

SEQUENCE LISTING

<110> The Governors of the University of Alberta

<120> LOW AFFINITY RED FLUORESCENT INDICATORS FOR IMAGING CA²⁺ IN
EXCITABLE AND NON-EXCITABLE CELLS

<130> 55326.272 PCT

<160> 21

<170> PatentIn version 3.5

<210> 1

<211> 1251

<212> DNA

<213> Homo sapiens

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Lys Ala Tyr Ile Lys His Pro Ala Asp Ile Pro Asp Tyr Phe Lys Leu
195 200 205

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

370

375

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<212> DNA

<213> Homo sapiens

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Ile His Val Asn Gln Asp Ser Ser Leu Gln Asp Gly Val Phe Ile Tyr
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Gln Lys Lys Thr Met Gly Trp Glu Ala Thr Arg Asp Gln Leu Thr Glu

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Lys Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Val Val Asp Ile
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Lys Leu Asp Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln
 385 390 395 400

Cys Glu Arg Ala Glu Gly Arg His Ser Thr Gly Gly Met Val Gly Leu
 405 410 415

Tyr Lys

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

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

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

Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser
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Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Ser Glu
195 200 205

Val Asp Ala Asp Gly Asp Gly Thr Phe Asp Phe Pro Glu Phe Leu Thr
210 215 220

Met Met Ala Arg Lys Met Asn Tyr Thr Asp Ser Glu Glu Glu Ile Arg
225 230 235 240

Glu Ala Phe Arg Val Ala Asp Lys Asp Gly Asn Gly Tyr Ile Gly Ala
245 250 255

Ala Glu Leu Arg His Ala Met Thr Asp Ile Gly Glu Lys Leu Thr Asp
260 265 270

Glu Glu Val Asp Glu Met Ile Arg Val Ala Asp Ile Asp Gly Asp Gly
275 280 285

Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys Gly Gly
290 295 300

Gly Gly Ser Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His
305 310 315 320

Ala Trp Arg Ala Ala Gly Arg Leu Ser Ser Pro Val Val Ser Glu Arg
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Met Tyr Pro Glu Asp Gly Ala Leu Lys Ser Glu Ile Lys Lys Gly Leu
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Arg Leu Lys Asp Gly Gly His Tyr Ala Ala Glu Val Lys Thr Thr Tyr

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Lys Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Val Val Asp Ile
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Lys Leu Asp Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln
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Cys Glu Arg Ala Glu Gly Arg His Ser Thr Gly Gly Met Val Gly Leu
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Tyr Lys

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35 40 45

Phe Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe
50 55 60

Ala Trp Asp Ile Leu Ser Pro Gln Phe Met Tyr Gly Ser Lys Ala Tyr
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Ile Lys His Pro Ala Asp Ile Pro Asp Tyr Phe Lys Leu Ser Phe Pro
85 90 95

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

Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Pro Asp Gly Pro Val Met

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135

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Gln Lys Lys Thr Met Gly Trp Glu Ala Thr Arg Asp Gln Leu Thr Glu
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Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp
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Gly Asp Gly Thr Met Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser
 180 185 190

Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Ser Glu
 195 200 205

Val Asp Ala Asp Gly Asp Gly Thr Phe Asp Phe Pro Glu Phe Leu Thr
 210 215 220

Met Met Ala Arg Lys Met Asn Tyr Thr Asp Ser Glu Glu Glu Ile Arg
 225 230 235 240

Glu Ala Phe Arg Val Ala Asp Lys Asp Gly Asn Gly Tyr Ile Gly Ala
 245 250 255

Ala Glu Leu Arg His Ala Met Thr Asp Ile Gly Glu Lys Leu Thr Asp
 260 265 270

Glu Glu Val Asp Glu Met Ile Arg Val Ala Asp Ile Asp Gly Asp Gly
 275 280 285

Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys Gly Gly
 290 295 300

Gly Gly Ser Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His
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Ala Trp Arg Ala Ile Gly Arg Leu Ser Ser Pro Val Val Ser Glu Arg
 325 330 335

Met Tyr Pro Glu Asp Gly Ala Leu Lys Ser Glu Ile Lys Lys Gly Leu
 340 345 350

Arg Leu Lys Asp Gly Gly His Tyr Ala Ala Glu Val Lys Thr Thr Tyr
 355 360 365

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

Lys Leu Asp Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln
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Cys Glu Arg Ala Glu Gly Arg His Ser Thr Gly Gly Met Val Gly Leu
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Tyr Lys

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His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr Glu Ala
35 40 45

Phe Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe
50 55 60

Ala Trp Asp Ile Leu Ser Pro Gln Phe Met Tyr Gly Ser Lys Ala Tyr
65 70 75 80

Ile Lys His Pro Ala Asp Ile Pro Asp Tyr Phe Lys Leu Ser Phe Pro
85 90 95

Glu Gly Phe Arg Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Ile
100 105 110

Ile His Val Asn Gln Asp Ser Ser Leu Gln Asp Gly Val Phe Ile Tyr
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Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Pro Asp Gly Pro Val Met
130 135 140

Gln Lys Lys Thr Met Gly Trp Glu Ala Thr Arg Asp Gln Leu Thr Glu
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Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp
165 170 175

Gly Asn Gly Thr Met Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser
180 185 190

Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Ser Glu
195 200 205

Val Asp Ala Asp Gly Asn Gly Thr Phe Asp Phe Pro Glu Phe Leu Thr
210 215 220

Met Met Ala Arg Lys Met Asn Tyr Thr Asp Ser Glu Glu Glu Ile Arg
225 230 235 240

Glu Ala Phe Arg Val Ala Asp Lys Asp Gly Asn Gly Tyr Ile Gly Ala
245 250 255

Ala Glu Leu Arg His Ala Met Thr Asp Ile Gly Glu Lys Leu Thr Asp
260 265 270

Glu Glu Val Asp Glu Met Ile Arg Val Ala Asp Ile Asp Gly Asp Gly
275 280 285

Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys Gly Gly
290 295 300

Gly Gly Ser Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His
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Ala Trp Arg Ala Ile Gly Arg Leu Ser Ser Pro Val Val Ser Glu Arg
325 330 335

Met Tyr Pro Glu Asp Gly Ala Leu Lys Ser Glu Ile Lys Lys Gly Leu

340

345

350

Arg Leu Lys Asp Gly Gly His Tyr Ala Ala Glu Val Lys Thr Thr Tyr
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Lys Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Val Val Asp Ile
 370 375 380

Lys Leu Asp Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln
 385 390 395 400

Cys Glu Arg Ala Glu Gly Arg His Ser Thr Gly Gly Met Val Gly Leu
 405 410 415

Tyr Lys

<210> 11
 <211> 1245
 <212> DNA
 <213> Homo sapiens

<400> 11
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 cgcccctacg aggcctttca gaccgctaag ctgaaggatga ccaagggtgg ccccctgccc 180
 ttgcctggg acatcctgtc cttcagttc atgtacggct ccaaggccta cattaagcac 240
 ccagccgaca tccccgacta cttcaagctg tccttccccg agggcttcag gtgggagcgc 300
 gtgatgatct tcgaggacgg cggcattatt cacgttaacc aggactcctc cctgcaggac 360
 ggcgtattca tctacaaggt gaagctgcgc ggcaccaact tcccccccga cggccccgta 420
 atgcagaaga agaccatggg ctgggagcct acgcgtgacc aactgactga agagcagatc 480
 gcagagttaa aagaggcttt ctccctatct gacaaggacg gggatgggac gatgacaacc 540
 aaggagctgg ggacggtggt gcggtctctg gggcagaacc ccacagaagc agagctgcag 600
 gacatgatca atgaagtaga tgccgacggg gacggcacat tcgacttccc tgagttcctg 660
 acgatgatgg caaggaaaat gaatgactca gacagtgaag aggaaattag agaagcgttc 720
 cgcgtggcgg ataaggacgg caatggctac atcggcgcag cagagcttcg ccacgcgatg 780

115

120

125

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

Thr Met Gly Trp Glu Pro Thr Arg Asp Gln Leu Thr Glu Glu Gln Ile
 145 150 155 160

Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly
 165 170 175

Thr Met Thr Thr Lys Glu Leu Gly Thr Val Leu Arg Ser Leu Gly Gln
 180 185 190

Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
 195 200 205

Asp Gly Asp Gly Thr Phe Asp Phe Pro Glu Phe Leu Thr Met Met Ala
 210 215 220

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

Arg Val Ala Asp Lys Asp Gly Asn Gly Tyr Ile Gly Ala Ala Glu Leu
 245 250 255

Arg His Ala Met Thr Asp Ile Gly Glu Lys Leu Thr Asp Glu Glu Val
 260 265 270

Asp Glu Met Ile Arg Val Ala Asp Ile Asp Gly Asp Gly Gln Val Asn
 275 280 285

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys Gly Gly Gly Gly Ser
 290 295 300

Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His Ala Trp Arg
 305 310 315 320

Ala Ile Gly Arg Leu Ser Ser Arg Trp Val Ser Glu Trp Met Tyr Pro
 325 330 335

Glu Asp Gly Ala Leu Lys Ser Val Ile Lys Glu Gly Leu Arg Leu Lys
340 345 350

Asp Gly Gly His Tyr Ala Ala Glu Val Arg Thr Thr Tyr Lys Ala Lys
355 360 365

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

Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Cys Glu Arg
385 390 395 400

Ala Glu Gly Arg His Ser Thr Gly Gly Met Asp Glu Leu Tyr Lys
405 410 415

<210> 13
<211> 1245
<212> DNA
<213> Homo sapiens

<400> 13
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gtgcacatgg agggctccgt gaacggccac gagttcgaga tcgagggcga gggcgagggc 120
cgcccctacg aggcctttca gaccgctaag ctgaaggtga ccaagggtgg ccccctgccc 180
ttcgcctggg acatcctgtc ctttcagttc atgtacggct ccaaggccta cattaagcac 240
ccagccgaca tccccgacta cttcaagctg tccttccccg agggcttcag gtgggagcgc 300
gtgatgatct tcgaggacgg cggcattatt cacgttaacc aggactcctc cctgcaggac 360
ggcgtattca tctacaaggt gaagctgcgc ggcaccaact tcccccccga cggccccgta 420
atgcagaaga agaccatggg ctgggagcct acgcgtgacc aactgactga agagcagatc 480
gcagagtta aagaggcttt ctccctatth gacaaggacg ggaatgggac gatgacaacc 540
aaggagctgg ggacggtgtt gcggtctctg gggcagaacc ccacagaagc agagctgcag 600
gacatgatca atgaagtaga tgccgacggg aacggcacat tcgacttccc tgagttcctg 660
acgatgatgg caaggaaaat gaatgactca gacagtgaag aggaaattag agaagcgttc 720
cgcgtggcgg ataaggacgg caatggctac atcggcgcag cagagcttcg ccacgcgatg 780
acagacattg gagagaagtt aacagatgag gaggttgatg aaatgatcag ggtagcagac 840

atcgatgggg atggtcaggt aaactacgaa gagtttgtac aaatgatgac agcgaagggt	900
ggcggagggtt ctgtcgactc atcacgtcgt aagtggaata aggcagggtca cgcatggaga	960
gctatagggtc ggctgagctc acgttgggtt tccgagtgga tgtaccccga ggacggcgcc	1020
ctgaagagcg tgatcaagga ggggttgagg ctgaaggacg gcggccacta cgccgccgag	1080
gtcaggacca cctacaaggc caaaaagccc gtgcagctgc ccggcgccta catcgtcgac	1140
atcaagttgg acatcgtgtc ccacaacgag gactacacca tcgtggaaca gtgcgaacgc	1200
gccgagggcc gccactccac cggcggcatg gacgagctgt acaag	1245

<210> 14
 <211> 415
 <212> PRT
 <213> Homo sapiens

<400> 14

Met Val Ser Lys Gly Glu Glu Asp Asn Met Ala Ile Ile Lys Glu Phe
1 5 10 15

Met Arg Phe Lys Val His Met Glu Gly Ser Val Asn Gly His Glu Phe
20 25 30

Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr Glu Ala Phe Gln Thr
35 40 45

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

Ile Leu Ser Leu Gln Phe Met Tyr Gly Ser Lys Ala Tyr Ile Lys His
65 70 75 80

Pro Ala Asp Ile Pro Asp Tyr Phe Lys Leu Ser Phe Pro Glu Gly Phe
85 90 95

Arg Trp Glu Arg Val Met Ile Phe Glu Asp Gly Gly Ile Ile His Val
100 105 110

Asn Gln Asp Ser Ser Leu Gln Asp Gly Val Phe Ile Tyr Lys Val Lys
115 120 125

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

Thr Met Gly Trp Glu Pro Thr Arg Asp Gln Leu Thr Glu Glu Gln Ile
145 150 155 160

Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asn Gly
165 170 175

Thr Met Thr Thr Lys Glu Leu Gly Thr Val Leu Arg Ser Leu Gly Gln
180 185 190

Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
195 200 205

Asp Gly Asn Gly Thr Phe Asp Phe Pro Glu Phe Leu Thr Met Met Ala
210 215 220

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

Arg Val Ala Asp Lys Asp Gly Asn Gly Tyr Ile Gly Ala Ala Glu Leu
245 250 255

Arg His Ala Met Thr Asp Ile Gly Glu Lys Leu Thr Asp Glu Glu Val
260 265 270

Asp Glu Met Ile Arg Val Ala Asp Ile Asp Gly Asp Gly Gln Val Asn
275 280 285

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys Gly Gly Gly Gly Ser
290 295 300

Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His Ala Trp Arg
305 310 315 320

Ala Ile Gly Arg Leu Ser Ser Arg Trp Val Ser Glu Trp Met Tyr Pro
325 330 335

Glu Asp Gly Ala Leu Lys Ser Val Ile Lys Glu Gly Leu Arg Leu Lys

340

345

350

Asp Gly Gly His Tyr Ala Ala Glu Val Arg Thr Thr Tyr Lys Ala Lys
 355 360 365

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

Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Cys Glu Arg
 385 390 395 400

Ala Glu Gly Arg His Ser Thr Gly Gly Met Asp Glu Leu Tyr Lys
 405 410 415

<210> 15

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 15

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gtgatcaagg aggggttgag gctgaaggac ggcggccact acgccgccga ggtcaggacc	180
acctacaagg ccaaaaagcc cgtgcagctg cccggcgcct acatcgtcga catcaagttg	240
gacatcgtgt cccacaacga ggactacacc atcgtggaac agtgcgaacg cgccgagggc	300
cgccacccca ccggcggcat ggtcgggctg tacaaggag gtacaggcgg gagtctggtg	360
agcaagggcg aggaggataa catggccatc atcaaggagt tcatgcgctt caaggtgcac	420
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tacgaggcct tttagaccgc taagctgaag gtgaccaagg gtggccccct gcccttcgcc	540
tgggacatcc tgtcccttca gttcatgtac ggctccaagg cctacattaa gcacccagcc	600
gacatccccg actacttcaa gctgtccttc cccgagggtc tcaggtggga gcgcgtgatg	660
atcttcgagg acggcggcat tattcacgtt aaccaggact cctccctgca ggacggcgta	720
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aagaagacca tgggctggga gcctacgcgt gaccaactga ctgaagagca gatcgcagaa	840
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ctggggacgg tgctgcggtc tctggggcag aacccacag aagcagagct ccaggacatg 960
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 tgggataagg atggcaatgg ctacatctct gcagcagacc ttcgccacgt gatgacaaac 1140
 cttggagaga agttaacaga tgaagagggt gatgaaatga tcagggaagc agatatcgat 1200
 ggagaagggtc aggtaaacta cgaagagttt gtacaaatga tgacagcgaa g 1251

<210> 16
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His Ala Val
 1 5 10 15

Arg Ala Ile Gly Arg Leu Ser Ser Arg Trp Val Ser Glu Trp Met Tyr
 20 25 30

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

Lys Asp Gly Gly His Tyr Ala Ala Glu Val Arg Thr Thr Tyr Lys Ala
 50 55 60

Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Ile Val Asp Ile Lys Leu
 65 70 75 80

Asp Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Cys Glu
 85 90 95

Arg Ala Glu Gly Arg His Pro Thr Gly Gly Met Val Gly Leu Tyr Lys
 100 105 110

Gly Gly Thr Gly Gly Ser Leu Val Ser Lys Gly Glu Glu Asp Asn Met
 115 120 125

Ala Ile Ile Lys Glu Phe Met Arg Phe Lys Val His Met Glu Gly Ser

130

135

140

Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro
 145 150 155 160

Tyr Glu Ala Phe Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro
 165 170 175

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

Lys Ala Tyr Ile Lys His Pro Ala Asp Ile Pro Asp Tyr Phe Lys Leu
 195 200 205

Ser Phe Pro Glu Gly Phe Arg Trp Glu Arg Val Met Ile Phe Glu Asp
 210 215 220

Gly Gly Ile Ile His Val Asn Gln Asp Ser Ser Leu Gln Asp Gly Val
 225 230 235 240

Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Pro Asp Gly
 245 250 255

Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Pro Thr Arg Asp Gln
 260 265 270

Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe
 275 280 285

Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Asp Leu Gly Thr Val
 290 295 300

Leu Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met
 305 310 315 320

Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Asp
 325 330 335

Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu
 340 345 350

Glu Ile Arg Glu Ala Phe Arg Val Trp Asp Lys Asp Gly Asn Gly Tyr
 355 360 365

Ile Ser Ala Ala Asp Leu Arg His Val Met Thr Asn Leu Gly Glu Lys
 370 375 380

Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp
 385 390 395 400

Gly Glu Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala
 405 410 415

Lys

<210> 17
 <211> 1245
 <212> DNA
 <213> Homo sapiens

<400> 17
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 cggccctacg aggcctttca gaccgctaag ctgaaggtga ccaagggtgg cccctgccc 180
 ttgcctggg acatcctgtc cttcagttc atgtacggct ccaaggccta cattaagcac 240
 ccagccgaca tccccgacta cttcaagctg tccttccccg agggcttcag gtgggagcgc 300
 gtgatgatct tcgaggacgg cggcattatt cacgttaacc aggactcctc cctgcaggac 360
 ggcgtattca tctacaaggt gaagctgcgc ggcaccaact tccccccga cggccccgta 420
 atgcagaaga agacatggg ctgggagcct actcgggacc aactgactga agagcagatc 480
 gcagaattta aagaggcttt ctccctatth gacaaggacg gggatgggac aataacaacc 540
 aaggatctgg ggacggtgct gcggtctctg gggcagaacc ccacagaagc agagctccag 600
 gacatgatca atgaagtaga tgccgacggg aatggcacia tcgacttccc tgatttcctg 660
 acaatgatgg caagaaaaat gaaagacaca gacagtgaag aagaaattcg cgaagcgttc 720
 cgtgtgtggg ataaggatgg caatggctac atctctgcag cagaccttcg ccacgtgatg 780
 acaaaccttg gagagaagtt aacagatgaa gaggttgatg aaatgatcag ggaagcagat 840

atcgatggag aaggtcaggt aaactacgaa gagtttgtac aaatgatgac agcgaagggt	900
ggcggagggtt ctgtcgactc atcacgtcgt aagtggaata aggcaggtca cgcagtcaga	960
gctataggctc ggctgagctc acgttgggtt tccgagtgga tgtaccccga ggacggcgcc	1020
ctgaagagcg tgatcaagga ggggttgagg ctgaaggacg gcggccacta cgccgccgag	1080
gtcaggacca cctacaaggc caaaaagccc gtgcagctgc ccggcgccta catcgtcgac	1140
atcaagttgg acatcgtgtc ccacaacgag gactacacca tcgtggaaca gtgcgaacgc	1200
gccgagggcc gccactccac cggcggcatg gacgagctgt acaag	1245

<210> 18
 <211> 415
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Val Ser Lys Gly Glu Glu Asp Asn Met Ala Ile Ile Lys Glu Phe
1 5 10 15

Met Arg Phe Lys Val His Met Glu Gly Ser Val Asn Gly His Glu Phe
20 25 30

Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr Glu Ala Phe Gln Thr
35 40 45

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

Ile Leu Ser Leu Gln Phe Met Tyr Gly Ser Lys Ala Tyr Ile Lys His
65 70 75 80

Pro Ala Asp Ile Pro Asp Tyr Phe Lys Leu Ser Phe Pro Glu Gly Phe
85 90 95

Arg Trp Glu Arg Val Met Ile Phe Glu Asp Gly Gly Ile Ile His Val
100 105 110

Asn Gln Asp Ser Ser Leu Gln Asp Gly Val Phe Ile Tyr Lys Val Lys
115 120 125

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

Thr Met Gly Trp Glu Pro Thr Arg Asp Gln Leu Thr Glu Glu Gln Ile
145 150 155 160

Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly
165 170 175

Thr Ile Thr Thr Lys Asp Leu Gly Thr Val Leu Arg Ser Leu Gly Gln
180 185 190

Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
195 200 205

Asp Gly Asn Gly Thr Ile Asp Phe Pro Asp Phe Leu Thr Met Met Ala
210 215 220

Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe
225 230 235 240

Arg Val Trp Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Asp Leu
245 250 255

Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val
260 265 270

Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Glu Gly Gln Val Asn
275 280 285

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys Gly Gly Gly Gly Ser
290 295 300

Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Ala Gly His Ala Val Arg
305 310 315 320

Ala Ile Gly Arg Leu Ser Ser Arg Trp Val Ser Glu Trp Met Tyr Pro
325 330 335

Glu Asp Gly Ala Leu Lys Ser Val Ile Lys Glu Gly Leu Arg Leu Lys

340

345

350

Asp Gly Gly His Tyr Ala Ala Glu Val Arg Thr Thr Tyr Lys Ala Lys
355 360 365

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

Ile Val Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Cys Glu Arg
385 390 395 400

Ala Glu Gly Arg His Ser Thr Gly Gly Met Asp Glu Leu Tyr Lys
405 410 415

<210> 19
<211> 17
<212> PRT
<213> Homo sapiens

<400> 19

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Ala Ala Ala
1 5 10 15

Asp

<210> 20
<211> 38
<212> DNA
<213> Homo sapiens

<400> 20
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38

<210> 21
<211> 34
<212> DNA
<213> Homo sapiens

<400> 21
gatcaagctt ttacttgtac agctcgtcca tgcc

34