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SEQUENCE LISTING

<110> Coda Biotherapeutics, Inc.
Greenberg, Kenneth P.
Keifer, Orion Jr.
Makinson, Stefanie
Lau, Anthony

<120> COMPOSITIONS AND METHODS FOR NEUROLOGICAL DISEASES

<130> SWCH-012/04WO 322917-2117

<150> 62/590,911

<151> 2017-11-27

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<151> 2018-04-19

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<170> PatentIn version 3.5

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

Ile Ser Leu Trp Arg Leu Pro Glu Lys Val Lys Ser Asp Arg Ser Val
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Arg Glu Phe Ser Met Glu Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe
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245 250 255

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Pro Pro Asn Ser Gly Glu Arg Val Ser Phe Lys Ile Thr Leu Leu Leu
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Gly Tyr Ser Val Phe Leu Ile Ile Val Ser Asp Thr Leu Pro Ala Thr
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Ala Ile Gly Thr Pro Leu Ile Gly Lys Ala Pro Pro Gly Ser Arg Ala
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Leu Leu Val Ile Ser Leu Ala Glu Thr Ile Phe Ile Val Arg Leu Val
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His Lys Gln Asp Leu Gln Gln Pro Val Pro Ala Trp Leu Arg His Leu
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Val Leu Glu Arg Ile Ala Trp Leu Leu Cys Leu Arg Glu Gln Ser Thr
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Ser Gln Arg Pro Pro Ala Thr Ser Gln Ala Thr Lys Thr Asp Asp Cys
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Ser Ala Met Gly Asn His Cys Ser His Met Gly Gly Pro Gln Asp Phe
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Glu Lys Ser Pro Arg Asp Arg Cys Ser Pro Pro Pro Pro Pro Arg Glu
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360990_1.txt

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 35 40 45

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Leu Ala Tyr Ser Gly Ile Pro Leu Asn Leu Thr Leu Asp Asn Arg Val
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Ala Asp Gln Leu Trp Val Pro Asp Thr Tyr Phe Leu Asn Asp Lys Lys
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Ser Phe Val His Gly Val Thr Val Lys Asn Arg Met Ile Arg Leu His
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Cys Met Met Asp Leu Arg Arg Tyr Pro Leu Asp Glu Gln Asn Cys Thr
165 170 175

Leu Glu Ile Glu Ser Tyr Gly Tyr Thr Thr Asp Asp Ile Glu Phe Tyr
180 185 190

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

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210 215 220

Phe Ala Thr Gly Ala Tyr Pro Arg Leu Ser Leu Ser Phe Arg Leu Lys
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360990_1.txt

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275 280 285

Ile Asn Thr His Leu Arg Glu Thr Leu Pro Lys Ile Pro Tyr Val Lys
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Ala Ile Asp Met Tyr Leu Met Gly Cys Phe Val Phe Val Phe Leu Ala
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325 330 335

Gln Arg Gln Lys Lys Leu Ala Glu Lys Thr Ala Lys Ala Lys Asn Asp
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355 360 365

Leu Thr Ser Leu Glu Val His Asn Glu Met Asn Glu Val Ser Gly Gly
370 375 380

Ile Gly Asp Thr Arg Asn Ser Ala Ile Ser Phe Asp Asn Ser Gly Ile
385 390 395 400

Gln Tyr Arg Lys Gln Ser Met Pro Arg Glu Gly His Gly Arg Phe Leu
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Gly Asp Arg Ser Leu Pro His Lys Lys Thr His Leu Arg Arg Arg Ser
420 425 430

360990_1.txt

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35 40 45

360990_1.txt

Val His Glu Asp Ala His Lys Gln Val Ser Pro Ile Leu Arg Arg Ser
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Pro Asp Ile Thr Lys Ser Pro Leu Thr Lys Ser Glu Gln Leu Leu Arg
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Ile Asp Asp His Asp Phe Ser Met Arg Pro Gly Phe Gly Gly Pro Ala
85 90 95

Ile Pro Val Gly Val Asp Val Gln Val Glu Ser Leu Asp Ser Ile Ser
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Glu Val Asp Met Asp Phe Thr Met Thr Leu Tyr Leu Arg His Tyr Trp
115 120 125

Lys Asp Glu Arg Leu Ser Phe Pro Ser Thr Asn Asn Leu Ser Met Thr
130 135 140

Phe Asp Gly Arg Leu Val Lys Lys Ile Trp Val Pro Asp Met Phe Phe
145 150 155 160

Val His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Thr Asp Asn Val
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Met Leu Arg Val Gln Pro Asp Gly Lys Val Leu Tyr Ser Leu Arg Val
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Thr Val Thr Ala Met Cys Asn Met Asp Phe Ser Arg Phe Pro Leu Asp
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Thr Gln Thr Cys Ser Leu Glu Ile Glu Ser Tyr Ala Tyr Thr Glu Asp
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Asp Leu Met Leu Tyr Trp Lys Lys Gly Asn Asp Ser Leu Lys Thr Asp
225 230 235 240

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Thr Lys Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Asn Arg Leu Tyr
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Tyr Phe Pro Ala Thr Leu Met Val Met Leu Ser Trp Val Ser Phe Trp
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Ile Asp Arg Arg Ala Val Pro Ala Arg Val Pro Leu Gly Ile Thr Thr
305 310 315 320

Val Leu Thr Met Ser Thr Ile Ile Thr Gly Val Asn Ala Ser Met Pro
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Arg Val Ser Tyr Ile Lys Ala Val Asp Ile Tyr Leu Trp Val Ser Phe
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Val Phe Val Phe Leu Ser Val Leu Glu Tyr Ala Ala Val Asn Tyr Leu
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Thr Thr Val Gln Glu Arg Lys Glu Gln Lys Leu Arg Glu Lys Leu Pro
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Cys Thr Ser Gly Leu Pro Pro Pro Arg Thr Ala Met Leu Asp Gly Asn
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Tyr Ser Asp Gly Glu Val Asn Asp Leu Asp Asn Tyr Met Pro Glu Asn
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Gly Glu Lys Pro Asp Arg Met Met Val Gln Leu Thr Leu Ala Ser Glu
420 425 430

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Arg Ser Ser Pro Gln Arg Lys Ser Gln Arg Ser Ser Tyr Val Ser Met
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360990_1.txt

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tggagtgcaa tggcttgatc ttggctcacc acaacctctg cctcccgggt tcaagcaatt	3720
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360990_1.txt

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<210> 12
 <211> 465
 <212> PRT
 <213> Homo sapiens

<400> 12

Met Pro Tyr Phe Thr Arg Leu Ile Leu Phe Leu Phe Cys Leu Met Val
 1 5 10 15

Leu Val Glu Ser Arg Lys Pro Lys Arg Lys Arg Trp Thr Gly Gln Val
 20 25 30

Glu Met Pro Lys Pro Ser His Leu Tyr Lys Lys Asn Leu Asp Val Thr
 35 40 45

360990_1.txt

Lys Ile Arg Lys Gly Lys Pro Gln Gln Leu Leu Arg Val Asp Glu His
50 55 60

Asp Phe Ser Met Arg Pro Ala Phe Gly Gly Pro Ala Ile Pro Val Gly
65 70 75 80

Val Asp Val Gln Val Glu Ser Leu Asp Ser Ile Ser Glu Val Asp Met
85 90 95

Asp Phe Thr Met Thr Leu Tyr Leu Arg His Tyr Trp Lys Asp Glu Arg
100 105 110

Leu Ala Phe Ser Ser Ala Ser Asn Lys Ser Met Thr Phe Asp Gly Arg
115 120 125

Leu Val Lys Lys Ile Trp Val Pro Asp Val Phe Phe Val His Ser Lys
130 135 140

Arg Ser Phe Thr His Asp Thr Thr Thr Asp Asn Ile Met Leu Arg Val
145 150 155 160

Phe Pro Asp Gly His Val Leu Tyr Ser Met Arg Ile Thr Val Thr Ala
165 170 175

Met Cys Asn Met Asp Phe Ser His Phe Pro Leu Asp Ser Gln Thr Cys
180 185 190

Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Thr Asp Glu Asp Leu Met Leu
195 200 205

Tyr Trp Lys Asn Gly Asp Glu Ser Leu Lys Thr Asp Glu Lys Ile Ser
210 215 220

Leu Ser Gln Phe Leu Ile Gln Lys Phe His Thr Thr Ser Arg Leu Ala
225 230 235 240

360990_1.txt

Phe Tyr Ser Ser Thr Gly Trp Tyr Asn Arg Leu Tyr Ile Asn Phe Thr
245 250 255

Leu Arg Arg His Ile Phe Phe Phe Leu Leu Gln Thr Tyr Phe Pro Ala
260 265 270

Thr Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile Asp Arg Arg
275 280 285

Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val Leu Thr Met
290 295 300

Thr Thr Ile Ile Thr Gly Val Asn Ala Ser Met Pro Arg Val Ser Tyr
305 310 315 320

Val Lys Ala Val Asp Ile Tyr Leu Trp Val Ser Phe Val Phe Val Phe
325 330 335

Leu Ser Val Leu Glu Tyr Ala Ala Val Asn Tyr Leu Thr Thr Val Gln
340 345 350

Glu Arg Lys Glu Arg Lys Leu Arg Glu Lys Phe Pro Cys Met Cys Gly
355 360 365

Met Leu His Ser Lys Thr Met Met Leu Asp Gly Ser Tyr Ser Glu Ser
370 375 380

Glu Ala Asn Ser Leu Ala Gly Tyr Pro Arg Ser His Ile Leu Thr Glu
385 390 395 400

Glu Glu Arg Gln Asp Lys Ile Val Val His Leu Gly Leu Ser Gly Glu
405 410 415

Ala Asn Ala Ala Arg Lys Lys Gly Leu Leu Lys Gly Gln Thr Gly Phe
420 425 430

360990_1.txt

Arg Ile Phe Gln Asn Thr His Ala Ile Asp Lys Tyr Ser Arg Leu Ile
435 440 445

Phe Pro Ala Ser Tyr Ile Phe Phe Asn Leu Ile Tyr Trp Ser Val Phe
450 455 460

Ser
465

<210> 13
<211> 1404
<212> DNA
<213> Homo sapiens

<400> 13
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gtttgtgctg cttctaacaat caagatgaca caccagcggg gctcctcttc aatgaaacaa
120
acctgcaaac aagaaactag aatgaagaaa gatgacagta ccaaagcgcg gcctcagaaa
180
tatgagcaac ttctccatat agaggacaac gatttcgcaa tgagacctgg atttggaggg
240
tctccagtgc cagtaggtat agatgtccat gttgaaagca ttgacagcat ttcagagact
300
aacatggact ttacaatgac tttttatctc aggcattact ggaaagacga gaggtctctc
360
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420
gtgcctgata tcttttttgt cactctaaa agatccttca tccatgatac aactatggag
480
aatatcatgc tgcgcgtaca ccctgatgga aacgtcctcc taagtctcag gataacgggt
540
tcggccatgt gctttatgga tttcagcagg tttcctcttg aactcaaaa ttgttctctt
600
gaactggaaa gctatgccta caatgaggat gacctaatgc tatactggaa acacggaaac
660
aagtccttaa atactgaaga acatatgtcc ctttctcagt tcttcattga agacttcagt
720
gcatctagtg gattagcttt ctatagcagc acaggttggg acaataggct tttcatcaac
780
tttgtgctaa ggaggcatgt tttcttcttt gtgtgcaaa cctatttccc agccatattg
840
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900

360990_1.txt

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gtgttcctgt cagtcattga gtatgcagct gtgaactacc tcaccacagt ggaagagcgg      1080
aaacaattca agaagacagg aaagatttct aggatgtaca atattgatgc agttcaagct      1140
atggcctttg atggttgta ccatgacagc gagattgaca tggaccagac ttccctctct      1200
ctaaactcag aagacttcat gagaagaaaa tcgatatgca gccccagcac cgattcatct      1260
cggataaaga gaagaaaatc cctaggagga catgttggta gaatcattct ggaaaacaac      1320
catgtcattg acacctattc taggatttta ttccccattg tgtatatattt atttaatttg      1380
ttttactggg gtgtatatgt atga                                             1404

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<210> 14
 <211> 467
 <212> PRT
 <213> Homo sapiens

<400> 14

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

Leu Lys Pro Asn Val Cys Ala Ala Ser Asn Ile Lys Met Thr His Gln
 20 25 30

Arg Cys Ser Ser Ser Met Lys Gln Thr Cys Lys Gln Glu Thr Arg Met
 35 40 45

Lys Lys Asp Asp Ser Thr Lys Ala Arg Pro Gln Lys Tyr Glu Gln Leu
 50 55 60

Leu His Ile Glu Asp Asn Asp Phe Ala Met Arg Pro Gly Phe Gly Gly
 65 70 75 80

Ser Pro Val Pro Val Gly Ile Asp Val His Val Glu Ser Ile Asp Ser
 85 90 95

360990_1.txt

Ile Ser Glu Thr Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His
100 105 110

Tyr Trp Lys Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser
115 120 125

Met Thr Phe Asp His Arg Leu Thr Arg Lys Ile Trp Val Pro Asp Ile
130 135 140

Phe Phe Val His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Met Glu
145 150 155 160

Asn Ile Met Leu Arg Val His Pro Asp Gly Asn Val Leu Leu Ser Leu
165 170 175

Arg Ile Thr Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro
180 185 190

Leu Asp Thr Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn
195 200 205

Glu Asp Asp Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn
210 215 220

Thr Glu Glu His Met Ser Leu Ser Gln Phe Phe Ile Glu Asp Phe Ser
225 230 235 240

Ala Ser Ser Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Asn Arg
245 250 255

Leu Phe Ile Asn Phe Val Leu Arg Arg His Val Phe Phe Phe Val Leu
260 265 270

Gln Thr Tyr Phe Pro Ala Ile Leu Met Val Met Leu Ser Trp Val Ser
275 280 285

360990_1.txt

Phe Trp Ile Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile
 290 295 300

Thr Thr Val Leu Thr Met Ser Thr Ile Ile Thr Ala Val Ser Ala Ser
 305 310 315 320

Met Pro Gln Val Ser Tyr Leu Lys Ala Val Asp Val Tyr Leu Trp Val
 325 330 335

Ser Ser Leu Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn
 340 345 350

Tyr Leu Thr Thr Val Glu Glu Arg Lys Gln Phe Lys Lys Thr Gly Lys
 355 360 365

Ile Ser Arg Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp
 370 375 380

Gly Cys Tyr His Asp Ser Glu Ile Asp Met Asp Gln Thr Ser Leu Ser
 385 390 395 400

Leu Asn Ser Glu Asp Phe Met Arg Arg Lys Ser Ile Cys Ser Pro Ser
 405 410 415

Thr Asp Ser Ser Arg Ile Lys Arg Arg Lys Ser Leu Gly Gly His Val
 420 425 430

Gly Arg Ile Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg
 435 440 445

Ile Leu Phe Pro Ile Val Tyr Ile Leu Phe Asn Leu Phe Tyr Trp Gly
 450 455 460

Val Tyr Val
 465

360990_1.txt

<210> 15
 <211> 1320
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 15
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 gagaggcccc tggccaatga ctcgcaacca ctaccgtct acttctccct gagcctcctg 180
 cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg 240
 tcttggacag atcactatit acagtggaat gtgtcagaat atccaggggt gaagactgtt 300
 cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360
 cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac 420
 ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat 480
 gtgcagcact gcaaactgaa gtttgggtcc tggctcttac gaggctgggt cttggatctg 540
 cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga 600
 atccccggca agaggagtga aaggttctat gagtgctgca aagagcccta ccccgatgtc 660
 accttcacag tgaccatgcg ccgcaggatg gggtactacc tgattcagat gtatattccc 720
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 gctcgtgtgg gcctaggcat caccactgtg ctccacctga ccaccagag ctccggctct 840
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 ctattccagg aggatgaagc tggagaaggc cgctttaact tctctgccta tgggatgggc 1080
 ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc 1140

360990_1.txt

accaaccccc ctcctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag 1200
 agggccaaga agatcgacaa aatatcccgcc attggcttcc ccatggcctt cctcattttc 1260
 aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccagtga 1320

<210> 16
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 16

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
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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

360990_1.txt

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 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

360990_1.txt

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

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 17
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 17

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

360990_1.txt

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

360990_1.txt

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

Thr Met Arg Arg Gln 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 Ser
 325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
 340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
 355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
 370 375 380

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

360990_1.txt

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 18
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 18

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

360990_1.txt

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

His Leu Glu Arg Gln 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

360990_1.txt

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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 19
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 19

360990_1.txt

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

360990_1.txt

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 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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

360990_1.txt

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 20
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 20
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gagaggcccc tggccaatga ctgcaacca ctaccgtct acttctccct gagcctcctg 180
cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg 240
tcttggacag atcactatit acagtggaat gtgtcagaat atccaggggt gaagactgtt 300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac 420
ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat 480
gtgcagcact gcaaactgaa gtttgggtcc tggctttacg gaggctgggt cttggatctg 540
cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga 600
atccccggca agaggagtga aagggttctat gagtgctgca aagagcccta ccccgatgtc 660
accttcacag tgacatgctg ccgcaggatg gggttactacc tgattcagat gtatattccc 720

360990_1.txt

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agcctgctca ttgtcatcct ctcatggatc tccttctgga tcaacatgga tgctgcacct      780
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gagatcatgc ccgcaacatc cgattcggta tcctatgtga aagccattga catttggaatg      900
gcagtttgcc tgctctttgt gttctcagcc ctattagaat atgctgccgt taactttgtg      960
tctcggcaac ataaggagct gctccgattc aggaggaagc ggagacatca caagagcccc     1020
atgttgaatc tattccagga ggatgaagct ggagaaggcc gctttaactt ctctgcctat     1080
gggatgggccc cagcctgtct acaggccaag gatggcatct cagtcaaggg cgccaacaac     1140
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ttcatccaga gggccaagaa gatcgacaaa atatcccgca ttggcttccc catggccttc     1260
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aaccagtga                                           1329

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<210> 21
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 21

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

```

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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

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360990_1.txt

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 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

360990_1.txt

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 Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

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

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

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

His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu
340 345 350

Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln
355 360 365

Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr
370 375 380

Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys Leu
385 390 395 400

Phe Ile Gln Arg Ala Lys Lys Ile Asp Lys Ile Ser Arg Ile Gly Phe
405 410 415

Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr Lys
420 425 430

Ile Val Arg Arg Glu Asp Val His Asn Gln
435 440

<210> 22
 <211> 1332
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 22
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 gagaggcccc tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg 180
 cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg 240
 tcttggacag atcactatit acagtggaat gtgtcagaat atccaggggt gaagactgtt 300
 cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360
 cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac 420
 ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat 480
 gtgcagcact gcaaactgaa gtttgggtcc tggctcttac gaggctgggt cttggatctg 540
 cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga 600
 atccccggca agaggagtga aaggttctat gagtgctgca aagagcccta ccccgatgtc 660
 accttcacag tgaccatgcg ccgcaggatg gggttactacc tgattcagat gtatattccc 720
 agcctgctca ttgtcatcct ctcattgatc tccttctgga tcaacatgga tgctgcacct 780
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 gtgtctcggc aacataagga gctgctccga ttcaggagga agcggagaca tcacaagagc 1020
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 tatgggatgg gccagcctg tctacaggcc aaggatggca tctcagtcaa gggcgccaac 1140

360990_1.txt

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 ctcttcatcc agagggccaa gaagatcgac aaaatatccc gcattggctt ccccatggcc 1260
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 cacaaccagt ga 1332

<210> 23
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 23

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

360990_1.txt

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 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 Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

Ser Val Pro Leu Ile Ala Gln Ala Ile Asp Ile Trp Met Ala Val Cys
290 295 300

360990_1.txt

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

Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg
325 330 335

His His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly
340 345 350

Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu
355 360 365

Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr
370 375 380

Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys
385 390 395 400

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

Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr
420 425 430

Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
435 440

<210> 24
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 24
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ctgcaaggcg agttccagag gaagctttac aaggagctgg tcaagaacta caatcccttg 120

360990_1.txt

gagaggcccg tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg	180
cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaagt	240
tcttggacag atcactatit acagtggaat gtgtcagaat atccaggggt gaagactgtt	300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag	360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac	420
ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat	480
gtgcagcact gcaaactgaa gtttgggtcc tggctttacg gaggctgggt cttggatctg	540
cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga	600
atccccggca agaggagtga aaggttctat gagtgctgca aagagcccta ccccgatgtc	660
accttcacag tgaccatgcg ccgcaggatg gggttactacc tgattcagat gtatattccc	720
agcctgctca ttgtcatcct ctcattgatc tccttctgga tcaacatgga tgctgcacct	780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccaccagag ctccggctct	840
cgagcatctc tgccaaggt gtccgattcg gtaccattga ttgacatttg gatggcagtt	900
tgctgtctct ttgtgttctc agccctatta gaatatgctg ccgttaactt tgtgtctcgg	960
caacataagg agctgtccg attcaggagg aagcggagac atcacaagag ccccatgttg	1020
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ggcccagcct gtctacaggc caaggatggc atctcagtca agggcgccaa caacagtaac	1140
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cagagggccca agaagatcga caaaatatcc cgcattggct tccccatggc cttcctcatt	1260
ttcaacatgt tctactggat catctacaag attgtccgta gagaggacgt ccacaaccag	1320
tga	1323

<210> 25
 <211> 440
 <212> PRT
 <213> Artificial Sequence

360990_1.txt

<220>

<223> synthetic sequence of chimeric LGIC

<400> 25

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

360990_1.txt

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 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

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

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

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

Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg
340 345 350

Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys
355 360 365

360990_1.txt

Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro
370 375 380

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

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

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

Arg Arg Glu Asp Val His Asn Gln
435 440

<210> 26
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 26
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gagaggcccc tggccaatga ctcgcaacca ctcaccgtct acttctccct gaggctcctg 180
cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg 240
tcttggacag atcactatit acagtggaat gtgtcagaat atccaggggt gaagactgtt 300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac 420
ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat 480
gtgcagcact gcaaactgaa gtttgggtcc tggctttacg gaggctgggt cttggatctg 540

360990_1.txt

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accttcacag tgaccatgga gcggcagatg ggttactacc tgattcagat gtatattccc      720
agcctgctca ttgtcatcct ctcatggatc tccttctgga tcaacatgga tgctgcacct      780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccacccagag ctccggctct      840
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gtgtctcggc aacataagga gctgctccga ttcaggagga agcggagaca tcacaagagc     1020
cccatgttga atctattcca ggaggatgaa gctggagaag gccgctttaa cttctctgcc     1080
tatgggatgg gcccagcctg tctacaggcc aaggatggca tctcagtcaa gggcgccaac     1140
aacagtaaca ccaccaaccc ccctcctgca ccatctaagt cccagagga gatgcgaaaa     1200
ctcttcatcc agaggggcaa gaagatcgac aaaatatccc gcattggctt ccccatggcc     1260
ttcctcattt tcaacatggt ctactggatc atctacaaga ttgtccgtag agaggacgtc     1320
cacaaccagt ga                                                             1332

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<210> 27
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 27

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		

360990_1.txt

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

360990_1.txt

Thr Met Glu Arg Gln 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 Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

Ser Val Pro Leu Ile Ala Gln Ala Ile Asp Ile Trp Met Ala Val Cys
290 295 300

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

Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg
325 330 335

His His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly
340 345 350

Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu
355 360 365

Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr
370 375 380

Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys
385 390 395 400

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

360990_1.txt

Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr
 420 425 430

Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
 435 440

<210> 28
 <211> 1332
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 28
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 gagaggcccc tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg 180
 cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg 240
 tcttggacag atcactatct acagtgggaat gtgtcagaat atccaggggt gaagactgtt 300
 cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360
 cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac 420
 ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat 480
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 cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga 600
 atccccggca agaggagtga aaggttctat gagtgtgca aagagcccta ccccgatgtc 660
 accttcacag tgacatgacg ccgcaggacg gggttactacc tgattcagat gtatattccc 720
 agcctgctca ttgtcatcct ctcattgatc tccttctgga tcaacatgga tgctgcacct 780
 gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccaccagag ctccggctct 840
 gagatcatgc ccgcaacatc cgattcggtg ccattgatag cccaggccat tgacatttgg 900
 atggcagttt gcctgctctt tgtgttctca gccctattag aatatgctgc cgtaacttt 960

360990_1.txt

gtgtctcggc aacataagga gctgctccga ttcaggagga agcggagaca tcacaagagc 1020
 cccatgttga atctattcca ggaggatgaa gctggagaag gccgctttaa cttctctgcc 1080
 tatgggatgg gcccagcctg tctacaggcc aaggatggca tctcagtcaa gggcgccaac 1140
 aacagtaaca ccaccaaccc ccctcctgca ccatctaagt ccccagagga gatgcgaaaa 1200
 ctcttcatcc agagggccaa gaagatcgac aaaatatccc gcattggctt ccccatggcc 1260
 ttcttcattt tcaacatggt ctactggatc atctacaaga ttgtccgtag agaggacgtc 1320
 cacaaccagt ga 1332

<210> 29
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 29

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

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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 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 Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

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Ser Val Pro Leu Ile Ala Gln Ala Ile Asp Ile Trp Met Ala Val Cys
 290 295 300

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

Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg
 325 330 335

His His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly
 340 345 350

Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu
 355 360 365

Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr
 370 375 380

Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys
 385 390 395 400

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

Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr
 420 425 430

Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
 435 440

<210> 30

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence of chimeric LGIC

<400> 30

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gagaggcccc tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg      180
cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg      240
tcttggacag atcactatit acagtggaaat gtgtcagaat atccaggggt gaagactgtt      300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag      360
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tatgggatgg gcccagcctg tctacaggcc aaggatggca tctcagtcaa gggcgccaac     1140
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ctcttcatcc agagggccaa gaagatcgac aaaatatccc gcattggctt ccccatggcc     1260
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cacaaccagt ga                                                                1332

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<210> 31
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 31

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

360990_1.txt

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 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 Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

Ser Val Pro Leu Ile Ala Gln Ala Ile Asp Ile Trp Met Ala Val Cys
290 295 300

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

Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg
325 330 335

360990_1.txt

His His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly
340 345 350

Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu
355 360 365

Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr
370 375 380

Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys
385 390 395 400

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

Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr
420 425 430

Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
435 440

<210> 32
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

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cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaatg 240
tcttggacag atcactatctt acagtgggaat gtgtcagaat atccaggggt gaagactgtt 300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360

360990_1.txt

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ctgcctccag gcatattcaa gagttcctgc cccatggact tgaagaattt ccccatggat 480
gtccagacat gcaaactgaa gtttgggtcc tggctttacg gaggctggtc cttggatctg 540
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agcctgctca ttgtcatcct ctcatggatc tccttctgga tcaacatgga tgctgcacct 780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccaccagag ctccggctct 840
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ctgctctttg tgttctcagc cctattagaa tatgctgccg ttaactttgt gtctcggcaa 960
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ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc 1140
accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag 1200
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aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccagtga 1320

<210> 33
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 33

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
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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 Pro Met Asp Leu Lys Asn Phe Pro Met Asp
145 150 155 160

Val Gln Thr 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

360990_1.txt

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr 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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

360990_1.txt

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 34
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 34
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cagatcatgg acgtggatga gaagaaccaa gttttaacca ccaacatttg gctgcaaattg 240
tcttggacag atcactatct acagtggatg gtgtcagaat atccaggggt gaagactgtt 300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac 420
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gctcgtgtgg gcctaggcat caccactgtg ctcacatga ccaccagag ctccggctct 840

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 accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag 1200
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<210> 35
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 35

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

360990_1.txt

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 Pro Met Asp Leu Lys Asn 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 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

360990_1.txt

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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 36
<211> 1320
<212> DNA
<213> Artificial Sequence

360990_1.txt

<220>

<223> synthetic sequence of chimeric LGIC

<400> 36

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gagaggcccc tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg	180
cagatcatgg acgtggatga gacaaccatg gttttaacca ccaacatttg gctgcaaatg	240
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atccccggca agaggagtga aaggttctat gagtgtgca aagagcccta ccccgatgtc	660
accttcacag tgaccatgcg ccgcaggatg gggttactacc tgattcagat gtatattccc	720
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ctgctctttg tgttctcagc cctattagaa tatgctgccg ttaactttgt gtctcgga	960
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ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc	1140
accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag	1200
agggccaaaga agatcgacaa aatatccgc attggcttcc ccatggcctt cctcattttc	1260
aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccagtga	1320

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<210> 37
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 37

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 Thr Thr Met 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

360990_1.txt

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 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 Ser
 325 330 335

360990_1.txt

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 38
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 38
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cagatcatgg acattgctga gacaaccatg gacttaacca ccaacatttg gctgcaaatg 240
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cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360

360990_1.txt

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ctgcctccag gcatattcaa gagttcctgc cccatggact tgaagaattt ccccatggat 480
gtccagacat gcaaactgaa gtttgggtcc tggctttacg gaggctggtc cttggatctg 540
cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga 600
atccccggca agaggagtga aaggttctat gagtgtgca aagagcccta ccccgatgtc 660
accttcacag tgacatgacg ccgcaggatg gggttactacc tgattcagat gtatattccc 720
agcctgctca ttgtcatcct ctcattgatc tccttctgga tcaacatgga tgctgcacct 780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccaccagag ctccggctct 840
cgagcatctc tgcccaaggt gtcctatgtg aaagccattg acatttggat ggagttttgc 900
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cataaggagc tgctccgatt caggaggaag cggagacatc acaagagccc catgttgaat 1020
ctattccagg aggatgaagc tggagaaggc cgctttaact tctctgccta tgggatgggc 1080
ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc 1140
accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag 1200
agggccaaga agatcgacaa aatatccgc attggcttcc ccatggcctt cctcattttc 1260
aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccagtga 1320

<210> 39
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 39

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

360990_1.txt

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

Ile Ala Glu Thr Thr Met Asp 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 Pro Met Asp Leu Lys Asn Phe Pro Met Asp
145 150 155 160

Val Gln Thr 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

360990_1.txt

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr 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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

360990_1.txt

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 40

<211> 1320

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence of chimeric LGIC

<400> 40

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ctgcaaggcg agttccagag gaagctttac aaggagctgg tcaagaacta caatcccttg	120
gagaggccccg tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg	180
cagatcatgg acgtggatga gacaaccatg gttttaacca ccaacatttg gctgcaaattg	240
tcttggacag atcactatctt acagtgggaat gtgtcagaat atccaggggt gaagactgtt	300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag	360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac	420
ctgcctccag gcatattcaa gagttcctgc cccatggact tgaagaattt ccccatggat	480
gtccagacat gcaaaactgaa gtttgggtcc tggctcttacg gaggctgggtc cttggatctg	540
cagatgcagg aggcagatat cagtggctat atccccaatg gagaatggga cctagtggga	600
atccccggca agaggagtga aaggttctat gaggctgca aagagcccta cccgatgtc	660
accttcacag tgaccatgcg ccgcaggatg ggttactacc tgattcagat gtatattccc	720
agcctgtctca ttgtcatcct ctcatggatc tccttctgga tcaacatgga tgctgcacct	780
gctcgtgtgg gcctaggcat caccactgtg ctcacatga ccaccagag ctccggctct	840

360990_1.txt

cgagcatctc tgcccaaggt gtcctatgtg aaagccattg acatttggat ggcagtttgc 900
 ctgctctttg tgttctcagc cctattagaa tatgctgccg ttaactttgt gtctcggcaa 960
 cataaggagc tgctccgatt caggaggaag cggagacatc acaagagccc catgttgaat 1020
 ctattccagg aggatgaagc tggagaaggc cgctttaact tctctgccta tgggatgggc 1080
 ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc 1140
 accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag 1200
 agggccaaga agatcgacaa aatatccgc attggcttcc ccatggcctt cctcattttc 1260
 aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccagtga 1320

<210> 41
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 41

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

360990_1.txt

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 Pro Met Asp Leu Lys Asn Phe Pro Met Asp
145 150 155 160

Val Gln Thr 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 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

360990_1.txt

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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 42
<211> 1317
<212> DNA
<213> Artificial Sequence

360990_1.txt

<220>

<223> synthetic sequence of chimeric LGIC

<400> 42

atgcgctgct cgccgggagg cgtctggctg gcgctggccg cgtcgctcct gcacgtgtcc	60
ctgcaaggcg agttccagag gaagctttac aaggagctgg tcaagaacta caatcccttg	120
gagaggcccc tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg	180
cagatcatgg acgtggatga gacaaccatg gttttaacca ccaacatttg gctgcaaatg	240
tcttggacag atcactatit acagtggaat gtgtcagaat atccaggggt gaagactgtt	300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag	360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac	420
ctgcctccag gcatattcaa gagttcctgc cccatggact tgaagaattt ccccatggat	480
gtccagacat gcaaaactgaa gtttgggtcc tggctttacg gaggctggtc cttggatctg	540
cagatgcagg aggcagatat cagtggctat atccccaatg gagaatggga cctagtggga	600
atccccggca agaggagtga aaggttctat gagtgtgca aagagcccta ccccgatgtc	660
accttcacag tgaccatgga gcggcagatg ggttactacc tgattcagat gtatattccc	720
agcctgtca ttgtcatcct ctcatggatc tccttctgga tcaacatgga tgctgcacct	780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccacccagag ctccggctct	840
cgagcatctc tgcccaaggt gtcctatgtg aaagccattg acatttggat ggcagtttgc	900
ctgctctttg tgttctcagc cctattagaa tatgctgccg ttaactttgt gtctcgga	960
cataaggagc tgctccgatt caggaggaag cggagacatc acaagagccc catgttgaat	1020
ctattccagg aggatgaagc tggagaaggc cgctttaact tctctgccta tgggatgggc	1080
ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc	1140
accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag	1200
agggccaaaga agatcgacaa aatatccgc attggcttcc ccatggcctt cctcattttc	1260
aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccag	1317

360990_1.txt

<210> 43
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 43

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 Thr Thr Met 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

360990_1.txt

Ile Phe Lys Ser Ser Cys Pro Met Asp Leu Lys Asn Phe Pro Met Asp
 145 150 155 160

Val Gln Thr 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 Glu Arg Gln 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 Ser
 325 330 335

360990_1.txt

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 44
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 44
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ctgcaaggcg agttccagag gaagctttac aaggagctgg tcaagaacta caatcccttg 120
gagaggcccg tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg 180
cagatcatgg acattgctga gacaaccatg gacttaacca ccaacatttg gctgcaaatg 240
tcttggacag atcactatct acagtgggaat gtgtcagaat atccaggggt gaagactgtt 300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag 360

360990_1.txt

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cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac      420
ctgcctccag gcatattcaa gagttcctgc cccatggact tgaagaattt ccccatggat      480
gtccagacat gcaaactgaa gtttgggtcc tggctttacg gaggctgggc cttggatctg      540
cagatgcagg aggagatat cagtggctat atccccaatg gagaatggga cctagtggga      600
atccccggca agaggagtga aaggttctat gagtgctgca aagagcccta ccccgatgtc      660
accttcacag tgacatgga gcggcagatg gggttactacc tgattcagat gtatattccc      720
agcctgctca ttgtcatcct ctcattgatc tccttctgga tcaacatgga tgctgcacct      780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccaccagag ctccggctct      840
cgagcatctc tgcccaaggt gtcctatgtg aaagccattg acatttggat ggagtttgc      900
ctgctctttg tgttctcagc cctattagaa tatgctgccg ttaactttgt gtctcggcaa      960
cataaggagc tgctccgatt caggaggaag cggagacatc acaagagccc catgttgaat     1020
ctattccagg aggatgaagc tggagaaggc cgctttaact tctctgccta tgggatgggc     1080
ccagcctgtc tacaggccaa ggatggcatc tcagtcaagg gcgccaacaa cagtaacacc     1140
accaaccccc ctctgcacc atctaagtcc ccagaggaga tgcgaaaact cttcatccag     1200
agggccaaga agatcgacaa aatatccgc attggcttcc ccatggcctt cctcattttc     1260
aacatgttct actggatcat ctacaagatt gtccgtagag aggacgtcca caaccag       1317

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<210> 45
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence of chimeric LGIC

<400> 45

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

360990_1.txt

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

Ile Ala Glu Thr Thr Met Asp 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 Pro Met Asp Leu Lys Asn Phe Pro Met Asp
145 150 155 160

Val Gln Thr 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

360990_1.txt

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

Thr Met Glu Arg Gln 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 Ser
325 330 335

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
340 345 350

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
355 360 365

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
370 375 380

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

360990_1.txt

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

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

Arg Glu Asp Val His Asn Gln
435

<210> 46

<211> 1329

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence of chimeric LGIC

<400> 46

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gagaggccccg tggccaatga ctcgcaacca ctcaccgtct acttctccct gagcctcctg	180
cagatcatgg acgtggatga gacaaccatg gttttaacca ccaacatttg gctgcaaattg	240
tcttggacag atcactatctt acagtgggaat gtgtcagaat atccaggggt gaagactgtt	300
cgtttcccag atggccagat ttggaaacca gacattcttc tctataacag tgctgatgag	360
cgctttgacg ccacattcca cactaacgtg ttggtgaact cttctgggca ttgccagtac	420
ctgcctccag gcatattcaa gagttcctgc tacatcgatg tacgctgggt tccctttgat	480
gtgcagcact gcaaaactgaa gtttgggtcc tggctcttacg gaggctgggtc cttggatctg	540
cagatgcagg aggcagatat cagtggctat atccccaatg gagaatggga cctagtggga	600
atccccggca agaggagtga aaggttctat gagtgctgca aagagcccta cccgatgtc	660
accttcacag tgaccatgcg ccgcaggatg gggttactacc tgattcagat gtatattccc	720
agcctgtcga ttgtcatcct ctcattggatc tccttctgga tcaacatgga tgctgcacct	780
gctcgtgtgg gcctaggcat caccactgtg ctcaccatga ccaccagag ctccggctct	840

360990_1.txt

gagatcatgc ccgcaacatc cgattcggta ccattgatag cccaggccat tgacatttgg 900
atggcagttt gcctgctctt tgtgttctca gccctattag aatatgctgc cgtaaacttt 960
gtgtctcggc aacataagga gctgctccga ttcaggagga agcggagaca tcacaagagc 1020
cccatgttga atctattcca ggaggatgaa gctggagaag gccgctttaa cttctctgcc 1080
tatgggatgg gcccagcctg tctacaggcc aaggatggca tctcagtcaa gggcgccaac 1140
aacagtaaca ccaccaaccc cctcctgca ccattctaagt cccagagga gatgcgaaaa 1200
ctcttcatcc agagggccaa gaagatcgac aaaatatccc gcattggctt cccatggcc 1260
ttcctcattt tcaacatgtt ctactggatc atctacaaga ttgtccgtag agaggacgtc 1320
cacaaccag 1329

<210> 47
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 47

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

360990_1.txt

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 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

360990_1.txt

Met Thr Thr Gln Ser Ser Gly Ser Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

Ser Val Pro Leu Ile Ala Gln Ala Ile Asp Ile Trp Met Ala Val Cys
290 295 300

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

Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg
325 330 335

His His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly
340 345 350

Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu
355 360 365

Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr
370 375 380

Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys
385 390 395 400

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

Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr
420 425 430

Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
435 440

<210> 48

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence of chimeric LGIC

<400> 48

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360990_1.txt

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cacaaccagt ga 1332

<210> 49

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence of chimeric LGIC

<400> 49

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

360990_1.txt

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 Pro Met Asp Leu Lys Asn Phe Pro Met Asp
145 150 155 160

Val Gln Thr 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 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 Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

Ser Val Pro Leu Ile Ala Gln Ala Ile Asp Ile Trp Met Ala Val Cys
290 295 300

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

360990_1.txt

Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg
325 330 335

His His Lys Ser Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly
340 345 350

Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu
355 360 365

Gln Ala Lys Asp Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr
370 375 380

Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys
385 390 395 400

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

Phe Pro Met Ala Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr
420 425 430

Lys Ile Val Arg Arg Glu Asp Val His Asn Gln
435 440

<210> 50

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence of chimeric LGIC

<400> 50

Met Leu Leu Trp Val Gln Gln Ala Leu Leu Ala Leu Leu Leu Pro Thr
1 5 10 15

Leu Leu Ala Gln Gly Glu Ala Arg Arg Ser Arg Asn Thr Thr Arg Pro
20 25 30

360990_1.txt

Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu Thr Asn Tyr Arg Lys Gly
35 40 45

Val Arg Pro Val Arg Asp Trp Arg Lys Pro Thr Thr Val Ser Ile Asp
50 55 60

Val Ile Val Tyr Ala Ile Leu Asn Val Asp Glu Lys Asn Gln Val Leu
65 70 75 80

Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu Gln
85 90 95

Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro Thr
100 105 110

Asp Ser Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp Val
115 120 125

Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln Gly Glu
130 135 140

Val Gln Asn Tyr Lys Pro Leu Gln Val Val Thr Ala Cys Ser Leu Asp
145 150 155 160

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

Ser Trp Leu His Thr Ile Gln Asp Ile Asn Ile Ser Leu Trp Arg Leu
180 185 190

Pro Glu Lys Val Lys Ser Asp Arg Ser Val Phe Met Asn Gln Gly Glu
195 200 205

Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe Arg Glu Phe Ser Met Glu
210 215 220

360990_1.txt

Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe Tyr Val Val Ile Arg Arg
225 230 235 240

Arg Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile
245 250 255

Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met Asp Ala Ala Pro
260 265 270

Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln
275 280 285

Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala
290 295 300

Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe Ser Ala Leu
305 310 315 320

Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln His Lys Glu Leu
325 330 335

Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Ser Pro Met Leu Asn
340 345 350

Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala
355 360 365

Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val
370 375 380

Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro Pro Ala Pro Ser
385 390 395 400

Lys Ser Pro Glu Glu Met Arg Lys Leu Phe Ile Gln Arg Ala Lys Lys
405 410 415

360990_1.txt

Ile Asp Lys Ile Ser Arg Ile Gly Phe Pro Met Ala Phe Leu Ile Phe
420 425 430

Asn Met Phe Tyr Trp Ile Ile Tyr Lys Ile Val Arg Arg Glu Asp Val
435 440 445

His Asn Gln
450

<210> 51
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence of chimeric LGIC

<400> 51

Met Leu Leu Trp Val Gln Gln Ala Leu Leu Ala Leu Leu Leu Pro Thr
1 5 10 15

Leu Leu Ala Gln Gly Glu Ala Arg Arg Ser Arg Asn Thr Thr Arg Pro
20 25 30

Ala Leu Leu Arg Leu Ser Asp Tyr Leu Leu Thr Asn Tyr Arg Lys Gly
35 40 45

Val Arg Pro Val Arg Asp Trp Arg Lys Pro Thr Thr Val Ser Ile Asp
50 55 60

Val Ile Val Tyr Ala Ile Leu Asn Val Asp Glu Lys Asn Gln Val Leu
65 70 75 80

Thr Thr Tyr Ile Trp Tyr Arg Gln Tyr Trp Thr Asp Glu Phe Leu Gln
85 90 95

360990_1.txt

Trp Asn Pro Glu Asp Phe Asp Asn Ile Thr Lys Leu Ser Ile Pro Thr
100 105 110

Asp Ser Ile Trp Val Pro Asp Ile Leu Ile Asn Glu Phe Val Asp Val
115 120 125

Gly Lys Ser Pro Asn Ile Pro Tyr Val Tyr Ile Arg His Gln Gly Glu
130 135 140

Val Gln Asn Tyr Lys Pro Leu Gln Val Val Thr Ala Cys Ser Leu Asp
145 150 155 160

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

Ser Trp Leu His Thr Ile Gln Asp Ile Asn Ile Ser Leu Trp Arg Leu
180 185 190

Pro Glu Lys Val Lys Ser Asp Arg Ser Val Phe Met Asn Gln Gly Glu
195 200 205

Trp Glu Leu Leu Gly Val Leu Pro Tyr Phe Arg Glu Phe Ser Met Glu
210 215 220

Ser Ser Asn Tyr Tyr Ala Glu Met Lys Phe Tyr Val His Leu Glu Arg
225 230 235 240

Gln Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile
245 250 255

Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met Asp Ala Ala Pro
260 265 270

Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln
275 280 285

360990_1.txt

Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala
290 295 300

Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val Phe Ser Ala Leu
305 310 315 320

Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln His Lys Glu Leu
325 330 335

Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Ser Pro Met Leu Asn
340 345 350

Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala
355 360 365

Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val
370 375 380

Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro Pro Ala Pro Ser
385 390 395 400

Lys Ser Pro Glu Glu Met Arg Lys Leu Phe Ile Gln Arg Ala Lys Lys
405 410 415

Ile Asp Lys Ile Ser Arg Ile Gly Phe Pro Met Ala Phe Leu Ile Phe
420 425 430

Asn Met Phe Tyr Trp Ile Ile Tyr Lys Ile Val Arg Arg Glu Asp Val
435 440 445

His Asn Gln
450

<210> 52
<211> 455
<212> PRT
<213> Artificial Sequence

360990_1.txt

<220>

<223> synthetic sequence of chimeric LGIC

<400> 52

Met Trp Gly Leu Ala Gly Gly Arg Leu Phe Gly Ile Phe Ser Ala Pro
1 5 10 15

Val Leu Val Ala Val Val Cys Cys Ala Gln Ser Val Asn Asp Pro Gly
20 25 30

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

Asp Ile Arg Leu Arg Pro Asp Phe Gly Gly Pro Pro Val Cys Val Gly
50 55 60

Met Asn Ile Asp Ile Ala Ser Ile Asp Met Val Ser Glu Val Asn Met
65 70 75 80

Asp Tyr Thr Leu Thr Met Tyr Phe Gln Gln Tyr Trp Arg Asp Lys Arg
85 90 95

Leu Ala Tyr Ser Gly Ile Pro Leu Asn Leu Thr Leu Asp Asn Arg Val
100 105 110

Ala Asp Gln Leu Trp Val Pro Asp Thr Tyr Phe Leu Asn Asp Lys Lys
115 120 125

Ser Phe Val His Gly Val Thr Val Lys Asn Arg Met Ile Arg Leu His
130 135 140

Pro Asp Gly Thr Val Leu Tyr Gly Leu Arg Ile Thr Thr Thr Ala Ala
145 150 155 160

Cys Met Met Asp Leu Arg Arg Tyr Pro Leu Asp Glu Gln Asn Cys Thr
165 170 175

360990_1.txt

Leu Glu Ile Glu Ser Tyr Gly Tyr Thr Thr Asp Asp Ile Glu Phe Tyr
180 185 190

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

Pro Gln Phe Ser Ile Val Glu His Arg Leu Val Ser Arg Asn Val Val
210 215 220

Phe Ala Thr Gly Ala Tyr Pro Arg Leu Ser Leu Ser Phe Arg Leu Lys
225 230 235 240

Arg Asn Ile Gly Tyr Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile Pro
245 250 255

Ser Leu Leu Ile Val Ile Leu Ser Trp Ile Ser Phe Trp Ile Asn Met
260 265 270

Asp Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu Thr
275 280 285

Met Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val Ser
290 295 300

Tyr Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe Val
305 310 315 320

Phe Ser Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg Gln
325 330 335

His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg His His Lys Ser
340 345 350

Pro Met Leu Asn Leu Phe Gln Glu Asp Glu Ala Gly Glu Gly Arg Phe
355 360 365

360990_1.txt

Asn Phe Ser Ala Tyr Gly Met Gly Pro Ala Cys Leu Gln Ala Lys Asp
 370 375 380

Gly Ile Ser Val Lys Gly Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro
 385 390 395 400

Pro Ala Pro Ser Lys Ser Pro Glu Glu Met Arg Lys Leu Phe Ile Gln
 405 410 415

Arg Ala Lys Lys Ile Asp Lys Ile Ser Arg Ile Gly Phe Pro Met Ala
 420 425 430

Phe Leu Ile Phe Asn Met Phe Tyr Trp Ile Ile Tyr Lys Ile Val Arg
 435 440 445

Arg Glu Asp Val His Asn Gln
 450 455

<210> 53
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C-terminal amino acids of GABAR1

<400> 53

Ile Asp Arg Leu Ser Arg Ile Ala Phe Pro Leu Leu Phe Gly Ile Phe
 1 5 10 15

Asn Leu Val Tyr Trp Ala Thr Tyr Leu Asn Arg Glu Pro Gln Leu
 20 25 30

<210> 54
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid residues 260-281 of human CHRNA7

<400> 54

Glu	Lys	Ile	Ser	Leu	Gly	Ile	Thr	Val	Leu	Leu	Ser	Leu	Thr	Val	Phe
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Met	Leu	Leu	Val	Ala	Glu
			20		

<210> 55

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide sequence

<400> 55

Pro	Ala	Lys	Ile	Gly	Leu	Gly	Ile	Thr	Val	Leu	Leu	Ser	Leu	Thr	Thr
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Phe	Met	Ser	Gly	Val	Ala	Asn
			20			

<210> 56

<211> 1780

<212> DNA

<213> Homo sapiens

<400> 56

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cagaaatatc	ataaagaagt	gagacctgtt	tacaactgga	ccaaggccac	cacagtctac	180
ctggacctgt	tcgtccatgc	tatatgggat	gtggatgcag	agaatcaaat	attaaagaca	240
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360990_1.txt

gatgagatta gagagatctc cctacctcta agtgccatct gggcccccga tatcatcatc	360
aatgagtttg tggacattga aagataccct gaccttcctt atgtttatgt gaactcatct	420
gggaccattg agaactataa gcccattccag gtggctctctg cgtgcagttt agagacatat	480
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ggtgggagga ttgcttgagc ccaggatttc aaggctgcag tgagccatga ttgcaccact	1680
gcaccccagc ctgggtgaca gagcaagacc ctgtctcaaa aaaaataaaa taaaaggctt	1740

tctgccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

1780

<210> 57
 <211> 441
 <212> PRT
 <213> Homo sapiens
 <400> 57

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

Ala Gly Ile Leu Ala Thr Asp Thr His His Pro Gln Asp Ser Ala Leu
 20 25 30

Tyr His Leu Ser Lys Gln Leu Leu Gln Lys Tyr His Lys Glu Val Arg
 35 40 45

Pro Val Tyr Asn Trp Thr Lys Ala Thr Thr Val Tyr Leu Asp Leu Phe
 50 55 60

Val His Ala Ile Leu Asp Val Asp Ala Glu Asn Gln Ile Leu Lys Thr
 65 70 75 80

Ser Val Trp Tyr Gln Glu Val Trp Asn Asp Glu Phe Leu Ser Trp Asn
 85 90 95

Ser Ser Met Phe Asp Glu Ile Arg Glu Ile Ser Leu Pro Leu Ser Ala
 100 105 110

Ile Trp Ala Pro Asp Ile Ile Ile Asn Glu Phe Val Asp Ile Glu Arg
 115 120 125

Tyr Pro Asp Leu Pro Tyr Val Tyr Val Asn Ser Ser Gly Thr Ile Glu
 130 135 140

Asn Tyr Lys Pro Ile Gln Val Val Ser Ala Cys Ser Leu Glu Thr Tyr
 145 150 155 160

360990_1.txt

Ala Phe Pro Phe Asp Val Gln Asn Cys Ser Leu Thr Phe Lys Ser Ile
165 170 175

Leu His Thr Val Glu Asp Val Asp Leu Ala Phe Leu Arg Ser Pro Glu
180 185 190

Asp Ile Gln His Asp Lys Lys Ala Phe Leu Asn Asp Ser Glu Trp Glu
195 200 205

Leu Leu Ser Val Ser Ser Thr Tyr Ser Ile Leu Gln Ser Ser Ala Gly
210 215 220

Gly Phe Ala Gln Ile Gln Phe Asn Val Val Met Arg Arg His Pro Leu
225 230 235 240

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

Asp Leu Gly Ser Phe Tyr Leu Pro Pro Asn Cys Arg Ala Arg Ile Val
260 265 270

Phe Lys Thr Ser Val Leu Val Gly Tyr Thr Val Phe Arg Val Asn Met
275 280 285

Ser Asn Gln Val Pro Arg Ser Val Gly Ser Thr Pro Leu Ile Gly His
290 295 300

Phe Phe Thr Ile Cys Met Ala Phe Leu Val Leu Ser Leu Ala Lys Ser
305 310 315 320

Ile Val Leu Val Lys Phe Leu His Asp Glu Gln Arg Gly Gly Gln Glu
325 330 335

Gln Pro Phe Leu Cys Leu Arg Gly Asp Thr Asp Ala Asp Arg Pro Arg
340 345 350

360990_1.txt

Val Glu Pro Arg Ala Gln Arg Ala Val Val Thr Glu Ser Ser Leu Tyr
 355 360 365

Gly Glu His Leu Ala Gln Pro Gly Thr Leu Lys Glu Val Trp Ser Gln
 370 375 380

Leu Gln Ser Ile Ser Asn Tyr Leu Gln Thr Gln Asp Gln Thr Asp Gln
 385 390 395 400

Gln Glu Ala Glu Trp Leu Val Leu Leu Ser Arg Phe Asp Arg Leu Leu
 405 410 415

Phe Gln Ser Tyr Leu Phe Met Leu Gly Ile Tyr Thr Ile Thr Leu Cys
 420 425 430

Ser Leu Trp Ala Leu Trp Gly Gly Val
 435 440