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GGTGTGCTTC TGTGGTTAGG TTTATCAGAG TGCTGAGATC CCTATAGTCA GGTTCGCCTT   4039

TCCTATCCCT GCTTCCATTC TCCTCTTCTG TTCTATCCCA TCCAACAGTC CAGAGATAAA   4099

ACCATGGCTT TAAGATACCC ACCTATTCCC CCTAGGGTCT TATTTGTTGT TTTTGTTGCT   4159

GTTGTTTTGG TTTGATTTTT GTTTTTAATG TTGAAACGTC TGCCCTGAAC TTTGCAGACA   4219

GCCTGGTCCA AAAACAAACC TGTGCAGAGT GACAGGACCT CCTATGGGCA CCACTAGAGT   4279

TGAGTGCGAA AGACAGAATG TCGCCAGCGC TGCCCAACAC CTTGACAGTG GGAAGAACTT   4339

GAAATGTCCA GAGCTGTAAG ATGAATGTGT CCCCTCCTAT TTATGAAAAA TGTTAAATAT   4399

GTGGTTTCCT ACTTGCTGCT GCTGTCACGT GACATGGAGA AGGTTAGCAT CCATCCTCCA   4459

GCAGTATGTC TGATCTTGTC CAGAGTGTGA TGGTGATGCC ACGTTTAGAT TCCAATATCT   4519

CAGGAATCAC CTCAGCCTGC ATGAATCCAA TGAGCTGTAT CTGTAATTAA TATTGTCATA   4579

TGTAGCTTTA TCCTTAAGAA AATGTGTTTG TTTTAATAGT CCGTGGAAAA TATAAGCTGG   4639

AAAAAATGTC CCAGTCTGGT TGATATAAGG CAGTATTATT GAGTCCCGTT TTCTTTGCCC   4699

GCCCCACCAC CCACACCCCA ATGAGCTAAG CCCTAAATGA GCCCTTTCAG GGCCCAGGGA   4759

TCCAGAAGCT CCCTCTTTCT CCACCCCAAA CGCTTCCTGA AGTCAGATCC ATGCCTTTCC   4819

CTGTGAAGAA TAAGCTCCCA GTCTCTGACC TCCTACCAGT TTCTGGGGTA AGAACACGTG   4879

GTTCCAAGAG AGCTCTCATG GGATATTACT CTTGGCACCC CCCAATGCCA TACTTAGGTT   4939

CCCTCCAGCA GTGGGATCTG CCCATGGGTA GTTACAAGAT TGAACGTTGA ATGGCATACT   4999

GCTGAACAGT CAGTTCTGGA GCTAGAGAGG CCTGGGGTCA AGTGCTGGGT TTGTCACTCA   5059

CAAGTTGGGT GACCACAGGC AGGGAACCTT GACCTCACTC AGCCCCAGCT TCTTTGTGTC   5119

TAAAATGGAG GTAATAATCA TCCTTTTCCC GCAGAGCTCT TATGTGGGTT AAATGAGATA   5179

AATGTATGTA AAGTATTTTA GCATGGTGCC TAGCCCATAG TAAGCACGCA ATAAATATTA   5239

GTTAATATTA AAAAAAAAAA AAAAAAAAAA AAAAAA                             5275
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 436..3699
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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GCTGCTGTGG CCGGACCCGA AGGCGGGCGC CGGGAGCGCA GCGAGCCAGA CGCGCCTCTC     60

CAAGACCGTG ACCTTGGCAT AGGGAGCGGG GCTGCGCGCA GTCCTGAGAT CAGACCAGAG    120

CTCATCCTCG TGGAGACCCA CGGCCGAGGG GCCGGAGCTG CCTCTGTGCG AGGGAGCCCT    180

GGCCGCGGCG CAGAAGGCAT CACAGGAGGC CTCTGCATGA TGTGGCTTCC AAAGACTCAA    240

GGACCACCCA CATTACAAGT CTGGATTGAG GAAGGCAGAA ATGGAGATTC AAACACCACG    300

TCTTCTATTA TTTTATTAAT CAATCTGTAG ACATGTGTCC CCACTGCAGG GAGTGAACTG    360

CTCCAAGGGA GAAACTTCTG GGAGCCTCCA AACTCCTAGC TGTCTCATCC CTTGCCCTGG    420

AGAGACGGCA GAACC ATG GCA TTT TAT AGC TGC TGC TGG GTC CTC TTG GCA     471
                 Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala
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                1               5                   10

CTC ACC TGG CAC ACC TCT GCC TAC GGG CCA GAC CAG CGA GCC CAA AAG      519
Leu Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys
        15                  20                  25

AAG GGG GAC ATT ATC CTT GGG GGG CTC TTT CCT ATT CAT TTT GGA GTA      567
Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val
    30                  35                  40

GCA GCT AAA GAT CAA GAT CTC AAA TCA AGG CCG GAG TCT GTG GAA TGT      615
Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys
45                  50                  55                  60

ATC AGG TAT AAT TTC CGT GGG TTT CGC TGG TTA CAG GCT ATG ATA TTT      663
Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe
                65                  70                  75

GCC ATA GAG GAG ATA AAC AGC AGC CCA GCC CTT CTT CCC AAC TTG ACG      711
Ala Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr
            80                  85                  90

CTG GGA TAC AGG ATA TTT GAC ACT TGC AAC ACC GTT TCT AAG GCC TTG      759
Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu
        95                  100                 105

GAA GCC ACC CTG AGT TTT GTT GCT CAA AAC AAA ATT GAT TCT TTG AAC      807
Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn
    110                 115                 120

CTT GAT GAG TTC TGC AAC TGC TCA GAG CAC ATT CCC TCT ACG ATT GCT      855
Leu Asp Glu Phe Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala
125                 130                 135                 140

GTG GTG GGA GCA ACT GGC TCA GGC GTC TCC ACG GCA GTG GCA AAT CTG      903
Val Val Gly Ala Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu
                145                 150                 155

CTG GGG CTC TTC TAC ATT CCC CAG GTC AGT TAT GCC TCC TCC AGC AGA      951
Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg
            160                 165                 170

CTC CTC AGC AAC AAG AAT CAA TTC AAG TCT TTC CTC CGA ACC ATC CCC      999
Leu Leu Ser Asn Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro
        175                 180                 185

AAT GAT GAG CAC CAG GCC ACT GCC ATG GCA GAC ATC ATC GAG TAT TTC     1047
Asn Asp Glu His Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe
    190                 195                 200

CGC TGG AAC TGG GTG GGC ACA ATT GCA GCT GAT GAC GAC TAT GGG CGG     1095
Arg Trp Asn Trp Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg
205                 210                 215                 220

CCG GGG ATT GAG AAA TTC CGA GAG GAA GCT GAG GAA AGG GAT ATC TGC     1143
Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys
                225                 230                 235

ATC GAC TTC AGT GAA CTC ATC TCC CAG TAC TCT GAT GAG GAA GAG ATC     1191
Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile
            240                 245                 250

CAG CAT GTG GTA GAG GTG ATT CAA AAT TCC ACG GCC AAA GTC ATC GTG     1239
Gln His Val Val Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val
        255                 260                 265

GTT TTC TCC AGT GGC CCA GAT CTT GAG CCC CTC ATC AAG GAG ATT GTC     1287
Val Phe Ser Ser Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val
    270                 275                 280

CGG CGC AAT.ATC ACG GGC AAG ATC TGG CTG GCC AGC GAG GCC TGG GCC     1335
Arg Arg Asn Ile Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala
285                 290                 295                 300

AGC TCC TCC CTG ATC GCC ATG CCT CAG TAC TTC CAC GTG GTT GGC GGC     1383
Ser Ser Ser Leu Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly
                305                 310                 315

ACC ATT GGA TTC GCT CTG AAG GCT GGG CAG ATC CCA GGC TTC CGG GAA     1431
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Thr Ile Gly Phe Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu
            320                 325                 330

TTC CTG AAG AAG GTC CAT CCC AGG AAG TCT GTC CAC AAT GGT TTT GCC     1479
Phe Leu Lys Lys Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala
        335                 340                 345

AAG GAG TTT TGG GAA GAA ACA TTT AAC TGC CAC CTC CAA GAA GGT GCA     1527
Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala
    350                 355                 360

AAA GGA CCT TTA CCT GTG GAC ACC TTT CTG AGA GGT CAC GAA GAA AGT     1575
Lys Gly Pro Leu Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser
365                 370                 375                 380

GGC GAC AGG TTT AGC AAC AGC TCG ACA GCC TTC CGA CCC CTC TGT ACA     1623
Gly Asp Arg Phe Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr
                385                 390                 395

GGG GAT GAG AAC ATC AGC AGT GTC GAG ACC CCT TAC ATA GAT TAC ACG     1671
Gly Asp Glu Asn Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr
            400                 405                 410

CAT TTA CGG ATA TCC TAC AAT GTG TAC TTA GCA GTC TAC TCC ATT GCC     1719
His Leu Arg Ile Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala
        415                 420                 425

CAC GCC TTG CAA GAT ATA TAT ACC TGC TTA CCT GGG AGA GGG CTC TTC     1767
His Ala Leu Gln Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe
    430                 435                 440

ACC AAT GGC TCC TGT GCA GAC ATC AAG AAA GTT GAG GCG TGG CAG GTC     1815
Thr Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val
445                 450                 455                 460

CTG AAG CAC CTA CGG CAT CTA AAC TTT ACA AAC AAT ATG GGG GAG CAG     1863
Leu Lys His Leu Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln
                465                 470                 475

GTG ACC TTT GAT GAG TGT GGT GAC CTG GTG GGG AAC TAT TCC ATC ATC     1911
Val Thr Phe Asp Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile
            480                 485                 490

AAC TGG CAC CTC TCC CCA GAG GAT GGC TCC ATC GTG TTT AAG GAA GTC     1959
Asn Trp His Leu Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val
        495                 500                 505

GGG TAT TAC AAC GTC TAT GCC AAG AAG GGA GAA AGA CTC TTC ATC AAC     2007
Gly Tyr Tyr Asn Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn
    510                 515                 520

GAG GAG AAA ATC CTG TGG AGT GGG TTC TCC AGG GAG CCA CTC ACC TTT     2055
Glu Glu Lys Ile Leu Trp Ser Gly Phe Ser Arg Glu Pro Leu Thr Phe
525                 530                 535                 540

GTG CTG TCT GTC CTC CAG GTG CCC TTC TCC AAC TGC AGC CGA GAC TGC     2103
Val Leu Ser Val Leu Gln Val Pro Phe Ser Asn Cys Ser Arg Asp Cys
                545                 550                 555

CTG GCA GGG ACC AGG AAA GGG ATC ATT GAG GGG GAG CCC ACC TGC TGC     2151
Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys
            560                 565                 570

TTT GAG TGT GTG GAG TGT CCT GAT GGG GAG TAT AGT GAT GAG ACA GAT     2199
Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu Thr Asp
        575                 580                 585

GCC AGT GCC TGT AAC AAG TGC CCA GAT GAC TTC TGG TCC AAT GAG AAC     2247
Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn Glu Asn
    590                 595                 600

CAC ACC TCC TGC ATT GCC AAG GAG ATC GAG TTT CTG TCG TGG ACG GAG     2295
His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu
605                 610                 615                 620

CCC TTT GGG ATC GCA CTC ACC CTC TTT GCC GTG CTG GGC ATT TTC CTG     2343
Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile Phe Leu
                625                 630                 635
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ACA GCC TTT GTG CTG GGT GTG TTT ATC AAG TTC CGC AAC ACA CCC ATT      2391
Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile
            640                 645                 650

GTC AAG GCC ACC AAC CGA GAG CTC TCC TAC CTC CTC CTC TTC TCC CTG      2439
Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu
        655                 660                 665

CTC TGC TGC TTC TCC AGC TCC CTG TTC TTC ATC GGG GAG CCC CAG GAC      2487
Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp
    670                 675                 680

TGG ACG TGC CGC CTG CGC CAG CCG GCC TTT GGC ATC AGC TTC GTG CTC      2535
Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu
685                 690                 695                 700

TGC ATC TCA TGC ATC CTG GTG AAA ACC AAC CGT GTC CTC CTG GTG TTT      2583
Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe
                705                 710                 715

GAG GCC AAG ATC CCC ACC AGC TTC CAC CGC AAG TGG TGG GGG CTC AAC      2631
Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn
            720                 725                 730

CTG CAG TTC CTG CTG GTT TTC CTC TGC ACC TTC ATG CAG ATT GTC ATC      2679
Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile Val Ile
        735                 740                 745

TGT GTG ATC TGG CTC TAC ACC GCG CCC CCC TCA AGC TAC CGC AAC CAG      2727
Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln
    750                 755                 760

GAG CTG GAG GAT GAG ATC ATC TTC ATC ACG TGC CAC GAG GGC TCC CTC      2775
Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu
765                 770                 775                 780

ATG GCC CTG GGC TTC CTG ATC GGC TAC ACC TGC CTG CTG GCT GCC ATC      2823
Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile
                785                 790                 795

TGC TTC TTC TTT GCC TTC AAG TCC CGG AAG CTG CCG GAG AAC TTC AAT      2871
Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn
            800                 805                 810

GAA GCC AAG TTC ATC ACC TTC AGC ATG CTC ATC TTC TTC ATC GTC TGG      2919
Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp
        815                 820                 825

ATC TCC TTC ATT CCA GCC TAT GCC AGC ACC TAT GGC AAG TTT GTC TCT      2967
Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser
    830                 835                 840

GCC GTA GAG GTG ATT GCC ATC CTG GCA GCC AGC TTT GGC TTG CTG GCG      3015
Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala
845                 850                 855                 860

TGC ATC TTC TTC AAC AAG ATC TAC ATC ATT CTC TTC AAG CCA TCC CGC      3063
Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe Lys Pro Ser Arg
                865                 870                 875

AAC ACC ATC GAG GAG GTG CGT TGC AGC ACC GCA GCT CAC GCT TTC AAG      3111
Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys
            880                 885                 890

GTG GCT GCC CGG GCC ACG CTG CGC CGC AGC AAC GTC TCC CGC AAG CGG      3159
Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg
        895                 900                 905

TCC AGC AGC CTT GGA GGC TCC ACG GGA TCC ACC CCC TCC TCC TCC ATC      3207
Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile
    910                 915                 920

AGC AGC AAG AGC AAC AGC GAA GAC CCA TTC CCA CGG CCC GAG AGG CAG      3255
Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Arg Pro Glu Arg Gln
925                 930                 935                 940

AAG CAG CAG CAG CCG CTG GCC CTA ACC CAG CAA GAG CAG CAG CAG CAG      3303
Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln
                945                 950                 955
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CCC CTG ACC CTC CCA CAG CAG CAA CGA TCT CAG CAG CAG CCC AGA TGC      3351
Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys
            960                 965                 970

AAG CAG AAG GTC ATC TTT GGC AGC GGC ACG GTC ACC TTC TCA CTG AGC      3399
Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser
        975                 980                 985

TTT GAT GAG CCT CAG AAG AAC GCC ATG GCC CAC AGG AAT TCT ACG CAC      3447
Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn Ser Thr His
    990                 995                 1000

CAG AAC TCC CTG GAG GCC CAG AAA AGC AGC GAT ACG CTG ACC CGA CAC      3495
Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His
1005                1010                1015                1020

CAG CCA TTA CTC CCG CTG CAG TGC GGG GAA ACG GAC TTA GAT CTG ACC      3543
Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr
                1025                1030                1035

GTC CAG GAA ACA GGT CTG CAA GGA CCT GTG GGT GGA GAC CAG CGG CCA      3591
Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro
            1040                1045                1050

GAG GTG GAG GAC CCT GAA GAG TTG TCC CCA GCA CTT GTA GTG TCC AGT      3639
Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser
        1055                1060                1065

TCA CAG AGC TTT GTC ATC AGT GGT GGA GGC AGC ACT GTT ACA GAA AAC      3687
Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn
    1070                1075                1080

GTA GTG AAT TCA TAAAATGGAA GGAGAAGACT GGGCTAGGGA GAATGCAGAG          3739
Val Val Asn Ser
1085

AGGTTTCTTG GGGTCCCAGG GATGAGGAAT CGCCCCAGAC TCCTTTCCTC TGAGGAAGAA   3799

GGGATAATAG ACACATCAAA TGCCCCGAAT TTAGTCACAC CATCTTAAAT GACAGTGAAT   3859

TGACCCATGT TCCCTTTAAA ATTAAAAAAA AGAAGAGCCT TGTGTTTCTG TGGTTGCATT   3919

TGTCAAAGCA TTGAGATCTC CACGGTCAGA TTTGCTGTTC ACCCACATCT AATGTCTCTT   3979

CCTCTGTTCT ATCCCACCCA ACAGCTCAGA GATGAAACTA TGGCTTTAAA CTACCCTCCA   4039

GAGTGTGCAG ACTGATGGGA CATCAAATTT GCCACCACTA GAGCTGAGAG TCTGAAAGAC   4099

AGAATGTCAC CAGTCCTGCC CAATGCCTTG ACAACAGACT GAATTTTAAA TGTTCACAAC   4159

ATAAGGAGAA TGTATCTCCT CCTATTTATG AAAACCATAT GATATTTTGT CTCCTACCTG   4219

CTGCTGCTAT TATGTAACAT CCAGAAGGTT TGCACCCCTC CTATACCATA TGTCTGGTTC   4279

TGTCCAGGAC ATGATACTGA TGCCATGTTT AGATTCCAGG ATCACAAGAA TCACCTCAAA   4339

TTGTTAGGAA GGGACTGCAT AAACCAATGA GCTGTATCTG TAATTAATAT TCCTATATGT   4399

AGCTTTATCC TTAGGAAAAT GCTTCTGTTG TAATAGTCCA TGGACAATAT AAACTGAAAA   4459

ATGTCAGTCT GGTTTATATA AGGCAGTATT ATTGAGCTCT ATTTCCCCAC CCCACTATCC   4519

TCACTCCCAT AAGCTAAGCC TTATGTGAGC CCCTTCAGGG ACTCAAGGGT CCAGAAGTCC   4579

CTCCCATCTC TACCCCAAAG AATTCCTGAA GCCAGATCCA CCCTATCCCT GTACAGAGTA   4639

AGTTCTCAAT TATTGGCCTG CTAATAGCTG CTAGGGTAGG AAAGCGTGGT TCCAAGAAAG   4699

ATCCACCCTC AAATGTCGGA GCTATGTTCC CTCCAGCAGT GGTATTAATA CTGCCGGTCA   4759

CCCAGGCTCT GGAGCCAGAG AGACAGACCG GGGTTCAAGC CATGGCTTCG TCATTTGCAA   4819

GCTGAGTGAC TGTAGGCAGG GAACCTTAAC CTCTCTAAGC CACAGCTTCT TCATCTTTAA   4879

AATAAGGATA ATAATCATTC CTTCCCCTCA GAGCTCTTAT GTGGATTAAA CGAGATAATG   4939

TATATAAAGT ACTTTAGCCT GGTACCTAGC ACACAATAAG CATTCAATAA ATATTAGTTA   4999
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ATATTAT                                                                5006

(2) INFORMATION FOR SEQ ID NO: 3:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:                3809 base pairs
          (B) TYPE:                  nucleic acid
          (C) STRANDEDNESS:          single
          (D) TOPOLOGY:              linear

    (ii) MOLECULE TYPE:              cDNA to mRNA

    (ix) FEATURE:
          (A) NAME/KEY:              CDS
          (B) LOCATION:              373..3606
          (D) OTHER INFORMATION:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAACAGGCAC CTGGCTGCAG CCAGGAAGGA CCGCACGCCC TTTCGCGCAG GAGAGTGGAA      60

GGAGGGAGCT GTTTGCCAGC ACCGAGGTCT TGCGGCACAG GCAACGCTTG ACCTGAGTCT     120

TGCAGAATGA AAGGCATCAC AGGAGGCCTC TGCATGATGT GGCTTCCAAA GACTCAAGGA     180

CCACCCACAT TACAAGTCTG GATTGAGGAA GGCAGAAATG GAGATTCAAA CACCACGTCT     240

TCTATTATTT TATTAATCAA TCTGTAGACA TGTGTCCCCA CTGCAGGGAG TGAACTGCTC     300

CAAGGGAGAA ACTTCTGGGA GCCTCCAAAC TCCTAGCTGT CTCATCCCTT GCCCTGGAGA     360

GACGGCAGAA CC ATG GCA TTT TAT AGC TGC TGC TGG GTC CTC TTG GCA          408
              Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala
               1               5                  10

CTC ACC TGG CAC ACC TCT GCC TAC GGG CCA GAC CAG CGA GCC CAA AAG        456
Leu Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys
        15                  20                  25

AAG GGG GAC ATT ATC CTT GGG GGG CTC TTT CCT ATT CAT TTT GGA GTA        504
Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val
    30                  35                  40

GCA GCT AAA GAT CAA GAT CTC AAA TCA AGG CCG GAG TCT GTG GAA TGT        552
Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys
45                  50                  55                  60

ATC AGG TAT AAT TTC CGT GGG TTT CGC TGG TTA CAG GCT ATG ATA TTT        600
Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe
            65                  70                  75

GCC ATA GAG GAG ATA AAC AGC AGC CCA GCC CTT CTT CCC AAC TTG ACG        648
Ala Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr
            80                  85                  90

CTG GGA TAC AGG ATA TTT GAC ACT TGC AAC ACC GTT TCT AAG GCC TTG        696
Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu
        95                  100                 105

GAA GCC ACC CTG AGT TTT GTT GCT CAA AAC AAA ATT GAT TCT TTG AAC        744
Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn
    110                 115                 120

CTT GAT GAG TTC TGC AAC TGC TCA GAG CAC ATT CCC TCT ACG ATT GCT        792
Leu Asp Glu Phe Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala
125                 130                 135                 140

GTG GTG GGA GCA ACT GGC TCA GGC GTC TCC ACG GCA GTG GCA AAT CTG        840
Val Val Gly Ala Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu
                145                 150                 155

CTG GGG CTC TTC TAC ATT CCC CAG GTC AGT TAT GCC TCC TCC AGC AGA        888
Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg
            160                 165                 170

CTC CTC AGC AAC AAG AAT CAA TTC AAG TCT TTC CTC CGA ACC ATC CCC        936
Leu Leu Ser Asn Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro
        175                 180                 185
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AAT GAT GAG CAC CAG GCC ACT GCC ATG GCA GAC ATC ATC GAG TAT TTC      984
Asn Asp Glu His Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe
    190                 195                 200

CGC TGG AAC TGG GTG GGC ACA ATT GCA GCT GAT GAC GAC TAT GGG CGG     1032
Arg Trp Asn Trp Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg
205                 210                 215                 220

CCG GGG ATT GAG AAA TTC CGA GAG GAA GCT GAG GAA AGG GAT ATC TGC     1080
Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys
                225                 230                 235

ATC GAC TTC AGT GAA CTC ATC TCC CAG TAC TCT GAT GAG GAA GAG ATC     1128
Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile
            240                 245                 250

CAG CAT GTG GTA GAG GTG ATT CAA AAT TCC ACG GCC AAA GTC ATC GTG     1176
Gln His Val Val Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val
        255                 260                 265

GTT TTC TCC AGT GGC CCA GAT CTT GAG CCC CTC ATC AAG GAG ATT GTC     1224
Val Phe Ser Ser Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val
    270                 275                 280

CGG CGC AAT ATC ACG GGC AAG ATC TGG CTG GCC AGC GAG GCC TGG GCC     1272
Arg Arg Asn Ile Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala
285                 290                 295                 300

AGC TCC TCC CTG ATC GCC ATG CCT CAG TAC TTC CAC GTG GTT GGC GGC     1320
Ser Ser Ser Leu Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly
                305                 310                 315

ACC ATT GGA TTC GCT CTG AAG GCT GGG CAG ATC CCA GGC TTC CGG GAA     1368
Thr Ile Gly Phe Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu
            320                 325                 330

TTC CTG AAG AAG GTC CAT CCC AGG AAG TCT GTC CAC AAT GGT TTT GCC     1416
Phe Leu Lys Lys Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala
        335                 340                 345

AAG GAG TTT TGG GAA GAA ACA TTT AAC TGC CAC CTC CAA GAA GGT GCA     1464
Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala
    350                 355                 360

AAA GGA CCT TTA CCT GTG GAC ACC TTT CTG AGA GGT CAC GAA GAA AGT     1512
Lys Gly Pro Leu Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser
365                 370                 375                 380

GGC GAC AGG TTT AGC AAC AGC TCG ACA GCC TTC CGA CCC CTC TGT ACA     1560
Gly Asp Arg Phe Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr
                385                 390                 395

GGG GAT GAG AAC ATC AGC AGT GTC GAG ACC CCT TAC ATA GAT TAC ACG     1608
Gly Asp Glu Asn Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr
            400                 405                 410

CAT TTA CGG ATA TCC TAC AAT GTG TAC TTA GCA GTC TAC TCC ATT GCC     1656
His Leu Arg Ile Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala
        415                 420                 425

CAC GCC TTG CAA GAT ATA TAT ACC TGC TTA CCT GGG AGA GGG CTC TTC     1704
His Ala Leu Gln Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe
    430                 435                 440

ACC AAT GGC TCC TGT GCA GAC ATC AAG AAA GTT GAG GCG TGG CAG GTC     1752
Thr Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val
445                 450                 455                 460

CTG AAG CAC CTA CGG CAT CTA AAC TTT ACA AAC AAT ATG GGG GAG CAG     1800
Leu Lys His Leu Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln
                465                 470                 475

GTG ACC TTT GAT GAG TGT GGT GAC CTG GTG GGG AAC TAT TCC ATC ATC     1848
Val Thr Phe Asp Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile
            480                 485                 490

AAC TGG CAC CTC TCC CCA GAG GAT GGC TCC ATC GTG TTT AAG GAA GTC     1896
Asn Trp His Leu Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val
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        495                 500                 505

GGG TAT TAC AAC GTC TAT GCC AAG AAG GGA GAA AGA CTC TTC ATC AAC     1944
Gly Tyr Tyr Asn Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn
    510                 515                 520

GAG GAG AAA ATC CTG TGG AGT GGG TTC TCC AGG GAG GTG CCC TTC TCC     1992
Glu Glu Lys Ile Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser
525                 530                 535                 540

AAC TGC AGC CGA GAC TGC CTG GCA GGG ACC AGG AAA GGG ATC ATT GAG     2040
Asn Cys Ser Arg Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu
                545                 550                 555

GGG GAG CCC ACC TGC TGC TTT GAG TGT GTG GAG TGT CCT GAT GGG GAG     2088
Gly Glu Pro Thr Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu
            560                 565                 570

TAT AGT GAT GAG ACA GAT GCC AGT GCC TGT AAC AAG TGC CCA GAT GAC     2136
Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp
        575                 580                 585

TTC TGG TCC AAT GAG AAC CAC ACC TCC TGC ATT GCC AAG GAG ATC GAG     2184
Phe Trp Ser Asn Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu
    590                 595                 600

TTT CTG TCG TGG ACG GAG CCC TTT GGG ATC GCA CTC ACC CTC TTT GCC     2232
Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala
605                 610                 615                 620

GTG CTG GGC ATT TTC CTG ACA GCC TTT GTG CTG GGT GTG TTT ATC AAG     2280
Val Leu Gly Ile Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys
                625                 630                 635

TTC CGC AAC ACA CCC ATT GTC AAG GCC ACC AAC CGA GAG CTC TCC TAC     2328
Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr
            640                 645                 650

CTC CTC CTC TTC TCC CTG CTC TGC TGC TTC TCC AGC TCC CTG TTC TTC     2376
Leu Leu Leu Phe Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe
        655                 660                 665

ATC GGG GAG CCC CAG GAC TGG ACG TGC CGC CTG CGC CAG CCG GCC TTT     2424
Ile Gly Glu Pro Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe
    670                 675                 680

GGC ATC AGC TTC GTG CTC TGC ATC TCA TGC ATC CTG GTG AAA ACC AAC     2472
Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn
685                 690                 695                 700

CGT GTC CTC CTG GTG TTT GAG GCC AAG ATC CCC ACC AGC TTC CAC CGC     2520
Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg
                705                 710                 715

AAG TGG TGG GGG CTC AAC CTG CAG TTC CTG CTG GTT TTC CTC TGC ACC     2568
Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr
            720                 725                 730

TTC ATG CAG ATT GTC ATC TGT GTG ATC TGG CTC TAC ACC GCG CCC CCC     2616
Phe Met Gln Ile Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro
        735                 740                 745

TCA AGC TAC CGC AAC CAG GAG CTG GAG GAT GAG ATC ATC TTC ATC ACG     2664
Ser Ser Tyr Arg Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr
    750                 755                 760

TGC CAC GAG GGC TCC CTC ATG GCC CTG GGC TTC CTG ATC GGC TAC ACC     2712
Cys His Glu Gly Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr
765                 770                 775                 780

TGC CTG CTG GCT GCC ATC TGC TTC TTC TTT GCC TTC AAG TCC CGG AAG     2760
Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys
                785                 790                 795

CTG CCG GAG AAC TTC AAT GAA GCC AAG TTC ATC ACC TTC AGC ATG CTC     2808
Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu
            800                 805                 810

ATC TTC TTC ATC GTC TGG ATC TCC TTC ATT CCA GCC TAT GCC AGC ACC     2856
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Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr
        815                 820                 825

TAT GGC AAG TTT GTC TCT GCC GTA GAG GTG ATT GCC ATC CTG GCA GCC     2904
Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala
    830                 835                 840

AGC TTT GGC TTG CTG GCG TGC ATC TTC TTC AAC AAG ATC TAC ATC ATT     2952
Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile
845                 850                 855                 860

CTC TTC AAG CCA TCC CGC AAC ACC ATC GAG GAG GTG CGT TGC AGC ACC     3000
Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr
                865                 870                 875

GCA GCT CAC GCT TTC AAG GTG GCT GCC CGG GCC ACG CTG CGC CGC AGC     3048
Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser
            880                 885                 890

AAC GTC TCC CGC AAG CGG TCC AGC AGC CTT GGA GGC TCC ACG GGA TCC     3096
Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser
        895                 900                 905

ACC CCC TCC TCC TCC ATC AGC AGC AAG AGC AAC AGC GAA GAC CCA TTC     3144
Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe
    910                 915                 920

CCA CAG CCC GAG AGG CAG AAG CAG CAG CAG CCG CTG GCC CTA ACC CAG     3192
Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln
925                 930                 935                 940

CAA GAG CAG CAG CAG CAG CCC CTG ACC CTC CCA CAG CAG CAA CGA TCT     3240
Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser
                945                 950                 955

CAG CAG CAG CCC AGA TGC AAG CAG AAG GTC ATC TTT GGC AGC GGC ACG     3288
Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr
            960                 965                 970

GTC ACC TTC TCA CTG AGC TTT GAT GAG CCT CAG AAG AAC GCC ATG GCC     3336
Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala
        975                 980                 985

CAC GGG AAT TCT ACG CAC CAG AAC TCC CTG GAG GCC CAG AAA AGC AGC     3384
His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser
    990                 995                 1000

GAT ACG CTG ACC CGA CAC CAG CCA TTA CTC CCG CTG CAG TGC GGG GAA     3432
Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu
1005                1010                1015                1020

ACG GAC TTA GAT CTG ACC GTC CAG GAA ACA GGT CTG CAA GGA CCT GTG     3480
Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val
                1025                1030                1035

GGT GGA GAC CAG CGG CCA GAG GTG GAG GAC CCT GAA GAG TTG TCC CCA     3528
Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro
            1040                1045                1050

GCA CTT GTA GTG TCC AGT TCA CAG AGC TTT GTC ATC AGT GGT GGA GGC     3576
Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly
        1055                1060                1065

AGC ACT GTT ACA GAA AAC GTA GTG AAT TCA TAAAATGGAA GGAGAAGACT       3626
Ser Thr Val Thr Glu Asn Val Val Asn Ser
    1070                1075

GGGCTAGGGA GAATGCAGAG AGGTTTCTTG GGGTCCCAGG GATGAGGAAT CGCCCCAGAC   3686

TCCTTTCCTC TGAGGAAGAA GGGATAATAG ACACATCAAA TGCCCCGAAT TTAGTCACAC   3746

CATCTTAAAT GACAGTGAAT TGACCCATGT TCCCTTTAAA AAAAAAAAAA AAAAAGCGGC   3806

CGC                                                                 3809
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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 4131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 574..3810
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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CGGGACTCTC CAGGCCGGCT CAGGCACCGG ACTGTAGGTG TATTTGGAGG GATTTGGAGG      60

CTGGAGACCC CAGGAAGCAC GCAGGCGGGA GCAGGCAAGG GGCGGAGCCC CGGGCCCGGC     120

CAAGGTGGCC GTCAGAGGGT CTGCGGGGAG GCAGTAGCTT GACCCAAGGC GACCAGGGAA     180

CTTCAGACGG TAGCACGCCA CTCAAACAAA TTAACTTGAC ATCGCAAGCT GGGCGGGCTG     240

GTACGACATC CTGACTTCAG CATCCAGCTG TTCCTGGGCA GACAGAGGGC CAACAGGTGT     300

TCCTGTGGAA GAAGCCAGGA CAAGGACTCC AGAAAACATC TCGGGCAGCC TCTACATGAT     360

GTCACTTCTC AGGACTCGAG GACCAGCCAC CCTACACCTC TACTACAGAG AAGGCAGAAA     420

TGGAGACCCA AAGGCCATCA CTCCTGCTCT GTCACTAACC ACTCTGTAAT CATGTCTCCC     480

CACCAGAAGG TGTGAACCGC ACCAGGGCCG TGGAGTTCTC GGGCTCCCAA TCCACTGACA     540

CCTTTACCTG TCCCCTGAAG AGAAGGCAAC GCT ATG GCA TCG TAC AGC TGC TGT      594
                                     Met Ala Ser Tyr Ser Cys Cys
                                      1               5

TTG GCC CTA TTG GCT CTT GCC TGG CAC TCC TCT GCC TAT GGG CCT GAC       642
Leu Ala Leu Leu Ala Leu Ala Trp His Ser Ser Ala Tyr Gly Pro Asp
        10                  15                  20

CAG CGA GCC CAA AAG AAG GGG GAC ATT ATC CTA GGA GGT CTC TTT CCT       690
Gln Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro
    25                  30                  35

ATC CAT TTT GGA GTA GCA GCC AAA GAT CAA GAT CTG AAG TCA AGA CCA       738
Ile His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro
40                  45                  50                  55

GAG TCT GTG GAG TGC ATT AGG TAT AAC TTC CGT GGA TTC CGA TGG TTA       786
Glu Ser Val Glu Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu
                60                  65                  70

CAA GCC ATG ATA TTC GCC ATA GAG GAG ATA AAC AGC AGC CCC TCC CTT       834
Gln Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Ser Ser Pro Ser Leu
            75                  80                  85

CTT CCC AAC ATG ACA CTG GGA TAT AGG ATA TTT GAC ACC TGT AAC ACC       882
Leu Pro Asn Met Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr
        90                  95                  100

GTC TCC AAG GCG CTG GAA GCC ACC TTG AGT TTT GTT GCC CAG AAC AAA       930
Val Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys
    105                 110                 115

ATC GAT TCT TTG AAC CTG GAC GAG TTC TGC AAC TGC TCT GAG CAC ATC       978
Ile Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Glu His Ile
120                 125                 130                 135

CCT TCG ACC ATT GCC GTG GTG GGA GCC ACC GGC TCC GGT GTC TCC ACG      1026
Pro Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Val Ser Thr
                140                 145                 150

GCG GTA GCC AAC CTG CTG GGA CTT TTC TAC ATC CCC CAG GTG AGC TAC      1074
Ala Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr
            155                 160                 165

GCC TCC TCC AGC AGG CTC CTC AGC AAT AAG AAC CAG TAC AAA TCC TTC      1122
Ala Ser Ser Ser Arg Leu Leu Ser Asn Lys Asn Gln Tyr Lys Ser Phe
        170                 175                 180
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CTC CGC ACC ATT CCC AAT GAC GAA CAC CAG GCA ACC GCG ATG GCC GAC     1170
Leu Arg Thr Ile Pro Asn Asp Glu His Gln Ala Thr Ala Met Ala Asp
    185                 190                 195

ATC ATC GAG TAC TTC CGC TGG AAC TGG GTG GGC ACA ATT GCA GCT GAT     1218
Ile Ile Glu Tyr Phe Arg Trp Asn Trp Val Gly Thr Ile Ala Ala Asp
200                 205                 210                 215

GAC GAC TAT GGC AGA CCT GGC ATT GAG AAG TTC CGA GAG GAA GCC GAA     1266
Asp Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala Glu
                220                 225                 230

GAG AGG GAT ATC TGC ATT GAT TTT AGC GAG CTC ATC TCC CAG TAC TCT     1314
Glu Arg Asp Ile Cys Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser
            235                 240                 245

GAC GAG GAA GAG ATC CAG CAG GTG GTC GAA GTG ATC CAA AAC TCT ACG     1362
Asp Glu Glu Glu Ile Gln Gln Val Val Glu Val Ile Gln Asn Ser Thr
        250                 255                 260

GCC AAG GTC ATT GTC GTT TTC TCC AGC GGC CCG GAC CTA GAA CCT CTC     1410
Ala Lys Val Ile Val Val Phe Ser Ser Gly Pro Asp Leu Glu Pro Leu
    265                 270                 275

ATC AAG GAG ATT GTG CGG CGT AAC ATC ACA GGC AGG ATC TGG CTG GCT     1458
Ile Lys Glu Ile Val Arg Arg Asn Ile Thr Gly Arg Ile Trp Leu Ala
280                 285                 290                 295

AGC GAG GCC TGG GCC AGT TCC TCG CTG ATT GCT ATG CCT GAG TAT TTC     1506
Ser Glu Ala Trp Ala Ser Ser Ser Leu Ile Ala Met Pro Glu Tyr Phe
                300                 305                 310

CAT GTA GTC GGG GGC ACC ATT GGG TTC GGT CTG AAG GCT GGG CAG ATT     1554
His Val Val Gly Gly Thr Ile Gly Phe Gly Leu Lys Ala Gly Gln Ile
            315                 320                 325

CCA GGC TTC AGA GAA TTC CTA CAG AAA GTT CAT CCT AGG AAG TCT GTC     1602
Pro Gly Phe Arg Glu Phe Leu Gln Lys Val His Pro Arg Lys Ser Val
        330                 335                 340

CAC AAT GGT TTT GCC AAA GAG TTT TGG GAA GAA ACT TTT AAT TGC CAC     1650
His Asn Gly Phe Ala Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys His
    345                 350                 355

CTC CAA GAA GGC GCA AAA GGA CCT TTA CCT GTG GAC ACC TTC GTG AGA     1698
Leu Gln Glu Gly Ala Lys Gly Pro Leu Pro Val Asp Thr Phe Val Arg
360                 365                 370                 375

AGT CAC GAA GAA GGT GGC AAC AGG TTA CTC AAT AGC TCT ACT GCC TTC     1746
Ser His Glu Glu Gly Gly Asn Arg Leu Leu Asn Ser Ser Thr Ala Phe
                380                 385                 390

CGA CCC CTC TGC ACA GGG GAT GAG AAC ATC AAC AGT GTG GAG ACC CCT     1794
Arg Pro Leu Cys Thr Gly Asp Glu Asn Ile Asn Ser Val Glu Thr Pro
            395                 400                 405

TAC ATG GAT TAC GAA CAT TTA CGG ATA TCC TAC AAT GTG TAC TTA GCC     1842
Tyr Met Asp Tyr Glu His Leu Arg Ile Ser Tyr Asn Val Tyr Leu Ala
        410                 415                 420

GTC TAC TCC ATT GCG CAT GCC CTA CAA GAT ATA TAC ACC TGC TTA CCC     1890
Val Tyr Ser Ile Ala His Ala Leu Gln Asp Ile Tyr Thr Cys Leu Pro
    425                 430                 435

GGA AGA GGG CTT TTC ACC AAC GGG TCC TGT GCA GAC ATC AAG AAG GTT     1938
Gly Arg Gly Leu Phe Thr Asn Gly Ser Cys Ala Asp Ile Lys Lys Val
440                 445                 450                 455

GAG GCC TGG CAG GTC TTG AAG CAC CTA CGG CAC CTG AAC TTC ACC AAC     1986
Glu Ala Trp Gln Val Leu Lys His Leu Arg His Leu Asn Phe Thr Asn
                460                 465                 470

AAC ATG GGG GAG CAG GTG ACC TTC GAT GAG TGT GGT GAT CTG GTG GGG     2034
Asn Met Gly Glu Gln Val Thr Phe Asp Glu Cys Gly Asp Leu Val Gly
            475                 480                 485

AAC TAT TCT ATC ATC AAC TGG CAC CTC TCC CCA GAG GAC GGC TCC ATT     2082
Asn Tyr Ser Ile Ile Asn Trp His Leu Ser Pro Glu Asp Gly Ser Ile
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        490                 495                 500

GTG TTC AAG GAA GTT GGG TAC TAC AAT GTG TAT GCC AAG AAG GGA GAA     2130
Val Phe Lys Glu Val Gly Tyr Tyr Asn Val Tyr Ala Lys Lys Gly Glu
    505                 510                 515

AGA CTC TTC ATC AAT GAG GAG AAG ATC TTG TGG AGT GGG TTC TCC AGA     2178
Arg Leu Phe Ile Asn Glu Glu Lys Ile Leu Trp Ser Gly Phe Ser Arg
520                 525                 530                 535

GAG GTG CCT TTC TCC AAT TGC AGC CGG GAC TGT CAG GCA GGG ACC AGG     2226
Glu Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Gln Ala Gly Thr Arg
                540                 545                 550

AAG GGG ATC ATC GAG GGA GAG CCC ACC TGC TGC TTT GAG TGT GTG GAG     2274
Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe Glu Cys Val Glu
            555                 560                 565

TGT CCT GAT GGA GAG TAC AGT GGA GAG ACA GAT GCG AGT GCC TGT GAC     2322
Cys Pro Asp Gly Glu Tyr Ser Gly Glu Thr Asp Ala Ser Ala Cys Asp
        570                 575                 580

AAG TGC CCG GAT GAC TTC TGG TCC AAT GAG AAC CAC ACT TCT TGC ATT     2370
Lys Cys Pro Asp Asp Phe Trp Ser Asn Glu Asn His Thr Ser Cys Ile
    585                 590                 595

GCC AAG GAG ATT GAG TTT CTG GCG TGG ACC GAG CCC TTT GGA ATC GCT     2418
Ala Lys Glu Ile Glu Phe Leu Ala Trp Thr Glu Pro Phe Gly Ile Ala
600                 605                 610                 615

CTC ACT CTC TTT GCG GTG CTG GGC ATT TTC CTG ACC GCC TTT GTG CTG     2466
Leu Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala Phe Val Leu
                620                 625                 630

GGT GTC TTC ATC AAG TTC CGA AAC ACA CCT ATC GTC AAG GCC ACC AAC     2514
Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn
            635                 640                 645

CGA GAA CTG TCC TAC CTC CTG CTC TTC TCC CTA CTC TGC TGC TTC TCC     2562
Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Leu Cys Cys Phe Ser
        650                 655                 660

AGC TCC TTG TTC TTC ATT GGG GAG CCC CAG GAC TGG ACG TGC CGC CTG     2610
Ser Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr Cys Arg Leu
    665                 670                 675

CGA CAG CCT GCT TTC GGC ATC AGC TTT GTG CTC TGT ATC TCG TGC ATC     2658
Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile
680                 685                 690                 695

TTG GTG AAG ACC AAT CGC GTC CTC CTG GTA TTT GAA GCC AAG ATA CCC     2706
Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro
                700                 705                 710

ACC AGC TTC CAC CGG AAG TGG TGG GGG CTC AAC CTG CAG TTC CTG CTG     2754
Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu
            715                 720                 725

GTT TTC CTC TGC ACC TTC ATG CAG ATC CTC ATC TGC ATC ATC TGG CTC     2802
Val Phe Leu Cys Thr Phe Met Gln Ile Leu Ile Cys Ile Ile Trp Leu
        730                 735                 740

TAC ACG GCG CCC CCC TCT AGC TAC CGC AAC CAT GAG CTG GAA GAC GAA     2850
Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp Glu
    745                 750                 755

ATC ATC TTC ATC ACG TGC CAT GAG GGC TCA CTC ATG GCA CTT GGC TCC     2898
Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala Leu Gly Ser
760                 765                 770                 775

CTG ATC GGC TAT ACC TGC CTG CTG GCT GCC ATC TGC TTC TTC TTT GCC     2946
Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala
                780                 785                 790

TTC AAG TCC AGG AAG TTA CCA GAG AAC TTC AAC GAA GCC AAG TTC ATT     2994
Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile
            795                 800                 805

ACC TTC AGC ATG CTC ATC TTC TTC ATC GTC TGG ATC TCC TTC ATT CCA     3042
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Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro
        810                 815                 820

GCC TAT GCC AGC ACC TAC GGC AAG TTT GTC TCT GCC GTA GAG GTG ATC     3090
Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile
    825                 830                 835

GCC ATT TTG GCA GCC AGC TTT GGC TTA CTA GCC TGC ATC TTC TTC AAC     3138
Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn
840                 845                 850                 855

AAG GTC TAC ATT ATC CTC TTC AAG CCT TCC CGG AAC ACC ATT GAG GAA     3186
Lys Val Tyr Ile Ile Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu
                860                 865                 870

GTC CGC TCC AGC ACC GCA GCA CAT GCT TTC AAA GTA GCA GCC CGC GCC     3234
Val Arg Ser Ser Thr Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala
            875                 880                 885

ACT CTA CGC CGT CCC AAC ATC TCC CGG AAG CGG TCC AGC AGC CTT GGA     3282
Thr Leu Arg Arg Pro Asn Ile Ser Arg Lys Arg Ser Ser Ser Leu Gly
        890                 895                 900

GGC TCC ACC GGC TCC ATT CCC TCC TCC TCC ATC AGC AGC AAA AGC AAC     3330
Gly Ser Thr Gly Ser Ile Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn
    905                 910                 915

AGC GAA GAC CGG TTC CCG CAG CCA GAG AGG CAG AAG CAA CAG CAA CCG     3378
Ser Glu Asp Arg Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro
920                 925                 930                 935

CTG TCC CTG ACC CAG CAA GAA CAG CAG CAG CAG CCC CTG ACC CTC CAC     3426
Leu Ser Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu His
                940                 945                 950

CCA CAG CAA CAG CAG CAG CCA CAG CAG CCG AGA TGC AAA CAG AAG GTC     3474
Pro Gln Gln Gln Gln Gln Pro Gln Gln Pro Arg Cys Lys Gln Lys Val
            955                 960                 965

ATC TTC GGC AGT GGT ACG GTC ACC TTC TCT CTG AGT TTT GAC GAG CCT     3522
Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro
        970                 975                 980

CAG AAG AAT GCC ATG GCC CAC AGG AAC TCC ATG CGT CAG AAC TCC CTG     3570
Gln Lys Asn Ala Met Ala His Arg Asn Ser Met Arg Gln Asn Ser Leu
    985                 990                 995

GAG GCC CAG AGG AGC AAC GAC ACC TTG GGC AGA CAC CAG GCC CTG CTT     3618
Glu Ala Gln Arg Ser Asn Asp Thr Leu Gly Arg His Gln Ala Leu Leu
1000                1005                1010                1015

CCC CTA CAG TGT GCA GAT GCG GAC TCA GAA ATG ACC ATT CAG GAA ACG     3666
Pro Leu Gln Cys Ala Asp Ala Asp Ser Glu Met Thr Ile Gln Glu Thr
                1020                1025                1030

GGC CTG CAA GGG CCC ATG GTG GGG GAC CAC CAG CCA GAA ATG GAA AGC     3714
Gly Leu Gln Gly Pro Met Val Gly Asp His Gln Pro Glu Met Glu Ser
            1035                1040                1045

TCA GAT GAA ATG TCC CCA GCG CTG GTC ATG TCC ACC TCT CGG AGC TTC     3762
Ser Asp Glu Met Ser Pro Ala Leu Val Met Ser Thr Ser Arg Ser Phe
        1050                1055                1060

GTC ATT AGT GGT GGA GGT AGC TCT GTG ACG GAA AAC GTA TTA CAC TCC     3810
Val Ile Ser Gly Gly Gly Ser Ser Val Thr Glu Asn Val Leu His Ser
    1065                1070                1075

TAATGGAGGG AAAGGCTATC CAGTTGAGAG GTTTTTCTTA GAGCCCTGAG CAAAAGGATG   3870

GGTCCTTCCT TTCTTCCCAG GAAGCCAGGG AGAGTAGGTA CGTCAAAGCC TGTACTCAGT   3930

TGCACTGCTT TGAATGACAG TGAACTGACT GGTGTGCTCT TTAGAGTTAA AAGAAGAGCC   3990

ATGTTTTGGG GTCGTTTTCC AGAGCTCAGT ATCACACCTG GGTTTGCTGA AGTCTTTTCC   4050

TCTGCTCTAT CCACCATCAG TTCAGACGAA AGCAAGGCTC TAAGCTACCC ATCTGCTTCC   4110

CTCAAAAAAA AAAAAAAAAA A                                             4131
```

-continued

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1085 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
Met Ala Leu Tyr Ser Cys Cys Trp Ile Leu Leu Ala Phe Ser Thr Trp
1               5                   10                  15

Cys Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp
            20                  25                  30

Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Val Lys
        35                  40                  45

Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr
    50                  55                  60

Asn Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu
65                  70                  75                  80

Glu Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Met Thr Leu Gly Tyr
                85                  90                  95

Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr
            100                 105                 110

Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu
        115                 120                 125

Phe Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly
    130                 135                 140

Ala Thr Gly Ser Gly Ile Ser Thr Ala Val Ala Asn Leu Leu Gly Leu
145                 150                 155                 160

Phe Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser
                165                 170                 175

Asn Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu
            180                 185                 190

His Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn
        195                 200                 205

Trp Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile
    210                 215                 220

Glu Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe
225                 230                 235                 240

Ser Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Lys Ile Gln Gln Val
                245                 250                 255

Val Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser
            260                 265                 270

Ser Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn
        275                 280                 285

Ile Thr Gly Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser
    290                 295                 300

Leu Ile Ala Met Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile Gly
305                 310                 315                 320

Phe Gly Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Gln
                325                 330                 335

Lys Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe
            340                 345                 350

Trp Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro
```

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```
        355                 360                 365

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

Leu Ser Asn Ser Pro Thr Ala Phe Arg Pro Leu Cys Thr Gly Glu Glu
385                 390                 395                 400

Asn Ile Ser Ser Val Glu Thr Pro Tyr Met Asp Tyr Thr His Leu Arg
                405                 410                 415

Ile Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu
            420                 425                 430

Gln Asp Ile Tyr Thr Cys Ile Pro Gly Arg Gly Leu Phe Thr Asn Gly
        435                 440                 445

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

Leu Arg His Leu Asn Phe Thr Ser Asn Met Gly Glu Gln Val Thr Phe
465                 470                 475                 480

Asp Glu Cys Gly Asp Leu Ala Gly Asn Tyr Ser Ile Ile Asn Trp His
                485                 490                 495

Leu Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr
            500                 505                 510

Asn Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Asp Glu Lys
        515                 520                 525

Ile Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser
    530                 535                 540

Arg Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro
545                 550                 555                 560

Thr Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp
                565                 570                 575

Glu Thr Asp Ala Ser Ala Cys Asp Lys Cys Pro Asp Asp Phe Trp Ser
            580                 585                 590

Asn Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser
        595                 600                 605

Trp Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly
    610                 615                 620

Ile Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn
625                 630                 635                 640

Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu
                645                 650                 655

Phe Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu
            660                 665                 670

Pro Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser
        675                 680                 685

Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu
    690                 695                 700

Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp
705                 710                 715                 720

Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln
                725                 730                 735

Ile Val Ile Cys Ala Ile Trp Leu Asn Thr Ala Pro Pro Ser Ser Tyr
            740                 745                 750

Arg Asn His Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu
        755                 760                 765

Gly Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu
    770                 775                 780
```

-continued

```
Ala Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu
785                 790                 795                 800

Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe
                805                 810                 815

Ile Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys
            820                 825                 830

Phe Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly
        835                 840                 845

Leu Leu Ala Cys Ile Phe Phe Asn Lys Val Tyr Ile Ile Leu Phe Lys
    850                 855                 860

Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His
865                 870                 875                 880

Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser
                885                 890                 895

Arg Gln Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser
            900                 905                 910

Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Gln
        915                 920                 925

Gln Pro Lys Arg Gln Lys Gln Pro Gln Pro Leu Ala Leu Ser Pro His
    930                 935                 940

Asn Ala Gln Gln Pro Gln Pro Arg Pro Pro Ser Thr Pro Gln Pro Gln
945                 950                 955                 960

Pro Gln Ser Gln Gln Pro Pro Arg Cys Lys Gln Lys Val Ile Phe Gly
                965                 970                 975

Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Thr
            980                 985                 990

Ala Val Ala His Arg Asn Ser Thr His Gln Thr Ser Leu Glu Ala Gln
        995                 1000                1005

Lys Asn Asn Asp Ala Leu Thr Lys His Gln Ala Leu Leu Pro Leu Gln
    1010                1015                1020

Cys Gly Glu Thr Asp Ser Glu Leu Thr Ser Gln Glu Thr Gly Leu Gln
1025                1030                1035                1040

Gly Pro Val Gly Glu Asp His Gln Leu Glu Met Glu Asp Pro Glu Glu
                1045                1050                1055

Met Ser Pro Ala Leu Val Val Ser Asn Ser Arg Ser Phe Val Ile Ser
            1060                1065                1070

Gly Gly Gly Ser Thr Val Thr Glu Asn Met Leu Arg Ser
        1075                1080                1085
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1088 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
1               5                   10                  15

Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
            20                  25                  30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
        35                  40                  45
```

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```
Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
    50                  55                  60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
65                  70                  75                  80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
                85                  90                  95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
            100                 105                 110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
        115                 120                 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
    130                 135                 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145                 150                 155                 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
                165                 170                 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
            180                 185                 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
        195                 200                 205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
    210                 215                 220

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

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
                245                 250                 255

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
            260                 265                 270

Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
        275                 280                 285

Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
    290                 295                 300

Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
305                 310                 315                 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
                325                 330                 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
            340                 345                 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
        355                 360                 365

Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
    370                 375                 380

Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
385                 390                 395                 400

Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
                405                 410                 415

Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
            420                 425                 430

Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
        435                 440                 445

Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
    450                 455                 460

Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
```

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```
465                 470                 475                 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
                485                 490                 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
            500                 505                 510

Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
        515                 520                 525

Leu Trp Ser Gly Phe Ser Arg Glu Pro Leu Thr Phe Val Leu Ser Val
    530                 535                 540

Leu Gln Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Leu Ala Gly Thr
545                 550                 555                 560

Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe Glu Cys Val
                565                 570                 575

Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys
            580                 585                 590

Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn Glu Asn His Thr Ser Cys
        595                 600                 605

Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile
    610                 615                 620

Ala Leu Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala Phe Val
625                 630                 635                 640

Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr
                645                 650                 655

Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Leu Cys Cys Phe
            660                 665                 670

Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr Cys Arg
        675                 680                 685

Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys
    690                 695                 700

Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile
705                 710                 715                 720

Pro Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu
                725                 730                 735

Leu Val Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val Ile Trp
            740                 745                 750

Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu Glu Asp
        755                 760                 765

Glu Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala Leu Gly
    770                 775                 780

Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe
785                 790                 795                 800

Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe
                805                 810                 815

Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser Phe Ile
            820                 825                 830

Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val Glu Val
        835                 840                 845

Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe
    850                 855                 860

Asn Lys Ile Tyr Ile Ile Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu
865                 870                 875                 880

Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val Ala Ala Arg
                885                 890                 895
```

-continued

```
Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu
            900                 905                 910

Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser
        915                 920                 925

Asn Ser Glu Asp Pro Phe Pro Arg Pro Glu Arg Gln Lys Gln Gln Gln
    930                 935                 940

Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu
945                 950                 955                 960

Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val
                965                 970                 975

Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro
            980                 985                 990

Gln Lys Asn Ala Met Ala His Arg Asn Ser Thr His Gln Asn Ser Leu
        995                 1000                1005

Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu
    1010                1015                1020

Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr
1025                1030                1035                1040

Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp
                1045                1050                1055

Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe
            1060                1065                1070

Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser
        1075                1080                1085
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1078 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
  1               5                  10                  15

Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
             20                  25                  30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
         35                  40                  45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
     50                  55                  60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
 65                  70                  75                  80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
                 85                  90                  95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
            100                 105                 110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
        115                 120                 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
    130                 135                 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145                 150                 155                 160
```

-continued

```
Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
                165                 170                 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
            180                 185                 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
        195                 200                 205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
    210                 215                 220

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

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
                245                 250                 255

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
            260                 265                 270

Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
        275                 280                 285

Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
    290                 295                 300

Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
305                 310                 315                 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
                325                 330                 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
            340                 345                 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
        355                 360                 365

Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
    370                 375                 380

Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
385                 390                 395                 400

Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
                405                 410                 415

Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
            420                 425                 430

Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
        435                 440                 445

Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
    450                 455                 460

Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
465                 470                 475                 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
                485                 490                 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
            500                 505                 510

Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
        515                 520                 525

Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
    530                 535                 540

Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
545                 550                 555                 560

Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
                565                 570                 575

Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
```

-continued

```
            580                 585                 590

Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
        595                 600                 605

Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile
    610                 615                 620

Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr
625                 630                 635                 640

Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe
                645                 650                 655

Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro
            660                 665                 670

Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe
        675                 680                 685

Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu
    690                 695                 700

Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly
705                 710                 715                 720

Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile
                725                 730                 735

Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg
            740                 745                 750

Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly
        755                 760                 765

Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala
    770                 775                 780

Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn
785                 790                 795                 800

Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile
                805                 810                 815

Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe
            820                 825                 830

Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu
        835                 840                 845

Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe Lys Pro
    850                 855                 860

Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala
865                 870                 875                 880

Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg
                885                 890                 895

Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser
            900                 905                 910

Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu
        915                 920                 925

Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln
    930                 935                 940

Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro
945                 950                 955                 960

Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser
                965                 970                 975

Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser
            980                 985                 990

Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr
        995                 1000                1005
```

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```
Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp
    1010                1015                1020

Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln
1025                1030                1035                1040

Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val
                1045                1050                1055

Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr
            1060                1065                1070

Glu Asn Val Val Asn Ser
        1075


(2) INFORMATION FOR SEQ ID NO: 8:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:              1079 amino acids
          (B) TYPE:                amino acid
          (D) TOPOLOGY:            linear

    (ii) MOLECULE TYPE:            protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Ser Tyr Ser Cys Cys Leu Ala Leu Leu Ala Leu Ala Trp His
  1               5                  10                  15

Ser Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
             20                  25                  30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
         35                  40                  45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
     50                  55                  60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
 65                  70                  75                  80

Ile Asn Ser Ser Pro Ser Leu Leu Pro Asn Met Thr Leu Gly Tyr Arg
                 85                  90                  95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
            100                 105                 110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
        115                 120                 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
    130                 135                 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145                 150                 155                 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
                165                 170                 175

Lys Asn Gln Tyr Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
            180                 185                 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
        195                 200                 205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
    210                 215                 220

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

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln Gln Val Val
                245                 250                 255

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
            260                 265                 270
```

-continued

```
Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
        275                 280                 285

Thr Gly Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
    290                 295                 300

Ile Ala Met Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
305                 310                 315                 320

Gly Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Gln Lys
                325                 330                 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
            340                 345                 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
        355                 360                 365

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

Leu Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
385                 390                 395                 400

Ile Asn Ser Val Glu Thr Pro Tyr Met Asp Tyr Glu His Leu Arg Ile
                405                 410                 415

Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
            420                 425                 430

Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
        435                 440                 445

Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
    450                 455                 460

Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
465                 470                 475                 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
                485                 490                 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
            500                 505                 510

Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
        515                 520                 525

Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
    530                 535                 540

Asp Cys Gln Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
545                 550                 555                 560

Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Gly Glu
                565                 570                 575

Thr Asp Ala Ser Ala Cys Asp Lys Cys Pro Asp Asp Phe Trp Ser Asn
            580                 585                 590

Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ala Trp
        595                 600                 605

Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile
    610                 615                 620

Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr
625                 630                 635                 640

Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe
                645                 650                 655

Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro
            660                 665                 670

Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe
        675                 680                 685

Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu
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-continued

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    690                 695                 700

Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly
705                 710                 715                 720

Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile
                725                 730                 735

Leu Ile Cys Ile Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg
            740                 745                 750

Asn His Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly
        755                 760                 765

Ser Leu Met Ala Leu Gly Ser Leu Ile Gly Tyr Thr Cys Leu Leu Ala
    770                 775                 780

Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn
785                 790                 795                 800

Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile
                805                 810                 815

Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe
            820                 825                 830

Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu
        835                 840                 845

Leu Ala Cys Ile Phe Phe Asn Lys Val Tyr Ile Ile Leu Phe Lys Pro
    850                 855                 860

Ser Arg Asn Thr Ile Glu Glu Val Arg Ser Ser Thr Ala Ala His Ala
865                 870                 875                 880

Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Pro Asn Ile Ser Arg
                885                 890                 895

Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Ile Pro Ser Ser
            900                 905                 910

Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Arg Phe Pro Gln Pro Glu
        915                 920                 925

Arg Gln Lys Gln Gln Gln Pro Leu Ser Leu Thr Gln Gln Glu Gln Gln
    930                 935                 940

Gln Gln Pro Leu Thr Leu His Pro Gln Gln Gln Gln Gln Pro Gln Gln
945                 950                 955                 960

Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe
                965                 970                 975

Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn
            980                 985                 990

Ser Met Arg Gln Asn Ser Leu Glu Ala Gln Arg Ser Asn Asp Thr Leu
        995                 1000                1005

Gly Arg His Gln Ala Leu Leu Pro Leu Gln Cys Ala Asp Ala Asp Ser
    1010                1015                1020

Glu Met Thr Ile Gln Glu Thr Gly Leu Gln Gly Pro Met Val Gly Asp
1025                1030                1035                1040

His Gln Pro Glu Met Glu Ser Ser Asp Glu Met Ser Pro Ala Leu Val
                1045                1050                1055

Met Ser Thr Ser Arg Ser Phe Val Ile Ser Gly Gly Gly Ser Ser Val
            1060                1065                1070

Thr Glu Asn Val Leu His Ser
        1075
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

-continued

```
          (B) TYPE:                  amino acids
          (C) STRANDEDNESS:          single
          (D) TOPOLOGY:              linear

    (ii) MOLECULE TYPE:              peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Tyr Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys
  1               5                  10                  15


(2) INFORMATION FOR SEQ ID NO:10:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:                23 amino acids
          (B) TYPE:                  amino acids
          (C) STRANDEDNESS:          single
          (D) TOPOLOGY:              linear

    (ii) MOLECULE TYPE:              peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu
  1               5                  10                  15

Ala Glu Glu Arg Asp Ile Cys
            20


(2) INFORMATION FOR SEQ ID NO:11:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:                19 amino acids
          (B) TYPE:                  amino acids
          (C) STRANDEDNESS:          single
          (D) TOPOLOGY:              linear

    (ii) MOLECULE TYPE:              peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Lys
  1               5                  10                  15

Ile Gln Gln


(2) INFORMATION FOR SEQ ID NO:12:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:                16 amino acids
          (B) TYPE:                  amino acids
          (C) STRANDEDNESS:          single
          (D) TOPOLOGY:              linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr His Asn Gly Phe Ala Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys
  1               5                  10                  15


(2) INFORMATION FOR SEQ ID NO:13:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:                13 amino acids
          (B) TYPE:                  amino acids
          (C) STRANDEDNESS:          single
          (D) TOPOLOGY:              linear

    (ii) MOLECULE TYPE:              peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Glu Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys
  1               5                  10
```

-continued

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Arg Asn His Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Tyr Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(iii) FEATURE:
(A) NAME/KEY: Modified Base
(B) LOCATION: 13...13
(C) OTHER INFORMATION: Inosine

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGCTCGAG ACNARYCGGG ARCTYTSCTA YMT 33

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(iii) FEATURE:

-continued

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        (A) NAME/KEY: Modified Base
        (B) LOCATION: 13...13
        (C) OTHER INFORMATION: Inosine

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAATTCCG TTNCGGGWYT TGAASGCRWA S                                  31


(2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:                 32 base pairs
        (B) TYPE:                   nucleic
        (C) STRANDEDNESS:           single
        (D) TOPOLOGY:               linear

    (ii) MOLECULE TYPE:             nucleic acid

   (iii) FEATURE:
        (A) NAME/KEY: Modified Base
        (B) LOCATION: 24...24
        (C) OTHER INFORMATION: Inosine

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTGCTCGAG TCAAGGCTAC GRRNMGNGAR YT                                 32


(2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:                 34 base pairs
        (B) TYPE:                   nucleic
        (C) STRANDEDNESS:           single
        (D) TOPOLOGY:               linear

    (ii) MOLECULE TYPE:             nucleic acid

   (iii) FEATURE:
        (A) NAME/KEY: Modified Base
        (B) LOCATION: 26...26
        (C) OTHER INFORMATION: Inosine

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGAATTCCA TTTGGCTTCG TTGAANKTNK CNGG                               34
```
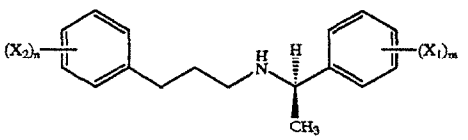

What is claimed is:

1. A compound having the chemical formula:



wherein each X_1 and X_2 is one or more substituents independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, acetoxy, or acetyl, or two of X_1 are together a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy, or two of X_2 are together are a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy; provided that $(X_2)_n$ is not 3-t-butyl; n is between 0 and 5 inclusive, and m is between 1 and 5 inclusive; or a pharmaceutically acceptable salt thereof.

2. The compound of claim 1, wherein each said X_1 and X_2 is independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, i-butyl, or acetoxy, or two of X_1 are together a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy, or two of X_2 are together a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy.

3. The compound of claim 1, wherein each said X_1 and X_2 is independently selected from the group consisting of: CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2 and CH_3CH_2.

4. The compound of claim 3, wherein each said X_1 and X_2 is independently selected from the group consisting of: CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH and CH_3CH_2.

5. The compound of claim 4, wherein each said X_1 and X_2 is independently selected from the group consisting of: Cl, F, CF_3, CH_3 and CH_3O.

6. The compound of claim 5, wherein said n is 0 or 1.

7. The compound of claim 6, wherein said X_1 is meta; and said n is 0 or 1, provided that if n is 1 then X_2 is either meta or ortho.

8. The compound of claim 3, wherein n is 1.

9. The compound of claim 1, wherein said X_1 is meta.

10. The compound of claim 1, wherein said compound is selected from the group consisting of:

NPS R-467 which is represented by the chemical formula (R)-N-(3-phenylpropyl)-1-(3-methoxyphenyl) ethylamine;

NPS R-568 which is represented by the chemical formula (R)-N-(3-(2-chlorophenyl)propyl)- 1-(3-methoxyphenyl)ethylamine;

R-4M which is represented be the chemical formula (R)-N-(3-(2-fluorophenyl)propyl)-1-(3-methoxyphenyl)ethylamine;

4N which is represented by the chemical formula (R)-N-(3-(3-fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine;

4P which is represented by the chemical formula (R)-N-(3-(4-fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine;

R-4V which is represented by the chemical formula (R)-N-(3-(2-trifluoromethyl)phenyl)propyl-1-(3-methoxyphenyl)ethylamine;

R-4W which is represented by the chemical formula (R)-N-(3-(3-trifluoromethyl)phenyl)propyl-1-(3-methoxyphenyl)ethylamine; and

6X which is represented by the chemical formula (R)-N-(3-(3-chlorophenyl)propyl-1-(3-methoxyphenyl) ethylamine;

or a pharmaceutically acceptable salt thereof.

11. The compound of claim **10**, wherein said compound is NPS R-568 which is represented by the chemical formula (R)-N-(3-(2-chlorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

12. The compound of claim **10**, wherein said compound is NPS R-467 which is represented by the chemical formula (R)-N-(3-phenylpropyl)-1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

13. The compound of claim **10**, wherein said compound is R-4M which is represented by the chemical formula (R)-N-(3-(2-fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

14. The compound of claim **10**, wherein said compound is 4N which is represented by the chemical formula (R)-N-(3-(3- fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

15. The compound of claim **10**, wherein said compound is 4P which is represented by the chemical formula (R)-N-(3-(4-fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

16. The compound of claim **10**, wherein said compound is R-4V which is represented by the chemical formula (R)-N-(3-(2-trifluoromethyl)phenyl)propyl- 1 -(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

17. The compound of claim **10**, wherein said compound is R-4W which is represented by the chemical formula (R)-N-(3-(3-trifluoromethyl)phenyl)propyl- 1 -(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

18. The compound of claim **10**, wherein said compound is 6X which is represented by the chemical formula (R)-N-(3-(3-chlorophenyl)propyl-1-(3 -methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

19. The compound of claim **10**, wherein said compound is 21M (R)-N-(3-(3-(trifluoromethoxy)phenyl)propyl)-1-(3-methoxy-phenyl)ethylamine) or a pharmaceutically acceptable salt thereof.

20. The compound of claim **1**, wherein each X_1 and X_2 is one or more substituents independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, acetoxy, or acetyl, or two of X_1 are together a fused benzene or methylene dioxy, or two of X_2 are together a fused benzene or methylene dioxy: and m is at least 1.

21. The compound of claim **20**, wherein each said X_1 and X_2 is independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, or acetoxy, or two of X_1 are together a fused benzene or methylene dioxy or two of X_2 are together a fused benzene or methylene dioxy.

22. The compound of claim **21**, wherein each said X_1 and X_2 is independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2 or CH_3CH_2, or two of X_1 are together a fused benzene, or two of X_2 are together a fused benzene.

23. The compound of claim **22**, wherein n is at least 1.

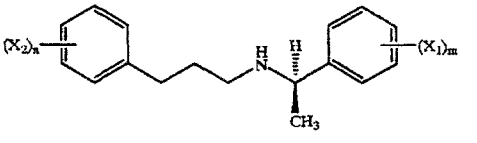
24. The compound of claim **22**, wherein two of X_1 are together a fused benzene.

25. The compound of claim **24**, wherein X_2 is selected from the group consisting of Cl, F, CF_3, CH_3 and CH_3O.

26. The compound of claim **1**, wherein said compound causes an increase in $(Ca^{2+})_i$ with an EC_{50} less than or equal to 5 μM as determined by measuring $(Ca^{2+})_i$ in bovine parathyroid cells using the Cytosolic Ca^{2+} Cell Assay.

27. The compound of claim **26**, wherein said EC_{50} is less than or equal to 1 μM.

28. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and a therapeutically effective amount of compound having the chemical formula:



wherein each X_1 and X_2 is one or more substituents independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, acetoxy, or acetyl, or two of X_1 are together a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy, or two of X_2 are together are a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy; provided that $(X_2)_n$ is not 3-t-butyl;

n is between 0 and 5 inclusive, and m is between 1 and 5 inclusive; or a pharmaceutically acceptable salt thereof.

29. The composition of claim **28**, wherein each said X_1 and X_2 is independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, or acetoxy, or two of X_1 are together a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy, or two of X_2 are together a fused cycloaliphatic ring, a fused aromatic ring or methylene dioxy.

30. The composition of claim **28**, wherein each said X_1 and X_2 is independently selected from the group consisting of: CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2 and CH_3CH_2.

31. The composition of claim **30**, wherein each said X_1 and X_2 is independently selected from the group consisting of: CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CHOH and CCH_2.

32. The composition of claim **31**, wherein each said X_1 and X_2 is independently selected from the group consisting of: Cl, F, CF_3, CH_3 and CH_3O.

33. The composition of claim 32, wherein said n is 0 or 1.

34. The composition of claim 33, wherein said X_1 is meta; and said n is 0 or 1, provided that if n is 1 then X_2 is either meta or ortho.

35. The composition of claim 30, wherein said X_1 is meta.

36. The composition of claim 30, wherein n is 1.

37. The composition of claim 28, wherein said X_1 is meta.

38. The composition of claim 28, wherein each X_1 and X_2 is one or more substituents independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, acetoxy, or acetyl, or two of X_1 are together a fused benzene or methylene dioxy, or two of X_2 are together a fused benzene or methylene dioxy.

39. The composition of claim 38 wherein each said X_1 and X_2 is independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, CH_3CH_2, propyl, isopropyl, butyl, isobutyl, t-butyl, or acetoxy, or two of X_1 are together a fused benzene or methylene dioxy, or two of X_2 together a fused benzene or methylene dioxy.

40. The composition of claim 39, wherein each said X_1 and X_2 is independently either CH_3, CH_3O, CH_3CH_2O, Br, Cl, F, CF_3, CHF_2, CH_2F, CF_3O, CH_3S, OH, CH_2OH, $CONH_2$, CN, NO_2 or CH_3CH_2, or two of X_1 are together a fused benzene, or two of X_2 are together a fused benzene.

41. The composition of claim 40, wherein two of X_1 are together a fused benzene.

42. The composition of claim 41, wherein X_2 is selected from the group consisting of Cl, F, CF_3, CH_3 and CH_3O.

43. The composition of claim 40, wherein n is at least 1.

44. The composition of claim 28, wherein said compound causes an increase in $(Ca^{2+})_i$ with an EC_{50} less than or equal to 5 μM as determined by measuring $(Ca^{2+})_i$ in bovine parathyroid cells using the Cytosolic Ca^{2+} Cell Assay.

45. The composition of claim 44, wherein said EC_{50} is less than or equal to 1 μM.

46. The compound of claim 28, wherein said compound is NPS R-568 which is represented by the chemical formula (R)-N-(3-(2-chlorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

47. The compound of claim 28, wherein said compound is NPS R-467 which is represented by the chemical formula (R)-N-(3-phenylpropyl)-1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

48. The compound of claim 28, wherein said compound is R-4M which is represented by the chemical formula (R)-N-(3-(2-fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

49. The compound of claim 8, wherein said compound is 4N which is represented by the chemical formula (R)-N-(3-(3- fluorophenyl)propyl)-1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

50. The compound of claim 28, wherein said compound is 4P which is represented by the chemical formula (R)-N-(3-(4-fluorophenyl)propyl)-1-(3-methoxyphenyl) ethylamine or a pharmaceutically acceptable salt thereof.

51. The compound of claim 28, wherein said compound is R-4V which is represented by the chemical formula (R)-N-(3-(2-trifluoromethyl)phenyl)propyl-1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

52. The compound of claim 28, wherein said compound is R-4W which is represented by the chemical formula (R)-N-(3-(3-trifluoromethyl)phenyl)propyl- 1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

53. The compound of claim 28, wherein said compound is 6X which is represented by the chemical formula (R)-N-(3-(3-chlorophenyl)propyl-1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

54. The compound of claim 28, wherein said compound is 21M which is represented by the chemical formula (R)-N-(3-(3-(trifluoromethoxy)phenyl)propyl)-1-(3-methoxyphenyl)ethylamine) or a pharmaceutically acceptable salt thereof.

55. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and a therapeutically effective amount of compound 4W which is represented by the chemical formula N-(3-(3-(trifluoromethyl)phenyl)propyl)-1-(3-methoxyphenyl)ethylamine or a pharmaceutically acceptable salt thereof.

* * * * *

ATTACHMENT B
COPY OF TERMINAL DISCLAIMER FOR US PATENT NO. 6,313,146