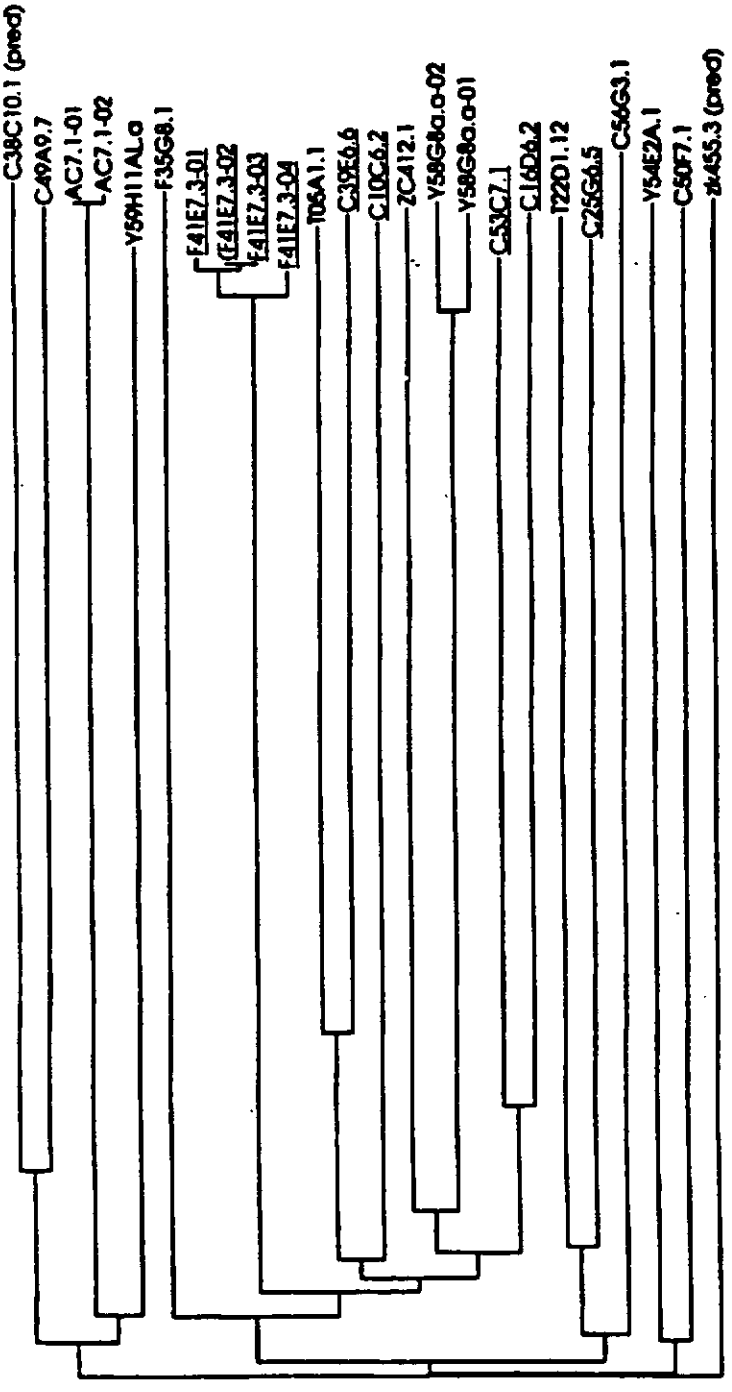

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FIG. 1

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<110> Lowery, David E.
Geary, Timothy G.
Kubiak, Teresa M.
Larsen, Martha J.

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gtg att ggt gga gct gga gtt ttg gca gaa gca ggc gaa gct gaa cta   96
Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu
             20                  25                  30

tct ggt gat gat gat ttt tat gag ctg act cct gta gaa ttg ata ata  144
Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile
         35                  40                  45

tgg tgc atg ctg tat gca att ata gcc ttc atg gca gtt gtt gga aat  192
Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
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ctt ctg gtt ctc tac ata aca ctg ttc aga tta aga gtc cgt tcc atc  240
Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
 65                  70                  75                  80

aca acc tac ttc att ctg aac ctc gga ttt gct gac ctc ttc act ggt  288
Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly
                 85                  90                  95

att ttt gcg att ccc ttc aag ttt cag gct gct ctt ttt caa gaa tgg  336
Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
            100                 105                 110

ttc ctg ccg cga tca ctc tgc cgg ata gtt cca tac gtg gaa aca gtt  384
Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val
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gct ctg aca gtt tca gtc ttc aca ctt gtg acg tca gca gtt cat gaa   432
Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu
    130                 135                 140

ttc cgt aca atg ttc ttc tcg aaa tgc tca caa atg agc cca aga tct   480
Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser
145                 150                 155                 160

gca aaa cga tgt gta ctt ttg ata tgg ata atg gcg gtt ctt gtg tct   528
Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser
                165                 170                 175

cta cca cat gga ttg ttc cat aat aca tac gaa ttt cca gat gac aat   576
Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn
            180                 185                 190

aat act tca att gta cag tgt ctc cca gta tat cct gat gct ggt tgg   624
Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp
        195                 200                 205

tgg aaa aca tac aat gtc tac ctt gtc ata atc caa tat ttt gtt cca   672
Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro
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atg att att ctt gac act gcg tac aca atg att gct gtt aaa ata tgg   720
Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp
225                 230                 235                 240

tca ttg agt cag tca aga gtt gaa ctt gat gaa aca aaa atg gca acc   768
Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr
                245                 250                 255

cag aag ctt atg cgt act ctc atc att gtc gtt gcc tgt ttc tca ttg   816
Gln Lys Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu
            260                 265                 270

tgt tgg ttt cca ttg gag acg tat cta ctt ttg aat gaa ttg aaa ccg   864
Cys Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro
        275                 280                 285

gaa att aat gga tgg aaa tac atc aat ttg gtg ttc ttc ttt tca cat   912
Glu Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His
    290                 295                 300

tgg ctg gcg atg agc aat tct tgt ctt aat cca att att tat gga ctt   960
Trp Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu
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tac aat aca aaa tac aac gag gaa tat cgt cgt ttg ttt cgc caa att  1008
Tyr Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile
                325                 330                 335

gga tgc att tgg caa cgg cag aaa agt ttg gac gat tcg atg aaa ccg  1056
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Pro
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Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile
         35                  40                  45

Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
     50                  55                  60

Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
 65                  70                  75                  80

Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly
                 85                  90                  95

Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
            100                 105                 110

Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val
        115                 120                 125

Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu
    130                 135                 140

Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser
145                 150                 155                 160

Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser
                165                 170                 175

Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn
            180                 185                 190

Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp
        195                 200                 205

Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro
    210                 215                 220

Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp
225                 230                 235                 240

Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr
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                245                 250                 255

Gln Lys Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu
            260                 265                 270

Cys Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro
        275                 280                 285

Glu Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His
    290                 295                 300

Trp Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu
305                 310                 315                 320

Tyr Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile
                325                 330                 335

Gly Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro
            340                 345                 350

Glu Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile
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Pro
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Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu
             20                  25                  30

tct ggt gat gat gat ttt tat gag ctg act cct gta gaa ttg ata ata  144
Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile
         35                  40                  45

tgg tgc atg ctg tat gca att ata gcc ttc atg gca gtt gtt gga aat  192
Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
     50                  55                  60

ctt ctg gtt ctc tac ata aca ctg ttc aga tta aga gtc cgt tcc atc  240
Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
 65                  70                  75                  80
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aca acc tac ttc att ctg aac ctc gga ttt gct gac ctc ttc act ggt   288
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                85                  90                  95

att ttt gcg att ccc ttc aag ttt cag gct gct ctt ttt caa gaa tgg   336
Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
            100                 105                 110

ttc ctg ccg cga tca ctc tgc cgg ata gtt cca tac gtg gaa aca gtt   384
Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val
        115                 120                 125

gct ctg aca gtt tca gtc ttc aca ctt gtg acg tca gca gtt cat gaa   432
Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu
    130                 135                 140

ttc cgt aca atg ttc ttc tcg aaa tgc tca caa atg agc cca aga tct   480
Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser
145                 150                 155                 160

gca aaa cga tgt gta ctt ttg ata tgg ata atg gcg gtt ctt gtg tct   528
Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser
                165                 170                 175

cta cca cat gga ttg ttc cat aat aca tac gaa ttt cca gat gac aat   576
Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn
            180                 185                 190

aat act tca att gta cag tgt ctc cca gta tat cct gat gct ggt tgg   624
Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp
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tgg aaa aca tac aat gtc tac ctt gtc ata atc caa tat ttt gtt cca   672
Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro
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atg att att ctt gac act gcg tac aca atg att gct gtt aaa ata tgg   720
Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp
225                 230                 235                 240

tca ttg agt cag tca aga gtt gaa ctt gat gaa aca aaa atg gca acc   768
Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr
                245                 250                 255

cag aag ata tca gtg gta tca atg gtt tca cca aac act caa tta tcg   816
Gln Lys Ile Ser Val Val Ser Met Val Ser Pro Asn Thr Gln Leu Ser
            260                 265                 270

cag ctt atg cgt act ctc atc att gtc gtt gcc tgt ttc tca ttg tgt   864
Gln Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu Cys
        275                 280                 285

tgg ttt cca ttg gag acg tat cta ctt ttg aat gaa ttg aaa ccg gaa   912
Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro Glu
    290                 295                 300

att aat gga tgg aaa tac atc aat ttg gtg ttc ttc ttt tca cat tgg   960
Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His Trp
305                 310                 315                 320
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ctg gcg atg agc aat tct tgt ctt aat cca att att tat gga ctt tac   1008
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aat aca aaa tac aac gag gaa tat cgt cgt ttg ttt cgc caa att gga   1056
Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile Gly
            340                 345                 350

tgc att tgg caa cgg cag aaa agt ttg gac gat tcg atg aaa ccg gag   1104
Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro Glu
        355                 360                 365

cgt cgt tgg aat tct tca aat gat tgt caa gat caa cag gaa att gat   1152
Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile Asp
    370                 375                 380

caa att gtt gat att cca cca gtt att tct aca aat aat ctt tct ccc   1200
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             20                  25                  30

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         35                  40                  45

Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn
     50                  55                  60

Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile
 65                  70                  75                  80

Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly
                 85                  90                  95

Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp
            100                 105                 110

Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val
        115                 120                 125

Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu
    130                 135                 140

Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser
145                 150                 155                 160

Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser
                165                 170                 175
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Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn
            180                 185                 190

Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp
        195                 200                 205

Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro
    210                 215                 220

Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp
225                 230                 235                 240

Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr
                245                 250                 255

Gln Lys Ile Ser Val Val Ser Met Val Ser Pro Asn Thr Gln Leu Ser
            260                 265                 270

Gln Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu Cys
        275                 280                 285

Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro Glu
    290                 295                 300

Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His Trp
305                 310                 315                 320

Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu Tyr
                325                 330                 335

Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile Gly
            340                 345                 350

Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro Glu
        355                 360                 365

Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile Asp
    370                 375                 380

Gln Ile Val Asp Ile Pro Pro Val Ile Ser Thr Asn Asn Leu Ser Pro
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  1               5                  10                  15
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aca cct tca tat caa agt aca tgt aaa atc aaa aac aac ccc atg gaa   96
Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
             20                  25                  30

atg gaa tat ttc cgc cca ttc ttt att tct atg tat tgt gct gtt ttt  144
Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
         35                  40                  45

ttg gtt gct agt tcc ggt aat ttt ttg gtg gtg tac gtt gtg atg acg  192
Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
     50                  55                  60

aac aag cga atg cag acg atc acc aac att ttt att aca aat ctc gca  240
Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
 65                  70                  75                  80

gtt tct gat ata atg gtt aac ttt aca tcg ttg tgg ctt aca cca aca  288
Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                 85                  90                  95

tac acc tca ata gga cat tgg ata ttc gga ggt gga ttg tgt cat ggt  336
Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
            100                 105                 110

tta ccc ctg ttc caa ggt aca agt atc ttc atc agt acg tgg aca ctt  384
Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
        115                 120                 125

acg gct ata gcc ata gat cga tac ata gtg atc gtg cac aac tca tca  432
Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

aat atc aat ata aat gat aga atg tcc atg aga tct tgc ctt tcg ttc  480
Asn Ile Asn Ile Asn Asp Arg Met Ser Met Arg Ser Cys Leu Ser Phe
145                 150                 155                 160

att gtc ctc att tgg cta tgc tca ttg ctt ctg gtc act ccg tat gcc  528
Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

atc aac atg aag ctc aac tac att cat gaa cca tgt gat ttt ctg ata  576
Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190

tgt agt gag gac tgg agc aat gcc gaa ttt cga tct att ttt gga att  624
Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

gtg gtg atg att ctt caa ttc att ttg cca ttt gta ctc att gcc att  672
Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220

agt tac ata aaa ata tgg ttg ttc cta aat agc cgt caa agt atg acc  720
Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

gag aga aaa tcc gat atc aag cgc aaa aag cgt tta cta cgg atg ttg  768
Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
                245                 250                 255
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att gtc atg gtg gtc atc ttc gca att tgc tgg ttc cca ttc aac ctc   816
Ile Val Met Val Val Ile Phe Ala Ile Cys Trp Phe Pro Phe Asn Leu
            260                 265                 270

tta aac tgt ctc cga gat ctc aag ttg gat aat ttc atg cgt ggc tac   864
Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285

ttc agt ttt gtt ttc ctt tcc gtg cat ttg atg agt atg aca gct acc   912
Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

gcc tgg aat cca atc ctc tac gca ttc atg aat gag acc ttc cgt gag   960
Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

gag ttc gca aaa gtt gtt ccc tgc ttg ttt gcg cgt cgt cct gga act   1008
Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335

ggt cca att cgc gtc atc act gaa cgc acc gct atg ata act aac ccg   1056
Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

ttt cga cgt gca aac cga aaa aaa aaa gtg gag gaa cag cct gtt acg   1104
Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365

gtg att tct gat tca gag agt cca ctt caa act gca gtg gag ccg cag   1152
Val Ile Ser Asp Ser Glu Ser Pro Leu Gln Thr Ala Val Glu Pro Gln
    370                 375                 380

cgc agt atc gtg tat ctc gat gag cct gag aac gga tca agt tgt cag   1200
Arg Ser Ile Val Tyr Leu Asp Glu Pro Glu Asn Gly Ser Ser Cys Gln
385                 390                 395                 400

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Thr Leu Leu Leu
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Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
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Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
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Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
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Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
100 105 110

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

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

Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
165 170 175

Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
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Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
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Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
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Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
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Ile Val Met Val Val Ile Phe Ala Ile Cys Trp Phe Pro Phe Asn Leu
260 265 270

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

Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
340 345 350

Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
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Val Ile Ser Asp Ser Glu Ser Pro Leu Gln Thr Ala Val Glu Pro Gln
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Thr Leu Leu Leu

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<211> 1208
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1206)

<220>
<223> Clone identifier: CEGPCR12h

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Met Ser Asn Asp Leu Val Pro Ser Val Ser Ser Ile Leu Asn Glu Thr
  1               5                  10                  15

aca cct tca tat caa agt aca tgt aaa atc aaa aac aac ccc atg gaa   96
Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
            20                  25                  30

atg gaa tat ttc cgc cca ttc ttt att tct atg tat tgt gct gtt ttt   144
Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
        35                  40                  45

ttg gtt gct agt tcc ggt aat ttt ttg gtg gtg tac gtt gtg atg acg   192
Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
    50                  55                  60

aac aag cga atg cag acg atc acc aac att ttt att aca aat ctc gca   240
Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
65                  70                  75                  80

gtt tct gat ata atg gtt aac ttt aca tcg ttg tgg ctt aca cca aca   288
Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                85                  90                  95

tac acc tca ata gga cat tgg ata ttc gga ggt gga ttg tgt cat ggt   336
Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
            100                 105                 110

tta ccc ctg ttc caa ggt aca agt atc ttc atc agt acg tgg aca ctt   384
Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
        115                 120                 125

acg gct ata gcc ata gat cga tac ata gtg atc gtg cac aac tca tca   432
Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

aat atc aat ata aat gat aga atg tcc atg aga tct tgc ctt tcg ttc   480
Asn Ile Asn Ile Asn Asp Arg Met Ser Met Arg Ser Cys Leu Ser Phe
145                 150                 155                 160

att gtc ctc att tgg cta tgc tca ttg ctt ctg gtc act ccg tat gcc   528
Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

atc aac atg aag ctc aac tac att cat gaa cca tgt gat ttt ctg ata   576
Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190
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tgt agt gag gac tgg agc aat gcc gaa ttt cga tct att ttt gga att   624
Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

gtg gtg atg att ctt caa ttc att ttg cca ttt gta ctc att gcc att   672
Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220

agt tac ata aaa ata tgg ttg ttc cta aat agc cgt caa agt atg acc   720
Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

gag aga aaa tcc gat atc aag cgc aaa aag cgt tta cta cgg atg ttg   768
Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
            245                 250                 255

att gtc atg gtg gtc atc ttc gca att tgc tgg ttc cca ttc aac ctc   816
Ile Val Met Val Val Ile Phe Ala Ile Cys Trp Phe Pro Phe Asn Leu
            260                 265                 270

tta aac tgt ctc cga gat ctc aag ttg gat aat ttc atg cgt ggc tac   864
Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285

ttc agt ttt gtt ttc ctt tcc gtg cat ttg atg agt atg aca gct acc   912
Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

gcc tgg aat cca atc ctc tac gca ttc atg aat gag acc ttc cgt gag   960
Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

gag ttc gca aaa gtt gtt ccc tgc ttg ttt gcg cgt cgt cct gga act  1008
Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335

ggt cca att cgc gtc atc act gaa cgc acc gct atg ata act aac ccg  1056
Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

ttt cga cgt gca aac cga aaa aaa aaa gtg gag gaa cag cct gtt acg  1104
Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365

gtg att tct gag agt cca ctt caa act gca gtg gag ccg cag cgc agt  1152
Val Ile Ser Glu Ser Pro Leu Gln Thr Ala Val Glu Pro Gln Arg Ser
    370                 375                 380

atc gtg tat ctc gat gag cct gag aac gga tca agt tgt cag acg ctt  1200
Ile Val Tyr Leu Asp Glu Pro Glu Asn Gly Ser Ser Cys Gln Thr Leu
385                 390                 395                 400

ctg ctt ta                                                      1208
Leu Leu
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<210> 8
<211> 402
<212> PRT
<213> Homo sapiens

<400> 8

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Met Ser Asn Asp Leu Val Pro Ser Val Ser Ser Ile Leu Asn Glu Thr
 1               5                  10                  15

Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
            20                  25                  30

Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
        35                  40                  45

Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
    50                  55                  60

Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
65                  70                  75                  80

Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                85                  90                  95

Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
            100                 105                 110

Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
        115                 120                 125

Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

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

Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190

Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220

Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
                245                 250                 255

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

Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285

Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335
```

```
Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365

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

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

Leu Leu
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<210> 9
<211> 1220
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1218)

<220>
<223> Clone identifier: CEGPCR12u

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Met Ser Asn Asp Leu Val Pro Ser Val Ser Ser Ile Leu Asn Glu Thr
  1               5                  10                  15

aca cct tca tat caa agt aca tgt aaa atc aaa aac aac ccc atg gaa   96
Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
             20                  25                  30

atg gaa tat ttc cgc cca ttc ttt att tct atg tat tgt gct gtt ttt   144
Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
         35                  40                  45

ttg gtt gct agt tcc ggt aat ttt ttg gtg gtg tac gtt gtg atg acg   192
Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
     50                  55                  60

aac aag cga atg cag acg atc acc aac att ttt att aca aat ctc gca   240
Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
 65                  70                  75                  80

gtt tct gat ata atg gtt aac ttt aca tcg ttg tgg ctt aca cca aca   288
Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                 85                  90                  95

tac acc tca ata gga cat tgg ata ttc gga ggt gga ttg tgt cat ggt   336
Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
            100                 105                 110

tta ccc ctg ttc caa ggt aca agt atc ttc atc agt acg tgg aca ctt   384
Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
        115                 120                 125
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acg gct ata gcc ata gat cga tac ata gtg atc gtg cac aac tca tca   432
Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

aat atc aat ata aat gat aga atg tcc atg aga tct tgc ctt tcg ttc   480
Asn Ile Asn Ile Asn Asp Arg Met Ser Met Arg Ser Cys Leu Ser Phe
145                 150                 155                 160

att gtc ctc att tgg cta tgc tca ttg ctt ctg gtc act ccg tat gcc   528
Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

atc aac atg aag ctc aac tac att cat gaa cca tgt gat ttt ctg ata   576
Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190

tgt agt gag gac tgg agc aat gcc gaa ttt cga tct att ttt gga att   624
Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

gtg gtg atg att ctt caa ttc att ttg cca ttt gta ctc att gcc att   672
Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220

agt tac ata aaa ata tgg ttg ttc cta aat agc cgt caa agt atg acc   720
Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

gag aga aaa tcc gat atc aag cgc aaa aag cgt tta cta cgg atg ttg   768
Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
                245                 250                 255

att gtc atg gtg gtc atc ttc gca att tgc tgg ttc cca ttc aac ctc   816
Ile Val Met Val Val Ile Phe Ala Ile Cys Trp Phe Pro Phe Asn Leu
            260                 265                 270

tta aac tgt ctc cga gat ctc aag ttg gat aat ttc atg cgt ggc tac   864
Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285

ttc agt ttt gtt ttc ctt tcc gtg cat ttg atg agt atg aca gct acc   912
Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

gcc tgg aat cca atc ctc tac gca ttc atg aat gag acc ttc cgt gag   960
Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

gag ttc gca aaa gtt gtt ccc tgc ttg ttt gcg cgt cgt cct gga act  1008
Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335

ggt cca att cgc gtc atc act gaa cgc acc gct atg ata act aac ccg  1056
Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

ttt cga cgt gca aac cga aaa aaa aaa gtg gag gaa cag cct gtt acg  1104
Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365
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gtg att tct gaa aca gat tca gag agt cca ctt caa act gca gtg gag   1152
Val Ile Ser Glu Thr Asp Ser Glu Ser Pro Leu Gln Thr Ala Val Glu
    370                 375                 380

ccg cag cgc agt atc gtg tat ctc gat gag cct gag aac gga tca agt   1200
Pro Gln Arg Ser Ile Val Tyr Leu Asp Glu Pro Glu Asn Gly Ser Ser
385                 390                 395                 400

tgt cag acg ctt ctg ctt ta                                       1220
Cys Gln Thr Leu Leu Leu
                405
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<210> 10
<211> 406
<212> PRT
<213> Homo sapiens

<400> 10

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Met Ser Asn Asp Leu Val Pro Ser Val Ser Ser Ile Leu Asn Glu Thr
  1               5                  10                  15

Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
             20                  25                  30

Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
         35                  40                  45

Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
     50                  55                  60

Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
 65                  70                  75                  80

Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                 85                  90                  95

Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
            100                 105                 110

Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
        115                 120                 125

Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

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

Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190

Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220
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```
Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
                245                 250                 255

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

Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285

Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335

Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365

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

Pro Gln Arg Ser Ile Val Tyr Leu Asp Glu Pro Glu Asn Gly Ser Ser
385                 390                 395                 400

Cys Gln Thr Leu Leu Leu
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<210> 11
<211> 1318
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1143)

<220>
<223> Clone identifier: CEGPCR12v

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  1               5                  10                  15

aca cct tca tat caa agt aca tgt aaa atc aaa aac aac ccc atg gaa   96
Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
            20                  25                  30

atg gaa tat ttc cgc cca ttc ttt att tct atg tat tgt gct gtt ttt   144
Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
        35                  40                  45
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ttg gtt gct agt tcc ggt aat ttt ttg gtg gtg tac gtt gtg atg acg   192
Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
     50                  55                  60

aac aag cga atg cag acg atc acc aac att ttt att aca aat ctc gca   240
Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
 65                  70                  75                  80

gtt tct gat ata atg gtt aac ttt aca tcg ttg tgg ctt aca cca aca   288
Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                 85                  90                  95

tac acc tca ata gga cat tgg ata ttc gga ggt gga ttg tgt cat ggt   336
Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
            100                 105                 110

tta ccc ctg ttc caa ggt aca agt atc ttc atc agt acg tgg aca ctt   384
Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
        115                 120                 125

acg gct ata gcc ata gat cga tac ata gtg atc gtg cac aac tca tca   432
Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

aat atc aat ata aat gat aga atg tcc atg aga tct tgc ctt tcg ttc   480
Asn Ile Asn Ile Asn Asp Arg Met Ser Met Arg Ser Cys Leu Ser Phe
145                 150                 155                 160

att gtc ctc att tgg cta tgc tca ttg ctt ctg gtc act ccg tat gcc   528
Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

atc aac atg aag ctc aac tac att cat gaa cca tgt gat ttt ctg ata   576
Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190

tgt agt gag gac tgg agc aat gcc gaa ttt cga tct att ttt gga att   624
Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

gtg gtg atg att ctt caa ttc att ttg cca ttt gta ctc att gcc att   672
Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220

agt tac ata aaa ata tgg ttg ttc cta aat agc cgt caa agt atg acc   720
Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

gag aga aaa tcc gat atc aag cgc aaa aag cgt tta cta cgg atg ttg   768
Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
                245                 250                 255

att gtc atg gtg gtc atc ttc gca att tgc tgg ttc cca ttc aac ctc   816
Ile Val Met Val Val Ile Phe Ala Ile Cys Trp Phe Pro Phe Asn Leu
            260                 265                 270

tta aac tgt ctc cga gat ctc aag ttg gat aat ttc atg cgt ggc tac   864
Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285
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```
ttc agt ttt gtt ttc ctt tcc gtg cat ttg atg agt atg aca gct acc   912
Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

gcc tgg aat cca atc ctc tac gca ttc atg aat gag acc ttc cgt gag   960
Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

gag ttc gca aaa gtt gtt ccc tgc ttg ttt gcg cgt cgt cct gga act   1008
Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335

ggt cca att cgc gtc atc act gaa cgc acc gct atg ata act aac ccg   1056
Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

ttt cga cgt gca aac cga aaa aaa aaa gtg gag gaa cag cct gtt acg   1104
Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365

gtg att tct gaa ctt tta cac ccg aca tcc aac gaa gaa taggaagcca   1153
Val Ile Ser Glu Leu Leu His Pro Thr Ser Asn Glu Glu
    370                 375                 380

ttcattccct gcatgcactc gttgtcagtg aacttttcaa caaaccagca atctttagaa 1213

acagattcag agagtccact tcaaactgca gtggagccgc agcgcagtat cgtgtatctc 1273

gatgagcctg agaacggatc aagttgtcag acgcttctgc tttaa                 1318
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<210> 12
<211> 381
<212> PRT
<213> Homo sapiens

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Thr Pro Ser Tyr Gln Ser Thr Cys Lys Ile Lys Asn Asn Pro Met Glu
             20                  25                  30

Met Glu Tyr Phe Arg Pro Phe Phe Ile Ser Met Tyr Cys Ala Val Phe
         35                  40                  45

Leu Val Ala Ser Ser Gly Asn Phe Leu Val Val Tyr Val Val Met Thr
     50                  55                  60

Asn Lys Arg Met Gln Thr Ile Thr Asn Ile Phe Ile Thr Asn Leu Ala
 65                  70                  75                  80

Val Ser Asp Ile Met Val Asn Phe Thr Ser Leu Trp Leu Thr Pro Thr
                 85                  90                  95

Tyr Thr Ser Ile Gly His Trp Ile Phe Gly Gly Gly Leu Cys His Gly
             100                 105                 110

Leu Pro Leu Phe Gln Gly Thr Ser Ile Phe Ile Ser Thr Trp Thr Leu
         115                 120                 125
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Thr Ala Ile Ala Ile Asp Arg Tyr Ile Val Ile Val His Asn Ser Ser
    130                 135                 140

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

Ile Val Leu Ile Trp Leu Cys Ser Leu Leu Leu Val Thr Pro Tyr Ala
                165                 170                 175

Ile Asn Met Lys Leu Asn Tyr Ile His Glu Pro Cys Asp Phe Leu Ile
            180                 185                 190

Cys Ser Glu Asp Trp Ser Asn Ala Glu Phe Arg Ser Ile Phe Gly Ile
        195                 200                 205

Val Val Met Ile Leu Gln Phe Ile Leu Pro Phe Val Leu Ile Ala Ile
    210                 215                 220

Ser Tyr Ile Lys Ile Trp Leu Phe Leu Asn Ser Arg Gln Ser Met Thr
225                 230                 235                 240

Glu Arg Lys Ser Asp Ile Lys Arg Lys Lys Arg Leu Leu Arg Met Leu
                245                 250                 255

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

Leu Asn Cys Leu Arg Asp Leu Lys Leu Asp Asn Phe Met Arg Gly Tyr
        275                 280                 285

Phe Ser Phe Val Phe Leu Ser Val His Leu Met Ser Met Thr Ala Thr
    290                 295                 300

Ala Trp Asn Pro Ile Leu Tyr Ala Phe Met Asn Glu Thr Phe Arg Glu
305                 310                 315                 320

Glu Phe Ala Lys Val Val Pro Cys Leu Phe Ala Arg Arg Pro Gly Thr
                325                 330                 335

Gly Pro Ile Arg Val Ile Thr Glu Arg Thr Ala Met Ile Thr Asn Pro
            340                 345                 350

Phe Arg Arg Ala Asn Arg Lys Lys Lys Val Glu Glu Gln Pro Val Thr
        355                 360                 365

Val Ile Ser Glu Leu Leu His Pro Thr Ser Asn Glu Glu
    370                 375                 380
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<210> 13
<211> 1163
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1161)

<220>
<223> Clone identifier: CEGPCR13

<400> 13

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Met Ile Asn Glu Thr Glu Glu Thr Cys Asp Arg Tyr Ile Asp Lys His
  1               5                  10                  15

cca gat atg aca aat gaa cca aca gtc ctt gtc aca ttc tcc ctg ctt   96
Pro Asp Met Thr Asn Glu Pro Thr Val Leu Val Thr Phe Ser Leu Leu
            20                  25                  30

tat ctt cat att ttt ctt ctt gga atc cta gga aat tcg gct gtt cta  144
Tyr Leu His Ile Phe Leu Leu Gly Ile Leu Gly Asn Ser Ala Val Leu
        35                  40                  45

tat ctt aca atg aaa cat cgt caa tta caa act gtt caa aat ata ttt  192
Tyr Leu Thr Met Lys His Arg Gln Leu Gln Thr Val Gln Asn Ile Phe
    50                  55                  60

att ttg aac tta tgc gca tcg aat gtt tta atg tgc ttg acg agt ctt  240
Ile Leu Asn Leu Cys Ala Ser Asn Val Leu Met Cys Leu Thr Ser Leu
65                  70                  75                  80

cca atc aca ttt atc aca aat gtc tac aaa caa tgg ttc ttc tca tcg  288
Pro Ile Thr Phe Ile Thr Asn Val Tyr Lys Gln Trp Phe Phe Ser Ser
                85                  90                  95

cct gtt tgt aaa ctt att cca ttg gtt cag gga gct tca atc ttt gtc  336
Pro Val Cys Lys Leu Ile Pro Leu Val Gln Gly Ala Ser Ile Phe Val
            100                 105                 110

tcc act ttc tcc ctt tcc gcc att gca ctt gac cga tac aac ctc gtg  384
Ser Thr Phe Ser Leu Ser Ala Ile Ala Leu Asp Arg Tyr Asn Leu Val
        115                 120                 125

gtt cgt cct cat aaa caa aaa ctc agt tca cga agt gca atg atg att  432
Val Arg Pro His Lys Gln Lys Leu Ser Ser Arg Ser Ala Met Met Ile
    130                 135                 140

gct ctt ctc att tgg gtt att agt gta gtt gtt tgt atg cca tat gga  480
Ala Leu Leu Ile Trp Val Ile Ser Val Val Val Cys Met Pro Tyr Gly
145                 150                 155                 160

tgg tac atg gat gtg gag aag ctc aat gga tta tgt gga gag tac tgt  528
Trp Tyr Met Asp Val Glu Lys Leu Asn Gly Leu Cys Gly Glu Tyr Cys
                165                 170                 175

tct gag cac tgg cca tta gca gaa gta cga aag gga tat act ttt ttg  576
Ser Glu His Trp Pro Leu Ala Glu Val Arg Lys Gly Tyr Thr Phe Leu
            180                 185                 190

gtg tta atc act caa ttt ttg ttt cct ttt gct acg atg gct ttt tgc  624
Val Leu Ile Thr Gln Phe Leu Phe Pro Phe Ala Thr Met Ala Phe Cys
        195                 200                 205

tat tat aat att ttt tca aga ctc aga caa cga gtg gaa acg aaa ctg  672
Tyr Tyr Asn Ile Phe Ser Arg Leu Arg Gln Arg Val Glu Thr Lys Leu
    210                 215                 220

aag aaa tta tca gaa aga tct caa ctt ttg gag aat agt aca aca tgt  720
Lys Lys Leu Ser Glu Arg Ser Gln Leu Leu Glu Asn Ser Thr Thr Cys
225                 230                 235                 240
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gga acc act aac cac att gtt agc att aac gcg gaa gca gtt caa aat   768
Gly Thr Thr Asn His Ile Val Ser Ile Asn Ala Glu Ala Val Gln Asn
                245                 250                 255

ggt ctg gaa aac aaa caa aga tta gct gtt ctt gct caa caa aga agg   816
Gly Leu Glu Asn Lys Gln Arg Leu Ala Val Leu Ala Gln Gln Arg Arg
            260                 265                 270

aca act act att tta tcg tgc atg gtt ctt ctt ttt gca ttt aca tgg   864
Thr Thr Thr Ile Leu Ser Cys Met Val Leu Leu Phe Ala Phe Thr Trp
        275                 280                 285

ctt cca cat aat gtt gtc act ttg atg ata gaa tac gat gga ttc ttt   912
Leu Pro His Asn Val Val Thr Leu Met Ile Glu Tyr Asp Gly Phe Phe
    290                 295                 300

ttt cat tct gat gag aca tcg gca acc agt acc gat cat aca tat att   960
Phe His Ser Asp Glu Thr Ser Ala Thr Ser Thr Asp His Thr Tyr Ile
305                 310                 315                 320

gtt tca atg act gct cat tta ata tcc atg tta aca aat gta acc aac  1008
Val Ser Met Thr Ala His Leu Ile Ser Met Leu Thr Asn Val Thr Asn
                325                 330                 335

cca ttt ctg tat gct tgg ctt aac cca atg ttc aaa gaa atg ctt att  1056
Pro Phe Leu Tyr Ala Trp Leu Asn Pro Met Phe Lys Glu Met Leu Ile
            340                 345                 350

aaa act ctc aga ggt gga agt aaa tcc ccg aaa cca gct gac atc aag  1104
Lys Thr Leu Arg Gly Gly Ser Lys Ser Pro Lys Pro Ala Asp Ile Lys
        355                 360                 365

caa act tca ttc att cga atg ccg aat agt ggt gcg cca agt caa tct  1152
Gln Thr Ser Phe Ile Arg Met Pro Asn Ser Gly Ala Pro Ser Gln Ser
    370                 375                 380

tcc tac ctg tg                                                  1163
Ser Tyr Leu
385
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<210> 14
<211> 387
<212> PRT
<213> Homo sapiens

<400> 14

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Met Ile Asn Glu Thr Glu Glu Thr Cys Asp Arg Tyr Ile Asp Lys His
  1               5                  10                  15

Pro Asp Met Thr Asn Glu Pro Thr Val Leu Val Thr Phe Ser Leu Leu
            20                  25                  30

Tyr Leu His Ile Phe Leu Leu Gly Ile Leu Gly Asn Ser Ala Val Leu
        35                  40                  45

Tyr Leu Thr Met Lys His Arg Gln Leu Gln Thr Val Gln Asn Ile Phe
    50                  55                  60

Ile Leu Asn Leu Cys Ala Ser Asn Val Leu Met Cys Leu Thr Ser Leu
65                  70                  75                  80
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Pro Ile Thr Phe Ile Thr Asn Val Tyr Lys Gln Trp Phe Phe Ser Ser
85 90 95

Pro Val Cys Lys Leu Ile Pro Leu Val Gln Gly Ala Ser Ile Phe Val
100 105 110

Ser Thr Phe Ser Leu Ser Ala Ile Ala Leu Asp Arg Tyr Asn Leu Val
115 120 125

Val Arg Pro His Lys Gln Lys Leu Ser Ser Arg Ser Ala Met Met Ile
130 135 140

Ala Leu Leu Ile Trp Val Ile Ser Val Val Val Cys Met Pro Tyr Gly
145 150 155 160

Trp Tyr Met Asp Val Glu Lys Leu Asn Gly Leu Cys Gly Glu Tyr Cys
165 170 175

Ser Glu His Trp Pro Leu Ala Glu Val Arg Lys Gly Tyr Thr Phe Leu
180 185 190

Val Leu Ile Thr Gln Phe Leu Phe Pro Phe Ala Thr Met Ala Phe Cys
195 200 205

Tyr Tyr Asn Ile Phe Ser Arg Leu Arg Gln Arg Val Glu Thr Lys Leu
210 215 220

Lys Lys Leu Ser Glu Arg Ser Gln Leu Leu Glu Asn Ser Thr Thr Cys
225 230 235 240

Gly Thr Thr Asn His Ile Val Ser Ile Asn Ala Glu Ala Val Gln Asn
245 250 255

Gly Leu Glu Asn Lys Gln Arg Leu Ala Val Leu Ala Gln Gln Arg Arg
260 265 270

Thr Thr Thr Ile Leu Ser Cys Met Val Leu Leu Phe Ala Phe Thr Trp
275 280 285

Leu Pro His Asn Val Val Thr Leu Met Ile Glu Tyr Asp Gly Phe Phe
290 295 300

Phe His Ser Asp Glu Thr Ser Ala Thr Ser Thr Asp His Thr Tyr Ile
305 310 315 320

Val Ser Met Thr Ala His Leu Ile Ser Met Leu Thr Asn Val Thr Asn
325 330 335

Pro Phe Leu Tyr Ala Trp Leu Asn Pro Met Phe Lys Glu Met Leu Ile
340 345 350

Lys Thr Leu Arg Gly Gly Ser Lys Ser Pro Lys Pro Ala Asp Ile Lys
355 360 365

Gln Thr Ser Phe Ile Arg Met Pro Asn Ser Gly Ala Pro Ser Gln Ser
370 375 380

Ser Tyr Leu
385

<210> 15

<211> 1352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1350)

<220>
<223> Clone identifier: CEGPCR14

<400> 15

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Met Gly Asp Ala Glu Ser His His Cys Ile Asp Val Asn Ala Ile Leu
  1               5                  10                  15

cag cag ttc aat gat tgg aca gtc ctc ttt gaa gtt cgg ctt gga tat   96
Gln Gln Phe Asn Asp Trp Thr Val Leu Phe Glu Val Arg Leu Gly Tyr
             20                  25                  30

tca gta cta tac ttt ctc ata tta ata atc gga ttg gtt gga aat ggg   144
Ser Val Leu Tyr Phe Leu Ile Leu Ile Ile Gly Leu Val Gly Asn Gly
         35                  40                  45

cta ttg atc act tca att tta atg cga aag aaa ctt tcc gtg gca aac   192
Leu Leu Ile Thr Ser Ile Leu Met Arg Lys Lys Leu Ser Val Ala Asn
     50                  55                  60

ata ttc ttg ata aac ctg gca gtt tct gat ttg ctt ctt tgc atc acg   240
Ile Phe Leu Ile Asn Leu Ala Val Ser Asp Leu Leu Leu Cys Ile Thr
 65                  70                  75                  80

gcg gtg ccg atc act cca gta ttg gcg ttt atg aag cga tgg ata ttt   288
Ala Val Pro Ile Thr Pro Val Leu Ala Phe Met Lys Arg Trp Ile Phe
                 85                  90                  95

gga ata att atg tgt aaa ttg gtt cca act tgt cag gcg ttt tcg gtg   336
Gly Ile Ile Met Cys Lys Leu Val Pro Thr Cys Gln Ala Phe Ser Val
            100                 105                 110

ctc att tct tca tgg tct ttg tgt tac atc gca att gat aga tat cga   384
Leu Ile Ser Ser Trp Ser Leu Cys Tyr Ile Ala Ile Asp Arg Tyr Arg
        115                 120                 125

agt att gtg acg cca ctc cgg gaa cca tgg tct gat agg cat gca agg   432
Ser Ile Val Thr Pro Leu Arg Glu Pro Trp Ser Asp Arg His Ala Arg
    130                 135                 140

tgg ctt ctg atg ttc aca tgg gtg gtc gcc ttc ctt gct agt tat cct   480
Trp Leu Leu Met Phe Thr Trp Val Val Ala Phe Leu Ala Ser Tyr Pro
145                 150                 155                 160

cta tat tac tca cag aac ttg aaa aca atg gtt att gaa aat gtg aca   528
Leu Tyr Tyr Ser Gln Asn Leu Lys Thr Met Val Ile Glu Asn Val Thr
                165                 170                 175

tta tgt gga gat ttt tgc ggc gag ttc aat tgg cag tcg gat gaa ata   576
Leu Cys Gly Asp Phe Cys Gly Glu Phe Asn Trp Gln Ser Asp Glu Ile
            180                 185                 190
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tcc aag ttg aca tat act acg agt tta ttg att att cag ctg att att   624
Ser Lys Leu Thr Tyr Thr Thr Ser Leu Leu Ile Ile Gln Leu Ile Ile
        195                 200                 205

cca gca att atc atg tct ttt tgt tat tta atg att cta caa aag gta   672
Pro Ala Ile Ile Met Ser Phe Cys Tyr Leu Met Ile Leu Gln Lys Val
    210                 215                 220

caa acc gac tgg ctt gtc gac gag gga tcc atg ttg act gcc gca caa   720
Gln Thr Asp Trp Leu Val Asp Glu Gly Ser Met Leu Thr Ala Ala Gln
225                 230                 235                 240

cag gct caa aca gca gtt cga aag cga cga gtg atg tac gtg ttg att   768
Gln Ala Gln Thr Ala Val Arg Lys Arg Arg Val Met Tyr Val Leu Ile
                245                 250                 255

cta atg gtt att gtt ttt atg gct tgc tgg ttc ccg ttg tcc gcc gtg   816
Leu Met Val Ile Val Phe Met Ala Cys Trp Phe Pro Leu Ser Ala Val
            260                 265                 270

aat ttg ttc aga gat ctc gga atg cga ttc gag ttc tgt caa act gtt   864
Asn Leu Phe Arg Asp Leu Gly Met Arg Phe Glu Phe Cys Gln Thr Val
        275                 280                 285

tac aag gtt tta atg atg gac caa atg tat ttc aag ttg ctc aat gtg   912
Tyr Lys Val Leu Met Met Asp Gln Met Tyr Phe Lys Leu Leu Asn Val
    290                 295                 300

cac gtc atc gcg atg act tcg atc gta tgg aat ccg gtg ctc tat ttc   960
His Val Ile Ala Met Thr Ser Ile Val Trp Asn Pro Val Leu Tyr Phe
305                 310                 315                 320

tgg atg agc aag cgt cat cga cga gcc ctg aaa gac gac atg acg tgg  1008
Trp Met Ser Lys Arg His Arg Arg Ala Leu Lys Asp Asp Met Thr Trp
                325                 330                 335

ctc acc aat gct cgc cgt cat aca aac gtc ggc gtt ctg tct cgc ttc  1056
Leu Thr Asn Ala Arg Arg His Thr Asn Val Gly Val Leu Ser Arg Phe
            340                 345                 350

aca cct tct cca tca gtt tca gtg gtt tac aga cga act ctg gag cga  1104
Thr Pro Ser Pro Ser Val Ser Val Val Tyr Arg Arg Thr Leu Glu Arg
        355                 360                 365

cat cta ggt gtc aat cat ttc cgc cgt ggc aca ctt gcg gac ccg aca  1152
His Leu Gly Val Asn His Phe Arg Arg Gly Thr Leu Ala Asp Pro Thr
    370                 375                 380

tgc act tca cgt gaa cga agt ctt ccg cga gaa ctt caa tca aat tgt  1200
Cys Thr Ser Arg Glu Arg Ser Leu Pro Arg Glu Leu Gln Ser Asn Cys
385                 390                 395                 400

ttc ctt ctt gtt ccg ctt atg cca tta tgt caa tct gtg acg agg aag  1248
Phe Leu Leu Val Pro Leu Met Pro Leu Cys Gln Ser Val Thr Arg Lys
                405                 410                 415

aat agt cat cta gca atc aat cga gac ggg atc gtc att cca caa gcc  1296
Asn Ser His Leu Ala Ile Asn Arg Asp Gly Ile Val Ile Pro Gln Ala
            420                 425                 430
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aat ggc tca agt cgt cgg ccg agc agc gtg aat acc aat tca act cga   1344
Asn Gly Ser Ser Arg Arg Pro Ser Ser Val Asn Thr Asn Ser Thr Arg
        435                 440                 445

gac tgg tg                                                      1352
Asp Trp
    450
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<210> 16
<211> 450
<212> PRT
<213> Homo sapiens

<400> 16

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Met Gly Asp Ala Glu Ser His His Cys Ile Asp Val Asn Ala Ile Leu
  1               5                  10                  15

Gln Gln Phe Asn Asp Trp Thr Val Leu Phe Glu Val Arg Leu Gly Tyr
             20                  25                  30

Ser Val Leu Tyr Phe Leu Ile Leu Ile Ile Gly Leu Val Gly Asn Gly
         35                  40                  45

Leu Leu Ile Thr Ser Ile Leu Met Arg Lys Lys Leu Ser Val Ala Asn
     50                  55                  60

Ile Phe Leu Ile Asn Leu Ala Val Ser Asp Leu Leu Leu Cys Ile Thr
 65                  70                  75                  80

Ala Val Pro Ile Thr Pro Val Leu Ala Phe Met Lys Arg Trp Ile Phe
                 85                  90                  95

Gly Ile Ile Met Cys Lys Leu Val Pro Thr Cys Gln Ala Phe Ser Val
            100                 105                 110

Leu Ile Ser Ser Trp Ser Leu Cys Tyr Ile Ala Ile Asp Arg Tyr Arg
        115                 120                 125

Ser Ile Val Thr Pro Leu Arg Glu Pro Trp Ser Asp Arg His Ala Arg
    130                 135                 140

Trp Leu Leu Met Phe Thr Trp Val Val Ala Phe Leu Ala Ser Tyr Pro
145                 150                 155                 160

Leu Tyr Tyr Ser Gln Asn Leu Lys Thr Met Val Ile Glu Asn Val Thr
                165                 170                 175

Leu Cys Gly Asp Phe Cys Gly Glu Phe Asn Trp Gln Ser Asp Glu Ile
            180                 185                 190

Ser Lys Leu Thr Tyr Thr Thr Ser Leu Leu Ile Ile Gln Leu Ile Ile
        195                 200                 205

Pro Ala Ile Ile Met Ser Phe Cys Tyr Leu Met Ile Leu Gln Lys Val
    210                 215                 220

Gln Thr Asp Trp Leu Val Asp Glu Gly Ser Met Leu Thr Ala Ala Gln
225                 230                 235                 240

Gln Ala Gln Thr Ala Val Arg Lys Arg Arg Val Met Tyr Val Leu Ile
                245                 250                 255
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Leu Met Val Ile Val Phe Met Ala Cys Trp Phe Pro Leu Ser Ala Val
            260                 265                 270

Asn Leu Phe Arg Asp Leu Gly Met Arg Phe Glu Phe Cys Gln Thr Val
        275                 280                 285

Tyr Lys Val Leu Met Met Asp Gln Met Tyr Phe Lys Leu Leu Asn Val
    290                 295                 300

His Val Ile Ala Met Thr Ser Ile Val Trp Asn Pro Val Leu Tyr Phe
305                 310                 315                 320

Trp Met Ser Lys Arg His Arg Arg Ala Leu Lys Asp Asp Met Thr Trp
                325                 330                 335

Leu Thr Asn Ala Arg Arg His Thr Asn Val Gly Val Leu Ser Arg Phe
            340                 345                 350

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

His Leu Gly Val Asn His Phe Arg Arg Gly Thr Leu Ala Asp Pro Thr
    370                 375                 380

Cys Thr Ser Arg Glu Arg Ser Leu Pro Arg Glu Leu Gln Ser Asn Cys
385                 390                 395                 400

Phe Leu Leu Val Pro Leu Met Pro Leu Cys Gln Ser Val Thr Arg Lys
                405                 410                 415

Asn Ser His Leu Ala Ile Asn Arg Asp Gly Ile Val Ile Pro Gln Ala
            420                 425                 430

Asn Gly Ser Ser Arg Arg Pro Ser Ser Val Asn Thr Asn Ser Thr Arg
        435                 440                 445

Asp Trp
    450


<210> 17
<211> 1652
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1650)

<220>
<223> Clone identifier: CEGPCR18a

<400> 17
atg acc gac gag gag ttg ttc gag atc gct ctt ccc ggc ttc tta tat   48
Met Thr Asp Glu Glu Leu Phe Glu Ile Ala Leu Pro Gly Phe Leu Tyr
  1               5                  10                  15

ctc act gtt ttt cta gtt gga act att gga aac tct atg gta ata ttt   96
Leu Thr Val Phe Leu Val Gly Thr Ile Gly Asn Ser Met Val Ile Phe
             20                  25                  30
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gtt gta aac cga ttc aaa cga atg cgc aac gta acg aac atc ttt ctc   144
Val Val Asn Arg Phe Lys Arg Met Arg Asn Val Thr Asn Ile Phe Leu
          35                  40                  45

gcc tcg ctc agc acc gcc gac ttg tgc ctt atc tgg ttt tgt gtg cct   192
Ala Ser Leu Ser Thr Ala Asp Leu Cys Leu Ile Trp Phe Cys Val Pro
      50                  55                  60

ata atg ttc atg aag tat atg tcg cat acg tgg tcg atg ggc agg ttt   240
Ile Met Phe Met Lys Tyr Met Ser His Thr Trp Ser Met Gly Arg Phe
 65                  70                  75                  80

gcg tgc tat tct gtg cac tac att caa cag ttt aca tgc ttc tgc tcg   288
Ala Cys Tyr Ser Val His Tyr Ile Gln Gln Phe Thr Cys Phe Cys Ser
                 85                  90                  95

gtg ctc acg atg act atg att agt ttt gag agg ttt ctt gca ata gca   336
Val Leu Thr Met Thr Met Ile Ser Phe Glu Arg Phe Leu Ala Ile Ala
            100                 105                 110

tat cct atg cga aat atc tgg ttt tca tcc ata gga cga gct aaa aaa   384
Tyr Pro Met Arg Asn Ile Trp Phe Ser Ser Ile Gly Arg Ala Lys Lys
        115                 120                 125

gta atc cta ctc atc tgg atg tca tcc gcg gta ctg gcc gtc cca acc   432
Val Ile Leu Leu Ile Trp Met Ser Ser Ala Val Leu Ala Val Pro Thr
    130                 135                 140

gct gtt cgg atg gat tat gag acc aat ctt tca ttg tcc ggg cag agg   480
Ala Val Arg Met Asp Tyr Glu Thr Asn Leu Ser Leu Ser Gly Gln Arg
145                 150                 155                 160

gtg cat tgg tgt cga aga cgg ttt ccc gcg caa ttt tta gga tat cct   528
Val His Trp Cys Arg Arg Arg Phe Pro Ala Gln Phe Leu Gly Tyr Pro
                165                 170                 175

agg aca tcg ttg aat aaa gca tat gcc atg tat cag ttg ttg cta ctt   576
Arg Thr Ser Leu Asn Lys Ala Tyr Ala Met Tyr Gln Leu Leu Leu Leu
            180                 185                 190

atc ata ttc ccg gtg ctc aca atg tcc ata tgt tat gct cgt gta tct   624
Ile Ile Phe Pro Val Leu Thr Met Ser Ile Cys Tyr Ala Arg Val Ser
        195                 200                 205

gca ata gtg tac aag tcg tcg aaa gat cgt gta ata ctt tcc caa gct   672
Ala Ile Val Tyr Lys Ser Ser Lys Asp Arg Val Ile Leu Ser Gln Ala
    210                 215                 220

atg gtc gca ttt tca aag gcc gcc act gac gcc gtt acc ttc tcc ggc   720
Met Val Ala Phe Ser Lys Ala Ala Thr Asp Ala Val Thr Phe Ser Gly
225                 230                 235                 240

tac tct gca atc ccc atg att aca act tcc cgg aac ttg aaa acc gcc   768
Tyr Ser Ala Ile Pro Met Ile Thr Thr Ser Arg Asn Leu Lys Thr Ala
                245                 250                 255

aac acg acc atc aag tcc tac agt aat cac aga aat aat cgc gtg gca   816
Asn Thr Thr Ile Lys Ser Tyr Ser Asn His Arg Asn Asn Arg Val Ala
            260                 265                 270
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gag gcg aat aag aaa cag ata gtt caa atg tta atc tcc atc gtc tgc   864
Glu Ala Asn Lys Lys Gln Ile Val Gln Met Leu Ile Ser Ile Val Cys
        275                 280                 285

atg tac acg gtt tgc tgg ctc cca acg atc gtc gac gag ctt ctg acg   912
Met Tyr Thr Val Cys Trp Leu Pro Thr Ile Val Asp Glu Leu Leu Thr
    290                 295                 300

tcc ttc ggg tac att tgt cga aca tca aat acg cag aca ttg aag cat   960
Ser Phe Gly Tyr Ile Cys Arg Thr Ser Asn Thr Gln Thr Leu Lys His
305                 310                 315                 320

atg cgg atg gga ttt aat gcg ctg acc tat tgc caa tca tgc att aat   1008
Met Arg Met Gly Phe Asn Ala Leu Thr Tyr Cys Gln Ser Cys Ile Asn
                325                 330                 335

cct atc ctg tat gcc ttc att tct cag aat ttc cgg tcc acg ttc aag   1056
Pro Ile Leu Tyr Ala Phe Ile Ser Gln Asn Phe Arg Ser Thr Phe Lys
            340                 345                 350

acc gcc tat tcg aga atg aaa agt cgt ctt cag ggc gtg gaa gaa atg   1104
Thr Ala Tyr Ser Arg Met Lys Ser Arg Leu Gln Gly Val Glu Glu Met
        355                 360                 365

cgc tct cgt atg gga tcg tgc tct tcg gcg agc atg atg tcg acc cgc   1152
Arg Ser Arg Met Gly Ser Cys Ser Ser Ala Ser Met Met Ser Thr Arg
    370                 375                 380

aac cag cac cga atc tac ggg tcc agc ttc aac aca ctc aca gtg ccc   1200
Asn Gln His Arg Ile Tyr Gly Ser Ser Phe Asn Thr Leu Thr Val Pro
385                 390                 395                 400

ggt cgc tcc atg atc act ccg aac atg tca cgc gac gtc tca cag ttg   1248
Gly Arg Ser Met Ile Thr Pro Asn Met Ser Arg Asp Val Ser Gln Leu
                405                 410                 415

tca ttg tgc agg ccg acg tcg caa atg tcg ttc tgc cga ccg aag agt   1296
Ser Leu Cys Arg Pro Thr Ser Gln Met Ser Phe Cys Arg Pro Lys Ser
            420                 425                 430

cca atg gcc gga gac tct ccg tcg act ttc atg aga cat cgt cct aga   1344
Pro Met Ala Gly Asp Ser Pro Ser Thr Phe Met Arg His Arg Pro Arg
        435                 440                 445

tcg cca acc gac gtg tcc cat gat tcc gga aga cca cgt agc ccc acg   1392
Ser Pro Thr Asp Val Ser His Asp Ser Gly Arg Pro Arg Ser Pro Thr
    450                 455                 460

gat ctt tcg cag tcg aca aag cct tcg cga cga tcc tcc tct ata aga   1440
Asp Leu Ser Gln Ser Thr Lys Pro Ser Arg Arg Ser Ser Ser Ile Arg
465                 470                 475                 480

ccc cgt agc cca aca tcg aca tct caa atg tct acc ata gtc cga tcg   1488
Pro Arg Ser Pro Thr Ser Thr Ser Gln Met Ser Thr Ile Val Arg Ser
                485                 490                 495

aga agt cct aca ggc gca tcg gac acc tct tca ttg ttc cca tca aga   1536
Arg Ser Pro Thr Gly Ala Ser Asp Thr Ser Ser Leu Phe Pro Ser Arg
            500                 505                 510
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aca aga agt cca act ctc caa tca aac aca tct ggt caa tcc atg gaa   1584
Thr Arg Ser Pro Thr Leu Gln Ser Asn Thr Ser Gly Gln Ser Met Glu
        515                 520                 525

cga acc acg gac cga ctg agt gtc cgt gac gct gtc cga cca aaa aca   1632
Arg Thr Thr Asp Arg Leu Ser Val Arg Asp Ala Val Arg Pro Lys Thr
    530                 535                 540

ccg cca gca gtg gtt gtc ta                                      1652
Pro Pro Ala Val Val Val
545                 550
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<210> 18
<211> 550
<212> PRT
<213> Homo sapiens

<400> 18

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Met Thr Asp Glu Glu Leu Phe Glu Ile Ala Leu Pro Gly Phe Leu Tyr
  1               5                  10                  15

Leu Thr Val Phe Leu Val Gly Thr Ile Gly Asn Ser Met Val Ile Phe
             20                  25                  30

Val Val Asn Arg Phe Lys Arg Met Arg Asn Val Thr Asn Ile Phe Leu
         35                  40                  45

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

Ile Met Phe Met Lys Tyr Met Ser His Thr Trp Ser Met Gly Arg Phe
 65                  70                  75                  80

Ala Cys Tyr Ser Val His Tyr Ile Gln Gln Phe Thr Cys Phe Cys Ser
                 85                  90                  95

Val Leu Thr Met Thr Met Ile Ser Phe Glu Arg Phe Leu Ala Ile Ala
            100                 105                 110

Tyr Pro Met Arg Asn Ile Trp Phe Ser Ser Ile Gly Arg Ala Lys Lys
        115                 120                 125

Val Ile Leu Leu Ile Trp Met Ser Ser Ala Val Leu Ala Val Pro Thr
    130                 135                 140

Ala Val Arg Met Asp Tyr Glu Thr Asn Leu Ser Leu Ser Gly Gln Arg
145                 150                 155                 160

Val His Trp Cys Arg Arg Arg Phe Pro Ala Gln Phe Leu Gly Tyr Pro
                165                 170                 175

Arg Thr Ser Leu Asn Lys Ala Tyr Ala Met Tyr Gln Leu Leu Leu Leu
            180                 185                 190

Ile Ile Phe Pro Val Leu Thr Met Ser Ile Cys Tyr Ala Arg Val Ser
        195                 200                 205

Ala Ile Val Tyr Lys Ser Ser Lys Asp Arg Val Ile Leu Ser Gln Ala
    210                 215                 220
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Met Val Ala Phe Ser Lys Ala Ala Thr Asp Ala Val Thr Phe Ser Gly
225 230 235 240

Tyr Ser Ala Ile Pro Met Ile Thr Thr Ser Arg Asn Leu Lys Thr Ala
245 250 255

Asn Thr Thr Ile Lys Ser Tyr Ser Asn His Arg Asn Asn Arg Val Ala
260 265 270

Glu Ala Asn Lys Lys Gln Ile Val Gln Met Leu Ile Ser Ile Val Cys
275 280 285

Met Tyr Thr Val Cys Trp Leu Pro Thr Ile Val Asp Glu Leu Leu Thr
290 295 300

Ser Phe Gly Tyr Ile Cys Arg Thr Ser Asn Thr Gln Thr Leu Lys His
305 310 315 320

Met Arg Met Gly Phe Asn Ala Leu Thr Tyr Cys Gln Ser Cys Ile Asn
325 330 335

Pro Ile Leu Tyr Ala Phe Ile Ser Gln Asn Phe Arg Ser Thr Phe Lys
340 345 350

Thr Ala Tyr Ser Arg Met Lys Ser Arg Leu Gln Gly Val Glu Glu Met
355 360 365

Arg Ser Arg Met Gly Ser Cys Ser Ser Ala Ser Met Met Ser Thr Arg
370 375 380

Asn Gln His Arg Ile Tyr Gly Ser Ser Phe Asn Thr Leu Thr Val Pro
385 390 395 400

Gly Arg Ser Met Ile Thr Pro Asn Met Ser Arg Asp Val Ser Gln Leu
405 410 415

Ser Leu Cys Arg Pro Thr Ser Gln Met Ser Phe Cys Arg Pro Lys Ser
420 425 430

Pro Met Ala Gly Asp Ser Pro Ser Thr Phe Met Arg His Arg Pro Arg
435 440 445

Ser Pro Thr Asp Val Ser His Asp Ser Gly Arg Pro Arg Ser Pro Thr
450 455 460

Asp Leu Ser Gln Ser Thr Lys Pro Ser Arg Arg Ser Ser Ser Ile Arg
465 470 475 480

Pro Arg Ser Pro Thr Ser Thr Ser Gln Met Ser Thr Ile Val Arg Ser
485 490 495

Arg Ser Pro Thr Gly Ala Ser Asp Thr Ser Ser Leu Phe Pro Ser Arg
500 505 510

Thr Arg Ser Pro Thr Leu Gln Ser Asn Thr Ser Gly Gln Ser Met Glu
515 520 525

Arg Thr Thr Asp Arg Leu Ser Val Arg Asp Ala Val Arg Pro Lys Thr
530 535 540

Pro Pro Ala Val Val Val
545 550

<210> 19
<211> 0
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<400> 19
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<210> 20
<211> 0
<212> PRT
<213> synthetic

<400> 20
000

<210> 21
<211> 1130
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1128)

<220>
<223> Clone identifier: CEGPCR4

<400> 21

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atg aat ggc tcc gat tgt ctg aat ctc aac tca gaa tta tgg ttg tat   48
Met Asn Gly Ser Asp Cys Leu Asn Leu Asn Ser Glu Leu Trp Leu Tyr
  1               5                  10                  15

cga gaa gat ttg tca tca agg tgg tac ata atg tta gtg ttt gca ttt   96
Arg Glu Asp Leu Ser Ser Arg Trp Tyr Ile Met Leu Val Phe Ala Phe
             20                  25                  30

ctc tac ctg ata atc att gcc gcc gga ata att gga aac tca tgt gtg   144
Leu Tyr Leu Ile Ile Ile Ala Ala Gly Ile Ile Gly Asn Ser Cys Val
         35                  40                  45

att ttg gca atc aca agg aac aaa tca ctt caa act gtt ccg aat ctg   192
Ile Leu Ala Ile Thr Arg Asn Lys Ser Leu Gln Thr Val Pro Asn Leu
     50                  55                  60

ttt att ctt tct tta tca tgt tct gat att gtg gta tgc tgc aca tct   240
Phe Ile Leu Ser Leu Ser Cys Ser Asp Ile Val Val Cys Cys Thr Ser
 65                  70                  75                  80

gca aca atc act ccg att act gca ttc aag aaa gaa tgg atc ttt gga   288
Ala Thr Ile Thr Pro Ile Thr Ala Phe Lys Lys Glu Trp Ile Phe Gly
                 85                  90                  95

gag gct tta tgc cga att gca cca ttc att gct ggt atc agc ctt tgt   336
Glu Ala Leu Cys Arg Ile Ala Pro Phe Ile Ala Gly Ile Ser Leu Cys
            100                 105                 110

ttc tca act ttc aca ttg act gca atc tcc atc gac aga tac atc ctg   384
Phe Ser Thr Phe Thr Leu Thr Ala Ile Ser Ile Asp Arg Tyr Ile Leu
```

```
        115                 120                 125

att cga ttt ccg atg agg aaa cct att acg cat tat caa gcg gtt gga   432
Ile Arg Phe Pro Met Arg Lys Pro Ile Thr His Tyr Gln Ala Val Gly
    130                 135                 140

gtg att gct att att tgc gct ttt gct gca acc atc aca tcc cca ata   480
Val Ile Ala Ile Ile Cys Ala Phe Ala Ala Thr Ile Thr Ser Pro Ile
145                 150                 155                 160

atg ttc aag caa aag ctg gga gag ttt gag aat ttt tgt ggg cag tac   528
Met Phe Lys Gln Lys Leu Gly Glu Phe Glu Asn Phe Cys Gly Gln Tyr
                165                 170                 175

tgc acg gaa aac tgg gga gcc aat gaa agc cag aga aaa att tat ggt   576
Cys Thr Glu Asn Trp Gly Ala Asn Glu Ser Gln Arg Lys Ile Tyr Gly
            180                 185                 190


gca gct ctg atg ttt ctt cag ctc gtc att ccg ctt acc atc atc atc   624
Ala Ala Leu Met Phe Leu Gln Leu Val Ile Pro Leu Thr Ile Ile Ile
        195                 200                 205

ata tcc tac act gcg att tct ttg aag atc gga caa agc atg att ctc   672
Ile Ser Tyr Thr Ala Ile Ser Leu Lys Ile Gly Gln Ser Met Ile Leu
    210                 215                 220

aaa ggg gcg aaa aag caa aaa aca gac aat tgg gaa atg gaa tta agt   720
Lys Gly Ala Lys Lys Gln Lys Thr Asp Asn Trp Glu Met Glu Leu Ser
225                 230                 235                 240

gat caa caa aga atc gct gtg aag aga aga caa aga act aat aga atg   768
Asp Gln Gln Arg Ile Ala Val Lys Arg Arg Gln Arg Thr Asn Arg Met
                245                 250                 255

ctt att ggt atg gta gtc gca ttc gct tgc agc tgg att tgg tca gtg   816
Leu Ile Gly Met Val Val Ala Phe Ala Cys Ser Trp Ile Trp Ser Val
            260                 265                 270

acg ttc aac att ctg agg gac tat gaa tat ttg cca gag ctc atc aaa   864
Thr Phe Asn Ile Leu Arg Asp Tyr Glu Tyr Leu Pro Glu Leu Ile Lys
        275                 280                 285

act caa gaa tat atc ttt gga att gct aca cat tgc att gca atg acc   912
Thr Gln Glu Tyr Ile Phe Gly Ile Ala Thr His Cys Ile Ala Met Thr
    290                 295                 300

tca acg gta tgg aac ccg tta ctc tac gca gtg ctc aac ctc caa ctg   960
Ser Thr Val Trp Asn Pro Leu Leu Tyr Ala Val Leu Asn Leu Gln Leu
305                 310                 315                 320

cgt gca gca ttc att gac ctg atg cct cac tgg ctt cgt cgt cat tta  1008
Arg Ala Ala Phe Ile Asp Leu Met Pro His Trp Leu Arg Arg His Leu
                325                 330                 335

aac ctg gaa gga gac aac agc tct cca ttg ctc aac cat ccg acg atg  1056
Asn Leu Glu Gly Asp Asn Ser Ser Pro Leu Leu Asn His Pro Thr Met
            340                 345                 350

aca att aca aac aaa ccg tca aag caa cat aca tta ata cca gca atg  1104
Thr Ile Thr Asn Lys Pro Ser Lys Gln His Thr Leu Ile Pro Ala Met
```

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        355                 360                 365

gac aac cat acg tgt caa caa gtt ta                          1130
Asp Asn His Thr Cys Gln Gln Val
    370                 375
```

<210> 22
<211> 376
<212> PRT
<213> Homo sapiens

<400> 22

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Met Asn Gly Ser Asp Cys Leu Asn Leu Asn Ser Glu Leu Trp Leu Tyr
  1               5                  10                  15

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

Leu Tyr Leu Ile Ile Ile Ala Ala Gly Ile Ile Gly Asn Ser Cys Val
         35                  40                  45

Ile Leu Ala Ile Thr Arg Asn Lys Ser Leu Gln Thr Val Pro Asn Leu
     50                  55                  60

Phe Ile Leu Ser Leu Ser Cys Ser Asp Ile Val Val Cys Cys Thr Ser
 65                  70                  75                  80

Ala Thr Ile Thr Pro Ile Thr Ala Phe Lys Lys Glu Trp Ile Phe Gly
                 85                  90                  95

Glu Ala Leu Cys Arg Ile Ala Pro Phe Ile Ala Gly Ile Ser Leu Cys
            100                 105                 110

Phe Ser Thr Phe Thr Leu Thr Ala Ile Ser Ile Asp Arg Tyr Ile Leu
        115                 120                 125

Ile Arg Phe Pro Met Arg Lys Pro Ile Thr His Tyr Gln Ala Val Gly
    130                 135                 140

Val Ile Ala Ile Ile Cys Ala Phe Ala Ala Thr Ile Thr Ser Pro Ile
145                 150                 155                 160

Met Phe Lys Gln Lys Leu Gly Glu Phe Glu Asn Phe Cys Gly Gln Tyr
                165                 170                 175

Cys Thr Glu Asn Trp Gly Ala Asn Glu Ser Gln Arg Lys Ile Tyr Gly
            180                 185                 190

Ala Ala Leu Met Phe Leu Gln Leu Val Ile Pro Leu Thr Ile Ile Ile
        195                 200                 205

Ile Ser Tyr Thr Ala Ile Ser Leu Lys Ile Gly Gln Ser Met Ile Leu
    210                 215                 220

Lys Gly Ala Lys Lys Gln Lys Thr Asp Asn Trp Glu Met Glu Leu Ser
225                 230                 235                 240

Asp Gln Gln Arg Ile Ala Val Lys Arg Arg Gln Arg Thr Asn Arg Met
                245                 250                 255
```

```
Leu Ile Gly Met Val Val Ala Phe Ala Cys Ser Trp Ile Trp Ser Val
            260                 265                 270

Thr Phe Asn Ile Leu Arg Asp Tyr Glu Tyr Leu Pro Glu Leu Ile Lys
        275                 280                 285

Thr Gln Glu Tyr Ile Phe Gly Ile Ala Thr His Cys Ile Ala Met Thr
    290                 295                 300

Ser Thr Val Trp Asn Pro Leu Leu Tyr Ala Val Leu Asn Leu Gln Leu
305                 310                 315                 320

Arg Ala Ala Phe Ile Asp Leu Met Pro His Trp Leu Arg Arg His Leu
                325                 330                 335

Asn Leu Glu Gly Asp Asn Ser Ser Pro Leu Leu Asn His Pro Thr Met
            340                 345                 350

Thr Ile Thr Asn Lys Pro Ser Lys Gln His Thr Leu Ile Pro Ala Met
        355                 360                 365

Asp Asn His Thr Cys Gln Gln Val
    370                 375
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<210> 23
<211> 1125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1122)

<220>
<223> Clone identifier: CEGPCR6

<400> 23

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atg att att ttt tat ctt tac gta gca act caa gta ttt gtg gca att   48
Met Ile Ile Phe Tyr Leu Tyr Val Ala Thr Gln Val Phe Val Ala Ile
  1               5                  10                  15

gca ttt gtc ctt ctg atg gca act gca ata att gga aac tct gtc gtg   96
Ala Phe Val Leu Leu Met Ala Thr Ala Ile Ile Gly Asn Ser Val Val
             20                  25                  30

atg tgg ata att tat caa cac aaa gta atg cac tac ggc ttc aac tat   144
Met Trp Ile Ile Tyr Gln His Lys Val Met His Tyr Gly Phe Asn Tyr
         35                  40                  45

ttt ctt ttc aat atg gca ttc gct gat ctt ttg att gct ctc ttc aat   192
Phe Leu Phe Asn Met Ala Phe Ala Asp Leu Leu Ile Ala Leu Phe Asn
     50                  55                  60



gtt ggt act tca tgg acc tat aat tta tac tat gac tgg tgg tat ggt   240
Val Gly Thr Ser Trp Thr Tyr Asn Leu Tyr Tyr Asp Trp Trp Tyr Gly
 65                  70                  75                  80

gat cta tgt aca ctt act tcc ttc ttc ggt att gca cca act acc gta   288
Asp Leu Cys Thr Leu Thr Ser Phe Phe Gly Ile Ala Pro Thr Thr Val
```

```
                    85                  90                  95

tcc gtg tgc tca atg atg gct ctc agc tgg gat aga tgt caa gca gtc   336
Ser Val Cys Ser Met Met Ala Leu Ser Trp Asp Arg Cys Gln Ala Val
            100                 105                 110

gtg aat cct cta caa aaa cgt cca cta tct cga aaa aga tcc gtc att   384
Val Asn Pro Leu Gln Lys Arg Pro Leu Ser Arg Lys Arg Ser Val Ile
        115                 120                 125

gct att ctc atc att tgg gtt gtt tca acg gtt act gca ctt ccg ttt   432
Ala Ile Leu Ile Ile Trp Val Val Ser Thr Val Thr Ala Leu Pro Phe
    130                 135                 140

gca att gct gca tct gtc aac tct ctc tac aca tat gac gtg gtt aca   480
Ala Ile Ala Ala Ser Val Asn Ser Leu Tyr Thr Tyr Asp Val Val Thr
145                 150                 155                 160

tca act gtt tca aaa gct cac gtt tgt tca gca cca gtt aat act ttc   528
Ser Thr Val Ser Lys Ala His Val Cys Ser Ala Pro Val Asn Thr Phe
                165                 170                 175

ttt gaa aaa gtg ctc ttt ggg att caa tat gct cta cct ata atc att   576
Phe Glu Lys Val Leu Phe Gly Ile Gln Tyr Ala Leu Pro Ile Ile Ile
            180                 185                 190

ttg gga tca acg ttc aca cgg att gcc gtt gca ttt cga gca aca aat   624
Leu Gly Ser Thr Phe Thr Arg Ile Ala Val Ala Phe Arg Ala Thr Asn
        195                 200                 205

gaa gcc act gac agt agt ctg aag aac aat cac aca cgc gca aag agc   672
Glu Ala Thr Asp Ser Ser Leu Lys Asn Asn His Thr Arg Ala Lys Ser
    210                 215                 220

aag gca gta aaa atg ctc ttc cta atg gtc gtt gca ttc gtt gtc tgc   720
Lys Ala Val Lys Met Leu Phe Leu Met Val Val Ala Phe Val Val Cys
225                 230                 235                 240

tgg ctt cca tac cac att tat cac gca ttc gct ctt gaa gaa ttc ttc   768
Trp Leu Pro Tyr His Ile Tyr His Ala Phe Ala Leu Glu Glu Phe Phe
                245                 250                 255

gat gca gct cgt gga aaa tat gcg tat ttg ttg att tac tgg att gca   816
Asp Ala Ala Arg Gly Lys Tyr Ala Tyr Leu Leu Ile Tyr Trp Ile Ala
            260                 265                 270

atg tct agt tgt gca tac aat cca att att tat tgt ttt gcc aac gaa   864
Met Ser Ser Cys Ala Tyr Asn Pro Ile Ile Tyr Cys Phe Ala Asn Glu
        275                 280                 285

aga ttc cgc att ggc ttc cgg tac gtc ttc cga tgg att cca gtg att   912
Arg Phe Arg Ile Gly Phe Arg Tyr Val Phe Arg Trp Ile Pro Val Ile
    290                 295                 300


gac tgc aaa aag gaa caa tat gaa tat tca caa tta ttc ccg gat aaa   960
Asp Cys Lys Lys Glu Gln Tyr Glu Tyr Ser Gln Leu Phe Pro Asp Lys
305                 310                 315                 320

atg aga agt atg gct att tct ttg caa aaa gga aga gtg aac tct tcc  1008
Met Arg Ser Met Ala Ile Ser Leu Gln Lys Gly Arg Val Asn Ser Ser
```

```
                325                 330                 335

tgt ttg gat aaa aaa gtc aaa gag aat tct tct caa gat ttg gtt tgt   1056
Cys Leu Asp Lys Lys Val Lys Glu Asn Ser Ser Gln Asp Leu Val Cys
            340                 345                 350

gtg atg cat tcc gag aaa aat acg aag aaa tat tca aaa gta cat ctt   1104
Val Met His Ser Glu Lys Asn Thr Lys Lys Tyr Ser Lys Val His Leu
        355                 360                 365

ctg agt tgc cat gaa cgg tga                                      1125
Leu Ser Cys His Glu Arg
    370
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<210> 24
<211> 374
<212> PRT
<213> Homo sapiens

<400> 24

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

Ala Phe Val Leu Leu Met Ala Thr Ala Ile Ile Gly Asn Ser Val Val
            20                  25                  30

Met Trp Ile Ile Tyr Gln His Lys Val Met His Tyr Gly Phe Asn Tyr
        35                  40                  45

Phe Leu Phe Asn Met Ala Phe Ala Asp Leu Leu Ile Ala Leu Phe Asn
    50                  55                  60

Val Gly Thr Ser Trp Thr Tyr Asn Leu Tyr Tyr Asp Trp Trp Tyr Gly
65                  70                  75                  80

Asp Leu Cys Thr Leu Thr Ser Phe Phe Gly Ile Ala Pro Thr Thr Val
                85                  90                  95

Ser Val Cys Ser Met Met Ala Leu Ser Trp Asp Arg Cys Gln Ala Val
            100                 105                 110

Val Asn Pro Leu Gln Lys Arg Pro Leu Ser Arg Lys Arg Ser Val Ile
        115                 120                 125

Ala Ile Leu Ile Ile Trp Val Val Ser Thr Val Thr Ala Leu Pro Phe
    130                 135                 140

Ala Ile Ala Ala Ser Val Asn Ser Leu Tyr Thr Tyr Asp Val Val Thr
145                 150                 155                 160

Ser Thr Val Ser Lys Ala His Val Cys Ser Ala Pro Val Asn Thr Phe
                165                 170                 175

Phe Glu Lys Val Leu Phe Gly Ile Gln Tyr Ala Leu Pro Ile Ile Ile
            180                 185                 190

Leu Gly Ser Thr Phe Thr Arg Ile Ala Val Ala Phe Arg Ala Thr Asn
        195                 200                 205

Glu Ala Thr Asp Ser Ser Leu Lys Asn Asn His Thr Arg Ala Lys Ser
    210                 215                 220
```

```
Lys Ala Val Lys Met Leu Phe Leu Met Val Val Ala Phe Val Val Cys
225                 230                 235                 240

Trp Leu Pro Tyr His Ile Tyr His Ala Phe Ala Leu Glu Glu Phe Phe
                245                 250                 255

Asp Ala Ala Arg Gly Lys Tyr Ala Tyr Leu Leu Ile Tyr Trp Ile Ala
            260                 265                 270

Met Ser Ser Cys Ala Tyr Asn Pro Ile Ile Tyr Cys Phe Ala Asn Glu
        275                 280                 285

Arg Phe Arg Ile Gly Phe Arg Tyr Val Phe Arg Trp Ile Pro Val Ile
    290                 295                 300

Asp Cys Lys Lys Glu Gln Tyr Glu Tyr Ser Gln Leu Phe Pro Asp Lys
305                 310                 315                 320

Met Arg Ser Met Ala Ile Ser Leu Gln Lys Gly Arg Val Asn Ser Ser
                325                 330                 335

Cys Leu Asp Lys Lys Val Lys Glu Asn Ser Ser Gln Asp Leu Val Cys
            340                 345                 350

Val Met His Ser Glu Lys Asn Thr Lys Lys Tyr Ser Lys Val His Leu
        355                 360                 365

Leu Ser Cys His Glu Arg
    370
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<210> 25
<211> 1374
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1371)

<220>
<223> Clone identifier: CEGPCR7

<400> 25

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atg gaa gtt gaa aat ttt acc gac tgt caa gta tat tgg aaa gtg tat   48
Met Glu Val Glu Asn Phe Thr Asp Cys Gln Val Tyr Trp Lys Val Tyr
  1               5                  10                  15

cca gat cct tct caa agt ata tat gcg ata gtg cca ttt ctg acc gtg   96
Pro Asp Pro Ser Gln Ser Ile Tyr Ala Ile Val Pro Phe Leu Thr Val
             20                  25                  30

tac ctt ttt ctc ttt ttt ctt gga ctc ttt gga aat gtg acc ttg att   144
Tyr Leu Phe Leu Phe Phe Leu Gly Leu Phe Gly Asn Val Thr Leu Ile
         35                  40                  45

tac gta act tgc agc cat aaa gct tta ctg agc gtt caa aac ata ttc   192
Tyr Val Thr Cys Ser His Lys Ala Leu Leu Ser Val Gln Asn Ile Phe
     50                  55                  60

att ctg aac ctg gcg gcg agc gat tgc atg atg tgc ata tta tcg ctt   240
Ile Leu Asn Leu Ala Ala Ser Asp Cys Met Met Cys Ile Leu Ser Leu
```

```
 65                  70                  75                  80

cca atc act cca atc aca aat gtg tac aaa aac tgg tac ttt gga aat   288
Pro Ile Thr Pro Ile Thr Asn Val Tyr Lys Asn Trp Tyr Phe Gly Asn
                 85                  90                  95

cta ctc tgc cat ttg ata cca tgc att caa ggt atc agc att ttc gta   336
Leu Leu Cys His Leu Ile Pro Cys Ile Gln Gly Ile Ser Ile Phe Val
            100                 105                 110

tgc aca ttc agt ctc ggt gcg att gct ttg gat cgg tat atc ctt gta   384
Cys Thr Phe Ser Leu Gly Ala Ile Ala Leu Asp Arg Tyr Ile Leu Val
        115                 120                 125

gta aga cca cat tct aca cca cta tcc caa aga gga gca ttt ctt act   432
Val Arg Pro His Ser Thr Pro Leu Ser Gln Arg Gly Ala Phe Leu Thr
    130                 135                 140

act gtt cta ttg tgg atc ctc tct ttt gtt gta act cta ccc tat gcg   480
Thr Val Leu Leu Trp Ile Leu Ser Phe Val Val Thr Leu Pro Tyr Ala
145                 150                 155                 160


ttc aat atg caa atg att gaa tac aca gaa gag aga ata tgc ggc tac   528
Phe Asn Met Gln Met Ile Glu Tyr Thr Glu Glu Arg Ile Cys Gly Tyr
                165                 170                 175

ttt tgc act gaa aag tgg gaa tct gcc aag tct aga aga gcc tac aca   576
Phe Cys Thr Glu Lys Trp Glu Ser Ala Lys Ser Arg Arg Ala Tyr Thr
            180                 185                 190

atg atc gtg atg ctc gcc caa ttc gtg gtc cca ttc gct gtc atg gcc   624
Met Ile Val Met Leu Ala Gln Phe Val Val Pro Phe Ala Val Met Ala
        195                 200                 205

ttc tgc tat gca aat att gtt tcg gtg ctc agc aag cgt gct cag aca   672
Phe Cys Tyr Ala Asn Ile Val Ser Val Leu Ser Lys Arg Ala Gln Thr
    210                 215                 220

aag ata cgc aaa atg gtg gag aga aca agc gcg ttg gag agc tct tgc   720
Lys Ile Arg Lys Met Val Glu Arg Thr Ser Ala Leu Glu Ser Ser Cys
225                 230                 235                 240

gca ttc ccg tcg cat ggt ctt gaa cag tat gaa aat gag ttg aac gaa   768
Ala Phe Pro Ser His Gly Leu Glu Gln Tyr Glu Asn Glu Leu Asn Glu
                245                 250                 255

ttt cta gac aaa cag gaa aag gag aaa caa cga gtt gta ctt cag aac   816
Phe Leu Asp Lys Gln Glu Lys Glu Lys Gln Arg Val Val Leu Gln Asn
            260                 265                 270

aga aga aca acg tca atc cta gtt acc atg gtt gtc tgg ttt ggg ata   864
Arg Arg Thr Thr Ser Ile Leu Val Thr Met Val Val Trp Phe Gly Ile
        275                 280                 285

act tgg ctg cca cat aac gtc att tct ttg att att gaa tat gat gac   912
Thr Trp Leu Pro His Asn Val Ile Ser Leu Ile Ile Glu Tyr Asp Asp
    290                 295                 300

aca caa tcg ttt ttc cga ctt tat ggc aga gat gat tac gat atc agt   960
Thr Gln Ser Phe Phe Arg Leu Tyr Gly Arg Asp Asp Tyr Asp Ile Ser
```

```
305                 310                 315                 320

tat tta ctg aac ctt ttc act cac agt att gcc atg tcg aac aat gtt   1008
Tyr Leu Leu Asn Leu Phe Thr His Ser Ile Ala Met Ser Asn Asn Val
                325                 330                 335

tta aac ccg gta ctc tat gcg tgg ctg aac cca agt ttc cgt caa ctg   1056
Leu Asn Pro Val Leu Tyr Ala Trp Leu Asn Pro Ser Phe Arg Gln Leu
            340                 345                 350

gtc ata aag aca tat ttt gga gac cgg cgt aaa agt gac aga ata atc   1104
Val Ile Lys Thr Tyr Phe Gly Asp Arg Arg Lys Ser Asp Arg Ile Ile
        355                 360                 365

aat caa aca tca gtt tac aaa aca aag atc gtg cat gat acg aag cac   1152
Asn Gln Thr Ser Val Tyr Lys Thr Lys Ile Val His Asp Thr Lys His
    370                 375                 380

ttg aat gga aga gcc aaa att ggc ggt ggt ggt agc cac gag gcg ttg   1200
Leu Asn Gly Arg Ala Lys Ile Gly Gly Gly Gly Ser His Glu Ala Leu
385                 390                 395                 400


aag gag agg gag ctg aac tcg tgt tcg gaa aat tta agc tat cat gtg   1248
Lys Glu Arg Glu Leu Asn Ser Cys Ser Glu Asn Leu Ser Tyr His Val
                405                 410                 415

aac ggt cat acg agg act cct aca ccg gaa gtt cag ttg aat gaa gtt   1296
Asn Gly His Thr Arg Thr Pro Thr Pro Glu Val Gln Leu Asn Glu Val
            420                 425                 430

tca agt cct gaa ata agt aaa ctt gtt gct gag ccg gaa gaa ttg atc   1344
Ser Ser Pro Glu Ile Ser Lys Leu Val Ala Glu Pro Glu Glu Leu Ile
        435                 440                 445

gag ttc agc gtc aac gac acg cta gtc tga                           1374
Glu Phe Ser Val Asn Asp Thr Leu Val
    450                 455
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<210> 26
<211> 457
<212> PRT
<213> Homo sapiens

<400> 26

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Met Glu Val Glu Asn Phe Thr Asp Cys Gln Val Tyr Trp Lys Val Tyr
  1               5                  10                  15

Pro Asp Pro Ser Gln Ser Ile Tyr Ala Ile Val Pro Phe Leu Thr Val
             20                  25                  30

Tyr Leu Phe Leu Phe Phe Leu Gly Leu Phe Gly Asn Val Thr Leu Ile
         35                  40                  45

Tyr Val Thr Cys Ser His Lys Ala Leu Leu Ser Val Gln Asn Ile Phe
     50                  55                  60

Ile Leu Asn Leu Ala Ala Ser Asp Cys Met Met Cys Ile Leu Ser Leu
 65                  70                  75                  80
```

```
Pro Ile Thr Pro Ile Thr Asn Val Tyr Lys Asn Trp Tyr Phe Gly Asn
                85                  90                  95

Leu Leu Cys His Leu Ile Pro Cys Ile Gln Gly Ile Ser Ile Phe Val
            100                 105                 110

Cys Thr Phe Ser Leu Gly Ala Ile Ala Leu Asp Arg Tyr Ile Leu Val
        115                 120                 125

Val Arg Pro His Ser Thr Pro Leu Ser Gln Arg Gly Ala Phe Leu Thr
    130                 135                 140

Thr Val Leu Leu Trp Ile Leu Ser Phe Val Val Thr Leu Pro Tyr Ala
145                 150                 155                 160

Phe Asn Met Gln Met Ile Glu Tyr Thr Glu Glu Arg Ile Cys Gly Tyr
                165                 170                 175

Phe Cys Thr Glu Lys Trp Glu Ser Ala Lys Ser Arg Arg Ala Tyr Thr
            180                 185                 190

Met Ile Val Met Leu Ala Gln Phe Val Val Pro Phe Ala Val Met Ala
        195                 200                 205

Phe Cys Tyr Ala Asn Ile Val Ser Val Leu Ser Lys Arg Ala Gln Thr
    210                 215                 220

Lys Ile Arg Lys Met Val Glu Arg Thr Ser Ala Leu Glu Ser Ser Cys
225                 230                 235                 240

Ala Phe Pro Ser His Gly Leu Glu Gln Tyr Glu Asn Glu Leu Asn Glu
                245                 250                 255

Phe Leu Asp Lys Gln Glu Lys Glu Lys Gln Arg Val Val Leu Gln Asn
            260                 265                 270

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

Thr Trp Leu Pro His Asn Val Ile Ser Leu Ile Ile Glu Tyr Asp Asp
    290                 295                 300

Thr Gln Ser Phe Phe Arg Leu Tyr Gly Arg Asp Asp Tyr Asp Ile Ser
305                 310                 315                 320

Tyr Leu Leu Asn Leu Phe Thr His Ser Ile Ala Met Ser Asn Asn Val
                325                 330                 335

Leu Asn Pro Val Leu Tyr Ala Trp Leu Asn Pro Ser Phe Arg Gln Leu
            340                 345                 350

Val Ile Lys Thr Tyr Phe Gly Asp Arg Arg Lys Ser Asp Arg Ile Ile
        355                 360                 365

Asn Gln Thr Ser Val Tyr Lys Thr Lys Ile Val His Asp Thr Lys His
    370                 375                 380

Leu Asn Gly Arg Ala Lys Ile Gly Gly Gly Gly Ser His Glu Ala Leu
385                 390                 395                 400

Lys Glu Arg Glu Leu Asn Ser Cys Ser Glu Asn Leu Ser Tyr His Val
                405                 410                 415
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Asn Gly His Thr Arg Thr Pro Thr Pro Glu Val Gln Leu Asn Glu Val
            420                 425                 430

Ser Ser Pro Glu Ile Ser Lys Leu Val Ala Glu Pro Glu Glu Leu Ile
        435                 440                 445

Glu Phe Ser Val Asn Asp Thr Leu Val
    450                 455


<210> 27
<211> 1146
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1143)

<220>
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Met Asn Thr Ser Phe Val Glu Pro Leu Tyr Ala Asp Val Glu Gln Leu
  1               5                  10                  15

gaa cca gtc cct cta ctt aga cat tca tat caa cta act gtt ctt tat   96
Glu Pro Val Pro Leu Leu Arg His Ser Tyr Gln Leu Thr Val Leu Tyr
             20                  25                  30

aca gtt gca tat gga gct gta ttc ttc act ggt gta ctt gga aac acg   144
Thr Val Ala Tyr Gly Ala Val Phe Phe Thr Gly Val Leu Gly Asn Thr
         35                  40                  45

ttt gtt gtc tta gcg gtt tgg gct cat aag aat tta aat ata acc acg   192
Phe Val Val Leu Ala Val Trp Ala His Lys Asn Leu Asn Ile Thr Thr
     50                  55                  60

gat tat cta att ttg tct ctt gca ctt gct gat ctg ttt att tta tgg   240
Asp Tyr Leu Ile Leu Ser Leu Ala Leu Ala Asp Leu Phe Ile Leu Trp
 65                  70                  75                  80

att tgt ctg cca act acg ttg att aat agc att ttc aca gaa tgg ctt   288
Ile Cys Leu Pro Thr Thr Leu Ile Asn Ser Ile Phe Thr Glu Trp Leu
                 85                  90                  95

tgg ggt caa ttt ttc tgc cga ttg tcc aca tgg gct aac gca tct acg   336
Trp Gly Gln Phe Phe Cys Arg Leu Ser Thr Trp Ala Asn Ala Ser Thr
            100                 105                 110

tca ttt gca tca gtt tac acc ttg gtt gca gtg acg gct gat cgt tat   384
Ser Phe Ala Ser Val Tyr Thr Leu Val Ala Val Thr Ala Asp Arg Tyr
        115                 120                 125


cta gct att tgc cat acg ttg aaa tac aac act agc tgg gat cga gaa   432
Leu Ala Ile Cys His Thr Leu Lys Tyr Asn Thr Ser Trp Asp Arg Glu
    130                 135                 140

tat aca aaa tat gtt ata ttt gct gtt tgg cta gta gct gca ata ttc   480
Tyr Thr Lys Tyr Val Ile Phe Ala Val Trp Leu Val Ala Ala Ile Phe
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145                 150                 155                 160

gga ata cct aat tgg tat aac tat gat ttg ata gta tgg caa gaa ggc   528
Gly Ile Pro Asn Trp Tyr Asn Tyr Asp Leu Ile Val Trp Gln Glu Gly
                165                 170                 175

agt tat ggt tac cga tta tgt acg tca caa acg gat caa aaa tta tat   576
Ser Tyr Gly Tyr Arg Leu Cys Thr Ser Gln Thr Asp Gln Lys Leu Tyr
            180                 185                 190

ttt tta ttt gtt aac tta ttg ctg gct ttc ata gtt cca ttt ggt ttg   624
Phe Leu Phe Val Asn Leu Leu Leu Ala Phe Ile Val Pro Phe Gly Leu
        195                 200                 205

att tcg ggt cta tac acg aga ata ttt atc act gta tca aca cat aga   672
Ile Ser Gly Leu Tyr Thr Arg Ile Phe Ile Thr Val Ser Thr His Arg
    210                 215                 220

agt ctg gca gtt gat gca aga gcc cga gaa gat cga gta aaa cta cga   720
Ser Leu Ala Val Asp Ala Arg Ala Arg Glu Asp Arg Val Lys Leu Arg
225                 230                 235                 240


gtt gcc aca atg atg tta aca gta ata att gta ttt gct tgt tgc tgg   768
Val Ala Thr Met Met Leu Thr Val Ile Ile Val Phe Ala Cys Cys Trp
                245                 250                 255

tta cct ctc tat tgc atc ttc aca tat ttt ttc ttc ttt gct gat cag   816
Leu Pro Leu Tyr Cys Ile Phe Thr Tyr Phe Phe Phe Phe Ala Asp Gln
            260                 265                 270

cga tcg gat ctt ttt caa att act tca atg ttg att cgg cca ata ttc   864
Arg Ser Asp Leu Phe Gln Ile Thr Ser Met Leu Ile Arg Pro Ile Phe
        275                 280                 285

caa tgg atg tca tta cta tcg agt tct tta aat cca ata att tat att   912
Gln Trp Met Ser Leu Leu Ser Ser Ser Leu Asn Pro Ile Ile Tyr Ile
    290                 295                 300

gca tac agt cac aag tac aga aga gct ttc aaa agt ata tta ctg atg   960
Ala Tyr Ser His Lys Tyr Arg Arg Ala Phe Lys Ser Ile Leu Leu Met
305                 310                 315                 320

cca tgt aag aca aga tac gaa aga gtc cga agc aca ata ctc cgt cgt  1008
Pro Cys Lys Thr Arg Tyr Glu Arg Val Arg Ser Thr Ile Leu Arg Arg
                325                 330                 335

cac tct cgt ggc ttc aaa tca act gca aca att tca atg tct aat ttt  1056
His Ser Arg Gly Phe Lys Ser Thr Ala Thr Ile Ser Met Ser Asn Phe
            340                 345                 350

gga act gaa cca aca aat tta ggt gga gca tct agt tta ctt att gaa  1104
Gly Thr Glu Pro Thr Asn Leu Gly Gly Ala Ser Ser Leu Leu Ile Glu
        355                 360                 365

cta gat gga aaa cag gtg gaa aga tct act tct gat tgt taa          1146
Leu Asp Gly Lys Gln Val Glu Arg Ser Thr Ser Asp Cys
    370                 375                 380
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<210> 28

<211> 381
<212> PRT
<213> Homo sapiens

<400> 28

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Met Asn Thr Ser Phe Val Glu Pro Leu Tyr Ala Asp Val Glu Gln Leu
  1               5                  10                  15

Glu Pro Val Pro Leu Leu Arg His Ser Tyr Gln Leu Thr Val Leu Tyr
            20                  25                  30

Thr Val Ala Tyr Gly Ala Val Phe Phe Thr Gly Val Leu Gly Asn Thr
        35                  40                  45

Phe Val Val Leu Ala Val Trp Ala His Lys Asn Leu Asn Ile Thr Thr
    50                  55                  60

Asp Tyr Leu Ile Leu Ser Leu Ala Leu Ala Asp Leu Phe Ile Leu Trp
65                  70                  75                  80

Ile Cys Leu Pro Thr Thr Leu Ile Asn Ser Ile Phe Thr Glu Trp Leu
                85                  90                  95

Trp Gly Gln Phe Phe Cys Arg Leu Ser Thr Trp Ala Asn Ala Ser Thr
            100                 105                 110

Ser Phe Ala Ser Val Tyr Thr Leu Val Ala Val Thr Ala Asp Arg Tyr
        115                 120                 125

Leu Ala Ile Cys His Thr Leu Lys Tyr Asn Thr Ser Trp Asp Arg Glu
    130                 135                 140

Tyr Thr Lys Tyr Val Ile Phe Ala Val Trp Leu Val Ala Ala Ile Phe
145                 150                 155                 160

Gly Ile Pro Asn Trp Tyr Asn Tyr Asp Leu Ile Val Trp Gln Glu Gly
                165                 170                 175

Ser Tyr Gly Tyr Arg Leu Cys Thr Ser Glu Thr Asp Gln Lys Leu Tyr
            180                 185                 190

Phe Leu Phe Val Asn Leu Leu Leu Ala Phe Ile Val Pro Phe Gly Leu
        195                 200                 205

Ile Ser Gly Leu Tyr Thr Arg Ile Phe Ile Thr Val Ser Thr His Arg
    210                 215                 220

Ser Leu Ala Val Asp Ala Arg Ala Arg Glu Asp Arg Val Lys Leu Arg
225                 230                 235                 240

Val Ala Thr Met Met Leu Thr Val Ile Ile Val Phe Ala Cys Cys Trp
                245                 250                 255

Leu Pro Leu Tyr Cys Ile Phe Thr Tyr Phe Phe Phe Phe Ala Asp Gln
            260                 265                 270

Arg Ser Asp Leu Phe Gln Ile Thr Ser Met Leu Ile Arg Pro Ile Phe
        275                 280                 285

Gln Trp Met Ser Leu Leu Ser Ser Ser Leu Asn Pro Ile Ile Tyr Ile
    290                 295                 300
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Ala Tyr Ser His Lys Tyr Arg Arg Ala Phe Lys Ser Ile Leu Leu Met
305                 310                 315                 320

Pro Cys Lys Thr Arg Tyr Glu Arg Val Arg Ser Thr Ile Leu Arg Arg
                325                 330                 335

His Ser Arg Gly Phe Lys Ser Thr Ala Thr Ile Ser Met Ser Asn Phe
            340                 345                 350

Gly Thr Glu Pro Thr Asn Leu Gly Gly Ala Ser Ser Leu Leu Ile Glu
        355                 360                 365

Leu Asp Gly Lys Gln Val Glu Arg Ser Thr Ser Asp Cys
    370                 375                 380


<210> 29
<211> 1473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1470)

<220>
<223> Clone identifier: CEGPCR9

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Met Glu Val Lys Asp Ile Asp Asn Tyr Cys Asp Arg Gly Ile Ser Pro
  1               5                  10                  15

aat gca tcc aat tat ctc acg tac cca ttt gac ggg ctc tgt cta cag   96
Asn Ala Ser Asn Tyr Leu Thr Tyr Pro Phe Asp Gly Leu Cys Leu Gln
            20                  25                  30

aaa ttt ttt tat caa ctc caa act tct ttg cga agg ttc act cct tac   144
Lys Phe Phe Tyr Gln Leu Gln Thr Ser Leu Arg Arg Phe Thr Pro Tyr
        35                  40                  45

gaa gaa atc att tac aca aca gtt tac atc att atc tct gta gca gct   192
Glu Glu Ile Ile Tyr Thr Thr Val Tyr Ile Ile Ile Ser Val Ala Ala
    50                  55                  60

gtt att gga aat gga ttg gtg ata atg gct gta gta cgg aaa aag aca   240
Val Ile Gly Asn Gly Leu Val Ile Met Ala Val Val Arg Lys Lys Thr
65                  70                  75                  80

atg aga aca aac aga aat gtt ttg att tta aat ctc gcg ctt tca aac   288
Met Arg Thr Asn Arg Asn Val Leu Ile Leu Asn Leu Ala Leu Ser Asn
                85                  90                  95

ttg ata ctc gcc atc acc aac atc cca ttt cta tgg ctt ccg tca att   336
Leu Ile Leu Ala Ile Thr Asn Ile Pro Phe Leu Trp Leu Pro Ser Ile
            100                 105                 110

gat ttc gaa ttt ccg tac tct cga ttt ttc tgc aaa ttt gcc aat gtg   384
Asp Phe Glu Phe Pro Tyr Ser Arg Phe Phe Cys Lys Phe Ala Asn Val
        115                 120                 125

ctt ccg ggt agt aat atc tac tgc tca act tta acc atc tcg gtg atg   432
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Leu Pro Gly Ser Asn Ile Tyr Cys Ser Thr Leu Thr Ile Ser Val Met
    130                 135                 140

gca att gat aga tat tat tcg gtg aag aaa ttg aaa att gca tca aat   480
Ala Ile Asp Arg Tyr Tyr Ser Val Lys Lys Leu Lys Ile Ala Ser Asn
145                 150                 155                 160

cgt aaa caa tgt ttc cat gct gtt ttg gtt tca ttg gct att tgg att   528
Arg Lys Gln Cys Phe His Ala Val Leu Val Ser Leu Ala Ile Trp Ile
                165                 170                 175

gtg tca ttc atc ctc tcg tta cct ctg ctc ttg tac tat gaa acc tca   576
Val Ser Phe Ile Leu Ser Leu Pro Leu Leu Leu Tyr Tyr Glu Thr Ser
            180                 185                 190

atg ctc tac gtc atg aga gaa att cga gtt gtt gat caa agc ggt cag   624
Met Leu Tyr Val Met Arg Glu Ile Arg Val Val Asp Gln Ser Gly Gln
        195                 200                 205

gaa gtc atc cga agc tac gga tgg aga cag tgc cgt cta gtt tct gcc   672
Glu Val Ile Arg Ser Tyr Gly Trp Arg Gln Cys Arg Leu Val Ser Ala
    210                 215                 220

gga cga tta ccg gac atc acc caa agc atc cag ttg ctc atg tct att   720
Gly Arg Leu Pro Asp Ile Thr Gln Ser Ile Gln Leu Leu Met Ser Ile
225                 230                 235                 240

ctt caa gtc gct ttc cta tac atc gtt cca ctc ttt gtt ctt tca atc   768
Leu Gln Val Ala Phe Leu Tyr Ile Val Pro Leu Phe Val Leu Ser Ile
                245                 250                 255

ttc aac gtg aaa ctc acc cgg ttt tta aaa aca aat gcc aac aaa atg   816
Phe Asn Val Lys Leu Thr Arg Phe Leu Lys Thr Asn Ala Asn Lys Met
            260                 265                 270

agc aaa act cgt gct ccg cca aaa cga ttt gac aga tcc gat agc cac   864
Ser Lys Thr Arg Ala Pro Pro Lys Arg Phe Asp Arg Ser Asp Ser His
        275                 280                 285

cat aat tcg ttg aaa aat aac aac aac cac acg tct tct cta cgt tcg   912
His Asn Ser Leu Lys Asn Asn Asn Asn His Thr Ser Ser Leu Arg Ser
    290                 295                 300

cca tca atg ccc tca atc aga agt tcg ata acg gag aga aac aag acg   960
Pro Ser Met Pro Ser Ile Arg Ser Ser Ile Thr Glu Arg Asn Lys Thr
305                 310                 315                 320

aat cag aga aca aac aga act act tcg tta ctg att gca atg gcc gga  1008
Asn Gln Arg Thr Asn Arg Thr Thr Ser Leu Leu Ile Ala Met Ala Gly
                325                 330                 335

agc tat gcg gct ctt tgg ttt cca ttc act ctc atc act ttt ttg ata  1056
Ser Tyr Ala Ala Leu Trp Phe Pro Phe Thr Leu Ile Thr Phe Leu Ile
            340                 345                 350



gac ttc gag ttg atc atc aat caa gac tac gtg aac ttg gta gaa cga  1104
Asp Phe Glu Leu Ile Ile Asn Gln Asp Tyr Val Asn Leu Val Glu Arg
        355                 360                 365

att gac caa acc tgc aaa atg gta tcc atg ctg tcc att tgt gtg aac  1152
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Ile Asp Gln Thr Cys Lys Met Val Ser Met Leu Ser Ile Cys Val Asn
    370                 375                 380

cca ttt ctc tac gga ttc cta aat acc aat ttt cga cac gaa ttt tcc   1200
Pro Phe Leu Tyr Gly Phe Leu Asn Thr Asn Phe Arg His Glu Phe Ser
385                 390                 395                 400

gac atc tac tac cga tac att cgc tgt gaa aca aag agt cag cca gcc   1248
Asp Ile Tyr Tyr Arg Tyr Ile Arg Cys Glu Thr Lys Ser Gln Pro Ala
                405                 410                 415

ggc cga ttc cat cat gat gta tca tca atc gct cac cat aga caa gac   1296
Gly Arg Phe His His Asp Val Ser Ser Ile Ala His His Arg Gln Asp
            420                 425                 430

tct gtt tac aat gat gag gca aca ctt ttg act aca ggg cgt cag agt   1344
Ser Val Tyr Asn Asp Glu Ala Thr Leu Leu Thr Thr Gly Arg Gln Ser
        435                 440                 445

aat ggt aaa gat ggg agc tcg tct cca ata gga ttc cgc tct agc gtc   1392
Asn Gly Lys Asp Gly Ser Ser Ser Pro Ile Gly Phe Arg Ser Ser Val
    450                 455                 460


cgt gtt tgc tcg ggt caa aca aaa atg att gga gat cgc att gta ttg   1440
Arg Val Cys Ser Gly Gln Thr Lys Met Ile Gly Asp Arg Ile Val Leu
465                 470                 475                 480

gac gat gat atc gag aaa gat agt ttt gtc taa                      1473
Asp Asp Asp Ile Glu Lys Asp Ser Phe Val
                485                 490


<210> 30
<211> 490
<212> PRT
<213> Homo sapiens

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Met Glu Val Lys Asp Ile Asp Asn Tyr Cys Asp Arg Gly Ile Ser Pro
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Asn Ala Ser Asn Tyr Leu Thr Tyr Pro Phe Asp Gly Leu Cys Leu Gln
             20                  25                  30

Lys Phe Phe Tyr Gln Leu Gln Thr Ser Leu Arg Arg Phe Thr Pro Tyr
         35                  40                  45

Glu Glu Ile Ile Tyr Thr Thr Val Tyr Ile Ile Ile Ser Val Ala Ala
     50                  55                  60

Val Ile Gly Asn Gly Leu Val Ile Met Ala Val Val Arg Lys Lys Thr
 65                  70                  75                  80

Met Arg Thr Asn Arg Asn Val Leu Ile Leu Asn Leu Ala Leu Ser Asn
                 85                  90                  95

Leu Ile Leu Ala Ile Thr Asn Ile Pro Phe Leu Trp Leu Pro Ser Ile
             100                 105                 110

Asp Phe Glu Phe Pro Tyr Ser Arg Phe Phe Cys Lys Phe Ala Asn Val
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115 120 125

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

Ala Ile Asp Arg Tyr Tyr Ser Val Lys Lys Leu Lys Ile Ala Ser Asn
145 150 155 160

Arg Lys Gln Cys Phe His Ala Val Leu Val Ser Leu Ala Ile Trp Ile
165 170 175

Val Ser Phe Ile Leu Ser Leu Pro Leu Leu Leu Tyr Tyr Glu Thr Ser
180 185 190

Met Leu Tyr Val Met Arg Glu Ile Arg Val Val Asp Gln Ser Gly Gln
195 200 205

Glu Val Ile Arg Ser Tyr Gly Trp Arg Gln Cys Arg Leu Val Ser Ala
210 215 220

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

Leu Gln Val Ala Phe Leu Tyr Ile Val Pro Leu Phe Val Leu Ser Ile
245 250 255

Phe Asn Val Lys Leu Thr Arg Phe Leu Lys Thr Asn Ala Asn Lys Met
260 265 270

Ser Lys Thr Arg Ala Pro Pro Lys Arg Phe Asp Arg Ser Asp Ser His
275 280 285

His Asn Ser Leu Lys Asn Asn Asn Asn His Thr Ser Ser Leu Arg Ser
290 295 300

Pro Ser Met Pro Ser Ile Arg Ser Ser Ile Thr Glu Arg Asn Lys Thr
305 310 315 320

Asn Gln Arg Thr Asn Arg Thr Thr Ser Leu Leu Ile Ala Met Ala Gly
325 330 335

Ser Tyr Ala Ala Leu Trp Phe Pro Phe Thr Leu Ile Thr Phe Leu Ile
340 345 350

Asp Phe Glu Leu Ile Ile Asn Gln Asp Tyr Val Asn Leu Val Glu Arg
355 360 365

Ile Asp Gln Thr Cys Lys Met Val Ser Met Leu Ser Ile Cys Val Asn
370 375 380

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

Asp Ile Tyr Tyr Arg Tyr Ile Arg Cys Glu Thr Lys Ser Gln Pro Ala
405 410 415

Gly Arg Phe His His Asp Val Ser Ser Ile Ala His His Arg Gln Asp
420 425 430

Ser Val Tyr Asn Asp Glu Ala Thr Leu Leu Thr Thr Gly Arg Gln Ser
435 440 445

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Asn Gly Lys Asp Gly Ser Ser Ser Pro Ile Gly Phe Arg Ser Ser Val
    450                 455                 460

Arg Val Cys Ser Gly Gln Thr Lys Met Ile Gly Asp Arg Ile Val Leu
465                 470                 475                 480

Asp Asp Asp Ile Glu Lys Asp Ser Phe Val
                485                 490


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<212> DNA
<213> Homo sapiens

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<223> CeGPCR11 (F35G8.1)

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<222> (1)..(1128)

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Met Asn Ile Asp Ser Asn Leu Thr Asp Phe Gln Cys Glu Tyr Pro Ala
  1               5                  10                  15

att gac ata gga att cat atg aaa acc ttg tta gca gtc ggg tat ggt   96
Ile Asp Ile Gly Ile His Met Lys Thr Leu Leu Ala Val Gly Tyr Gly
             20                  25                  30

ttg gtg gga gcc ctg agc tta gtt gga aat ctt gct gta ttg ctc att   144
Leu Val Gly Ala Leu Ser Leu Val Gly Asn Leu Ala Val Leu Leu Ile
         35                  40                  45

gtg ata tgc agg aga gaa atg caa aca gtc acc aac att ttt ata agt   192
Val Ile Cys Arg Arg Glu Met Gln Thr Val Thr Asn Ile Phe Ile Ser
     50                  55                  60

agc gtc tcc gcg gct gac ttg gta ata aca agt ttc tcc tta tgg gcg   240
Ser Val Ser Ala Ala Asp Leu Val Ile Thr Ser Phe Ser Leu Trp Ala
 65                  70                  75                  80

acc cca tta gcc tat tat caa cgg gta tgg cat ttc gga aag tat atg   288
Thr Pro Leu Ala Tyr Tyr Gln Arg Val Trp His Phe Gly Lys Tyr Met
                85                  90                  95

tgc tat atg gtt tcc atc ata caa ggc tta tcc ctc atg tgg gta cca   336
Cys Tyr Met Val Ser Ile Ile Gln Gly Leu Ser Leu Met Trp Val Pro
            100                 105                 110

ctg acc cta gca gca gtt gca tta gat cgc tac tct cta gtt gct tct   384
Leu Thr Leu Ala Ala Val Ala Leu Asp Arg Tyr Ser Leu Val Ala Ser
        115                 120                 125

ccg ttc cgt cag cca atg tct aaa aag act tgc ttg ctg atc atc gct   432
Pro Phe Arg Gln Pro Met Ser Lys Lys Thr Cys Leu Leu Ile Ile Ala
    130                 135                 140

gga atc tgg atg gga ggg ttt gca gtt ttg tcg cca atg att cgg atg   480
Gly Ile Trp Met Gly Gly Phe Ala Val Leu Ser Pro Met Ile Arg Met
145                 150                 155                 160
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22 JUL 2004

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gta gat ttt gtt gac agc tat gga cca tgc cat ttt tgc ctg gaa tcc   528
Val Asp Phe Val Asp Ser Tyr Gly Pro Cys His Phe Cys Leu Glu Ser
                165                 170                 175

tgg gac cac gac aaa caa cac tac cga ctt ttc tac gga ctc tcg gtg   576
Trp Asp His Asp Lys Gln His Tyr Arg Leu Phe Tyr Gly Leu Ser Val
            180                 185                 190

ctc gtg atc cgc tcc gca att cca ctt gtt ctc att tcc ctg tgc cac   624
Leu Val Ile Arg Ser Ala Ile Pro Leu Val Leu Ile Ser Leu Cys His
        195                 200                 205

tgg aga atc gca gtt att ttg aac acg cag acg gag aaa ttc caa aca   672
Trp Arg Ile Ala Val Ile Leu Asn Thr Gln Thr Glu Lys Phe Gln Thr
    210                 215                 220

tta cgt agt gcc agc aca gtc acc caa tcg act gac atc cgc cgt aaa   720
Leu Arg Ser Ala Ser Thr Val Thr Gln Ser Thr Asp Ile Arg Arg Lys
225                 230                 235                 240

caa cgt ctt cag act ctc tta ttg gca atg gtg gtc ata ttt gcc gtg   768
Gln Arg Leu Gln Thr Leu Leu Leu Ala Met Val Val Ile Phe Ala Val
                245                 250                 255


tcc agt ctc cca ctg gac ctt tca aat gtt ctt caa gat ttg atc gta   816
Ser Ser Leu Pro Leu Asp Leu Ser Asn Val Leu Gln Asp Leu Ile Val
            260                 265                 270

gtg tac cag gtt cga cct gtc ccc gac aac gtt cgc cat ttt atc ttc   864
Val Tyr Gln Val Arg Pro Val Pro Asp Asn Val Arg His Phe Ile Phe
        275                 280                 285

ttc ttt tgc cat tgg acc gca atg gca gga aca ctt ctc aac ccg tta   912
Phe Phe Cys His Trp Thr Ala Met Ala Gly Thr Leu Leu Asn Pro Leu
    290                 295                 300

gtc tac gcg tac tac aac gaa aac ttc cgg cgt cag att caa aca tgc   960
Val Tyr Ala Tyr Tyr Asn Glu Asn Phe Arg Arg Gln Ile Gln Thr Cys
305                 310                 315                 320

ttt gga gaa atg cgt gga cag gga gag ttc aag cgg ggg cta tac tct  1008
Phe Gly Glu Met Arg Gly Gln Gly Glu Phe Lys Arg Gly Leu Tyr Ser
                325                 330                 335

att gtc tcc ggc aga tac tcc tac cga gca gac gac gag gaa aat cat  1056
Ile Val Ser Gly Arg Tyr Ser Tyr Arg Ala Asp Asp Glu Glu Asn His
            340                 345                 350

cac aga caa aac aca cgt atc gaa ctg gct aac aat caa act ggt gat  1104
His Arg Gln Asn Thr Arg Ile Glu Leu Ala Asn Asn Gln Thr Gly Asp
        355                 360                 365

atc gaa gtt ctc aga acg gat ctt ta                              1130
Ile Glu Val Leu Arg Thr Asp Leu
    370                 375
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<210> 32
<211> 376
<212> PRT

22 JUN 2004

<213> Homo sapiens

<400> 32

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Ile Asp Ile Gly Ile His Met Lys Thr Leu Leu Ala Val Gly Tyr Gly
            20                  25                  30

Leu Val Gly Ala Leu Ser Leu Val Gly Asn Leu Ala Val Leu Leu Ile
        35                  40                  45

Val Ile Cys Arg Arg Glu Met Gln Thr Val Thr Asn Ile Phe Ile Ser
    50                  55                  60

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

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

Cys Tyr Met Val Ser Ile Ile Gln Gly Leu Ser Leu Met Trp Val Pro
            100                 105                 110

Leu Thr Leu Ala Ala Val Ala Leu Asp Arg Tyr Ser Leu Val Ala Ser
        115                 120                 125

Pro Phe Arg Gln Pro Met Ser Lys Lys Thr Cys Leu Leu Ile Ile Ala
    130                 135                 140

Gly Ile Trp Met Gly Gly Phe Ala Val Leu Ser Pro Met Ile Arg Met
145                 150                 155                 160

Val Asp Phe Val Asp Ser Tyr Gly Pro Cys His Phe Cys Leu Glu Ser
                165                 170                 175

Trp Asp His Asp Lys Gln His Tyr Arg Leu Phe Tyr Gly Leu Ser Val
            180                 185                 190

Leu Val Ile Arg Ser Ala Ile Pro Leu Val Leu Ile Ser Leu Cys His
        195                 200                 205

Trp Arg Ile Ala Val Ile Leu Asn Thr Gln Thr Glu Lys Phe Gln Thr
    210                 215                 220

Leu Arg Ser Ala Ser Thr Val Thr Gln Ser Thr Asp Ile Arg Arg Lys
225                 230                 235                 240

Gln Arg Leu Gln Thr Leu Leu Leu Ala Met Val Val Ile Phe Ala Val
                245                 250                 255

Ser Ser Leu Pro Leu Asp Leu Ser Asn Val Leu Gln Asp Leu Ile Val
            260                 265                 270

Val Tyr Gln Val Arg Pro Val Pro Asp Asn Val Arg His Phe Ile Phe
        275                 280                 285

Phe Phe Cys His Trp Thr Ala Met Ala Gly Thr Leu Leu Asn Pro Leu
    290                 295                 300

Val Tyr Ala Tyr Tyr Asn Glu Asn Phe Arg Arg Gln Ile Gln Thr Cys
305                 310                 315                 320
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Phe Gly Glu Met Arg Gly Gln Gly Glu Phe Lys Arg Gly Leu Tyr Ser
                325                 330                 335

Ile Val Ser Gly Arg Tyr Ser Tyr Arg Ala Asp Asp Glu Glu Asn His
            340                 345                 350

His Arg Gln Asn Thr Arg Ile Glu Leu Ala Asn Asn Gln Thr Gly Asp
        355                 360                 365

Ile Glu Val Leu Arg Thr Asp Leu
    370                 375


<210> 33
<211> 1176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1173)

<220>
<223> Clone identifier: CEGPCR15

<400> 33
atg aca acg tgt ccc cta cca ccc agt tta gac gaa atg gat ctg cga   48
Met Thr Thr Cys Pro Leu Pro Pro Ser Leu Asp Glu Met Asp Leu Arg
  1               5                  10                  15

tta gct gcc gat aaa gtt cta aac ggt tca ctg atc aac tgt aca ttc   96
Leu Ala Ala Asp Lys Val Leu Asn Gly Ser Leu Ile Asn Cys Thr Phe
             20                  25                  30

caa tcg ttt tac gat caa atg tat caa aca cac gga gta tac ttc ata   144
Gln Ser Phe Tyr Asp Gln Met Tyr Gln Thr His Gly Val Tyr Phe Ile
         35                  40                  45

ttt gaa cca act ccg ttc gtt cat cca att gtt tca cag att ttc tat   192
Phe Glu Pro Thr Pro Phe Val His Pro Ile Val Ser Gln Ile Phe Tyr
     50                  55                  60

gga atc ctg ttc aca cta aca ata ttt ctg gcg tta atg ggc aat ttt   240
Gly Ile Leu Phe Thr Leu Thr Ile Phe Leu Ala Leu Met Gly Asn Phe
 65                  70                  75                  80

aca gtg atg tgg ata atc ctg tac cac cgt caa atg cga agc gtc aca   288
Thr Val Met Trp Ile Ile Leu Tyr His Arg Gln Met Arg Ser Val Thr
                 85                  90                  95

aat tac tat ctg ttc aac ttg gca gtg gcg gat gcc tcg att tca gtg   336
Asn Tyr Tyr Leu Phe Asn Leu Ala Val Ala Asp Ala Ser Ile Ser Val
            100                 105                 110

ttc aac acg gga ttc tca tgg tct tat aat tat tat tat gtt tgg aaa   384
Phe Asn Thr Gly Phe Ser Trp Ser Tyr Asn Tyr Tyr Tyr Val Trp Lys
        115                 120                 125


ttc gga agc ttt tac tgt cga ata aac aat ttg atg gga ata act ccg   432
Phe Gly Ser Phe Tyr Cys Arg Ile Asn Asn Leu Met Gly Ile Thr Pro
    130                 135                 140
```

```
att tgt gca agt gta ttc aca atg att gtc atg agc att gaa aga tat   480
Ile Cys Ala Ser Val Phe Thr Met Ile Val Met Ser Ile Glu Arg Tyr
145                 150                 155                 160

tat gcc ata atc cat cca ttg aaa aag cgt cca gga cga cga tca act   528
Tyr Ala Ile Ile His Pro Leu Lys Lys Arg Pro Gly Arg Arg Ser Thr
                165                 170                 175

gtt acc atc atc ata atg att tgg ttc atg gca ttt ttg ttc ggg gtt   576
Val Thr Ile Ile Ile Met Ile Trp Phe Met Ala Phe Leu Phe Gly Val
            180                 185                 190

cca gca ttt ctt gcg tca aag gtt gat gtc tat tac ttc tac gat ggt   624
Pro Ala Phe Leu Ala Ser Lys Val Asp Val Tyr Tyr Phe Tyr Asp Gly
        195                 200                 205



tac aca tta tac gag aat cca ctg tgc ctt gca gac aat tat ccc ggt   672
Tyr Thr Leu Tyr Glu Asn Pro Leu Cys Leu Ala Asp Asn Tyr Pro Gly
    210                 215                 220

gga aat gaa tca cta ctt gga cag gta tac aac aac gga ctg ata act   720
Gly Asn Glu Ser Leu Leu Gly Gln Val Tyr Asn Asn Gly Leu Ile Thr
225                 230                 235                 240

gtt caa tac att ctt cca cta tgc att tta tca gct gct tat tat cga   768
Val Gln Tyr Ile Leu Pro Leu Cys Ile Leu Ser Ala Ala Tyr Tyr Arg
                245                 250                 255

gtt ggt gtt gag ctg aga aag gat aaa acc gtc ggt gac gtg aga cat   816
Val Gly Val Glu Leu Arg Lys Asp Lys Thr Val Gly Asp Val Arg His
            260                 265                 270

gca aaa tca gtg gcc gca aag aag aag gcg tca atc atg ttg gca gtg   864
Ala Lys Ser Val Ala Ala Lys Lys Lys Ala Ser Ile Met Leu Ala Val
        275                 280                 285

gtt gtg ttc att ttc atg att gtc tgg ttc cca tac aat gcc tac tat   912
Val Val Phe Ile Phe Met Ile Val Trp Phe Pro Tyr Asn Ala Tyr Tyr
    290                 295                 300

ctc aca ttg cat tta gtt gag cca att ggg aat aaa atg ttg agt ctg   960
Leu Thr Leu His Leu Val Glu Pro Ile Gly Asn Lys Met Leu Ser Leu
305                 310                 315                 320

tac att tat atc aac atc tat tgg ttg gga atg tcg tca act gtc ttc  1008
Tyr Ile Tyr Ile Asn Ile Tyr Trp Leu Gly Met Ser Ser Thr Val Phe
                325                 330                 335

aat cct gtc atc tat tat ttt atg aac aaa cga ttc cgt gtc gga ttc  1056
Asn Pro Val Ile Tyr Tyr Phe Met Asn Lys Arg Phe Arg Val Gly Phe
            340                 345                 350

cat cac gca ttc cgt tgg ctt cca ttc gtt cgt tcc gat aaa gat gaa  1104
His His Ala Phe Arg Trp Leu Pro Phe Val Arg Ser Asp Lys Asp Glu
        355                 360                 365

tat caa aca att ctt tca cag aca cgt cca tct ctg atg cca ccc aca  1152
Tyr Gln Thr Ile Leu Ser Gln Thr Arg Pro Ser Leu Met Pro Pro Thr
    370                 375                 380
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acg atg gcg cat acg gat ttc tga                                          1176
Thr Met Ala His Thr Asp Phe
385                 390
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<210> 34
<211> 391
<212> PRT
<213> Homo sapiens

<400> 34

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Met Thr Thr Cys Pro Leu Pro Pro Ser Leu Asp Glu Met Asp Leu Arg
  1               5                  10                  15

Leu Ala Ala Asp Lys Val Leu Asn Gly Ser Leu Ile Asn Cys Thr Phe
            20                  25                  30

Gln Ser Phe Tyr Asp Gln Met Tyr Gln Thr His Gly Val Tyr Phe Ile
        35                  40                  45

Phe Glu Pro Thr Pro Phe Val His Pro Ile Val Ser Gln Ile Phe Tyr
    50                  55                  60

Gly Ile Leu Phe Thr Leu Thr Ile Phe Leu Ala Leu Met Gly Asn Phe
65                  70                  75                  80

Thr Val Met Trp Ile Ile Leu Tyr His Arg Gln Met Arg Ser Val Thr
                85                  90                  95

Asn Tyr Tyr Leu Phe Asn Leu Ala Val Ala Asp Ala Ser Ile Ser Val
            100                 105                 110

Phe Asn Thr Gly Phe Ser Trp Ser Tyr Asn Tyr Tyr Tyr Val Trp Lys
        115                 120                 125

Phe Gly Ser Phe Tyr Cys Arg Ile Asn Asn Leu Met Gly Ile Thr Pro
    130                 135                 140

Ile Cys Ala Ser Val Phe Thr Met Ile Val Met Ser Ile Glu Arg Tyr
145                 150                 155                 160

Tyr Ala Ile Ile His Pro Leu Lys Lys Arg Pro Gly Arg Arg Ser Thr
                165                 170                 175

Val Thr Ile Ile Ile Met Ile Trp Phe Met Ala Phe Leu Phe Gly Val
            180                 185                 190

Pro Ala Phe Leu Ala Ser Lys Val Asp Val Tyr Tyr Phe Tyr Asp Gly
        195                 200                 205

Tyr Thr Leu Tyr Glu Asn Pro Leu Cys Leu Ala Asp Asn Tyr Pro Gly
    210                 215                 220

Gly Asn Glu Ser Leu Leu Gly Gln Val Tyr Asn Asn Gly Leu Ile Thr
225                 230                 235                 240

Val Gln Tyr Ile Leu Pro Leu Cys Ile Leu Ser Ala Ala Tyr Tyr Arg
                245                 250                 255

Val Gly Val Glu Leu Arg Lys Asp Lys Thr Val Gly Asp Val Arg His
```

```
            260                 265                 270

Ala Lys Ser Val Ala Ala Lys Lys Lys Ala Ser Ile Met Leu Ala Val
        275                 280                 285

Val Val Phe Ile Phe Met Ile Val Trp Phe Pro Tyr Asn Ala Tyr Tyr
    290                 295                 300

Leu Thr Leu His Leu Val Glu Pro Ile Gly Asn Lys Met Leu Ser Leu
305                 310                 315                 320

Tyr Ile Tyr Ile Asn Ile Tyr Trp Leu Gly Met Ser Ser Thr Val Phe
                325                 330                 335

Asn Pro Val Ile Tyr Tyr Phe Met Asn Lys Arg Phe Arg Val Gly Phe
            340                 345                 350

His His Ala Phe Arg Trp Leu Pro Phe Val Arg Ser Asp Lys Asp Glu
        355                 360                 365

Tyr Gln Thr Ile Leu Ser Gln Thr Arg Pro Ser Leu Met Pro Pro Thr
    370                 375                 380

Thr Met Ala His Thr Asp Phe
385                 390

<210> 35
<211> 1098
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1095)

<220>
<223> Clone identifier: CEGPCR16

<400> 35
atg agt tct tcg aat cac tgc atc gac atc cgt gca tac ttg tgg cag   48
Met Ser Ser Ser Asn His Cys Ile Asp Ile Arg Ala Tyr Leu Trp Gln
  1               5                  10                  15

aca aag cat gac ctg acg ctc cac ccg att ccc atc gcg att ctt gca   96
Thr Lys His Asp Leu Thr Leu His Pro Ile Pro Ile Ala Ile Leu Ala
            20                  25                  30

acc atc tac act ata att gtc gta gtt ggc gta acc ggc aat ttg tta  144
Thr Ile Tyr Thr Ile Ile Val Val Val Gly Val Thr Gly Asn Leu Leu
        35                  40                  45

gta gtg atg tcg gtg atg agg ttc aaa gtt ctt caa tca gtc agg aac  192
Val Val Met Ser Val Met Arg Phe Lys Val Leu Gln Ser Val Arg Asn
    50                  55                  60

atg ttc atc gta tct ttg tca gtt tct gac att ttt gtg gcg att gtt  240
Met Phe Ile Val Ser Leu Ser Val Ser Asp Ile Phe Val Ala Ile Val
65                  70                  75                  80

agt ggt tca gta acg ccg ata acc gca ttc tct aaa gtt tgg tta ttt  288
Ser Gly Ser Val Thr Pro Ile Thr Ala Phe Ser Lys Val Trp Leu Phe
                85                  90                  95
```

```
ggt gga cca ttg tgt cat tta cta cct ttg tta cag ggt acc gcg ttg   336
Gly Gly Pro Leu Cys His Leu Leu Pro Leu Leu Gln Gly Thr Ala Leu
            100                 105                 110

agt ttt tcc acg tta acg ctc acc gca att gca att gac aga tat att   384
Ser Phe Ser Thr Leu Thr Leu Thr Ala Ile Ala Ile Asp Arg Tyr Ile
        115                 120                 125

ctc atc tgt cat ccg acg aaa gaa ccg ata cgc aaa gat caa gca ttg   432
Leu Ile Cys His Pro Thr Lys Glu Pro Ile Arg Lys Asp Gln Ala Leu
    130                 135                 140

aaa atg ata agt ttc aac agc gcc atc tca gtt ggg ctt tcg gta cca   480
Lys Met Ile Ser Phe Asn Ser Ala Ile Ser Val Gly Leu Ser Val Pro
145                 150                 155                 160

tta ttc atg aaa cag gaa ctt atg caa ttc cga aac tat tgc gga gaa   528
Leu Phe Met Lys Gln Glu Leu Met Gln Phe Arg Asn Tyr Cys Gly Glu
                165                 170                 175

tat tgc tca gaa aac tgg gga cca gat gct tat ttg aga agc gtt tat   576
Tyr Cys Ser Glu Asn Trp Gly Pro Asp Ala Tyr Leu Arg Ser Val Tyr
            180                 185                 190

gga aca gtg gtg ttc att att caa ttc gtg ttt cca ttg atc acc atc   624
Gly Thr Val Val Phe Ile Ile Gln Phe Val Phe Pro Leu Ile Thr Ile
        195                 200                 205

aca ttt tgc tat gca tct att tct atc aaa cta cga cgt ggt gtc ttt   672
Thr Phe Cys Tyr Ala Ser Ile Ser Ile Lys Leu Arg Arg Gly Val Phe
    210                 215                 220

gtg aga gga agc caa aaa gag ctg atg tct gag gca cgt cgt caa ttg   720
Val Arg Gly Ser Gln Lys Glu Leu Met Ser Glu Ala Arg Arg Gln Leu
225                 230                 235                 240

acg caa cgt cga ctt cgc aca aat cgg atg ctt att atc atg aca gtc   768
Thr Gln Arg Arg Leu Arg Thr Asn Arg Met Leu Ile Ile Met Thr Val
                245                 250                 255

aca ttc gct ctc tca tgg ctg cca tct gtt ggc ttc aac ttt ctc cgg   816
Thr Phe Ala Leu Ser Trp Leu Pro Ser Val Gly Phe Asn Phe Leu Arg
            260                 265                 270

gat tac tca gcg ctt ccc ggc att att gat tca caa gat tac cta ttc   864
Asp Tyr Ser Ala Leu Pro Gly Ile Ile Asp Ser Gln Asp Tyr Leu Phe
        275                 280                 285

gga att att ttc cat tgc att tca atg aca tcg gtg att gtg aat ccc   912
Gly Ile Ile Phe His Cys Ile Ser Met Thr Ser Val Ile Val Asn Pro
    290                 295                 300

ttc ctt tac ggt tac tgt aat gaa cac ttt cgt gct gca ttt gcg gct   960
Phe Leu Tyr Gly Tyr Cys Asn Glu His Phe Arg Ala Ala Phe Ala Ala
305                 310                 315                 320

ctt ctt gac acg gtg aag gca gct tgt gga atg aga cga gtg agt ccg   1008
Leu Leu Asp Thr Val Lys Ala Ala Cys Gly Met Arg Arg Val Ser Pro
                325                 330                 335
```

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ggc aat cca gcg tgc tcc cag cta ctc agt act cac ttt gaa agc acc   1056
Gly Asn Pro Ala Cys Ser Gln Leu Leu Ser Thr His Phe Glu Ser Thr
            340                 345                 350

aca aga cga tcc gtg act acc acg att cca agt tca att taa           1098
Thr Arg Arg Ser Val Thr Thr Thr Ile Pro Ser Ser Ile
        355                 360                 365
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<210> 36
<211> 365
<212> PRT
<213> Homo sapiens

<400> 36

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Met Ser Ser Ser Asn His Cys Ile Asp Ile Arg Ala Tyr Leu Trp Gln
  1               5                  10                  15

Thr Lys His Asp Leu Thr Leu His Pro Ile Pro Ile Ala Ile Leu Ala
            20                  25                  30

Thr Ile Tyr Thr Ile Ile Val Val Val Gly Val Thr Gly Asn Leu Leu
        35                  40                  45

Val Val Met Ser Val Met Arg Phe Lys Val Leu Gln Ser Val Arg Asn
    50                  55                  60

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

Ser Gly Ser Val Thr Pro Ile Thr Ala Phe Ser Lys Val Trp Leu Phe
                85                  90                  95

Gly Gly Pro Leu Cys His Leu Leu Pro Leu Leu Gln Gly Thr Ala Leu
            100                 105                 110

Ser Phe Ser Thr Leu Thr Leu Thr Ala Ile Ala Ile Asp Arg Tyr Ile
        115                 120                 125

Leu Ile Cys His Pro Thr Lys Glu Pro Ile Arg Lys Asp Gln Ala Leu
    130                 135                 140

Lys Met Ile Ser Phe Asn Ser Ala Ile Ser Val Gly Leu Ser Val Pro
145                 150                 155                 160

Leu Phe Met Lys Gln Glu Leu Met Gln Phe Arg Asn Tyr Cys Gly Glu
                165                 170                 175

Tyr Cys Ser Glu Asn Trp Gly Pro Asp Ala Tyr Leu Arg Ser Val Tyr
            180                 185                 190

Gly Thr Val Val Phe Ile Ile Gln Phe Val Phe Pro Leu Ile Thr Ile
        195                 200                 205

Thr Phe Cys Tyr Ala Ser Ile Ser Ile Lys Leu Arg Arg Gly Val Phe
    210                 215                 220

Val Arg Gly Ser Gln Lys Glu Leu Met Ser Glu Ala Arg Arg Gln Leu
225                 230                 235                 240

Thr Gln Arg Arg Leu Arg Thr Asn Arg Met Leu Ile Ile Met Thr Val
                245                 250                 255
```

```
Thr Phe Ala Leu Ser Trp Leu Pro Ser Val Gly Phe Asn Phe Leu Arg
            260                 265                 270

Asp Tyr Ser Ala Leu Pro Gly Ile Ile Asp Ser Gln Asp Tyr Leu Phe
        275                 280                 285

Gly Ile Ile Phe His Cys Ile Ser Met Thr Ser Val Ile Val Asn Pro
    290                 295                 300

Phe Leu Tyr Gly Tyr Cys Asn Glu His Phe Arg Ala Ala Phe Ala Ala
305                 310                 315                 320

Leu Leu Asp Thr Val Lys Ala Ala Cys Gly Met Arg Arg Val Ser Pro
                325                 330                 335

Gly Asn Pro Ala Cys Ser Gln Leu Leu Ser Thr His Phe Glu Ser Thr
            340                 345                 350

Thr Arg Arg Ser Val Thr Thr Thr Ile Pro Ser Ser Ile
        355                 360                 365


<210> 37
<211> 1176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1173)

<220>
<223> Clone identifier: CEGPCR17

<400> 37
atg caa ccg cca aac tct acg gga caa tgg aca gaa att cac tgc gat   48
Met Gln Pro Pro Asn Ser Thr Gly Gln Trp Thr Glu Ile His Cys Asp
  1               5                  10                  15

tgg ttt gca gaa atg caa aat tat cag aac agt ctc tac aaa ata aat   96
Trp Phe Ala Glu Met Gln Asn Tyr Gln Asn Ser Leu Tyr Lys Ile Asn
             20                  25                  30

ttt gat gga tcc cca ata gtg cca atg tat ggg ttg gtg tgc tca ttc   144
Phe Asp Gly Ser Pro Ile Val Pro Met Tyr Gly Leu Val Cys Ser Phe
         35                  40                  45

gga gct ctt gcc aac ttt atc gtt ctc ctc gca ttt gtc aga act gca   192
Gly Ala Leu Ala Asn Phe Ile Val Leu Leu Ala Phe Val Arg Thr Ala
     50                  55                  60

aat ctt cga aac ttg aga aac agt ttc att gtg aat ttg gca ttt tcc   240
Asn Leu Arg Asn Leu Arg Asn Ser Phe Ile Val Asn Leu Ala Phe Ser
 65                  70                  75                  80

gat ttg att ctg tgt gtg gtc aca gcg cca gtc act ctc tat acg agt   288
Asp Leu Ile Leu Cys Val Val Thr Ala Pro Val Thr Leu Tyr Thr Ser
                85                  90                  95

tta aat tta ttt tgg cca ttc gga gat tgg tcg tgc aag ttt ctc gct   336
Leu Asn Leu Phe Trp Pro Phe Gly Asp Trp Ser Cys Lys Phe Leu Ala
            100                 105                 110
```

```
ggt gtt caa gca gtg aac aca ttt gtt tca tca ctt act ctt gca ttc   384
Gly Val Gln Ala Val Asn Thr Phe Val Ser Ser Leu Thr Leu Ala Phe
        115                 120                 125

att gca atg gat cgt gtt ctt cta aca ctt tgt cca gtt cga tgg aga   432
Ile Ala Met Asp Arg Val Leu Leu Thr Leu Cys Pro Val Arg Trp Arg
    130                 135                 140

tta gca gca act gca cca ctt tta tgc tat ggt gtc gta tgg atc att   480
Leu Ala Ala Thr Ala Pro Leu Leu Cys Tyr Gly Val Val Trp Ile Ile
145                 150                 155                 160

tcg atc ata gtt gct ctt cca tat gca ttg gca gta agc tca aag ttg   528
Ser Ile Ile Val Ala Leu Pro Tyr Ala Leu Ala Val Ser Ser Lys Leu
                165                 170                 175

gct cca ttt gat cca tgg agt gat aga gca act ccc aaa atg cta acc   576
Ala Pro Phe Asp Pro Trp Ser Asp Arg Ala Thr Pro Lys Met Leu Thr
            180                 185                 190

tat tgc aac cgt caa gtg cca gaa ata tgt gca gag atg caa gaa gcc   624
Tyr Cys Asn Arg Gln Val Pro Glu Ile Cys Ala Glu Met Gln Glu Ala
        195                 200                 205

tgg gat aat gca att gtc tca aaa acc acg tac aca ttt gta gta ctt   672
Trp Asp Asn Ala Ile Val Ser Lys Thr Thr Tyr Thr Phe Val Val Leu
    210                 215                 220

ggt att caa tat att cta cca ctt gct gcc ttg gca tat gca tat ttc   720
Gly Ile Gln Tyr Ile Leu Pro Leu Ala Ala Leu Ala Tyr Ala Tyr Phe
225                 230                 235                 240

caa atc ggg tca aca att caa aaa cga tca aaa gta tca cgt aca gtg   768
Gln Ile Gly Ser Thr Ile Gln Lys Arg Ser Lys Val Ser Arg Thr Val
                245                 250                 255

gat aca aca aga aga atg caa atg caa aat aga aat cga aga gct ctt   816
Asp Thr Thr Arg Arg Met Gln Met Gln Asn Arg Asn Arg Arg Ala Leu
            260                 265                 270

ttg ttg ctc ttt ttg tta gta ctc aca tat gcc gtg tgt tgg gct cca   864
Leu Leu Leu Phe Leu Leu Val Leu Thr Tyr Ala Val Cys Trp Ala Pro
        275                 280                 285

atg aat att tat cat gtt ttg aat ggt ctc gag att att aac tat tca   912
Met Asn Ile Tyr His Val Leu Asn Gly Leu Glu Ile Ile Asn Tyr Ser
    290                 295                 300

caa aat atg tac atc ttc tgt cat ttg gtc gga atc tct tca acg tgt   960
Gln Asn Met Tyr Ile Phe Cys His Leu Val Gly Ile Ser Ser Thr Cys
305                 310                 315                 320

gtt aat cca ata gta tat gca ctg gtc aat gaa tca ttt aga aat gct  1008
Val Asn Pro Ile Val Tyr Ala Leu Val Asn Glu Ser Phe Arg Asn Ala
                325                 330                 335


tta caa tca atg att ctt caa ttc cgc ccg tgt tac gtc aca act acc  1056
Leu Gln Ser Met Ile Leu Gln Phe Arg Pro Cys Tyr Val Thr Thr Thr
            340                 345                 350
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ggt aca gca gcc acc aac gtg tat gca tat tct gcg act tcg aag gcg   1104
Gly Thr Ala Ala Thr Asn Val Tyr Ala Tyr Ser Ala Thr Ser Lys Ala
        355                 360                 365

gaa aat gtc act ttg atg cgt gat cct ttc tca aca act cct cgt cca   1152
Glu Asn Val Thr Leu Met Arg Asp Pro Phe Ser Thr Thr Pro Arg Pro
    370                 375                 380

aat gaa cgc cca gac agt gtt tga                                  1176
Asn Glu Arg Pro Asp Ser Val
385                 390
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<210> 38
<211> 391
<212> PRT
<213> Homo sapiens

<400> 38

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Met Gln Pro Pro Asn Ser Thr Gly Gln Trp Thr Glu Ile His Cys Asp
  1               5                  10                  15

Trp Phe Ala Glu Met Gln Asn Tyr Gln Asn Ser Leu Tyr Lys Ile Asn
            20                  25                  30

Phe Asp Gly Ser Pro Ile Val Pro Met Tyr Gly Leu Val Cys Ser Phe
        35                  40                  45

Gly Ala Leu Ala Asn Phe Ile Val Leu Leu Ala Phe Val Arg Thr Ala
    50                  55                  60

Asn Leu Arg Asn Leu Arg Asn Ser Phe Ile Val Asn Leu Ala Phe Ser
65                  70                  75                  80

Asp Leu Ile Leu Cys Val Val Thr Ala Pro Val Thr Leu Tyr Thr Ser
                85                  90                  95

Leu Asn Leu Phe Trp Pro Phe Gly Asp Trp Ser Cys Lys Phe Leu Ala
            100                 105                 110

Gly Val Gln Ala Val Asn Thr Phe Val Ser Ser Leu Thr Leu Ala Phe
        115                 120                 125

Ile Ala Met Asp Arg Val Leu Leu Thr Leu Cys Pro Val Arg Trp Arg
    130                 135                 140

Leu Ala Ala Thr Ala Pro Leu Leu Cys Tyr Gly Val Val Trp Ile Ile
145                 150                 155                 160

Ser Ile Ile Val Ala Leu Pro Tyr Ala Leu Ala Val Ser Ser Lys Leu
                165                 170                 175

Ala Pro Phe Asp Pro Trp Ser Asp Arg Ala Thr Pro Lys Met Leu Thr
            180                 185                 190

Tyr Cys Asn Arg Gln Val Pro Glu Ile Cys Ala Glu Met Gln Glu Ala
        195                 200                 205

Trp Asp Asn Ala Ile Val Ser Lys Thr Thr Tyr Thr Phe Val Val Leu
    210                 215                 220
```

```
Gly Ile Gln Tyr Ile Leu Pro Leu Ala Ala Leu Ala Tyr Ala Tyr Phe
225                 230                 235                 240

Gln Ile Gly Ser Thr Ile Gln Lys Arg Ser Lys Val Ser Arg Thr Val
                245                 250                 255

Asp Thr Thr Arg Arg Met Gln Met Gln Asn Arg Asn Arg Arg Ala Leu
            260                 265                 270

Leu Leu Leu Phe Leu Leu Val Leu Thr Tyr Ala Val Cys Trp Ala Pro
        275                 280                 285

Met Asn Ile Tyr His Val Leu Asn Gly Leu Glu Ile Ile Asn Tyr Ser
    290                 295                 300

Gln Asn Met Tyr Ile Phe Cys His Leu Val Gly Ile Ser Ser Thr Cys
305                 310                 315                 320

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

Leu Gln Ser Met Ile Leu Gln Phe Arg Pro Cys Tyr Val Thr Thr Thr
            340                 345                 350

Gly Thr Ala Ala Thr Asn Val Tyr Ala Tyr Ser Ala Thr Ser Lys Ala
        355                 360                 365

Glu Asn Val Thr Leu Met Arg Asp Pro Phe Ser Thr Thr Pro Arg Pro
    370                 375                 380

Asn Glu Arg Pro Asp Ser Val
385                 390

<210> 39
<211> 1500
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1497)

<220>
<223> Clone identifier: CEGPCR19

<400> 39
atg gag att att ctt tgt ttt ttg aac tac ctg gca cat ttt aaa gcg   48
Met Glu Ile Ile Leu Cys Phe Leu Asn Tyr Leu Ala His Phe Lys Ala
  1               5                  10                  15

ggt ttc gag att gat tta ttt aac ttc att aac ata aca att tat aag   96
Gly Phe Glu Ile Asp Leu Phe Asn Phe Ile Asn Ile Thr Ile Tyr Lys
             20                  25                  30

aaa ttt cct ttt ttt ttt cat cga ctg aaa ttt gat aga aaa ttg gat   144
Lys Phe Pro Phe Phe Phe His Arg Leu Lys Phe Asp Arg Lys Leu Asp
         35                  40                  45

ttt atg att aat ttc cag aac acg ctt ttc gat ttt ccc att tta gaa   192
Phe Met Ile Asn Phe Gln Asn Thr Leu Phe Asp Phe Pro Ile Leu Glu
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     50                  55                  60

aaa aac att ttt cga ttt tcg aat tta aaa aat tta aaa act cta aaa   240
Lys Asn Ile Phe Arg Phe Ser Asn Leu Lys Asn Leu Lys Thr Leu Lys
 65                  70                  75                  80

ttt tca acg ata ttt tta ttt tat gga ttt tat gca tgt aat ttt ctt   288
Phe Ser Thr Ile Phe Leu Phe Tyr Gly Phe Tyr Ala Cys Asn Phe Leu
                 85                  90                  95

caa aac aac ctt cga tgc atg gtt agt tcg gcg gcc acc att tcg acc   336
Gln Asn Asn Leu Arg Cys Met Val Ser Ser Ala Ala Thr Ile Ser Thr
            100                 105                 110

att tca acc aca acg act ccc tcc acc atc agc aac gtt atc aca agt   384
Ile Ser Thr Thr Thr Thr Pro Ser Thr Ile Ser Asn Val Ile Thr Ser
        115                 120                 125

cat tcg aac aat ggc tcg tgc att cag atc gct gag gcg att gcg gca   432
His Ser Asn Asn Gly Ser Cys Ile Gln Ile Ala Glu Ala Ile Ala Ala
    130                 135                 140

caa ggc atc gat gat att act gta gac ttt tac atc cga tca atc ttc   480
Gln Gly Ile Asp Asp Ile Thr Val Asp Phe Tyr Ile Arg Ser Ile Phe
145                 150                 155                 160

aca ttc ctc tac ggg ttc ctg ttt gta tta ggc att ttt gga aac ggc   528
Thr Phe Leu Tyr Gly Phe Leu Phe Val Leu Gly Ile Phe Gly Asn Gly
                165                 170                 175

ggc gta cta tgg gcg gtg gcg aga aac aag cgg ctc caa tcg gct cgc   576
Gly Val Leu Trp Ala Val Ala Arg Asn Lys Arg Leu Gln Ser Ala Arg
            180                 185                 190

aac gta ttt ctg ctc aac ttg atc ttc acc gat ttg ata ttg gtg ttc   624
Asn Val Phe Leu Leu Asn Leu Ile Phe Thr Asp Leu Ile Leu Val Phe
        195                 200                 205

aca gcg att cca gtc aca cca tgg tac gcg atg acc aaa gac tgg gca   672
Thr Ala Ile Pro Val Thr Pro Trp Tyr Ala Met Thr Lys Asp Trp Ala
    210                 215                 220

ttc ggg tca gtg atg tgc cat tta gtt cct ttg tca aat tcg tgt tcg   720
Phe Gly Ser Val Met Cys His Leu Val Pro Leu Ser Asn Ser Cys Ser
225                 230                 235                 240

gtg ttt gtg acg agt tgg agc ctc act gca atc tcc tta gat aaa ttt   768
Val Phe Val Thr Ser Trp Ser Leu Thr Ala Ile Ser Leu Asp Lys Phe
                245                 250                 255

ctg cat atc aac gat ccc acc aaa caa cca gtt tct att cgt caa gcg   816
Leu His Ile Asn Asp Pro Thr Lys Gln Pro Val Ser Ile Arg Gln Ala
            260                 265                 270

ttg gca ata aca ttt ctt atc tgg ata gtc tca aca ctg ata aat cta   864
Leu Ala Ile Thr Phe Leu Ile Trp Ile Val Ser Thr Leu Ile Asn Leu
        275                 280                 285

ccg tat ctt atg tct ttc gag cac gtc gat gga agc ttt tac gtt cag   912
Pro Tyr Leu Met Ser Phe Glu His Val Asp Gly Ser Phe Tyr Val Gln
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    290                 295                 300

ccc gga gaa act cca tac tgc ggg cac ttt tgc gac gag gcg aat tgg   960
Pro Gly Glu Thr Pro Tyr Cys Gly His Phe Cys Asp Glu Ala Asn Trp
305                 310                 315                 320

cag agc gaa aat agt cga aag att tac gga act acg gtt atg ttg tta   1008
Gln Ser Glu Asn Ser Arg Lys Ile Tyr Gly Thr Thr Val Met Leu Leu
                325                 330                 335

cag ttc gtc gtg ccg atg gca gtg atc acg tat tgc tac ttc aaa atc   1056
Gln Phe Val Val Pro Met Ala Val Ile Thr Tyr Cys Tyr Phe Lys Ile
            340                 345                 350

ttg caa aaa gtg tca aaa gac atg atc atc caa aat gct caa ttc tgt   1104
Leu Gln Lys Val Ser Lys Asp Met Ile Ile Gln Asn Ala Gln Phe Cys
        355                 360                 365

caa tca ctg aca caa aag cag aga agt gat gcg acg tca cga aag aag   1152
Gln Ser Leu Thr Gln Lys Gln Arg Ser Asp Ala Thr Ser Arg Lys Lys
    370                 375                 380

aaa gtg aat tat att cta att gca atg gtt gtc aca ttt atc ggg tgt   1200
Lys Val Asn Tyr Ile Leu Ile Ala Met Val Val Thr Phe Ile Gly Cys
385                 390                 395                 400

tgg ttg cct tta aca tta ctc aat ttg gtc aaa gat ttt aaa aaa gag   1248
Trp Leu Pro Leu Thr Leu Leu Asn Leu Val Lys Asp Phe Lys Lys Glu
                405                 410                 415

ccc gaa tgg cta aaa cgt cag ccg ttc ttc tgg gca ata aat gct cac   1296
Pro Glu Trp Leu Lys Arg Gln Pro Phe Phe Trp Ala Ile Asn Ala His
            420                 425                 430

gtc ata gcc atg tcc tta gtc gtc tgg aac cct ctg cta ttc ttt tgg   1344
Val Ile Ala Met Ser Leu Val Val Trp Asn Pro Leu Leu Phe Phe Trp
        435                 440                 445

ctg aca cga aaa caa aaa cgt tcc gga ctg tca aaa ata ctc aac tca   1392
Leu Thr Arg Lys Gln Lys Arg Ser Gly Leu Ser Lys Ile Leu Asn Ser
    450                 455                 460

aca gag ggt tcg aaa aaa gca ggt ggt tct gga ttg cga ggg atc cag   1440
Thr Glu Gly Ser Lys Lys Ala Gly Gly Ser Gly Leu Arg Gly Ile Gln
465                 470                 475                 480

cta cac gac ctc ctc ccg acc tct act cat tcg gac aga tgt gca ggc   1488
Leu His Asp Leu Leu Pro Thr Ser Thr His Ser Asp Arg Cys Ala Gly
                485                 490                 495

aac tct ttc taa                                                  1500
Asn Ser Phe


<210> 40
<211> 499
<212> PRT
<213> Homo sapiens

<400> 40
Met Glu Ile Ile Leu Cys Phe Leu Asn Tyr Leu Ala His Phe Lys Ala
  1               5                  10                  15
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Gly Phe Glu Ile Asp Leu Phe Asn Phe Ile Asn Ile Thr Ile Tyr Lys
20 25 30

Lys Phe Pro Phe Phe Phe His Arg Leu Lys Phe Asp Arg Lys Leu Asp
35 40 45

Phe Met Ile Asn Phe Gln Asn Thr Leu Phe Asp Phe Pro Ile Leu Glu
50 55 60

Lys Asn Ile Phe Arg Phe Ser Asn Leu Lys Asn Leu Lys Thr Leu Lys
65 70 75 80

Phe Ser Thr Ile Phe Leu Phe Tyr Gly Phe Tyr Ala Cys Asn Phe Leu
85 90 95

Gln Asn Asn Leu Arg Cys Met Val Ser Ser Ala Ala Thr Ile Ser Thr
100 105 110

Ile Ser Thr Thr Thr Thr Pro Ser Thr Ile Ser Asn Val Ile Thr Ser
115 120 125

His Ser Asn Asn Gly Ser Cys Ile Gln Ile Ala Glu Ala Ile Ala Ala
130 135 140

Gln Gly Ile Asp Asp Ile Thr Val Asp Phe Tyr Ile Arg Ser Ile Phe
145 150 155 160

Thr Phe Leu Tyr Gly Phe Leu Phe Val Leu Gly Ile Phe Gly Asn Gly
165 170 175

Gly Val Leu Trp Ala Val Ala Arg Asn Lys Arg Leu Gln Ser Ala Arg
180 185 190

Asn Val Phe Leu Leu Asn Leu Ile Phe Thr Asp Leu Ile Leu Val Phe
195 200 205

Thr Ala Ile Pro Val Thr Pro Trp Tyr Ala Met Thr Lys Asp Trp Ala
210 215 220

Phe Gly Ser Val Met Cys His Leu Val Pro Leu Ser Asn Ser Cys Ser
225 230 235 240

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

Leu His Ile Asn Asp Pro Thr Lys Gln Pro Val Ser Ile Arg Gln Ala
260 265 270

Leu Ala Ile Thr Phe Leu Ile Trp Ile Val Ser Thr Leu Ile Asn Leu
275 280 285

Pro Tyr Leu Met Ser Phe Glu His Val Asp Gly Ser Phe Tyr Val Gln
290 295 300

Pro Gly Glu Thr Pro Tyr Cys Gly His Phe Cys Asp Glu Ala Asn Trp
305 310 315 320

Gln Ser Glu Asn Ser Arg Lys Ile Tyr Gly Thr Thr Val Met Leu Leu
325 330 335

Gln Phe Val Val Pro Met Ala Val Ile Thr Tyr Cys Tyr Phe Lys Ile
340 345 350

```
Leu Gln Lys Val Ser Lys Asp Met Ile Ile Gln Asn Ala Gln Phe Cys
        355                 360                 365

Gln Ser Leu Thr Gln Lys Gln Arg Ser Asp Ala Thr Ser Arg Lys Lys
    370                 375                 380

Lys Val Asn Tyr Ile Leu Ile Ala Met Val Val Thr Phe Ile Gly Cys
385                 390                 395                 400

Trp Leu Pro Leu Thr Leu Leu Asn Leu Val Lys Asp Phe Lys Lys Glu
                405                 410                 415

Pro Glu Trp Leu Lys Arg Gln Pro Phe Phe Trp Ala Ile Asn Ala His
            420                 425                 430

Val Ile Ala Met Ser Leu Val Val Trp Asn Pro Leu Leu Phe Phe Trp
        435                 440                 445

Leu Thr Arg Lys Gln Lys Arg Ser Gly Leu Ser Lys Ile Leu Asn Ser
    450                 455                 460

Thr Glu Gly Ser Lys Lys Ala Gly Gly Ser Gly Leu Arg Gly Ile Gln
465                 470                 475                 480

Leu His Asp Leu Leu Pro Thr Ser Thr His Ser Asp Arg Cys Ala Gly
                485                 490                 495

Asn Ser Phe


<210> 41
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1332)

<220>
<223> Clone identifier: CEGPCR20

<400> 41
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Met Ser Leu Gly Asn Val Ile Ile Ala Ser Ser Val Asn Thr Arg Ser
  1               5                  10                  15

ccc ata gat tcc cac ttg ttt aga aaa att ttg tgt ttt aga att tat   96
Pro Ile Asp Ser His Leu Phe Arg Lys Ile Leu Cys Phe Arg Ile Tyr
             20                  25                  30

gac gac act atc agt ttt gag aga aaa att gga ata atc att cca aca   144
Asp Asp Thr Ile Ser Phe Glu Arg Lys Ile Gly Ile Ile Ile Pro Thr
         35                  40                  45

att ttt gcc gtt atc att ttg gtc gga ctt gtt ggt aat gct ctg gtg   192
Ile Phe Ala Val Ile Ile Leu Val Gly Leu Val Gly Asn Ala Leu Val
     50                  55                  60

gtg att gtt gct ttt gga cga caa atg aga aat tca acc aac act ctt   240
Val Ile Val Ala Phe Gly Arg Gln Met Arg Asn Ser Thr Asn Thr Leu
 65                  70                  75                  80
```

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att att gga ctt gcc ata tct gac ttg atg ttc ctt ttg ctt tgc gtt   288
Ile Ile Gly Leu Ala Ile Ser Asp Leu Met Phe Leu Leu Leu Cys Val
                85                  90                  95

cct ttc aca gct gtg gat tac gca gct ccg aca tgg atc ttt ccc gag   336
Pro Phe Thr Ala Val Asp Tyr Ala Ala Pro Thr Trp Ile Phe Pro Glu
            100                 105                 110

tgg aca tgc tct atg atc aat ttc ttc cag cat acg tct gca tac tgt   384
Trp Thr Cys Ser Met Ile Asn Phe Phe Gln His Thr Ser Ala Tyr Cys
        115                 120                 125

agt gtt tgg aca ttg acc ctt atg gcc ctc gat aga tat cta gca gtt   432
Ser Val Trp Thr Leu Thr Leu Met Ala Leu Asp Arg Tyr Leu Ala Val
    130                 135                 140

gta tat cca gtt gaa tca atg acg tta cga aca cca agg aac act gtg   480
Val Tyr Pro Val Glu Ser Met Thr Leu Arg Thr Pro Arg Asn Thr Val
145                 150                 155                 160

att gcg tta tgc ttc att tac atc att atc att gct tct cag att cct   528
Ile Ala Leu Cys Phe Ile Tyr Ile Ile Ile Ile Ala Ser Gln Ile Pro
                165                 170                 175

gtg gga cga atg cac ggg att tat gtg tat gac ttt att atg gaa aaa   576
Val Gly Arg Met His Gly Ile Tyr Val Tyr Asp Phe Ile Met Glu Lys
            180                 185                 190

cgg tca acg tgc gca att ctg aca att gcc act gca gag gct act ccg   624
Arg Ser Thr Cys Ala Ile Leu Thr Ile Ala Thr Ala Glu Ala Thr Pro
        195                 200                 205

acg atg gct cga aca tat ttt atg aca ttc aat gtg ttt ggt tac gtg   672
Thr Met Ala Arg Thr Tyr Phe Met Thr Phe Asn Val Phe Gly Tyr Val
    210                 215                 220

ctt cca ctg ggc att tct gtt gtc ctg tat ggt ctt atg ttg aga aaa   720
Leu Pro Leu Gly Ile Ser Val Val Leu Tyr Gly Leu Met Leu Arg Lys
225                 230                 235                 240

ctt tgg gac atg cca agg ccg ggt aac tct caa tct gtt ggt ggt aga   768
Leu Trp Asp Met Pro Arg Pro Gly Asn Ser Gln Ser Val Gly Gly Arg
                245                 250                 255

aat ctt aca aat cgt gat agt ggt tca agt att cgt cgg agg ccg gaa   816
Asn Leu Thr Asn Arg Asp Ser Gly Ser Ser Ile Arg Arg Arg Pro Glu
            260                 265                 270

gca act gct gcc aaa aga aaa gtt acc cgc ctt gta ctg tgt gtt ttg   864
Ala Thr Ala Ala Lys Arg Lys Val Thr Arg Leu Val Leu Cys Val Leu
        275                 280                 285

atc acc tgg gca ctt tgc tgg ctt cca cta aac gtg tgc ttt ttc atg   912
Ile Thr Trp Ala Leu Cys Trp Leu Pro Leu Asn Val Cys Phe Phe Met
    290                 295                 300


tct ggt ctc gcc tac ccg gaa cca ctt gtt ata tct cat ggt gtc atc   960
Ser Gly Leu Ala Tyr Pro Glu Pro Leu Val Ile Ser His Gly Val Ile
305                 310                 315                 320
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atg gta att gtt cag att gct agt caa gtt ctt gcc tac acc aat tcg   1008
Met Val Ile Val Gln Ile Ala Ser Gln Val Leu Ala Tyr Thr Asn Ser
                325                 330                 335

tgt ctt aat cca att cta tac gct ttg atg tcg cag agt ttc cgg gaa   1056
Cys Leu Asn Pro Ile Leu Tyr Ala Leu Met Ser Gln Ser Phe Arg Glu
            340                 345                 350

gga ttc att cga gtc atg aaa atg cta ata aat aag cta tcg cgt gga   1104
Gly Phe Ile Arg Val Met Lys Met Leu Ile Asn Lys Leu Ser Arg Gly
        355                 360                 365

agg ttc tgc act aat tac cga cga agt gct ctt cgg aca gag ctc aca   1152
Arg Phe Cys Thr Asn Tyr Arg Arg Ser Ala Leu Arg Thr Glu Leu Thr
    370                 375                 380



cac tat aac caa act cca gca cat cca gca aac act gtg gtt caa gtg   1200
His Tyr Asn Gln Thr Pro Ala His Pro Ala Asn Thr Val Val Gln Val
385                 390                 395                 400

tca aac gga gaa cga tcc tcg ctt ctg aaa gat aac tcg agc tct gcg   1248
Ser Asn Gly Glu Arg Ser Ser Leu Leu Lys Asp Asn Ser Ser Ser Ala
                405                 410                 415

acg tct gta caa cca ctt cgg acg tca att caa gcg aag aaa aca aag   1296
Thr Ser Val Gln Pro Leu Arg Thr Ser Ile Gln Ala Lys Lys Thr Lys
            420                 425                 430

aat gtc tgt gat acg atg ctc ttt gtg tgt ttc ttc taa               1335
Asn Val Cys Asp Thr Met Leu Phe Val Cys Phe Phe
        435                 440
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<210> 42
<211> 444
<212> PRT
<213> Homo sapiens

<400> 42

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Met Ser Leu Gly Asn Val Ile Ile Ala Ser Ser Val Asn Thr Arg Ser
  1               5                  10                  15

Pro Ile Asp Ser His Leu Phe Arg Lys Ile Leu Cys Phe Arg Ile Tyr
             20                  25                  30

Asp Asp Thr Ile Ser Phe Glu Arg Lys Ile Gly Ile Ile Ile Pro Thr
         35                  40                  45

Ile Phe Ala Val Ile Ile Leu Val Gly Leu Val Gly Asn Ala Leu Val
     50                  55                  60

Val Ile Val Ala Phe Gly Arg Gln Met Arg Asn Ser Thr Asn Thr Leu
 65                  70                  75                  80

Ile Ile Gly Leu Ala Ile Ser Asp Leu Met Phe Leu Leu Leu Cys Val
                 85                  90                  95

Pro Phe Thr Ala Val Asp Tyr Ala Ala Pro Thr Trp Ile Phe Pro Glu
            100                 105                 110
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Trp Thr Cys Ser Met Ile Asn Phe Phe Gln His Thr Ser Ala Tyr Cys
115 120 125

Ser Val Trp Thr Leu Thr Leu Met Ala Leu Asp Arg Tyr Leu Ala Val
130 135 140

Val Tyr Pro Val Glu Ser Met Thr Leu Arg Thr Pro Arg Asn Thr Val
145 150 155 160

Ile Ala Leu Cys Phe Ile Tyr Ile Ile Ile Ile Ala Ser Gln Ile Pro
165 170 175

Val Gly Arg Met His Gly Ile Tyr Val Tyr Asp Phe Ile Met Glu Lys
180 185 190

Arg Ser Thr Cys Ala Ile Leu Thr Ile Ala Thr Ala Glu Ala Thr Pro
195 200 205

Thr Met Ala Arg Thr Tyr Phe Met Thr Phe Asn Val Phe Gly Tyr Val
210 215 220

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

Leu Trp Asp Met Pro Arg Pro Gly Asn Ser Gln Ser Val Gly Gly Arg
245 250 255

Asn Leu Thr Asn Arg Asp Ser Gly Ser Ser Ile Arg Arg Arg Pro Glu
260 265 270

Ala Thr Ala Ala Lys Arg Lys Val Thr Arg Leu Val Leu Cys Val Leu
275 280 285

Ile Thr Trp Ala Leu Cys Trp Leu Pro Leu Asn Val Cys Phe Phe Met
290 295 300

Ser Gly Leu Ala Tyr Pro Glu Pro Leu Val Ile Ser His Gly Val Ile
305 310 315 320

Met Val Ile Val Gln Ile Ala Ser Gln Val Leu Ala Tyr Thr Asn Ser
325 330 335

Cys Leu Asn Pro Ile Leu Tyr Ala Leu Met Ser Gln Ser Phe Arg Glu
340 345 350

Gly Phe Ile Arg Val Met Lys Met Leu Ile Asn Lys Leu Ser Arg Gly
355 360 365

Arg Phe Cys Thr Asn Tyr Arg Arg Ser Ala Leu Arg Thr Glu Leu Thr
370 375 380

His Tyr Asn Gln Thr Pro Ala His Pro Ala Asn Thr Val Val Gln Val
385 390 395 400

Ser Asn Gly Glu Arg Ser Ser Leu Leu Lys Asp Asn Ser Ser Ser Ala
405 410 415

Thr Ser Val Gln Pro Leu Arg Thr Ser Ile Gln Ala Lys Lys Thr Lys
420 425 430

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Asn Val Cys Asp Thr Met Leu Phe Val Cys Phe Phe
        435                 440

<210> 43
<211> 1131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1128)

<220>
<223> Clone identifier: CEGPCR3

<400> 43
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Met Glu Gly Gly Arg Asn Cys Val Met Thr Val Gln Gln Trp Gln Pro
  1               5                  10                  15

gaa tac aat gat atg aac cag ata aga gca ata ttc tcg tta ctg tac   96
Glu Tyr Asn Asp Met Asn Gln Ile Arg Ala Ile Phe Ser Leu Leu Tyr
             20                  25                  30

ctt ctt gtt tgg gtt gga gct att gtt ggc aac act cta gta ctt tat   144
Leu Leu Val Trp Val Gly Ala Ile Val Gly Asn Thr Leu Val Leu Tyr
         35                  40                  45

gta ctc act ttt aat cag gta tca ctg tca gtt agg acg gta ttt gtt   192
Val Leu Thr Phe Asn Gln Val Ser Leu Ser Val Arg Thr Val Phe Val
     50                  55                  60

gga tgt cta gct ggt tca gac ctt cta atg tgc ctt ttc tcg ttg cca   240
Gly Cys Leu Ala Gly Ser Asp Leu Leu Met Cys Leu Phe Ser Leu Pro
 65                  70                  75                  80

att acc gcg att tct ata ttt tca aga gtt tgg gta ttt cct gct ata   288
Ile Thr Ala Ile Ser Ile Phe Ser Arg Val Trp Val Phe Pro Ala Ile
                 85                  90                  95

ttt tgc aag ttg atc gga gtt ttc cag ggc ggt acg att ttt gtc tca   336
Phe Cys Lys Leu Ile Gly Val Phe Gln Gly Gly Thr Ile Phe Val Ser
            100                 105                 110

tca ttc aca tta aca gtt att gct ctg gac aga tgt gta cta att cta   384
Ser Phe Thr Leu Thr Val Ile Ala Leu Asp Arg Cys Val Leu Ile Leu
        115                 120                 125

cgt cca aat cag gag ata gta aat ttc ccg aga gct gtc ttc att gtt   432
Arg Pro Asn Gln Glu Ile Val Asn Phe Pro Arg Ala Val Phe Ile Val
    130                 135                 140

ttc tgc att tgg ctt ctc gga tac tct cta gca ctt cct gta ggc atc   480
Phe Cys Ile Trp Leu Leu Gly Tyr Ser Leu Ala Leu Pro Val Gly Ile
145                 150                 155                 160

tac agc gac att gca gta tac gac gaa att tgc ggc aca ttc tgt gaa   528
Tyr Ser Asp Ile Ala Val Tyr Asp Glu Ile Cys Gly Thr Phe Cys Glu
                165                 170                 175

gag aat tgg cct gat ttc aat ccg gat act gga aga tcg gga att cga   576
Glu Asn Trp Pro Asp Phe Asn Pro Asp Thr Gly Arg Ser Gly Ile Arg
```

```
                180                 185                 190

aga gct tat gga ctt tct gtg ttg gta ctt caa ttt ggt att cct gca   624
Arg Ala Tyr Gly Leu Ser Val Leu Val Leu Gln Phe Gly Ile Pro Ala
        195                 200                 205

ttg ata agt tca att tgt tac tgg atg att agt cga gtg atg tca gat   672
Leu Ile Ser Ser Ile Cys Tyr Trp Met Ile Ser Arg Val Met Ser Asp
    210                 215                 220

caa tta gca aga aga aga ggg cac aat att cga ccg gaa tct gaa aca   720
Gln Leu Ala Arg Arg Arg Gly His Asn Ile Arg Pro Glu Ser Glu Thr
225                 230                 235                 240

aag ctg gtg aat cga aag aca aga gct aat cga atg atg atc gta atg   768
Lys Leu Val Asn Arg Lys Thr Arg Ala Asn Arg Met Met Ile Val Met
                245                 250                 255

gtt gtt gga ttc gtt ctc gcg tgg atg cca ttc aat gca gtc aat ctc   816
Val Val Gly Phe Val Leu Ala Trp Met Pro Phe Asn Ala Val Asn Leu
            260                 265                 270


tac cgt gac cta ttt gga att tct aaa tgg tat tct aca gtc ttt gcg   864
Tyr Arg Asp Leu Phe Gly Ile Ser Lys Trp Tyr Ser Thr Val Phe Ala
        275                 280                 285

ctt tgc cac gta tgc gca atg tgc tcc gct gtg ctc aac cca atc atc   912
Leu Cys His Val Cys Ala Met Cys Ser Ala Val Leu Asn Pro Ile Ile
    290                 295                 300

tat tcc tgg ttc aat cct caa ttc cga caa agt atc acc act ttg ttc   960
Tyr Ser Trp Phe Asn Pro Gln Phe Arg Gln Ser Ile Thr Thr Leu Phe
305                 310                 315                 320

aag ggt act gat gaa gct aga ttg atc aag aag aaa cca caa tct acc  1008
Lys Gly Thr Asp Glu Ala Arg Leu Ile Lys Lys Lys Pro Gln Ser Thr
                325                 330                 335

agt aaa atg gtt tcg tat ccg act aat ttc tcc gag atc cga aaa gaa  1056
Ser Lys Met Val Ser Tyr Pro Thr Asn Phe Ser Glu Ile Arg Lys Glu
            340                 345                 350

aca gaa att gca tcg aca aag aca aaa atc aca att gct gaa aac gac  1104
Thr Glu Ile Ala Ser Thr Lys Thr Lys Ile Thr Ile Ala Glu Asn Asp
        355                 360                 365

tat cga gct gga gat caa ctt tta taa                             1131
Tyr Arg Ala Gly Asp Gln Leu Leu
    370                 375
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<210> 44
<211> 376
<212> PRT
<213> Homo sapiens

<400> 44

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Met Glu Gly Gly Arg Asn Cys Val Met Thr Val Gln Gln Trp Gln Pro
  1               5                  10                  15
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Glu Tyr Asn Asp Met Asn Gln Ile Arg Ala Ile Phe Ser Leu Leu Tyr
20 25 30

Leu Leu Val Trp Val Gly Ala Ile Val Gly Asn Thr Leu Val Leu Tyr
35 40 45

Val Leu Thr Phe Asn Gln Val Ser Leu Ser Val Arg Thr Val Phe Val
50 55 60

Gly Cys Leu Ala Gly Ser Asp Leu Leu Met Cys Leu Phe Ser Leu Pro
65 70 75 80

Ile Thr Ala Ile Ser Ile Phe Ser Arg Val Trp Val Phe Pro Ala Ile
85 90 95

Phe Cys Lys Leu Ile Gly Val Phe Gln Gly Gly Thr Ile Phe Val Ser
100 105 110

Ser Phe Thr Leu Thr Val Ile Ala Leu Asp Arg Cys Val Leu Ile Leu
115 120 125

Arg Pro Asn Gln Glu Ile Val Asn Phe Pro Arg Ala Val Phe Ile Val
130 135 140

Phe Cys Ile Trp Leu Leu Gly Tyr Ser Leu Ala Leu Pro Val Gly Ile
145 150 155 160

Tyr Ser Asp Ile Ala Val Tyr Asp Glu Ile Cys Gly Thr Phe Cys Glu
165 170 175

Glu Asn Trp Pro Asp Phe Asn Pro Asp Thr Gly Arg Ser Gly Ile Arg
180 185 190

Arg Ala Tyr Gly Leu Ser Val Leu Val Leu Gln Phe Gly Ile Pro Ala
195 200 205

Leu Ile Ser Ser Ile Cys Tyr Trp Met Ile Ser Arg Val Met Ser Asp
210 215 220

Gln Leu Ala Arg Arg Arg Gly His Asn Ile Arg Pro Glu Ser Glu Thr
225 230 235 240

Lys Leu Val Asn Arg Lys Thr Arg Ala Asn Arg Met Met Ile Val Met
245 250 255

Val Val Gly Phe Val Leu Ala Trp Met Pro Phe Asn Ala Val Asn Leu
260 265 270

Tyr Arg Asp Leu Phe Gly Ile Ser Lys Trp Tyr Ser Thr Val Phe Ala
275 280 285

Leu Cys His Val Cys Ala Met Cys Ser Ala Val Leu Asn Pro Ile Ile
290 295 300

Tyr Ser Trp Phe Asn Pro Gln Phe Arg Gln Ser Ile Thr Thr Leu Phe
305 310 315 320

Lys Gly Thr Asp Glu Ala Arg Leu Ile Lys Lys Lys Pro Gln Ser Thr
325 330 335

Ser Lys Met Val Ser Tyr Pro Thr Asn Phe Ser Glu Ile Arg Lys Glu
340 345 350

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Thr Glu Ile Ala Ser Thr Lys Thr Lys Ile Thr Ile Ala Glu Asn Asp
        355                 360                 365

Tyr Arg Ala Gly Asp Gln Leu Leu
    370                 375


<210> 45
<211> 1209
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1209)

<220>
<223> Clone identifier: CEGPCR5

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Met Gly Ser Val Asn Glu Ser Cys Asp Asn Tyr Val Glu Ile Phe Asn
  1               5                  10                  15

aaa atc aac tac ttt ttt cga gat gat cag gtt atc aat ggg act gag   96
Lys Ile Asn Tyr Phe Phe Arg Asp Asp Gln Val Ile Asn Gly Thr Glu
             20                  25                  30

tat tca cca aaa gag ttc gga tat ttc atc aca ttc gca tac atg ctg   144
Tyr Ser Pro Lys Glu Phe Gly Tyr Phe Ile Thr Phe Ala Tyr Met Leu
         35                  40                  45

atc att ttg ttt gga gca ata ggc aac ttt ttg aca atc atc gta gtc   192
Ile Ile Leu Phe Gly Ala Ile Gly Asn Phe Leu Thr Ile Ile Val Val
     50                  55                  60

ata ctc aac cca gca atg cgg aca aca agg aac ttt ttc att tta aac   240
Ile Leu Asn Pro Ala Met Arg Thr Thr Arg Asn Phe Phe Ile Leu Asn
 65                  70                  75                  80

ttg gcg ctg tcg gac ttt ttt gtt tgt att gtg aca gcg ccg acc aca   288
Leu Ala Leu Ser Asp Phe Phe Val Cys Ile Val Thr Ala Pro Thr Thr
                 85                  90                  95

tta tac acg gtt ctc tac atg ttc tgg cca ttt agc agg aca tta tgc   336
Leu Tyr Thr Val Leu Tyr Met Phe Trp Pro Phe Ser Arg Thr Leu Cys
            100                 105                 110

aaa att gcg ggt tcg ctg caa ggc ttt aac ata ttt tta tcc aca ttc   384
Lys Ile Ala Gly Ser Leu Gln Gly Phe Asn Ile Phe Leu Ser Thr Phe
        115                 120                 125

tcg ata gcc tca att gct gtt gat aga tac gtg ctc att atc ttc cca   432
Ser Ile Ala Ser Ile Ala Val Asp Arg Tyr Val Leu Ile Ile Phe Pro
    130                 135                 140

acg aag cga gaa cga caa caa aat ctg tcg ttc tgc ttt ttt atc atg   480
Thr Lys Arg Glu Arg Gln Gln Asn Leu Ser Phe Cys Phe Phe Ile Met
145                 150                 155                 160

atc tgg gtg att tcc cta atc ctt gcg gtt cca ctt ctg cag gct tct   528
Ile Trp Val Ile Ser Leu Ile Leu Ala Val Pro Leu Leu Gln Ala Ser
```

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                    165                 170                 175

gat ttg aca ccg gtt ttc gtt gag cca tcg tgc gat ttg gct ctt tac   576
Asp Leu Thr Pro Val Phe Val Glu Pro Ser Cys Asp Leu Ala Leu Tyr
            180                 185                 190

att tgc cat gag caa aat gag ata tgg gaa aag atg atc ata tca aaa   624
Ile Cys His Glu Gln Asn Glu Ile Trp Glu Lys Met Ile Ile Ser Lys
        195                 200                 205

ggc acc tac acg ttg gca gtt ctt atc acc caa tac gca ttt ccc ctg   672
Gly Thr Tyr Thr Leu Ala Val Leu Ile Thr Gln Tyr Ala Phe Pro Leu
    210                 215                 220

ttt tca cta gtc ttc gcc tac tcc cgg ata gca cat cgg atg aag ctg   720
Phe Ser Leu Val Phe Ala Tyr Ser Arg Ile Ala His Arg Met Lys Leu
225                 230                 235                 240


aga ttt gca aac cga aat cag aat gtg aca aca aat acc aat acg agt   768
Arg Phe Ala Asn Arg Asn Gln Asn Val Thr Thr Asn Thr Asn Thr Ser
                245                 250                 255

cag agg aga cga tcc gtc gtg gaa cgt caa cga cgc acc cac ctc ctt   816
Gln Arg Arg Arg Ser Val Val Glu Arg Gln Arg Arg Thr His Leu Leu
            260                 265                 270

ctt gta tgc gtt gta gct gta ttc gcc gtc gcc tgg ctg cca ctc aac   864
Leu Val Cys Val Val Ala Val Phe Ala Val Ala Trp Leu Pro Leu Asn
        275                 280                 285

gtt ttt cat atc ttc aac aca ttc gag ctg gtc aac agt ttt tcc gtt   912
Val Phe His Ile Phe Asn Thr Phe Glu Leu Val Asn Ser Phe Ser Val
    290                 295                 300

aca acg ttc agc atc tgt cac tgc ttg gca atg tgc tcg gcg tgc ttg   960
Thr Thr Phe Ser Ile Cys His Cys Leu Ala Met Cys Ser Ala Cys Leu
305                 310                 315                 320

aat ccg ctg atc tat gca ttt ttc aat cat aac ttc cgg atc gaa ttt  1008
Asn Pro Leu Ile Tyr Ala Phe Phe Asn His Asn Phe Arg Ile Glu Phe
                325                 330                 335

atg cat ctt ttc gat aga gtt ggg ttg aga tcc ctt cga gtc gtg ata  1056
Met His Leu Phe Asp Arg Val Gly Leu Arg Ser Leu Arg Val Val Ile
            340                 345                 350

ttt gga gag caa gag tcg ctc aag aaa agt atg cgc act gaa ttc aga  1104
Phe Gly Glu Gln Glu Ser Leu Lys Lys Ser Met Arg Thr Glu Phe Arg
        355                 360                 365

agc cgt gga ggc tgt aag acg gta act act gca gag cca gca acc ttc  1152
Ser Arg Gly Gly Cys Lys Thr Val Thr Thr Ala Glu Pro Ala Thr Phe
    370                 375                 380

cag aga atg aat gaa agt atg att ctg agt gcg atg gag caa gat gag  1200
Gln Arg Met Asn Glu Ser Met Ile Leu Ser Ala Met Glu Gln Asp Glu
385                 390                 395                 400

cag ctg tga                                                     1209
Gln Leu
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<210> 46
<211> 402
<212> PRT
<213> Homo sapiens

<400> 46

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Met Gly Ser Val Asn Glu Ser Cys Asp Asn Tyr Val Glu Ile Phe Asn
  1               5                  10                  15

Lys Ile Asn Tyr Phe Phe Arg Asp Asp Gln Val Ile Asn Gly Thr Glu
             20                  25                  30

Tyr Ser Pro Lys Glu Phe Gly Tyr Phe Ile Thr Phe Ala Tyr Met Leu
         35                  40                  45

Ile Ile Leu Phe Gly Ala Ile Gly Asn Phe Leu Thr Ile Ile Val Val
     50                  55                  60

Ile Leu Asn Pro Ala Met Arg Thr Thr Arg Asn Phe Phe Ile Leu Asn
 65                  70                  75                  80

Leu Ala Leu Ser Asp Phe Phe Val Cys Ile Val Thr Ala Pro Thr Thr
                 85                  90                  95

Leu Tyr Thr Val Leu Tyr Met Phe Trp Pro Phe Ser Arg Thr Leu Cys
            100                 105                 110

Lys Ile Ala Gly Ser Leu Gln Gly Phe Asn Ile Phe Leu Ser Thr Phe
        115                 120                 125

Ser Ile Ala Ser Ile Ala Val Asp Arg Tyr Val Leu Ile Ile Phe Pro
    130                 135                 140

Thr Lys Arg Glu Arg Gln Gln Asn Leu Ser Phe Cys Phe Phe Ile Met
145                 150                 155                 160

Ile Trp Val Ile Ser Leu Ile Leu Ala Val Pro Leu Leu Gln Ala Ser
                165                 170                 175

Asp Leu Thr Pro Val Phe Val Glu Pro Ser Cys Asp Leu Ala Leu Tyr
            180                 185                 190

Ile Cys His Glu Gln Asn Glu Ile Trp Glu Lys Met Ile Ile Ser Lys
        195                 200                 205

Gly Thr Tyr Thr Leu Ala Val Leu Ile Thr Gln Tyr Ala Phe Pro Leu
    210                 215                 220

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

Arg Phe Ala Asn Arg Asn Gln Asn Val Thr Thr Asn Thr Asn Thr Ser
                245                 250                 255

Gln Arg Arg Arg Ser Val Val Glu Arg Gln Arg Arg Thr His Leu Leu
            260                 265                 270

Leu Val Cys Val Val Ala Val Phe Ala Val Ala Trp Leu Pro Leu Asn
        275                 280                 285
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Val Phe His Ile Phe Asn Thr Phe Glu Leu Val Asn Ser Phe Ser Val
290 295 300

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

Asn Pro Leu Ile Tyr Ala Phe Phe Asn His Asn Phe Arg Ile Glu Phe
325 330 335

Met His Leu Phe Asp Arg Val Gly Leu Arg Ser Leu Arg Val Val Ile
340 345 350

Phe Gly Glu Gln Glu Ser Leu Lys Lys Ser Met Arg Thr Glu Phe Arg
355 360 365

Ser Arg Gly Gly Cys Lys Thr Val Thr Thr Ala Glu Pro Ala Thr Phe
370 375 380

Gln Arg Met Asn Glu Ser Met Ile Leu Ser Ala Met Glu Gln Asp Glu
385 390 395 400

Gln Leu

<210> 47
<211> 31
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> AC7.1_F

<400> 47
gccgccatgc tgtatgcaat tatagccttc a 31

<210> 48
<211> 31
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> AC7.1_R

<400> 48
tctagatcag ggagaaagat tatttgtaga a 31

<210> 49
<211> 31
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C09B7.1_F

<400> 49
gccgccatgg cccgtgcagt caacatatct c 31

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C09B7.1_R

<400> 50
tctagattat gaataggtga aagtgttgaa t 31

<210> 51
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C10C6.2_F

<400> 51
gccgccatgg agggtggtcg aaactgtgta a 31

<210> 52
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C10C6.2_R

<400> 52
tctagattat aaaagttgat ctccagctcg a 31

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

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C16D6.2_F

<400> 53
gccgccatga atggctccga ttgtctgaat c 31

<210> 54
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C16D6.2_R

<400> 54
tctagatcac gtgcatagtg tcgtcgaacg g 31

<210> 55
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C25G6.5_F

<400> 55
gccgccatgg gatcggtgaa tgaatcatgt g 31

<210> 56
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C25G6.5_R

<400> 56
tctagatcaa ctcagtaccc cttcaactat a 31

<210> 57
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C38C10.1_F

<400> 57
gccgccatga ttatttttta tctttacgta g 31

<210> 58
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C38C10.1_R

<400> 58
tctagatcac cgttcatggc aactcagaag a 31

<210> 59
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C39E6.6_F

<400> 59
gccgccatgg aagttgaaaa ttttaccgac t 31

<210> 60
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C39E6.6_R

<400> 60
ctcgagtcag actagcgtgt cgttgacgct g 31

<210> 61
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<220>
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<220>
<223> C50F7.1_F

<400> 61
gccgccatga atacgtcatt tgtagagcca t 31

<210> 62

<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C50F7.1_R

<400> 62
tctagattaa caatcagaag tagatctttc c 31

<210> 63
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C56G3.1_F

<400> 63
gccgccatgg aagtgaaaga tatagataac t 31

<210> 64
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C56G3.1_R

<400> 64
tctagattag acaaaactat ctttctcgat a 31

<210> 65
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<220>
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<220>
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<400> 65
gccgccatgt gcttcgcaga aaaaggagaa g 31

<210> 66
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<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> F01E11.5_R

<400> 66
tctagattag acacgagaag ttgagctggg t 31

<210> 67
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> F35G8.1_F

<400> 67
gccgccatgg gactccaagg gcgtgcaatt a 31

<210> 68
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> F35G8.1_R

<400> 68
tctagattaa agatccgttc tgagaacttc g 31

<210> 69
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> F41E7.3_F

<400> 69
gccgccatgg aaatggaata tttccgccca t 31

<210> 70
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> F41E7.3_R

<400> 70
tctagattaa agcagaagcg tctgacaact t 31

<210> 71
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> T05A1.1_F

<400> 71
gccgccatga tcaacgaaac agaagagaca t 31

<210> 72
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

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<223> T05A1.1_R

<400> 72
ctcgagtcat tggcaaacaa aataagtata a 31

<210> 73
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> ZC412.1_F

<400> 73
gccgccatgg gtgatgctga atctcatcat t 31

<210> 74
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> ZC412.1_R

<400> 74
tctagattat tgtttcgttt cgaaacagac a 31

<210> 75
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C49A9.7_F

<400> 75
gccgccatga caacgtgtcc cctaccaccc a 31

<210> 76
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<223> C49A9.7_R

<400> 76
tctagatcag aaatccgtat gcgccatcgt t 31

<210> 77
<211> 12
<212> PRT
<213> Caenorhabditis elegans/flp 3

<220>
<221> MOD_RES
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<400> 77
Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe
1 5 10

<210> 78
<211> 8
<212> PRT
<213> Caenorhabditis elegans/flp 4

<220>
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<222> (8)
<223> AMIDATION

<400> 78
Ala Ser Pro Ser Phe Ile Arg Phe
1 5

<210> 79
<211> 8
<212> PRT
<213> A. suum

<220>
<223> AF3

<220>
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<400> 79
Ala Val Pro Gly Val Leu Arg Phe
1 5

<210> 80
<211> 8
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<213> Caenorhabditis elegans/flp 18

<220>
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<400> 80
Asp Val Pro Gly Val Leu Arg Phe
1 5

<210> 81
<211> 11
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<213> Caenorhabditis elegans/flp 3

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<400> 81
Glu Ala Glu Glu Pro Leu Gly Thr Met Arg Phe
1 5 10

<210> 82
<211> 12
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<220>
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<400> 82
Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 83
<211> 14
<212> PRT
<213> Caenorhabditis elegans/flp 14

<220>
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<222> (14)
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<400> 83
Glu Ile Val Phe His Gln Ile Ser Pro Ile Phe Phe Arg Phe
1 5 10

<210> 84
<211> 9
<212> PRT
<213> A. suum

<220>
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<220>
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<222> (9)
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<400> 84
Gly Asp Val Pro Gly Val Leu Arg Phe
1 5

<210> 85
<211> 9
<212> PRT
<213> Caenorhabditis elegans/flp15

<220>
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<222> (9)
<223> AMIDATION

<400> 85
Gly Gly Pro Gln Gly Pro Leu Arg Phe
1 5

<210> 86
<211> 9
<212> PRT
<213> A. suum/C.elegans (flp 21)

<220>
<223> AF9

<220>
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<223> AMIDATION

<400> 86
Gly Leu Gly Pro Arg Pro Leu Arg Phe
1 5

<210> 87
<211> 8
<212> PRT
<213> A. suum

<220>
<223> AF20

<220>
<221> MOD_RES
<222> (8)
<223> AMIDATION

<400> 87
Gly Met Pro Gly Val Leu Arg Phe
1 5

<210> 88
<211> 7
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<213> Manduca

<220>
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<223> AMIDATION

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Gly Asn Ser Phe Leu Arg Phe
1 5

<210> 89
<211> 8
<212> PRT
<213> Caenorhabditis elegans/flp 15

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<222> (8)
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<400> 89
Gly Pro Ser Gly Pro Leu Arg Phe
1 5

<210> 90
<211> 5
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<213> Artificial Sequence

<220>
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<220>
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<222> (5)
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<220>
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Ile Leu Xaa Arg Phe
1 5

<210> 91
<211> 7
<212> PRT
<213> Caenorhabditis elegans/flp 1

<220>
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<223> AMIDATION

<400> 91
Lys Pro Asn Phe Leu Arg Phe
1 5

<210> 92
<211> 9
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<213> Caenorhabditis elegans/flp 18

<220>
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<400> 92
Lys Ser Val Pro Gly Val Leu Arg Phe
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<210> 93
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<213> Caenorhabditis elegans/flp11

<220>
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<400> 93
Asn Gly Ala Pro Gln Pro Phe Val Arg Phe

1 5 10

<210> 94
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<212> PRT
<213> Locust

<220>
<223> SchistoFLRFa

<220>
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<400> 94
Pro Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 95
<211> 11
<212> PRT
<213> Locust

<220>
<223> leucomyosuppressin

<220>
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1 5 10

<210> 96
<211> 13
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<213> Caenorhabditis elegans/flp3

<220>
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<400> 96
Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 97
<211> 10
<212> PRT

<213> Caenorhabditis elegans/flp 3

<220>
<221> MOD_RES
<222> (10)
<223> AMIDATION

<400> 97
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1 5 10

<210> 98
<211> 9
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<220>
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<223> AMIDATION

<400> 98
Ser Glu Val Pro Gly Val Leu Arg Phe
1 5

<210> 99
<211> 8
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<213> Caenorhabditis elegans/flp 3

<220>
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<400> 99
Ser Pro Leu Gly Thr Met Arg Phe
1 5

<210> 100
<211> 8
<212> PRT
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<220>
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<223> AMIDATION

<400> 100
Ser Val Pro Gly Val Leu Arg Phe
1 5

<210> 101
<211> 10
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<213> Drosophila

<220>
<221> MOD_RES
<222> (10)
<223> AMIDATION

<400> 101
Thr Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 102
<211> 8
<212> PRT
<213> lobster

<220>
<223> Lobster peptide II

<220>
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<400> 102
Thr Asn Arg Asn Phe Leu Arg Phe
1 5

<210> 103
<211> 11
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<213> locust

<220>
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<222> (1)
<223> Xaa=IodoY

<220>
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<400> 103
Xaa Pro Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 104
<211> 1193
<212> DNA
<213> Homo sapiens

<220>
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<220>
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Met Val Ser Ser Ala Ala Thr Ile Ser Thr Ile Ser Thr Thr Thr Thr
1 5 10 15

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ccc tcc acc atc agc aac gtt atc aca agt cat tcg aac aat ggc tcg   96
Pro Ser Thr Ile Ser Asn Val Ile Thr Ser His Ser Asn Asn Gly Ser
            20                  25                  30

tgc att cag atc gct gag gcg att gcg gca caa ggc atc gat gat att  144
Cys Ile Gln Ile Ala Glu Ala Ile Ala Ala Gln Gly Ile Asp Asp Ile
        35                  40                  45

act gta gac ttt tac atc cga tca atc ttc aca ttc ctc tac ggg ttc  192
Thr Val Asp Phe Tyr Ile Arg Ser Ile Phe Thr Phe Leu Tyr Gly Phe
    50                  55                  60

ctg ttt gta tta ggc att ttt gga aac ggc ggc gta cta tgg gcg gtg  240
Leu Phe Val Leu Gly Ile Phe Gly Asn Gly Gly Val Leu Trp Ala Val
65                  70                  75                  80

gcg aga aac aag cgg ctc caa tcg gct cgc aac gta ttt ctg ctc aac  288
Ala Arg Asn Lys Arg Leu Gln Ser Ala Arg Asn Val Phe Leu Leu Asn
                85                  90                  95

ttg atc ttc acc gat ttg ata ttg gtg ttc aca gcg att cca gtc aca  336
Leu Ile Phe Thr Asp Leu Ile Leu Val Phe Thr Ala Ile Pro Val Thr
            100                 105                 110

cca tgg tac gcg atg acc aaa gac tgg gca ttc ggg tca gtg atg tgc  384
Pro Trp Tyr Ala Met Thr Lys Asp Trp Ala Phe Gly Ser Val Met Cys
        115                 120                 125

cat tta gtt cct ttg tca aat tcg tgt tcg gtg ttt gtg acg agt tgg  432
His Leu Val Pro Leu Ser Asn Ser Cys Ser Val Phe Val Thr Ser Trp
    130                 135                 140

agc ctc act gca atc tcc tta gat aaa ttt ctg cat atc aac gat ccc  480
Ser Leu Thr Ala Ile Ser Leu Asp Lys Phe Leu His Ile Asn Asp Pro
145                 150                 155                 160

acc aaa caa cca gtt tct att cgt caa gcg ttg gca ata aca ttt ctt  528
Thr Lys Gln Pro Val Ser Ile Arg Gln Ala Leu Ala Ile Thr Phe Leu
                165                 170                 175

atc tgg ata gtc tca aca ctg ata aat cta ccg tat ctt atg tct ttc  576
Ile Trp Ile Val Ser Thr Leu Ile Asn Leu Pro Tyr Leu Met Ser Phe
            180                 185                 190

gag cac gtc gat gga agc ttt tac gtt cag ccc gga gaa act cca tac  624
Glu His Val Asp Gly Ser Phe Tyr Val Gln Pro Gly Glu Thr Pro Tyr
        195                 200                 205

tgc ggg cac ttt tgc gac gag gcg aat tgg cag agc gaa aat agt cga  672
Cys Gly His Phe Cys Asp Glu Ala Asn Trp Gln Ser Glu Asn Ser Arg
    210                 215                 220

aag att tac gga act acg gtt atg ttg tta cag ttc gtc gtg ccg atg  720
Lys Ile Tyr Gly Thr Thr Val Met Leu Leu Gln Phe Val Val Pro Met
225                 230                 235                 240


gca gtg atc acg tat tgc tac ttc aaa atc ttg caa aaa gtg tca aaa  768
Ala Val Ile Thr Tyr Cys Tyr Phe Lys Ile Leu Gln Lys Val Ser Lys
                245                 250                 255
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gac atg atc atc caa aat gct caa ttc tgt caa tca ctg aca caa aag   816
Asp Met Ile Ile Gln Asn Ala Gln Phe Cys Gln Ser Leu Thr Gln Lys
            260                 265                 270

cag aga agt gat gcg acg tca cga aag aag aaa gtg aat tat att cta   864
Gln Arg Ser Asp Ala Thr Ser Arg Lys Lys Lys Val Asn Tyr Ile Leu
        275                 280                 285

att gca atg gtt gtc aca ttt atc ggg tgt tgg ttg cct tta aca tta   912
Ile Ala Met Val Val Thr Phe Ile Gly Cys Trp Leu Pro Leu Thr Leu
    290                 295                 300

ctc aat ttg gtc aaa gat ttt aaa aaa gag ccc gaa tgg cta aaa cgt   960
Leu Asn Leu Val Lys Asp Phe Lys Lys Glu Pro Glu Trp Leu Lys Arg
305                 310                 315                 320

cag ccg ttc ttc tgg gca ata aat gct cac gtc ata gcc atg tcc tta   1008
Gln Pro Phe Phe Trp Ala Ile Asn Ala His Val Ile Ala Met Ser Leu
                325                 330                 335

gtc gtc tgg aac cct ctg cta ttc ttt tgg ctg aca cga aaa caa aaa   1056
Val Val Trp Asn Pro Leu Leu Phe Phe Trp Leu Thr Arg Lys Gln Lys
            340                 345                 350

cgt tcc gga ctg tca aaa ata ctc aac tca aca gag ggt tcg aaa aaa   1104
Arg Ser Gly Leu Ser Lys Ile Leu Asn Ser Thr Glu Gly Ser Lys Lys
        355                 360                 365

gca ggt ggt tct gga ttg cga ggg atc cag cta cac gac ctc ctc ccg   1152
Ala Gly Gly Ser Gly Leu Arg Gly Ile Gln Leu His Asp Leu Leu Pro
    370                 375                 380

acc tct act cat tcg gac aga tgt gca ggc aac tct ttc ta           1193
Thr Ser Thr His Ser Asp Arg Cys Ala Gly Asn Ser Phe
385                 390                 395
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<210> 105
<211> 397
<212> PRT
<213> Homo sapiens

<400> 105

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Met Val Ser Ser Ala Ala Thr Ile Ser Thr Ile Ser Thr Thr Thr Thr
  1               5                  10                  15

Pro Ser Thr Ile Ser Asn Val Ile Thr Ser His Ser Asn Asn Gly Ser
             20                  25                  30

Cys Ile Gln Ile Ala Glu Ala Ile Ala Ala Gln Gly Ile Asp Asp Ile
         35                  40                  45

Thr Val Asp Phe Tyr Ile Arg Ser Ile Phe Thr Phe Leu Tyr Gly Phe
     50                  55                  60

Leu Phe Val Leu Gly Ile Phe Gly Asn Gly Gly Val Leu Trp Ala Val
 65                  70                  75                  80

Ala Arg Asn Lys Arg Leu Gln Ser Ala Arg Asn Val Phe Leu Leu Asn
                 85                  90                  95
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Leu Ile Phe Thr Asp Leu Ile Leu Val Phe Thr Ala Ile Pro Val Thr
100 105 110

Pro Trp Tyr Ala Met Thr Lys Asp Trp Ala Phe Gly Ser Val Met Cys
115 120 125

His Leu Val Pro Leu Ser Asn Ser Cys Ser Val Phe Val Thr Ser Trp
130 135 140

Ser Leu Thr Ala Ile Ser Leu Asp Lys Phe Leu His Ile Asn Asp Pro
145 150 155 160

Thr Lys Gln Pro Val Ser Ile Arg Gln Ala Leu Ala Ile Thr Phe Leu
165 170 175

Ile Trp Ile Val Ser Thr Leu Ile Asn Leu Pro Tyr Leu Met Ser Phe
180 185 190

Glu His Val Asp Gly Ser Phe Tyr Val Gln Pro Gly Glu Thr Pro Tyr
195 200 205

Cys Gly His Phe Cys Asp Glu Ala Asn Trp Gln Ser Glu Asn Ser Arg
210 215 220

Lys Ile Tyr Gly Thr Thr Val Met Leu Leu Gln Phe Val Val Pro Met
225 230 235 240

Ala Val Ile Thr Tyr Cys Tyr Phe Lys Ile Leu Gln Lys Val Ser Lys
245 250 255

Asp Met Ile Ile Gln Asn Ala Gln Phe Cys Gln Ser Leu Thr Gln Lys
260 265 270

Gln Arg Ser Asp Ala Thr Ser Arg Lys Lys Lys Val Asn Tyr Ile Leu
275 280 285

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

Leu Asn Leu Val Lys Asp Phe Lys Lys Glu Pro Glu Trp Leu Lys Arg
305 310 315 320

Gln Pro Phe Phe Trp Ala Ile Asn Ala His Val Ile Ala Met Ser Leu
325 330 335

Val Val Trp Asn Pro Leu Leu Phe Phe Trp Leu Thr Arg Lys Gln Lys
340 345 350

Arg Ser Gly Leu Ser Lys Ile Leu Asn Ser Thr Glu Gly Ser Lys Lys
355 360 365

Ala Gly Gly Ser Gly Leu Arg Gly Ile Gln Leu His Asp Leu Leu Pro
370 375 380

Thr Ser Thr His Ser Asp Arg Cys Ala Gly Asn Ser Phe
385 390 395

<210> 106
<211> 1301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1299)

<220>
<223> Clone identifier: CEGPCR19.1

<400> 106

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Met Val Ser Ser Ala Ala Thr Ile Ser Thr Ile Ser Thr Thr Thr Thr
  1               5                  10                  15

ccc tcc acc atc agc aac gtt atc aca agt cat tcg aac aat ggc tcg   96
Pro Ser Thr Ile Ser Asn Val Ile Thr Ser His Ser Asn Asn Gly Ser
            20                  25                  30

tgc att cag atc gct gag gcg att gcg gca caa ggc atc gat gat att  144
Cys Ile Gln Ile Ala Glu Ala Ile Ala Ala Gln Gly Ile Asp Asp Ile
        35                  40                  45

act gta gac ttt tac atc cga tca atc ttc aca ttc ctc tac ggg ttc  192
Thr Val Asp Phe Tyr Ile Arg Ser Ile Phe Thr Phe Leu Tyr Gly Phe
    50                  55                  60

ctg ttt gta tta ggc att ttt gga aac ggc ggc gta cta tgg gcg gtg  240
Leu Phe Val Leu Gly Ile Phe Gly Asn Gly Gly Val Leu Trp Ala Val
65                  70                  75                  80

gcg aga aac aag cgg ctc caa tcg gct cgc aac gta ttt ctg ctc aac  288
Ala Arg Asn Lys Arg Leu Gln Ser Ala Arg Asn Val Phe Leu Leu Asn
                85                  90                  95

ttg atc ttc acc gat ttg ata ttg gtg ttc aca gcg att cca gtc aca  336
Leu Ile Phe Thr Asp Leu Ile Leu Val Phe Thr Ala Ile Pro Val Thr
            100                 105                 110

cca tgg tac gcg atg acc aaa gac tgg gca ttc ggg tca gtg atg tgc  384
Pro Trp Tyr Ala Met Thr Lys Asp Trp Ala Phe Gly Ser Val Met Cys
        115                 120                 125

cat tta gtt cct ttg tca aat tcg tgt tcg gtg ttt gtg acg agt tgg  432
His Leu Val Pro Leu Ser Asn Ser Cys Ser Val Phe Val Thr Ser Trp
    130                 135                 140

agc ctc act gca atc tcc tta gat aaa ttt ctg cat atc aac gat ccc  480
Ser Leu Thr Ala Ile Ser Leu Asp Lys Phe Leu His Ile Asn Asp Pro
145                 150                 155                 160

acc aaa caa cca gtt tct att cgt caa gcg ttg gca ata aca ttt ctt  528
Thr Lys Gln Pro Val Ser Ile Arg Gln Ala Leu Ala Ile Thr Phe Leu
                165                 170                 175

atc tgg ata gtc tca aca ctg ata aat cta ccg tat ctt atg tct ttc  576
Ile Trp Ile Val Ser Thr Leu Ile Asn Leu Pro Tyr Leu Met Ser Phe
            180                 185                 190


gag cac gtc gat gga agc ttt tac gtt cag ccc gga gaa act cca tac  624
Glu His Val Asp Gly Ser Phe Tyr Val Gln Pro Gly Glu Thr Pro Tyr
        195                 200                 205

tgc ggg cac ttt tgc gac gag gcg aat tgg cag agc gaa aat agt cga  672
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Cys Gly His Phe Cys Asp Glu Ala Asn Trp Gln Ser Glu Asn Ser Arg
    210                 215                 220

aag att tac gga act acg gtt atg ttg tta cag ttc gtc gtg ccg atg   720
Lys Ile Tyr Gly Thr Thr Val Met Leu Leu Gln Phe Val Val Pro Met
225                 230                 235                 240

gca gtg atc acg tat tgc tac ttc aaa atc ttg caa aaa gtg tca aaa   768
Ala Val Ile Thr Tyr Cys Tyr Phe Lys Ile Leu Gln Lys Val Ser Lys
                245                 250                 255

gac atg atc atc caa aat gct caa ttc tgt caa tca ctg aca caa aag   816
Asp Met Ile Ile Gln Asn Ala Gln Phe Cys Gln Ser Leu Thr Gln Lys
            260                 265                 270

cag aga agt gat gcg acg tca cga aag aag aaa gtg aat tat att cta   864
Gln Arg Ser Asp Ala Thr Ser Arg Lys Lys Lys Val Asn Tyr Ile Leu
        275                 280                 285

att gca atg gtt gtc aca ttt atc ggg tgt tgg ttg cct tta aca tta   912
Ile Ala Met Val Val Thr Phe Ile Gly Cys Trp Leu Pro Leu Thr Leu
    290                 295                 300

ctc aat ttg gtc aaa gat ttt aaa aaa gag ccc gaa tgg cta aaa cgt   960
Leu Asn Leu Val Lys Asp Phe Lys Lys Glu Pro Glu Trp Leu Lys Arg
305                 310                 315                 320

cag ccg ttc ttc tgg gca ata aat gct cac gtc ata gcc atg tcc tta  1008
Gln Pro Phe Phe Trp Ala Ile Asn Ala His Val Ile Ala Met Ser Leu
                325                 330                 335

gtc gtc tgg aac cct ctg cta ttc ttt tgg ctg aca cga aaa caa aaa  1056
Val Val Trp Asn Pro Leu Leu Phe Phe Trp Leu Thr Arg Lys Gln Lys
            340                 345                 350

cgt tcc gga ctg tca aaa ata ctc aac tca aca gag att gtg tcc tcg  1104
Arg Ser Gly Leu Ser Lys Ile Leu Asn Ser Thr Glu Ile Val Ser Ser
        355                 360                 365

ttt gcc agt aga gtg agt aac tcg att cgg cgg tca acg ttt cgg aga  1152
Phe Ala Ser Arg Val Ser Asn Ser Ile Arg Arg Ser Thr Phe Arg Arg
    370                 375                 380

aac aat att gac agg gtt cga aaa aag cag gtg gtt ctg gat tgc gag  1200
Asn Asn Ile Asp Arg Val Arg Lys Lys Gln Val Val Leu Asp Cys Glu
385                 390                 395                 400

gga tcc agc tac acg acc tcc tcc cga cct cta ctc att cgg aca gat  1248
Gly Ser Ser Tyr Thr Thr Ser Ser Arg Pro Leu Leu Ile Arg Thr Asp
                405                 410                 415

gtg cag gca act ctt tct aat ggc tcg acg agt act acc cgc gag atg  1296
Val Gln Ala Thr Leu Ser Asn Gly Ser Thr Ser Thr Thr Arg Glu Met
            420                 425                 430

ctg ta                                                          1301
Leu
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<210> 107
<211> 433
<212> PRT

<213> Homo sapiens

<400> 107

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Met Val Ser Ser Ala Ala Thr Ile Ser Thr Ile Ser Thr Thr Thr Thr
 1               5                  10                  15

Pro Ser Thr Ile Ser Asn Val Ile Thr Ser His Ser Asn Asn Gly Ser
            20                  25                  30

Cys Ile Gln Ile Ala Glu Ala Ile Ala Ala Gln Gly Ile Asp Asp Ile
        35                  40                  45

Thr Val Asp Phe Tyr Ile Arg Ser Ile Phe Thr Phe Leu Tyr Gly Phe
    50                  55                  60

Leu Phe Val Leu Gly Ile Phe Gly Asn Gly Gly Val Leu Trp Ala Val
65                  70                  75                  80

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

Leu Ile Phe Thr Asp Leu Ile Leu Val Phe Thr Ala Ile Pro Val Thr
            100                 105                 110

Pro Trp Tyr Ala Met Thr Lys Asp Trp Ala Phe Gly Ser Val Met Cys
        115                 120                 125

His Leu Val Pro Leu Ser Asn Ser Cys Ser Val Phe Val Thr Ser Trp
    130                 135                 140

Ser Leu Thr Ala Ile Ser Leu Asp Lys Phe Leu His Ile Asn Asp Pro
145                 150                 155                 160

Thr Lys Gln Pro Val Ser Ile Arg Gln Ala Leu Ala Ile Thr Phe Leu
                165                 170                 175

Ile Trp Ile Val Ser Thr Leu Ile Asn Leu Pro Tyr Leu Met Ser Phe
            180                 185                 190

Glu His Val Asp Gly Ser Phe Tyr Val Gln Pro Gly Glu Thr Pro Tyr
        195                 200                 205

Cys Gly His Phe Cys Asp Glu Ala Asn Trp Gln Ser Glu Asn Ser Arg
    210                 215                 220

Lys Ile Tyr Gly Thr Thr Val Met Leu Leu Gln Phe Val Val Pro Met
225                 230                 235                 240

Ala Val Ile Thr Tyr Cys Tyr Phe Lys Ile Leu Gln Lys Val Ser Lys
                245                 250                 255

Asp Met Ile Ile Gln Asn Ala Gln Phe Cys Gln Ser Leu Thr Gln Lys
            260                 265                 270

Gln Arg Ser Asp Ala Thr Ser Arg Lys Lys Lys Val Asn Tyr Ile Leu
        275                 280                 285

Ile Ala Met Val Val Thr Phe Ile Gly Cys Trp Leu Pro Leu Thr Leu
    290                 295                 300
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Leu Asn Leu Val Lys Asp Phe Lys Lys Glu Pro Glu Trp Leu Lys Arg
305                 310                 315                 320

Gln Pro Phe Phe Trp Ala Ile Asn Ala His Val Ile Ala Met Ser Leu
                325                 330                 335

Val Val Trp Asn Pro Leu Leu Phe Phe Trp Leu Thr Arg Lys Gln Lys
            340                 345                 350

Arg Ser Gly Leu Ser Lys Ile Leu Asn Ser Thr Glu Ile Val Ser Ser
        355                 360                 365

Phe Ala Ser Arg Val Ser Asn Ser Ile Arg Arg Ser Thr Phe Arg Arg
    370                 375                 380

Asn Asn Ile Asp Arg Val Arg Lys Lys Gln Val Val Leu Asp Cys Glu
385                 390                 395                 400

Gly Ser Ser Tyr Thr Thr Ser Ser Arg Pro Leu Leu Ile Arg Thr Asp
                405                 410                 415

Val Gln Ala Thr Leu Ser Asn Gly Ser Thr Ser Thr Thr Arg Glu Met
            420                 425                 430

Leu
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<210> 108
<211> 1277
<212> DNA
<213> Homo sapiens

<220>
<223> Clone identifier: CEGPCR21 (F02E8.2)

<220>
<221> CDS
<222> (1)..(1275)

<400> 108

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Met Thr His Asp Asn Glu Tyr Gln Ser Ala Leu Val Phe Asp Arg Ile
  1               5                  10                  15

aga cga tta atc tta aac aac tcg aat acc cca ata acg aca aaa gag   96
Arg Arg Leu Ile Leu Asn Asn Ser Asn Thr Pro Ile Thr Thr Lys Glu
             20                  25                  30

ctt ata aag cat tgc ttt cat cca gat gtt cag ttt ctt gct cac atg   144
Leu Ile Lys His Cys Phe His Pro Asp Val Gln Phe Leu Ala His Met
         35                  40                  45

acc ctg aaa tcg ttg gat cat ccc ggt gaa cag ttt aat aat tca tca   192
Thr Leu Lys Ser Leu Asp His Pro Gly Glu Gln Phe Asn Asn Ser Ser
     50                  55                  60

aat caa ctt tta tta gat cgc gct ttt cta aac cca ata ctc aca ctc   240
Asn Gln Leu Leu Leu Asp Arg Ala Phe Leu Asn Pro Ile Leu Thr Leu
 65                  70                  75                  80

att ttt gtt ttt gtc ggg ctt gtg ggt ctc att ggc aat ttg ctc aca   288
Ile Phe Val Phe Val Gly Leu Val Gly Leu Ile Gly Asn Leu Leu Thr
                 85                  90                  95
```

```
gtt att gtg att ttc aag aca aat tcc ctg cac tcg cac aca aac tat   336
Val Ile Val Ile Phe Lys Thr Asn Ser Leu His Ser His Thr Asn Tyr
            100                 105                 110

ttc ttg gca aat ctt gct acc ggc gac ttc tgt ctc atc gtt gtt gga   384
Phe Leu Ala Asn Leu Ala Thr Gly Asp Phe Cys Leu Ile Val Val Gly
        115                 120                 125

gtt tcg ttt gac ttg gtg aat atc tgg aac gat gag gaa ccg ctg gac   432
Val Ser Phe Asp Leu Val Asn Ile Trp Asn Asp Glu Glu Pro Leu Asp
    130                 135                 140

att ttt gga tat tgc tct ctt aca agc act ttt ata tct ctg ttc aca   480
Ile Phe Gly Tyr Cys Ser Leu Thr Ser Thr Phe Ile Ser Leu Phe Thr
145                 150                 155                 160

ttt gct tca att ctc aca att gtt ctt ttg acg gca gaa aga ttt aca   528
Phe Ala Ser Ile Leu Thr Ile Val Leu Leu Thr Ala Glu Arg Phe Thr
                165                 170                 175

gcg att tgt tat cct ttt tcc cat aga aca att ttc gac gag aag cgt   576
Ala Ile Cys Tyr Pro Phe Ser His Arg Thr Ile Phe Asp Glu Lys Arg
            180                 185                 190

gtt aaa agg ttt ata ctg ctt att tgg ttc gta gca ctt ctt cca tca   624
Val Lys Arg Phe Ile Leu Leu Ile Trp Phe Val Ala Leu Leu Pro Ser
        195                 200                 205

att ttc att ggc tct atg ttc aaa cga gtg tct caa gac ttt tgt ggc   672
Ile Phe Ile Gly Ser Met Phe Lys Arg Val Ser Gln Asp Phe Cys Gly
    210                 215                 220

ttc aat cgc caa atg act tat atc ggt cga tgt gat ttg gtg aca tct   720
Phe Asn Arg Gln Met Thr Tyr Ile Gly Arg Cys Asp Leu Val Thr Ser
225                 230                 235                 240

cca gat agt ttc ttc cgg tac cca ttt gaa tca gca ata acc atc act   768
Pro Asp Ser Phe Phe Arg Tyr Pro Phe Glu Ser Ala Ile Thr Ile Thr
                245                 250                 255

ttt gta ctt ccc ttg ttc ttc att att tat tgt tac ttc cgg att cta   816
Phe Val Leu Pro Leu Phe Phe Ile Ile Tyr Cys Tyr Phe Arg Ile Leu
            260                 265                 270

gtc aca ttg aac gag atg tcc aat tcg act cat gtg cac act cca gtc   864
Val Thr Leu Asn Glu Met Ser Asn Ser Thr His Val His Thr Pro Val
        275                 280                 285

gga act gct cgt agt gat agt gga gct ttt cct ttt ccc cat aca tct   912
Gly Thr Ala Arg Ser Asp Ser Gly Ala Phe Pro Phe Pro His Thr Ser
    290                 295                 300

aat aac tct aac act caa agt ttc ccg cta aca gtc cat act aaa aat   960
Asn Asn Ser Asn Thr Gln Ser Phe Pro Leu Thr Val His Thr Lys Asn
305                 310                 315                 320


gtc caa ccg ccg cga agt caa caa gcc cag aaa atg gtc att aag atg  1008
Val Gln Pro Pro Arg Ser Gln Gln Ala Gln Lys Met Val Ile Lys Met
                325                 330                 335
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