

SEQUENCE LISTING

<110> Howard Hughes Medical Institute

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

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<160> 34

<170> PatentIn version 3.5

<210> 1

<211> 224

<212> PRT

<213> human

<400> 1

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

<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 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

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

<210> 14
<211> 437
<212> PRT
<213> artificial

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

<400> 14

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

<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

Phe Cys Tyr Glu Asn Glu Val
1 5

<210> 17

<211> 21

<212> PRT

<213> artificial

<220>

<223> CHRN4 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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gagaggccgg tggccaacga ctcgcagccg ctcaccgtgt acttctccct gagtctcctg 180
cagatcatgg atgtggatga gaagaaccaa gttttaacca ccaacatttg gctacaaatg 240
tcttggacag atcactatatt gcagtggaac atgtctgagt accccggagt gaagaatggt 300
cgttttccag atggccagat ttggaaacca gacattctcc tctataacag tgctgatgag 360
cgctttgatg ccacgttcca caccaatgtt ttggtgaatg catctgggca ttgccagtat 420

ctccctccag gcatattcaa gagctcctgc tacattgacg ttcgctggtt cccttttgat	480
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caaatgcaag aggagatat cagcagctat atccccaacg gagaatggga tctcatggga	600
atccctggca aaaggaatga gaagttctat gaggctgca aagagccata cccagatgtc	660
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tgtgtactca tttcagccct ggctctgctg gtattcttgc tgcctgcaga ctctggagag	780
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gagatcatgc cagcaacatc tgattctgtg cccttgatag cacaatactt cgccagcacc	900
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gaccctgatg gtggcaaaat gcctaagtgg accagaatca ttctcctgaa ctggtgtgca	1020
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cgctacatcg ccaaccgcaa ccgctgccag gacgagagtg aggtgatctg cagtgaatgg	1380
aagtttgag cctgcgtggt ggacccgctt tgcctcatgg ctttttcggt ctttaccatc	1440
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tttgcttaa	1509

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

<400> 20	
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ctgcaggggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taaccccctg	120
gagcggccgg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg	180
cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatattg gttgcagatg	240
tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta	300

agattccctg acggccaaat ctggaaacca gatatacctgc tgtacaacag cgcagacgaa	360
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ctgccccctg gaatcttcaa gtcctcatgc tatatcgacg tccgctgggt tcccttcgac	480
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caaatgcagg aggctgacat ctctgggttac atcccgaatg gggagtggga ccttgtggga	600
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 ctaatatattg gttgcagatg	240
tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta	300
agattccctg acggccaaat ctggaaacca gatatacctgc tgtacaacag cgcagacgaa	360
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gtccagcact gcaaactcaa attcgggagc tggagctacg gcggatggag cctggatctg	540
caaatgcagg aggctgacat ctctgggttac 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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ctgcaggggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taaccccctg	120
gagcggcccg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg	180
cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatattg gttgcagatg	240
tcctggaccg atcactactt gcagtggaaat gtgagcgaat acccaggtgt aaagactgta	300
agattccctg acggccaaat ctggaaacca gatatcctgc tgtacaacag cgcagacgaa	360
aggtttgatg caacatttca caccaacgtg ttgggtcaatt cttcaggcca ctgccagtac	420
ctgccccctg gaatcttcaa gtcctcatgc tatatcgacg tccgctgggtt tcccttcgac	480
gtccagcact gcaaaactcaa attcgggagc tggagctacg gcggatggag cctggatctg	540
caaatgcagg aggctgacat ctctgggttac atcccgaatg gggagtggga ctttgtggga	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 tacccttcct	180
gccacaatcg gcactccgct gataggagtg tatttcgtcg tgtgtatggc actcctgggtg	240
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cccgtgccag actggttgcg acaccttggt ctggacagaa ttgcatggat tctgtgtctt	360
ggcgagcaac ctatggccca ccggccacct gcaacctttc aagccaacaa gacagacgat	420
tgtagtgggt ctgatctggt gcctgctatg gggaatcact gctcccatgt tgggggacca	480
caagatttgg aaaagacccc acggggggcgg ggatcacccc ttctctctcc ccgagaagcc	540
tctctcgctg tccgggggct gctccaggaa ctgtcaagca tccgacattt tctggagaag	600
cgggacgaga tgagggaagt cgctagagac tggctgcgag tgggctacgt ccttgacagg	660
ctgctgtttc ggatctactt gctggcggtg ctggcttatt ccattactct ggtgacactc	720

tggtccatat ggcactacag ttag 744

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

<400> 24
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atgggtcatgg acatcgtggg cttttacctg ccaccaatt ctggcgagcg cgtgagcttc 120
aagatcacac tgctgctggg ctatagcgtg tttctgatca tcgtgtccga taccctgcct 180
gcaacagcaa tcggaacccc actgatcggc gtgtatttcg tgggtgtgcat ggccctgctg 240
gtcatcagcc tggccgagac aatctttatc gtgcggctgg tgcacaagca ggacctgcag 300
cagcctgtgc cagcatggct gaggcacctg gtgctggaga ggatcgcatt gctgctgtgc 360
ctgagagagc agtccacatc tcagaggcct ccagccacct ctcaggccac caagacagac 420
gattgctctg ccatgggcaa tcactgtagc cacatgggcg gccccagga ctttgagaag 480
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gaggtggcca gagattggct gaggggtggc agcgtgctgg ataagctgct gtttcacatc 660
tacctgctgg cagtcctggc ctattctatt accctgggtc tgctgtggtc catctggcag 720
tacgcc 726

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

<400> 25
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atctccttct ggattaatat ggacgccgct ccagctaggg tcggactggg catcaccaca 120
gtgctgacaa tgactactca gagctcaggc agccgagcca gcttgcccaa ggtttcttac 180
gtgaaggcca tcgatatctg gatggctgtc tgccttctgt ttgtcttcag cgactgctg 240
gaatacgccg ctgtcaattt tgtgtctcga cagcataaag agctgttgcg gttcagaaga 300
aaacgacgcc accacaaaga ggatgaggca ggagaaggac gcttcaactt tagcgcctat 360

ggtatgggac ctgcttgcc	ccaggctaaa gacggaattt	ccgtgaaggg agccaacaat	420
agcaacacaa ccaaccacc	ccctgctcca tctaagagcc	cggaggaaat gcgcaaactc	480
tttattcaga gagcgaaaaa	gatcgacaaa atctcccgga	tcggattccc catggctttc	540
ctgattttca acatgtttta	ttggatcatc tacaagattg	tgcgaaggga ggacgtacac	600
aaccagtaa			609

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

<400> 26			
cttttgcaaa cttactttcc	agcaaccctc atggtgatgc	tttcatgggt gtccttttgg	60
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agcaccataa tctactggagt	caatgcaagc atgcctagag	tgtcttacat aaaggccgtg	180
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tgcactagcg gactgccacc	gcccagaacc gctatgctcg	atggtaacta ttccgacggc	360
gaagttaatg acctcgataa	ctacatgcct gaaaatggcg	aaaagcccga caggatgatg	420
gtccagctga cactggcctc	agaaagggtc agtccacaga	gaaagtcaca gcgacacctc	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 taaccccctg	120
gagcggccgg tcgcaaatga	ttcccagcca ctgacagtgt	acttcagcct ctccttgctg	180
cagatcatgg acgtggatga	aaagaaccag gtgctgacca	ctaataatttg gttgcagatg	240

tcctggaccg atcactactt gcagtggaat gtgagcgaat acccaggtgt aaagactgta	300
agattccctg acggccaaat ctggaaacca gatatacctgc tgtacaacag cgcagacgaa	360
aggtttgatg caacatttca caccaacgtg ttgggtcaatt cttcaggcca ctgccagtac	420
ctgccccctg gaatcttcaa gtcctcatgc tatatcgacg tccgctgggt tcccttcgac	480
gtccagcact gcaaactcaa attcgggagc tggagctacg gcggatggag cctggatctg	540
caaatgcagg aggctgacat ctctgggttac atcccgaatg gggagtggga ccttgtggga	600
atccccggta aaagaagcga gcgattttat gaatgctgca aggaacccta ccctgacgta	660
acattcacag ttatcatcag aagaaggcca ttgttctacg ccgttagttt gttgctcccc	720
agtatttttc tcatggctgt ggacatcgtg ggattttgtc tcccacctga tagcggggag	780
agggtctcct ttaagattac cttgttgctc ggctattctg tatttctgat catcgtgtcc	840
gatacccttc ctgccacaat cggcactccg ctgataggag tgtatttcgt cgtgtgtatg	900
gcactcctgg tgataagtct ggcggaaact atcttcattg tacggctggt acataagcag	960
gacctgcaaa gaccctgtcc agactggttg cgacacctg tgctggacag aattgcatgg	1020
attctgtgtc ttggcgagca acctatggcc caccggccac ctgcaacctt tcaagccaac	1080
aagacagacg attgtagtgg gtctgatctg ttgcctgcta tggggaatca ctgctcccat	1140
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ccccgagaag cctctctcgc tgtccggggg ctgctccagg aactgtcaag catccgacat	1260
tttctggaga agcgggacga gatgaggga gtcgctagag actggctgcg agtgggctac	1320
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ctggtgacac tctggtccat atggcactac agttag	1416

<210> 28
 <211> 1296
 <212> DNA
 <213> artificial

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

<400> 28	
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ctgcagggtg agttccagcg caaactgtat aaggagcttg ttaagaatta taaccccctg	120

gagcggccgg tcgcaaatga ttcccagcca ctgacagtgt acttcagcct ctccttgctg	180
cagatcatgg acgtggatga aaagaaccag gtgctgacca ctaatatattg gttgcagatg	240
tcctggaccg atcactactt gcagtgggaat gtgagcgaat acccaggtgt aaagactgta	300
agattccctg acggccaaat ctggaaacca gatatcctgc tgtacaacag cgcagacgaa	360
aggtttgatg caacatttca caccaacgtg ttgggtcaatt cttcaggcca ctgccagtac	420
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gtccagcact gcaaactcaa attcgggagc tggagctacg gcggatggag cctggatctg	540
caaatgcagg aggctgacat ctctggttac atcccgaatg gggagtggga ctttgtggga	600
atccccggta aaagaagcga gcgattttat gaatgctgca aagagcccta cccagatgtc	660
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cgagccagct tgcccaaggt ttcttacgtg aaggccatcg atatctggat ggctgtctgc	900
cttctgtttg tcttcagcgc actgctggaa tacgccgctg tcaattttgt gtctcgacag	960
cataaagagc tgttgcggtt cagaagaaaa cgacgccacc acaaagagga tgaggcagga	1020
gaaggacgct tcaactttag cgcctatggg atgggacctg cttgcctcca ggctaaagac	1080
ggaatttccg tgaagggagc caacaatagc aacacaacca acccaccctt tgctccatct	1140
aagagcccgg aggaaatgcg caaactcttt attcagagag cgaaaaagat cgacaaaatc	1200
tcccgatcg gattccccat ggctttcctg attttcaaca tgttttattg gatcatctac	1260
aagattgtgc gaaggaggga cgtacacaac cagtaa	1296

<210> 29
 <211> 1287
 <212> DNA
 <213> artificial

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

<400> 29	
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