga gcgattttat gaatgctgca aagagcccta cccagatgtc 660

accttcacag tgaccatgcg gagacgc 687

<210> 22
<211> 699
<212> DNA
<213> human

<400> 22
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ctgcagggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taacccccctg 120

gagcggccgg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg 180

cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatttg gttgcagatg 240

tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta 300

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caaatgcagg aggctgacat ctctggttac atcccgaatg gggagtggga ccttgtggga 600

atccccggta aaagaagcga gcgattttat gaatgctgca aagagcccta cccagatgtc 660

accttcacag tgaccatgcg gagacgcaca ctgtattac 699

<210> 23
<211> 744

<212> DNA
<213> mouse

<400> 23
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aagattacct tgttgctcgg ctattctgta tttctgatca tcgtgtccga taccttcct 180

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cccgtgccag actggttgcg acaccttgtg ctggacagaa ttgcatggat tctgtgtctt 360

ggcgagcaac ctatggccca ccggccacct gcaacctttc aagccaacaa gacagacgat 420

tgtagtgggt ctgatctgtt gcctgctatg gggaatcact gctcccatgt tgggggacca 480

caagatttgg aaaagacccc acgggggcgg ggatcacccc ttcctcctcc ccgagaagcc 540

tctctcgctg tccgggggct gctccaggaa ctgtcaagca tccgacattt tctggagaag 600

cgggacgaga tgagggaagt cgctagagac tggctgcgag tgggctacgt ccttgacagg 660

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tggtccatat ggcactacag ttag 744

<210> 24
<211> 726
<212> DNA
<213> human

<400> 24
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gcaacagcaa tcggaacccc actgatcggc gtgtatttcg tggtgtgcat ggccctgctg 240

gtcatcagcc tggccgagac aatctttatc gtgcggctgg tgcacaagca ggacctgcag 300

cagcctgtgc cagcatggct gaggcacctg gtgctggaga ggatcgcatg gctgctgtgc 360

ctgagagagc agtccacatc tcagaggcct ccagccacct ctcaggccac caagacagac 420

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tacgcc 726

<210> 25
<211> 609
<212> DNA
<213> mouse

<400> 25
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gtgctgacaa tgactactca gagctcaggc agccgagcca gcttgcccaa ggtttcttac 180

gtgaaggcca tcgatatctg gatggctgtc tgccttctgt ttgtcttcag cgcactgctg 240

gaatacgccg ctgtcaattt tgtgtctcga cagcataaag agctgttgcg gttcagaaga 300

aaacgacgcc accacaaaga ggatgaggca ggagaaggac gcttcaactt tagcgcctat 360

ggtatgggac ctgcttgcct ccaggctaaa gacggaattt ccgtgaaggg agccaacaat 420

agcaacacaa ccaacccacc ccctgctcca tctaagagcc cggaggaaat gcgcaaactc 480

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ctgattttca acatgtttta ttggatcatc tacaagattg tgcgaaggga ggacgtacac 600

aaccagtaa 609

<210> 26
<211> 588
<212> DNA
<213> human

<400> 26
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gtgaactatc tgacaacagt tcaagagcgg aaagagcaga agttgaggga gaagctgcca 300

tgcactagcg gactgccacc gcccagaacc gctatgctcg atggtaacta ttccgacggc 360

gaagttaatg acctcgataa ctacatgcct gaaaatggcg aaaagcccga caggatgatg 420

gtccagctga cactggcctc agaaaggtcc agtccacaga gaaagtcaca gcgatcctct 480

tacgtcagca tgcgcatcga tacacatgcc atcgacaaat actctcgcat tatctttccg 540

gctgcttaca tattgttcaa ccttatctat tggagcattt tcagttga 588

<210> 27
<211> 1416
<212> DNA
<213> artificial

<220>
<223> alpha7-5HT3 chimeric receptor sequence

<400> 27
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ctgcagggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taacccccctg 120

gagcggccgg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg 180

cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatttg gttgcagatg 240

tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta 300

agattccctg acggccaaat ctggaaacca gatatcctgc tgtacaacag cgcagacgaa 360

aggtttgatg caacatttca caccaacgtg ttggtcaatt cttcaggcca ctgccagtac 420

ctgccccctg gaatcttcaa gtcctcatgc tatatcgacg tccgctggtt tcccttcgac 480

gtccagcact gcaaactcaa attcgggagc tggagctacg gcggatggag cctggatctg 540

caaatgcagg aggctgacat ctctggttac atcccgaatg gggagtggga ccttgtggga 600

atccccggta aaagaagcga gcgattttat gaatgctgca aggaacccta ccctgacgta 660

acattcacag ttatcatcag aagaaggcca ttgttctacg ccgttagttt gttgctcccc 720

agtatttttc tcatggtcgt ggacatcgtg ggattttgtc tcccacctga tagcggggag 780

agggtctcct ttaagattac cttgttgctc ggctattctg tatttctgat catcgtgtcc 840

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gcactcctgg tgataagtct ggcggaaact atcttcattg tacggctggt acataagcag 960

gacctgcaaa gacccgtgcc agactggttg cgacaccttg tgctggacag aattgcatgg 1020

attctgtgtc ttggcgagca acctatggcc caccggccac ctgcaacctt tcaagccaac 1080

aagacagacg attgtagtgg gtctgatctg ttgcctgcta tggggaatca ctgctcccat 1140

gttgggggac cacaagattt ggaaaagacc ccacgggggc ggggatcacc ccttcctcct 1200

ccccgagaag cctctctcgc tgtccggggg ctgctccagg aactgtcaag catccgacat 1260

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