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(54) **PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE BY TRANSFORMATION WITH AN ETR NUCLEIC ACID**

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Related U.S. Application Data

(63) Continuation of application No. 08/263,480, filed on Jun. 28, 1994, now abandoned, which is a continuation-in-part of application No. 08/086,555, filed on Jul. 1, 1993, now abandoned.

(51) **Int. Cl.**^{7} **A01H 5/00**; A01H 5/08; C12N 5/14; C12N 15/82

(52) **U.S. Cl.** **800/317.4**; 435/320.1; 435/419; 435/440; 536/23.6; 800/283; 800/298

(58) **Field of Search** .... 536/23.6; 435/172.3, 435/320.1, 419, 69.1, 468, 440, 283; 800/205, DIG. 15, DIG. 44, 69.1, 278, 298, 317.4, 287

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(57) **ABSTRACT**

The invention includes transformed plants having at least one cell transformed with a modified ETR nucleic acid. Such plants have a phenotype characterized by a decrease in the response of at least one transformed plant cell to ethylene as compared to a plant not containing the transformed plant cell. Tissue and/or temporal specificity for expression of the modified ETR nucleic acid is controlled by selecting appropriate expression regulation sequences to target the location and/or time of expression of the transformed nucleic acid. The plants are made by transforming at least one plant cell with an appropriate modified ETR nucleic acid, regenerating plants from one or more of the transformed plant cells and selecting at least one plant having the desired phenotype.

32 Claims, 65 Drawing Sheets

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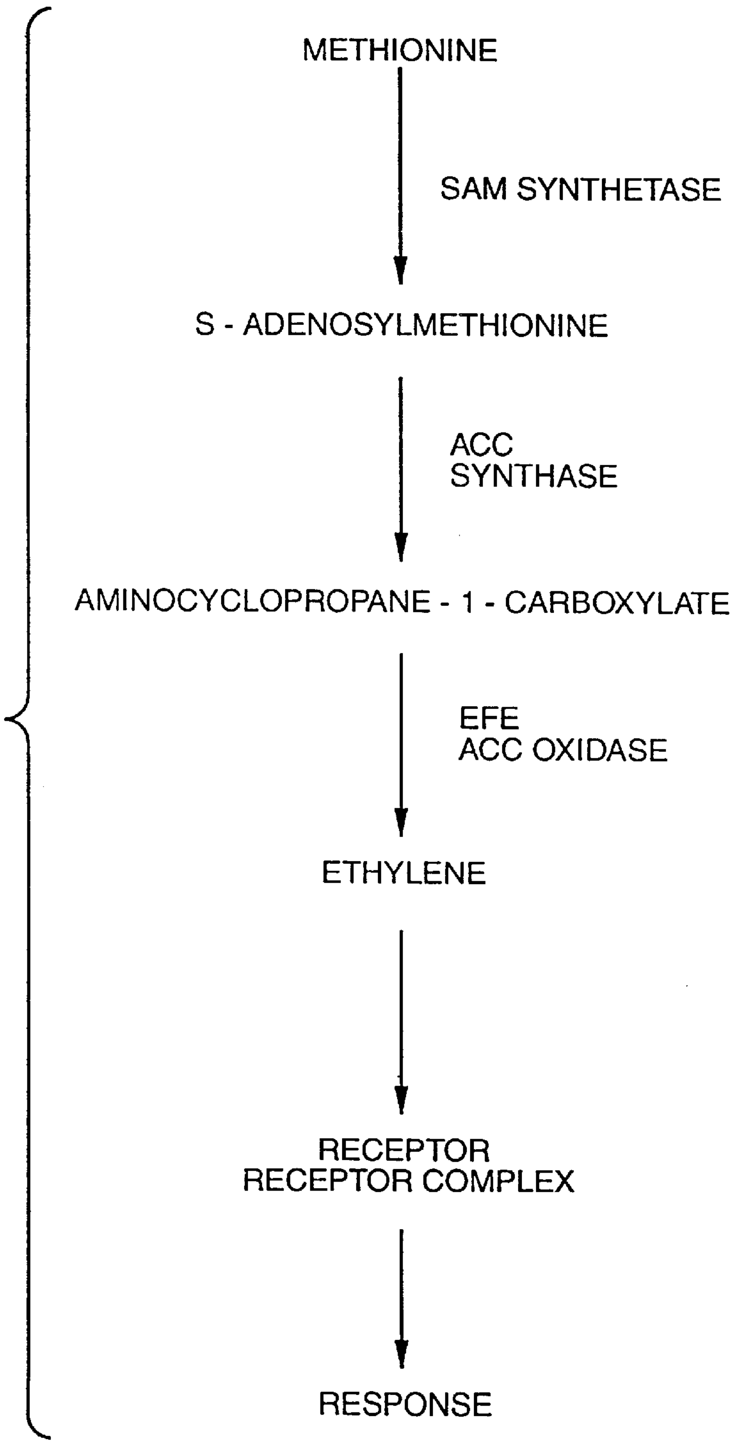
FIG. 1


METHIONINE
SAM SYNTHETASE
S - ADENOSYLMETHIONINE
ACC
SYNTHASE
AMINOCYCLOPROPANE - 1 - CARBOXYLATE
EFE
ACC OXIDASE
ETHYLENE
RECEPTOR
RECEPTOR COMPLEX
RESPONSE

AAAGATAGTA TTTGTTGATA AATATGGGGA TATTTATCCT ATATTATCTG 50
TATTTTTCTT ACCATTTTTA CTCTATTCCT TTATCTACAT TACGTCATTA 100
CACTATCATA AGATATTTGA ATGAACAAAT TCATGCACCC ACCAGCTATA 150
TTACCCTTTT TTATTAAAAA AAAACATCTG ATAATAATAA CAAAAAAATT 200
AGAGAAATGA CGTCGAAAAA AAAAGTAAGA ACGAAGAAGA AGTGTTAAAC 250
CCAACCAATT TTGACTTGAA AAAAAGCTTC AACGCTCCCC TTTTCTCCTT 300
CTCCGTCGCT CTCCGCCGCG TCCCAAATCC CCAATTCCTC CTCTTCTCCG 350
ATCAATTCTT CCCAAGTAAG CTTCTTCTTC CTCGATTCTC TCCTCAGATT 400
GTTTCGTGAC TTCTTTATAT ATATTCTTCA CTTCCACAGT TTTCTTCTGT 450
TGTTGTCGTC GATCTCAAAT CATAGAGATT GATTAACCTA ATTGGTCTTT 500
ATCTAGTGTA ATGCATCGTT ATTAGGAACT TTAAATTAAG ATTTAATCGT 550
TAATTTCATG ATTCGGATTC GAATTTTACT GTTCTCGAGA CTGAAATATG 600
CAACCTATTT TTTCGTAATC GTTGTGATCG AATTCGATTC TTCAGAATTT 650
ATAGCAATTT TGATGCTCAT GATCTGTCTA CGCTACGTTC TCGTCGTAAA 700
TCGAAGTTGA TAATGCTATG TGTTTGTTAC ACAGGTGTGT GTATGTGTGA 750
GAGAGGAACT ATAGTGTAAA AAATTCATAA TGGAAGTCTG CAATTGTATT 800
GAACCGCAAT GGCCAGCGGA TGAATTGTTA ATGAAATACC AATACATCTC 850
CGATTTCTTC ATTGCGATTG CGTATTTTTC GATTCCTCTT GAGTTGATTT 900
ACTTTGTGAA GAAATCAGCC GTGTTTCCGT ATAGATGGGT ACTTGTTCAG 950
TTTGGTGCTT TTATCGTTCT TTGTGGAGCA ACTCATCTTA TTAACTTATG 1000
GACTTTCACT ACGCATTCGA GAACCGTGGC GCTTGTGATG ACTACCGCGA 1050
AGGTGTTAAC CGCTGTTGTC TCGTGTGCTA CTGCGTTGAT GCTTGTTCAT 1100
ATTATTCCTG ATCTTTTGAG TGTTAAGACT CGGGAGCTTT TCTTGAAAAA 1150
TAAAGCTGCT GAGCTCGATA GAGAAATGGG ATTGATTCGA ACTCAGGAAG 1200
AAACCGGAAG GCATGTGAGA ATGTTGACTC ATGAGATTAG AAGCACTTTA 1250
GATAGACATA CTATTTTAAA GACTACACTT GTTGAGCTTG GTAGGACATT 1300
AGCTTTGGAG GAGTGTGCAT TGTGGATGCC TACTAGAACT GGGTTAGAGC 1350
TACAGCTTTC TTATACACTT CGTCATCAAC ATCCCGTGGA GTATACGGTT 1400
CCTATTCAAT TACCGGTGAT TAACCAAGTG TTTGGTACTA GTAGGGCTGT 1450
AAAAATATCT CCTAATTCTC CTGTGGCTAG GTTGAGACCT GTTTCTGGGA 1500
AATATATGCT AGGGGAGGTG GTCGCTGTGA GGGTTCCGCT TCTCCACCTT 1550

FIG. 2A

```
TCTAATTTTC AGATTAATGA CTGGCCTGAG CTTTCAACAA AGAGATATGC    1600
TTTGATGGTT TTGATGCTTC CTTCAGATAG TGCAAGGCAA TGGCATGTCC    1650
ATGAGTTGGA ACTCGTTGAA GTCGTCGCTG ATCAGGTTTT ACATTGCTGA    1700
GAATTTCTCT TCTTTGCTAT GTTCATGATC TTGTCTATAA CTTTTCTTCT    1750
CTTATTATAG GTGGCTGTAG CTCTCTCACA TGCTGCGATC CTAGAAGAGT    1800
CGATGCGAGC TAGGGACCTT CTCATGGAGC AGAATGTTGC TCTTGATCTA    1850
GCTAGACGAG AAGCAGAAAC AGCAATCCGT GCCCGCAATG ATTTCCTAGC    1900
GGTTATGAAC CATGAAATGC GAACACCGAT GCATGCGATT ATTGCACTCT    1950
CTTCCTTACT CCAAGAAACG GAACTAACCC CTGAACAAAG ACTGATGGTG    2000
GAAACAATAC TTAAAAGTAG TAACCTTTTG GCAACTTTGA TGAATGATGT    2050
CTTAGATCTT TCAAGGTTAG AAGATGGAAG TCTTCAACTT GAACTTGGGA    2100
CATTCAATCT TCATACATTA TTTAGAGAGG TAACTTTTGA ACAGCTCTAT    2150
GTTTCATAAG TTTATACTAT TTGTGTACTT GATTGTCATA TTGAATCTTG    2200
TTGCAGGTCC TCAATCTGAT AAAGCCTATA GCGGTTGTTA AGAAATTACC    2250
CATCACACTA AATCTTGCAC CAGATTTGCC AGAATTTGTT GTTGGGGATG    2300
AGAAACGGCT AATGCAGATA ATATTAAATA TAGTTGGTAA TGCTGTGAAA    2350
TTCTCCAAAC AAGGTAGTAT CTCCGTAACC GCTCTTGTCA CCAAGTCAGA    2400
CACACGAGCT GCTGACTTTT TTGTCGTGCC AACTGGGAGT CATTTCTACT    2450
TGAGAGTGAA GGTTATTATC TTGTATCTTG GGATCTTATA CCATAGCTGA    2500
AAGTATTTCT TAGGTCTTAA TTTTGATGAT TATTCAAATA TAGGTAAAAG    2550
ACTCTGGAGC AGGAATAAAT CCTCAAGACA TTCCAAAGAT TTTCACTAAA    2600
TTTGCTCAAA CACAATCTTT AGCGACGAGA AGCTCGGGTG GTAGTGGGCT    2650
TGGCCTCGCC ATCTCCAAGA GGTTTGAGCC TTATTAAAAG ACGTTTTTTT    2700
CCAACTTTTT CTTGTCTTCT GTGTTGTTAA AAGTTTACTC ATAAGCGTTT    2750
AATATGACAA GGTTTGTGAA TCTGATGGAG GGTAACATTT GGATTGAGAG    2800
CGATGGTCTT GGAAAAGGAT GCACGGCTAT CTTTGATGTT AAACTTGGGA    2850
TCTCAGAACG TTCAAACGAA TCTAAACAGT CGGGCATACC GAAAGTTCCA    2900
GCCATTCCCC GACATTCAAA TTTCACTGGA CTTAAGGTTC TTGTCATGGA    2950
TGAGAACGGG TTAGTATAAG CTTCTCACCT TTCTCTTTGC AAAATCTCTC    3000
GCCTTACTTC TTGCAAATGC AGATATTGGC GTTTAGAAAA AACGCAAATT    3050
TAATCTTATG AGAAACCGAT GATTATTTTG GTTGCAGGGT AAGTAGAATG    3100
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FIG. 2B

```
GTGACGAAGG GACTTCTTGT ACACCTTGGG TGCGAAGTGA CCACGGTGAG    3150
TTCAAACGAG GAGTGTCTCC GAGTTGTGTC CCATGAGCAC AAAGTGGTCT    3200
TCATGGACGT GTGCATGCCC GGGGTCGAAA ACTACCAAAT CGCTCTCCGT    3250
ATTCACGAGA AATTCACAAA ACAACGCCAC CAACGGCCAC TACTTGTGGC    3300
ACTCAGTGGT AACACTGACA AATCCACAAA AGAGAAATGC ATGAGCTTTG    3350
GTCTAGACGG TGTGTTGCTC AAACCCGTAT CACTAGACAA CATAAGAGAT    3400
GTTCTGTCTG ATCTTCTCGA GCCCCGGGTA CTGTACGAGG GCATGTAAAG    3450
GCGATGGATG CCCCATGCCC CAGAGGAGTA ATTCCGCTCC CGCCTTCTTC    3500
TCCCGTAAAA CATCGGAAGC TGATGTTCTC TGGTTTAATT GTGTACATAT    3550
CAGAGATTGT CGGAGCGTTT TGGATGATAT CTTAAAACAG AAAGGGAATA    3600
ACAAAATAGA AACTCTAAAC CGGTATGTGT CCGTGGCGAT TTCGGTTATA    3650
GAGGAACAAG ATGGTGGTGG TATAATCATA CCATTTCAGA TTACATGTTT    3700
GACTAATGTT GTATCCTTAT ATATGTAGTT ACATTCTTAT AAGAATTTGG    3750
ATCGAGTTAT GGATGCTTGT TGCGTGCATG TATGACATTG ATGCAGTATT    3800
ATGGCGTCAG CTTTGCGCCG CTTAGTAGAA CAACAACAAT GGCGTTACTT    3850
AGTTTCTCAA TCAACCCGAT CTCCAAAAC                           3879
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FIG. 2C

```
AGTAAGAACG AAGAAGAAGT GTTAAACCCA ACCAATTTTG ACTTGAAAAA      50

AAGCTTCAAC GCTCCCCTTT TCTCCTTCTC CGTCGCTCTC CGCCGCGTCC     100

CAAATCCCCA ATTCCTCCTC TTCTCCGATC AATTCTTCCC AAGTGTGTGT     150

ATGTGTGAGA GAGGAACTAT AGTGTAAAAA ATTCATA ATG GAA GTC TGC   199
                                         Met Glu Val Cys
                                          1

AAT TGT ATT GAA CCG CAA TGG CCA GCG GAT GAA TTG TTA ATG    241
Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu Leu Met
 5                   10                  15

AAA TAC CAA TAC ATC TCC GAT TTC TTC ATT GCG ATT GCG TAT    283
Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
     20                  25                  30

TTT TCG ATT CCT CTT GAG TTG ATT TAC TTT GTG AAG AAA TCA    325
Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
         35                  40                  45

GCC GTG TTT CCG TAT AGA TGG GTA CTT GTT CAG TTT GGT GCT    367
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala
             50                  55                  60

TTT ATC GTT CTT TGT GGA GCA ACT CAT CTT ATT AAC TTA TGG    409
Phe Ile Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp
                 65                  70

ACT TTC ACT ACG CAT TCG AGA ACC GTG GCG CTT GTG ATG ACT    451
Thr Phe Thr Thr His Ser Arg Thr Val Ala Leu Val Met Thr
75                  80                  85

ACC GCG AAG GTG TTA ACC GCT GTT GTC TCG TGT GCT ACT GCG    493
Thr Ala Lys Val Leu Thr Ala Val Val Ser Cys Ala Thr Ala
     90                  95                 100

TTG ATG CTT GTT CAT ATT ATT CCT GAT CTT TTG AGT GTT AAG    535
Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
        105                 110                 115

ACT CGG GAG CTT TTC TTG AAA AAT AAA GCT GCT GAG CTC GAT    577
Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp
            120                 125                 130

AGA GAA ATG GGA TTG ATT CGA ACT CAG GAA GAA ACC GGA AGG    619
Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
                135                 140

CAT GTG AGA ATG TTG ACT CAT GAG ATT AGA AGC ACT TTA GAT    661
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
145                 150                 155

AGA CAT ACT ATT TTA AAG ACT ACA CTT GTT GAG CTT GGT AGG    703
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg
    160                 165                 170

ACA TTA GCT TTG GAG GAG TGT GCA TTG TGG ATG CCT ACT AGA    745
Thr Leu Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg
        175                 180                 185
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FIG. 3A

```
ACT GGG TTA GAG CTA CAG CTT TCT TAT ACA CTT CGT CAT CAA       787
Thr Gly Leu Glu Leu Gln Leu Ser Tyr Thr Leu Arg His Gln
            190                 195                 200

CAT CCC GTG GAG TAT ACG GTT CCT ATT CAA TTA CCG GTG ATT       829
His Pro Val Glu Tyr Thr Val Pro Ile Gln Leu Pro Val Ile
                205                 210

AAC CAA GTG TTT GGT ACT AGT AGG GCT GTA AAA ATA TCT CCT       871
Asn Gln Val Phe Gly Thr Ser Arg Ala Val Lys Ile Ser Pro
215                 220                 225

AAT TCT CCT GTG GCT AGG TTG AGA CCT GTT TCT GGG AAA TAT       913
Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly Lys Tyr
    230                 235                 240

ATG CTA GGG GAG GTG GTC GCT GTG AGG GTT CCG CTT CTC CAC       955
Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
        245                 250                 255

CTT TCT AAT TTT CAG ATT AAT GAC TGG CCT GAG CTT TCA ACA       997
Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
            260                 265                 270

AAG AGA TAT GCT TTG ATG GTT TTG ATG CTT CCT TCA GAT AGT      1039
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser
                275                 280

GCA AGG CAA TGG CAT GTC CAT GAG TTG GAA CTC GTT GAA GTC      1081
Ala Arg Gln Trp His Val His Glu Leu Glu Leu Val Glu Val
285                 290                 295

GTC GCT GAT CAG GTG GCT GTA GCT CTC TCA CAT GCT GCG ATC      1123
Val Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile
    300                 305                 310

CTA GAA GAG TCG ATG CGA GCT AGG GAC CTT CTC ATG GAG CAG      1165
Leu Glu Glu Ser Met Arg Ala Arg Asp Leu Leu Met Glu Gln
        315                 320                 325

AAT GTT GCT CTT GAT CTA GCT AGA CGA GAA GCA GAA ACA GCA      1207
Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala Glu Thr Ala
            330                 335                 340

ATC CGT GCC CGC AAT GAT TTC CTA GCG GTT ATG AAC CAT GAA      1249
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu
                345                 350

ATG CGA ACA CCG ATG CAT GCG ATT ATT GCA CTC TCT TCC TTA      1291
Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
355                 360                 365

CTC CAA GAA ACG GAA CTA ACC CCT GAA CAA AGA CTG ATG GTG      1333
Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
    370                 375                 380

GAA ACA ATA CTT AAA AGT AGT AAC CTT TTG GCA ACT TTG ATG      1375
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met
        385                 390                 395
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FIG. 3B

```
AAT GAT GTC TTA GAT CTT TCA AGG TTA GAA GAT GGA AGT CTT     1417
Asn Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu
            400                 405                 410

CAA CTT GAA CTT GGG ACA TTC AAT CTT CAT ACA TTA TTT AGA     1459
Gln Leu Glu Leu Gly Thr Phe Asn Leu His Thr Leu Phe Arg
                415                 420

GAG GTC CTC AAT CTG ATA AAG CCT ATA GCG GTT GTT AAG AAA     1501
Glu Val Leu Asn Leu Ile Lys Pro Ile Ala Val Val Lys Lys
425                 430                 435

TTA CCC ATC ACA CTA AAT CTT GCA CCA GAT TTG CCA GAA TTT     1543
Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu Pro Glu Phe
    440                 445                 450

GTT GTT GGG GAT GAG AAA CGG CTA ATG CAG ATA ATA TTA AAT     1585
Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu Asn
        455                 460                 465

ATA GTT GGT AAT GCT GTG AAA TTC TCC AAA CAA GGT AGT ATC     1621
Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
            470                 475                 480

TCC GTA ACC GCT CTT GTC ACC AAG TCA GAC ACA CGA GCT GCT     1669
Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
                485                 490

GAC TTT TTT GTC GTG CCA ACT GGG AGT CAT TTC TAC TTG AGA     1711
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg
495                 500                 505

GTG AAG GTA AAA GAC TCT GGA GCA GGA ATA AAT CCT CAA GAC     1753
Val Lys Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp
    510                 515                 520

ATT CCA AAG ATT TTC ACT AAA TTT GCT CAA ACA CAA TCT TTA     1795
Ile Pro Lys Ile Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu
        525                 530                 535

GCG ACG AGA AGC TCG GGT GGT AGT GGG CTT GGC CTC GCC ATC     1837
Ala Thr Arg Ser Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
            540                 545                 550

TCC AAG AGG TTT GTG AAT CTG ATG GAG GGT AAC ATT TGG ATT     1879
Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn Ile Trp Ile
                555                 560

GAG AGC GAT GGT CTT GGA AAA GGA TGC ACG GCT ATC TTT GAT     1921
Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile Phe Asp
565                 570                 575

GTT AAA CTT GGG ATC TCA GAA CGT TCA AAC GAA TCT AAA CAG     1963
Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
    580                 585                 590

TCG GGC ATA CCG AAA GTT CCA GCC ATT CCC CGA CAT TCA AAT     2005
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
        595                 600                 605
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FIG. 3C

```
TTC ACT GGA CTT AAG GTT CTT GTC ATG GAT GAG AAC GGG GTA      2047
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val
            610                 615                 620

AGT AGA ATG GTG ACG AAG GGA CTT CTT GTA CAC CTT GGG TGC      2089
Ser Arg Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys
                625                 630

GAA GTG ACC ACG GTG AGT TCA AAC GAG GAG TGT CTC CGA GTT      2131
Glu Val Thr Thr Val Ser Ser Asn Glu Glu Cys Leu Arg Val
635                 640                 645

GTG TCC CAT GAG CAC AAA GTG GTC TTC ATG GAC GTG TGC ATG      2173
Val Ser His Glu His Lys Val Val Phe Met Asp Val Cys Met
    650                 655                 660

CCC GGG GTC GAA AAC TAC CAA ATC GCT CTC CGT ATT CAC GAG      2215
Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg Ile His Glu
        665                 670                 675

AAA TTC ACA AAA CAA CGC CAC CAA CGG CCA CTA CTT GTG GCA      2257
Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val Ala
            680                 685                 690

CTC AGT GGT AAC ACT GAC AAA TCC ACA AAA GAG AAA TGC ATG      2299
Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
                695                 700

AGC TTT GGT CTA GAC GGT GTG TTG CTC AAA CCC GTA TCA CTA      2341
Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
705                 710                 715

GAC AAC ATA AGA GAT GTT CTG TCT GAT CTT CTC GAG CCC CGG      2383
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg
    720                 725                 730

GTA CTG TAC GAG GGC ATG TAAAGGCGAT GGATGCCCCA                2421
Val Leu Tyr Glu Gly Met
        735

TGCCCCAGAG GAGTAATTCC GCTCCCGCCT TCTTCTCCCG TAAAACATCG       2471

GAAGCTGATG TTCTCTGGTT TAATTGTGTA CATATCAGAG ATTGTCGGAG       2521

CGTTTTGGAT GATATCTTAA AACAGAAAGG GAATAACAAA ATAGAAACTC       2571

TAAACCGGTA TGTGTCCGTG GCGATTTCGG TTATAGAGGA ACAAGATGGT       2621

GGTGGTATAA TCATACCATT TCAGATTACA TGTTTGACTA ATGTTGTATC       2671

CTTATATATG TAGTTACATT CTTATAAGAA TTTGGATCGA GTTATGGATG       2721

CTTGTTGCGT GCATGTATGA CATTGATGCA GTATTATGGC GTCAGCTTTG       2771

CGCCGCTTAG TAGAAC                                            2787
```

FIG. 3D

```
AGTAAGAACG AAGAAGAAGT GTTAAACCCA ACCAATTTTG ACTTGAAAAA        50

AAGCTTCAAC GCTCCCCTTT TCTCCTTCTC CGTCGCTCTC CGCCGCGTCC       100

CAAATCCCCA ATTCCTCCTC TTCTCCGATC AATTCTTCCC AAGTGTGTGT       150

ATGTGTGAGA GAGGAACTAT AGTGTAAAAA ATTCATA ATG GAA GTC TGC     199
                                        Met Glu Val Cys
                                         1

AAT TGT ATT GAA CCG CAA TGG CCA GCG GAT GAA TTG TTA ATG      241
Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu Leu Met
 5                   10                  15

AAA TAC CAA TAC ATC TCC GAT TTC TTC ATT GCG ATT GTG TAT      283
Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Val Tyr
     20                  25                  30

TTT TCG ATT CCT CTT GAG TTG ATT TAC TTT GTG AAG AAA TCA      325
Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
         35                  40                  45

GCC GTG TTT CCG TAT AGA TGG GTA CTT GTT CAG TTT GGT GCT      367
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala
             50                  55                  60

TTT ATC GTT CTT TGT GGA GCA ACT CAT CTT ATT AAC TTA TGG      409
Phe Ile Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp
                 65                  70

ACT TTC ACT ACG CAT TCG AGA ACC GTG GCG CTT GTG ATG ACT      451
Thr Phe Thr Thr His Ser Arg Thr Val Ala Leu Val Met Thr
75                  80                  85

ACC GCG AAG GTG TTA ACC GCT GTT GTC TCG TGT GCT ACT GCG      493
Thr Ala Lys Val Leu Thr Ala Val Val Ser Cys Ala Thr Ala
     90                  95                 100

TTG ATG CTT GTT CAT ATT ATT CCT GAT CTT TTG AGT GTT AAG      535
Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
        105                 110                 115

ACT CGG GAG CTT TTC TTG AAA AAT AAA GCT GCT GAG CTC GAT      577
Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp
            120                 125                 130

AGA GAA ATG GGA TTG ATT CGA ACT CAG GAA GAA ACC GGA AGG      619
Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
                135                 140

CAT GTG AGA ATG TTG ACT CAT GAG ATT AGA AGC ACT TTA GAT      661
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
145                 150                 155

AGA CAT ACT ATT TTA AAG ACT ACA CTT GTT GAG CTT GGT AGG      703
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg
    160                 165                 170

ACA TTA GCT TTG GAG GAG TGT GCA TTG TGG ATG CCT ACT AGA      745
Thr Leu Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg
        175                 180                 185
```

FIG. 4A

```
ACT GGG TTA GAG CTA CAG CTT TCT TAT ACA CTT CGT CAT CAA       787
Thr Gly Leu Glu Leu Gln Leu Ser Tyr Thr Leu Arg His Gln
            190                 195                 200

CAT CCC GTG GAG TAT ACG GTT CCT ATT CAA TTA CCG GTG ATT       829
His Pro Val Glu Tyr Thr Val Pro Ile Gln Leu Pro Val Ile
                205                 210

AAC CAA GTG TTT GGT ACT AGT AGG GCT GTA AAA ATA TCT CCT       871
Asn Gln Val Phe Gly Thr Ser Arg Ala Val Lys Ile Ser Pro
215                 220                 225

AAT TCT CCT GTG GCT AGG TTG AGA CCT GTT TCT GGG AAA TAT       913
Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly Lys Tyr
    230                 235                 240

ATG CTA GGG GAG GTG GTC GCT GTG AGG GTT CCG CTT CTC CAC       955
Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
        245                 250                 255

CTT TCT AAT TTT CAG ATT AAT GAC TGG CCT GAG CTT TCA ACA       997
Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
            260                 265                 270

AAG AGA TAT GCT TTG ATG GTT TTG ATG CTT CCT TCA GAT AGT      1039
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser
                275                 280

GCA AGG CAA TGG CAT GTC CAT GAG TTG GAA CTC GTT GAA GTC      1081
Ala Arg Gln Trp His Val His Glu Leu Glu Leu Val Glu Val
285                 290                 295

GTC GCT GAT CAG GTG GCT GTA GCT CTC TCA CAT GCT GCG ATC      1123
Val Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile
    300                 305                 310

CTA GAA GAG TCG ATG CGA GCT AGG GAC CTT CTC ATG GAG CAG      1165
Leu Glu Glu Ser Met Arg Ala Arg Asp Leu Leu Met Glu Gln
        315                 320                 325

AAT GTT GCT CTT GAT CTA GCT AGA CGA GAA GCA GAA ACA GCA      1207
Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala Glu Thr Ala
            330                 335                 340

ATC CGT GCC CGC AAT GAT TTC CTA GCG GTT ATG AAC CAT GAA      1249
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu
                345                 350

ATG CGA ACA CCG ATG CAT GCG ATT ATT GCA CTC TCT TCC TTA      1291
Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
355                 360                 365

CTC CAA GAA ACG GAA CTA ACC CCT GAA CAA AGA CTG ATG GTG      1333
Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
    370                 375                 380

GAA ACA ATA CTT AAA AGT AGT AAC CTT TTG GCA ACT TTG ATG      1375
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met
        385                 390                 395
```

FIG. 4B

```
AAT GAT GTC TTA GAT CTT TCA AGG TTA GAA GAT GGA AGT CTT   1417
Asn Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu
            400                 405                 410

CAA CTT GAA CTT GGG ACA TTC AAT CTT CAT ACA TTA TTT AGA   1459
Gln Leu Glu Leu Gly Thr Phe Asn Leu His Thr Leu Phe Arg
                415                 420

GAG GTC CTC AAT CTG ATA AAG CCT ATA GCG GTT GTT AAG AAA   1501
Glu Val Leu Asn Leu Ile Lys Pro Ile Ala Val Val Lys Lys
425                 430                 435

TTA CCC ATC ACA CTA AAT CTT GCA CCA GAT TTG CCA GAA TTT   1543
Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu Pro Glu Phe
    440                 445                 450

GTT GTT GGG GAT GAG AAA CGG CTA ATG CAG ATA ATA TTA AAT   1585
Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu Asn
        455                 460                 465

ATA GTT GGT AAT GCT GTG AAA TTC TCC AAA CAA GGT AGT ATC   1627
Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
            470                 475                 480

TCC GTA ACC GCT CTT GTC ACC AAG TCA GAC ACA CGA GCT GCT   1669
Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
                485                 490

GAC TTT TTT GTC GTG CCA ACT GGG AGT CAT TTC TAC TTG AGA   1711
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg
495                 500                 505

GTG AAG GTA AAA GAC TCT GGA GCA GGA ATA AAT CCT CAA GAC   1753
Val Lys Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp
    510                 515                 520

ATT CCA AAG ATT TTC ACT AAA TTT GCT CAA ACA CAA TCT TTA   1795
Ile Pro Lys Ile Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu
        525                 530                 535

GCG ACG AGA AGC TCG GGT GGT AGT GGG CTT GGC CTC GCC ATC   1837
Ala Thr Arg Ser Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
            540                 545                 550

TCC AAG AGG TTT GTG AAT CTG ATG GAG GGT AAC ATT TGG ATT   1879
Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn Ile Trp Ile
                555                 560

GAG AGC GAT GGT CTT GGA AAA GGA TGC ACG GCT ATC TTT GAT   1921
Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile Phe Asp
565                 570                 575

GTT AAA CTT GGG ATC TCA GAA CGT TCA AAC GAA TCT AAA CAG   1963
Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
    580                 585                 590

TCG GGC ATA CCG AAA GTT CCA GCC ATT CCC CGA CAT TCA AAT   2005
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
        595                 600                 605
```

FIG. 4C

```
TTC ACT GGA CTT AAG GTT CTT GTC ATG GAT GAG AAC GGG GTA     2047
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val
            610                 615                 620

AGT AGA ATG GTG ACG AAG GGA CTT CTT GTA CAC CTT GGG TGC     2089
Ser Arg Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys
                625                 630

GAA GTG ACC ACG GTG AGT TCA AAC GAG GAG TGT CTC CGA GTT     2131
Glu Val Thr Thr Val Ser Ser Asn Glu Glu Cys Leu Arg Val
635                 640                 645

GTG TCC CAT GAG CAC AAA GTG GTC TTC ATG GAC GTG TGC ATG     2173
Val Ser His Glu His Lys Val Val Phe Met Asp Val Cys Met
    650                 655                 660

CCC GGG GTC GAA AAC TAC CAA ATC GCT CTC CGT ATT CAC GAG     2215
Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg Ile His Glu
        665                 670                 675

AAA TTC ACA AAA CAA CGC CAC CAA CGG CCA CTA CTT GTG GCA     2257
Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val Ala
            680                 685                 690

CTC AGT GGT AAC ACT GAC AAA TCC ACA AAA GAG AAA TGC ATG     2299
Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
                695                 700

AGC TTT GGT CTA GAC GGT GTG TTG CTC AAA CCC GTA TCA CTA     2341
Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
705                 710                 715

GAC AAC ATA AGA GAT GTT CTG TCT GAT CTT CTC GAG CCC CGG     2383
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg
    720                 725                 730

GTA CTG TAC GAG GGC ATG TAAAGGCGAT GGATGCCCCA               2421
Val Leu Tyr Glu Gly Met
        735

TGCCCCAGAG GAGTAATTCC GCTCCCGCCT TCTTCTCCCG TAAAACATCG      2471

GAAGCTGATG TTCTCTGGTT TAATTGTGTA CATATCAGAG ATTGTCGGAG      2521

CGTTTTGGAT GATATCTTAA AACAGAAAGG GAATAACAAA ATAGAAACTC      2571

TAAACCGGTA TGTGTCCGTG GCGATTTCGG TTATAGAGGA ACAAGATGGT      2621

GGTGGTATAA TCATACCATT TCAGATTACA TGTTTGACTA ATGTTGTATC      2671

CTTATATATG TAGTTACATT CTTATAAGAA TTTGGATCGA GTTATGGATG      2721

CTTGTTGCGT GCATGTATGA CATTGATGCA GTATTATGGC GTCAGCTTTG      2771

CGCCGCTTAG TAGAAC                                           2787
```

FIG. 4D

```
AGTAAGAACG AAGAAGAAGT GTTAAACCCA ACCAATTTTG ACTTGAAAAA    50

AAGCTTCAAC GCTCCCCTTT TCTCCTTCTC CGTCGCTCTC CGCCGCGTCC   100

CAAATCCCCA ATTCCTCCTC TTCTCCGATC AATTCTTCCC AAGTGTGTGT   150

ATGTGTGAGA GAGGAACTAT AGTGTAAAAA ATTCATA ATG GAA GTC TGC   199
                                         Met Glu Val Cys
                                          1

AAT TGT ATT GAA CCG CAA TGG CCA GCG GAT GAA TTG TTA ATG   241
Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu Leu Met
 5                   10                  15

AAA TAC CAA TAC ATC TCC GAT TTC TTC ATT GCG ATT GCG TAT   283
Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
     20                  25                  30

TTT TCG ATT CCT CTT GAG TTG ATT TAC TTT GTG AAG AAA TCA   325
Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
         35                  40                  45

GCC GTG TTT CCG TAT AGA TGG GTA CTT GTT CAG TTT GGT GCT   367
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala
             50                  55                  60

TTT TTC GTT CTT TGT GGA GCA ACT CAT CTT ATT AAC TTA TGG   409
Phe Phe Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp
                 65                  70

ACT TTC ACT ACG CAT TCG AGA ACC GTG GCG CTT GTG ATG ACT   451
Thr Phe Thr Thr His Ser Arg Thr Val Ala Leu Val Met Thr
 75                  80                  85

ACC GCG AAG GTG TTA ACC GCT GTT GTC TCG TGT GCT ACT GCG   493
Thr Ala Lys Val Leu Thr Ala Val Val Ser Cys Ala Thr Ala
     90                  95                 100

TTG ATG CTT GTT CAT ATT ATT CCT GAT CTT TTG AGT GTT AAG   535
Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
        105                 110                 115

ACT CGG GAG CTT TTC TTG AAA AAT AAA GCT GCT GAG CTC GAT   577
Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp
            120                 125                 130

AGA GAA ATG GGA TTG ATT CGA ACT CAG GAA GAA ACC GGA AGG   619
Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
                135                 140

CAT GTG AGA ATG TTG ACT CAT GAG ATT AGA AGC ACT TTA GAT   661
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
145                 150                 155

AGA CAT ACT ATT TTA AAG ACT ACA CTT GTT GAG CTT GGT AGG   703
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg
    160                 165                 170

ACA TTA GCT TTG GAG GAG TGT GCA TTG TGG ATG CCT ACT AGA   745
Thr Leu Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg
        175                 180                 185
```

FIG. 5A

```
ACT GGG TTA GAG CTA CAG CTT TCT TAT ACA CTT CGT CAT CAA       787
Thr Gly Leu Glu Leu Gln Leu Ser Tyr Thr Leu Arg His Gln
            190                 195                 200

CAT CCC GTG GAG TAT ACG GTT CCT ATT CAA TTA CCG GTG ATT       829
His Pro Val Glu Tyr Thr Val Pro Ile Gln Leu Pro Val Ile
                205                 210

AAC CAA GTG TTT GGT ACT AGT AGG GCT GTA AAA ATA TCT CCT       871
Asn Gln Val Phe Gly Thr Ser Arg Ala Val Lys Ile Ser Pro
215                 220                 225

AAT TCT CCT GTG GCT AGG TTG AGA CCT GTT TCT GGG AAA TAT       913
Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly Lys Tyr
    230                 235                 240

ATG CTA GGG GAG GTG GTC GCT GTG AGG GTT CCG CTT CTC CAC       955
Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
        245                 250                 255

CTT TCT AAT TTT CAG ATT AAT GAC TGG CCT GAG CTT TCA ACA       997
Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
            260                 265                 270

AAG AGA TAT GCT TTG ATG GTT TTG ATG CTT CCT TCA GAT AGT      1039
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser
                275                 280

GCA AGG CAA TGG CAT GTC CAT GAG TTG GAA CTC GTT GAA GTC      1081
Ala Arg Gln Trp His Val His Glu Leu Glu Leu Val Glu Val
285                 290                 295

GTC GCT GAT CAG GTG GCT GTA GCT CTC TCA CAT GCT GCG ATC      1123
Val Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile
    300                 305                 310

CTA GAA GAG TCG ATG CGA GCT AGG GAC CTT CTC ATG GAG CAG      1165
Leu Glu Glu Ser Met Arg Ala Arg Asp Leu Leu Met Glu Gln
        315                 320                 325

AAT GTT GCT CTT GAT CTA GCT AGA CGA GAA GCA GAA ACA GCA      1207
Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala Glu Thr Ala
            330                 335                 340

ATC CGT GCC CGC AAT GAT TTC CTA GCG GTT ATG AAC CAT GAA      1249
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu
                345                 350

ATG CGA ACA CCG ATG CAT GCG ATT ATT GCA CTC TCT TCC TTA      1291
Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
355                 360                 365

CTC CAA GAA ACG GAA CTA ACC CCT GAA CAA AGA CTG ATG GTG      1333
Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
    370                 375                 380

GAA ACA ATA CTT AAA AGT AGT AAC CTT TTG GCA ACT TTG ATG      1375
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met
        385                 390                 395
```

FIG. 5B

```
AAT GAT GTC TTA GAT CTT TCA AGG TTA GAA GAT GGA AGT CTT   1417
Asn Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu
            400                 405                 410

CAA CTT GAA CTT GGG ACA TTC AAT CTT CAT ACA TTA TTT AGA   1459
Gln Leu Glu Leu Gly Thr Phe Asn Leu His Thr Leu Phe Arg
                415                 420

GAG GTC CTC AAT CTG ATA AAG CCT ATA GCG GTT GTT AAG AAA   1501
Glu Val Leu Asn Leu Ile Lys Pro Ile Ala Val Val Lys Lys
425                 430                 435

TTA CCC ATC ACA CTA AAT CTT GCA CCA GAT TTG CCA GAA TTT   1543
Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu Pro Glu Phe
    440                 445                 450

GTT GTT GGG GAT GAG AAA CGG CTA ATG CAG ATA ATA TTA AAT   1585
Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu Asn
        455                 460                 465

ATA GTT GGT AAT GCT GTG AAA TTC TCC AAA CAA GGT AGT ATC   1627
Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
            470                 475                 480

TCC GTA ACC GCT CTT GTC ACC AAG TCA GAC ACA CGA GCT GCT   1669
Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
                485                 490

GAC TTT TTT GTC GTG CCA ACT GGG AGT CAT TTC TAC TTG AGA   1711
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg
495                 500                 505

GTG AAG GTA AAA GAC TCT GGA GCA GGA ATA AAT CCT CAA GAC   1753
Val Lys Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp
    510                 515                 520

ATT CCA AAG ATT TTC ACT AAA TTT GCT CAA ACA CAA TCT TTA   1795
Ile Pro Lys Ile Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu
        525                 530                 535

GCG ACG AGA AGC TCG GGT GGT AGT GGG CTT GGC CTC GCC ATC   1837
Ala Thr Arg Ser Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
            540                 545                 550

TCC AAG AGG TTT GTG AAT CTG ATG GAG GGT AAC ATT TGG ATT   1879
Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn Ile Trp Ile
                555                 560

GAG AGC GAT GGT CTT GGA AAA GGA TGC ACG GCT ATC TTT GAT   1921
Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile Phe Asp
565                 570                 575

GTT AAA CTT GGG ATC TCA GAA CGT TCA AAC GAA TCT AAA CAG   1963
Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
    580                 585                 590

TCG GGC ATA CCG AAA GTT CCA GCC ATT CCC CGA CAT TCA AAT   2005
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
        595                 600                 605
```

FIG. 5C

```
TTC ACT GGA CTT AAG GTT CTT GTC ATG GAT GAG AAC GGG GTA     2047
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val
            610                 615                 620

AGT AGA ATG GTG ACG AAG GGA CTT CTT GTA CAC CTT GGG TGC     2089
Ser Arg Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys
                625                 630

GAA GTG ACC ACG GTG AGT TCA AAC GAG GAG TGT CTC CGA GTT     2131
Glu Val Thr Thr Val Ser Ser Asn Glu Glu Cys Leu Arg Val
635                 640                 645

GTG TCC CAT GAG CAC AAA GTG GTC TTC ATG GAC GTG TGC ATG     2173
Val Ser His Glu His Lys Val Val Phe Met Asp Val Cys Met
    650                 655                 660

CCC GGG GTC GAA AAC TAC CAA ATC GCT CTC CGT ATT CAC GAG     2215
Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg Ile His Glu
        665                 670                 675

AAA TTC ACA AAA CAA CGC CAC CAA CGG CCA CTA CTT GTG GCA     2257
Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val Ala
            680                 685                 690

CTC AGT GGT AAC ACT GAC AAA TCC ACA AAA GAG AAA TGC ATG     2299
Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
                695                 700

AGC TTT GGT CTA GAC GGT GTG TTG CTC AAA CCC GTA TCA CTA     2341
Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
705                 710                 715

GAC AAC ATA AGA GAT GTT CTG TCT GAT CTT CTC GAG CCC CGG     2383
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg
    720                 725                 730

GTA CTG TAC GAG GGC ATG TAAAGGCGAT GGATGCCCCA               2421
Val Leu Tyr Glu Gly Met
        735

TGCCCCAGAG GAGTAATTCC GCTCCCGCCT TCTTCTCCCG TAAAACATCG      2471

GAAGCTGATG TTCTCTGGTT TAATTGTGTA CATATCAGAG ATTGTCGGAG      2521

CGTTTTGGAT GATATCTTAA AACAGAAAGG GAATAACAAA ATAGAAACTC      2571

TAAACCGGTA TGTGTCCGTG GCGATTTCGG TTATAGAGGA ACAAGATGGT      2621

GGTGGTATAA TCATACCATT TCAGATTACA TGTTTGACTA ATGTTGTATC      2671

CTTATATATG TAGTTACATT CTTATAAGAA TTTGGATCGA GTTATGGATG      2721

CTTGTTGCGT GCATGTATGA CATTGATGCA GTATTATGGC GTCAGCTTTG      2771

CGCCGCTTAG TAGAAC                                           2787
```

FIG. 5D

```
AGTAAGAACG AAGAAGAAGT GTTAAACCCA ACCAATTTTG ACTTGAAAAA         50

AAGCTTCAAC GCTCCCCTTT TCTCCTTCTC CGTCGCTCTC CGCCGCGTCC        100

CAAATCCCCA ATTCCTCCTC TTCTCCGATC AATTCTTCCC AAGTGTGTGT        150

ATGTGTGAGA GAGGAACTAT AGTGTAAAAA ATTCATA ATG GAA GTC TGC      199
                                         Met Glu Val Cys
                                           1

AAT TGT ATT GAA CCG CAA TGG CCA GCG GAT GAA TTG TTA ATG       241
Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu Leu Met
  5                  10                  15

AAA TAC CAA TAC ATC TCC GAT TTC TTC ATT GCG ATT GCG TAT       283
Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
     20                  25                  30

TTT TCG ATT CCT CTT GAG TTG ATT TAC TTT GTG AAG AAA TCA       325
Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
         35                  40                  45

GCC GTG TTT CCG TAT AGA TGG GTA CTT GTT CAG TTT GGT GCT       367
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala
             50                  55                  60

TTT ATC GTT CTT TAT GGA GCA ACT CAT CTT ATT AAC TTA TGG       409
Phe Ile Val Leu Tyr Gly Ala Thr His Leu Ile Asn Leu Trp
                 65                  70

ACT TTC ACT ACG CAT TCG AGA ACC GTG GCG CTT GTG ATG ACT       451
Thr Phe Thr Thr His Ser Arg Thr Val Ala Leu Val Met Thr
 75                  80                  85

ACC GCG AAG GTG TTA ACC GCT GTT GTC TCG TGT GCT ACT GCG       493
Thr Ala Lys Val Leu Thr Ala Val Val Ser Cys Ala Thr Ala
     90                  95                 100

TTG ATG CTT GTT CAT ATT ATT CCT GAT CTT TTG AGT GTT AAG       535
Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
        105                 110                 115

ACT CGG GAG CTT TTC TTG AAA AAT AAA GCT GCT GAG CTC GAT       577
Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp
            120                 125                 130

AGA GAA ATG GGA TTG ATT CGA ACT CAG GAA GAA ACC GGA AGG       619
Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
                135                 140

CAT GTG AGA ATG TTG ACT CAT GAG ATT AGA AGC ACT TTA GAT       661
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
145                 150                 155

AGA CAT ACT ATT TTA AAG ACT ACA CTT GTT GAG CTT GGT AGG       703
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg
    160                 165                 170

ACA TTA GCT TTG GAG GAG TGT GCA TTG TGG ATG CCT ACT AGA       745
Thr Leu Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg
        175                 180                 185
```

FIG. 6A

```
ACT GGG TTA GAG CTA CAG CTT TCT TAT ACA CTT CGT CAT CAA      787
Thr Gly Leu Glu Leu Gln Leu Ser Tyr Thr Leu Arg His Gln
            190                 195                 200

CAT CCC GTG GAG TAT ACG GTT CCT ATT CAA TTA CCG GTG ATT      829
His Pro Val Glu Tyr Thr Val Pro Ile Gln Leu Pro Val Ile
                205                 210

AAC CAA GTG TTT GGT ACT AGT AGG GCT GTA AAA ATA TCT CCT      871
Asn Gln Val Phe Gly Thr Ser Arg Ala Val Lys Ile Ser Pro
215                 220                 225

AAT TCT CCT GTG GCT AGG TTG AGA CCT GTT TCT GGG AAA TAT      913
Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly Lys Tyr
    230                 235                 240

ATG CTA GGG GAG GTG GTC GCT GTG AGG GTT CCG CTT CTC CAC      955
Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
        245                 250                 255

CTT TCT AAT TTT CAG ATT AAT GAC TGG CCT GAG CTT TCA ACA      997
Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
            260                 265                 270

AAG AGA TAT GCT TTG ATG GTT TTG ATG CTT CCT TCA GAT AGT     1039
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser
                275                 280

GCA AGG CAA TGG CAT GTC CAT GAG TTG GAA CTC GTT GAA GTC     1081
Ala Arg Gln Trp His Val His Glu Leu Glu Leu Val Glu Val
285                 290                 295

GTC GCT GAT CAG GTG GCT GTA GCT CTC TCA CAT GCT GCG ATC     1123
Val Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile
    300                 305                 310

CTA GAA GAG TCG ATG CGA GCT AGG GAC CTT CTC ATG GAG CAG     1165
Leu Glu Glu Ser Met Arg Ala Arg Asp Leu Leu Met Glu Gln
        315                 320                 325

AAT GTT GCT CTT GAT CTA GCT AGA CGA GAA GCA GAA ACA GCA     1207
Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala Glu Thr Ala
            330                 335                 340

ATC CGT GCC CGC AAT GAT TTC CTA GCG GTT ATG AAC CAT GAA     1249
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu
                345                 350

ATG CGA ACA CCG ATG CAT GCG ATT ATT GCA CTC TCT TCC TTA     1291
Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
355                 360                 365

CTC CAA GAA ACG GAA CTA ACC CCT GAA CAA AGA CTG ATG GTG     1333
Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
    370                 375                 380

GAA ACA ATA CTT AAA AGT AGT AAC CTT TTG GCA ACT TTG ATG     1375
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met
        385                 390                 395
```

FIG. 6B

```
AAT GAT GTC TTA GAT CTT TCA AGG TTA GAA GAT GGA AGT CTT   1417
Asn Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu
            400                 405                 410

CAA CTT GAA CTT GGG ACA TTC AAT CTT CAT ACA TTA TTT AGA   1459
Gln Leu Glu Leu Gly Thr Phe Asn Leu His Thr Leu Phe Arg
                415                 420

GAG GTC CTC AAT CTG ATA AAG CCT ATA GCG GTT GTT AAG AAA   1501
Glu Val Leu Asn Leu Ile Lys Pro Ile Ala Val Val Lys Lys
425                 430                 435

TTA CCC ATC ACA CTA AAT CTT GCA CCA GAT TTG CCA GAA TTT   1543
Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu Pro Glu Phe
    440                 445                 450

GTT GTT GGG GAT GAG AAA CGG CTA ATG CAG ATA ATA TTA AAT   1585
Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu Asn
        455                 460                 465

ATA GTT GGT AAT GCT GTG AAA TTC TCC AAA CAA GGT AGT ATC   1627
Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
            470                 475                 480

TCC GTA ACC GCT CTT GTC ACC AAG TCA GAC ACA CGA GCT GCT   1669
Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
                485                 490

GAC TTT TTT GTC GTG CCA ACT GGG AGT CAT TTC TAC TTG AGA   1711
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg
495                 500                 505

GTG AAG GTA AAA GAC TCT GGA GCA GGA ATA AAT CCT CAA GAC   1753
Val Lys Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp
    510                 515                 520

ATT CCA AAG ATT TTC ACT AAA TTT GCT CAA ACA CAA TCT TTA   1795
Ile Pro Lys Ile Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu
        525                 530                 535

GCG ACG AGA AGC TCG GGT GGT AGT GGG CTT GGC CTC GCC ATC   1837
Ala Thr Arg Ser Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
            540                 545                 550

TCC AAG AGG TTT GTG AAT CTG ATG GAG GGT AAC ATT TGG ATT   1879
Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn Ile Trp Ile
                555                 560

GAG AGC GAT GGT CTT GGA AAA GGA TGC ACG GCT ATC TTT GAT   1921
Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile Phe Asp
565                 570                 575

GTT AAA CTT GGG ATC TCA GAA CGT TCA AAC GAA TCT AAA CAG   1963
Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
    580                 585                 590

TCG GGC ATA CCG AAA GTT CCA GCC ATT CCC CGA CAT TCA AAT   2005
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
        595                 600                 605
```

FIG. 6C

```
TTC ACT GGA CTT AAG GTT CTT GTC ATG GAT GAG AAC GGG GTA    2047
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val
            610                 615                 620

AGT AGA ATG GTG ACG AAG GGA CTT CTT GTA CAC CTT GGG TGC    2089
Ser Arg Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys
                625                 630

GAA GTG ACC ACG GTG AGT TCA AAC GAG GAG TGT CTC CGA GTT    2131
Glu Val Thr Thr Val Ser Ser Asn Glu Glu Cys Leu Arg Val
635                 640                 645

GTG TCC CAT GAG CAC AAA GTG GTC TTC ATG GAC GTG TGC ATG    2173
Val Ser His Glu His Lys Val Val Phe Met Asp Val Cys Met
    650                 655                 660

CCC GGG GTC GAA AAC TAC CAA ATC GCT CTC CGT ATT CAC GAG    2215
Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg Ile His Glu
        665                 670                 675

AAA TTC ACA AAA CAA CGC CAC CAA CGG CCA CTA CTT GTG GCA    2257
Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val Ala
            680                 685                 690

CTC AGT GGT AAC ACT GAC AAA TCC ACA AAA GAG AAA TGC ATG    2299
Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
                695                 700

AGC TTT GGT CTA GAC GGT GTG TTG CTC AAA CCC GTA TCA CTA    2341
Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
705                 710                 715

GAC AAC ATA AGA GAT GTT CTG TCT GAT CTT CTC GAG CCC CGG    2383
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg
    720                 725                 730

GTA CTG TAC GAG GGC ATG TAAAGGCGAT GGATGCCCCA TGCCCCAGAG   2431
Val Leu Tyr Glu Gly Met
        735

GAGTAATTCC GCTCCCGCCT TCTTCTCCCG TAAAACATCG GAAGCTGATG     2481

TTCTCTGGTT TAATTGTGTA CATATCAGAG ATTGTCGGAG CGTTTTGGAT     2531

GATATCTTAA AACAGAAAGG GAATAACAAA ATAGAAACTC TAAACCGGTA     2581

TGTGTCCGTG GCGATTTCGG TTATAGAGGA ACAAGATGGT GGTGGTATAA     2631

TCATACCATT TCAGATTACA TGTTTGACTA ATGTTGTATC CTTATATATG     2681

TAGTTACATT CTTATAAGAA TTTGGATCGA GTTATGGATG CTTGTTGCGT     2731

GCATGTATGA CATTGATGCA GTATTATGGC GTCAGCTTTG CGCCGCTTAG     2781

TAGAAC                                                     2787
```

FIG. 6D

```
AGTAAGAACG AAGAAGAAGT GTTAAACCCA ACCAATTTTG ACTTGAAAAA      50

AAGCTTCAAC GCTCCCCTTT TCTCCTTCTC CGTCGCTCTC CGCCGCGTCC     100

CAAATCCCCA ATTCCTCCTC TTCTCCGATC AATTCTTCCC AAGTGTGTGT     150

ATGTGTGAGA GAGGAACTAT AGTGTAAAAA ATTCATA ATG GAA GTC TGC   199
                                         Met Glu Val Cys
                                          1

AAT TGT ATT GAA CCG CAA TGG CCA GCG GAT GAA TTG TTA ATG     241
Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu Leu Met
 5                   10                  15

AAA TAC CAA TAC ATC TCC GAT TTC TTC ATT GCG ATT GCG TAT     283
Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
     20                  25                  30

TTT TCG ATT CCT CTT GAG TTG ATT TAC TTT GTG AAG AAA TCA     325
Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
         35                  40                  45

GCC GTG TTT CCG TAT AGA TGG GTA CTT GTT CAG TTT GGT GCT     367
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala
             50                  55                  60

TTT ATC GTT CTT TGT GGA GCA ACT CAT CTT ATT AAC TTA TGG     409
Phe Ile Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp
                 65                  70

ACT TTC ACT ACG CAT TCG AGA ACC GTG GCG CTT GTG ATG ACT     451
Thr Phe Thr Thr His Ser Arg Thr Val Ala Leu Val Met Thr
 75                  80                  85

ACC GCG AAG GTG TTA ACC GCT GTT GTC TCG TGT GCT ACT ACG     493
Thr Ala Lys Val Leu Thr Ala Val Val Ser Cys Ala Thr Thr
     90                  95                 100

TTG ATG CTT GTT CAT ATT ATT CCT GAT CTT TTG AGT GTT AAG     535
Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
        105                 110                 115

ACT CGG GAG CTT TTC TTG AAA AAT AAA GCT GCT GAG CTC GAT     577
Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp
            120                 125                 130

AGA GAA ATG GGA TTG ATT CGA ACT CAG GAA GAA ACC GGA AGG     619
Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
                135                 140

CAT GTG AGA ATG TTG ACT CAT GAG ATT AGA AGC ACT TTA GAT     661
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
145                 150                 155

AGA CAT ACT ATT TTA AAG ACT ACA CTT GTT GAG CTT GGT AGG     703
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg
    160                 165                 170

ACA TTA GCT TTG GAG GAG TGT GCA TTG TGG ATG CCT ACT AGA     745
Thr Leu Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg
        175                 180                 185
```

FIG. 7A

```
ACT GGG TTA GAG CTA CAG CTT TCT TAT ACA CTT CGT CAT CAA      787
Thr Gly Leu Glu Leu Gln Leu Ser Tyr Thr Leu Arg His Gln
            190                 195                 200

CAT CCC GTG GAG TAT ACG GTT CCT ATT CAA TTA CCG GTG ATT      829
His Pro Val Glu Tyr Thr Val Pro Ile Gln Leu Pro Val Ile
                205                 210

AAC CAA GTG TTT GGT ACT AGT AGG GCT GTA AAA ATA TCT CCT      871
Asn Gln Val Phe Gly Thr Ser Arg Ala Val Lys Ile Ser Pro
215                 220                 225

AAT TCT CCT GTG GCT AGG TTG AGA CCT GTT TCT GGG AAA TAT      913
Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly Lys Tyr
    230                 235                 240

ATG CTA GGG GAG GTG GTC GCT GTG AGG GTT CCG CTT CTC CAC      955
Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
        245                 250                 255

CTT TCT AAT TTT CAG ATT AAT GAC TGG CCT GAG CTT TCA ACA      997
Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
            260                 265                 270

AAG AGA TAT GCT TTG ATG GTT TTG ATG CTT CCT TCA GAT AGT     1039
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser
                275                 280

GCA AGG CAA TGG CAT GTC CAT GAG TTG GAA CTC GTT GAA GTC     1081
Ala Arg Gln Trp His Val His Glu Leu Glu Leu Val Glu Val
285                 290                 295

GTC GCT GAT CAG GTG GCT GTA GCT CTC TCA CAT GCT GCG ATC     1123
Val Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile
    300                 305                 310

CTA GAA GAG TCG ATG CGA GCT AGG GAC CTT CTC ATG GAG CAG     1165
Leu Glu Glu Ser Met Arg Ala Arg Asp Leu Leu Met Glu Gln
        315                 320                 325

AAT GTT GCT CTT GAT CTA GCT AGA CGA GAA GCA GAA ACA GCA     1207
Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala Glu Thr Ala
            330                 335                 340

ATC CGT GCC CGC AAT GAT TTC CTA GCG GTT ATG AAC CAT GAA     1249
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu
                345                 350

ATG CGA ACA CCG ATG CAT GCG ATT ATT GCA CTC TCT TCC TTA     1291
Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
355                 360                 365

CTC CAA GAA ACG GAA CTA ACC CCT GAA CAA AGA CTG ATG GTG     1333
Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
    370                 375                 380

GAA ACA ATA CTT AAA AGT AGT AAC CTT TTG GCA ACT TTG ATG     1375
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met
        385                 390                 395
```

FIG. 7B

```
AAT GAT GTC TTA GAT CTT TCA AGG TTA GAA GAT GGA AGT CTT    1417
Asn Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu
            400                 405                 410

CAA CTT GAA CTT GGG ACA TTC AAT CTT CAT ACA TTA TTT AGA    1459
Gln Leu Glu Leu Gly Thr Phe Asn Leu His Thr Leu Phe Arg
                415                 420

GAG GTC CTC AAT CTG ATA AAG CCT ATA GCG GTT GTT AAG AAA    1501
Glu Val Leu Asn Leu Ile Lys Pro Ile Ala Val Val Lys Lys
425                 430                 435

TTA CCC ATC ACA CTA AAT CTT GCA CCA GAT TTG CCA GAA TTT    1543
Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu Pro Glu Phe
    440                 445                 450

GTT GTT GGG GAT GAG AAA CGG CTA ATG CAG ATA ATA TTA AAT    1585
Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu Asn
        455                 460                 465

ATA GTT GGT AAT GCT GTG AAA TTC TCC AAA CAA GGT AGT ATC    1627
Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
            470                 475                 480

TCC GTA ACC GCT CTT GTC ACC AAG TCA GAC ACA CGA GCT GCT    1669
Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
                485                 490

GAC TTT TTT GTC GTG CCA ACT GGG AGT CAT TTC TAC TTG AGA    1711
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg
495                 500                 505

GTG AAG GTA AAA GAC TCT GGA GCA GGA ATA AAT CCT CAA GAC    1753
Val Lys Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp
    510                 515                 520

ATT CCA AAG ATT TTC ACT AAA TTT GCT CAA ACA CAA TCT TTA    1795
Ile Pro Lys Ile Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu
        525                 530                 535

GCG ACG AGA AGC TCG GGT GGT AGT GGG CTT GGC CTC GCC ATC    1837
Ala Thr Arg Ser Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
            540                 545                 550

TCC AAG AGG TTT GTG AAT CTG ATG GAG GGT AAC ATT TGG ATT    1879
Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn Ile Trp Ile
                555                 560

GAG AGC GAT GGT CTT GGA AAA GGA TGC ACG GCT ATC TTT GAT    1921
Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile Phe Asp
565                 570                 575

GTT AAA CTT GGG ATC TCA GAA CGT TCA AAC GAA TCT AAA CAG    1963
Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
    580                 585                 590

TCG GGC ATA CCG AAA GTT CCA GCC ATT CCC CGA CAT TCA AAT    2005
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
        595                 600                 605
```

FIG. 7C

```
TTC ACT GGA CTT AAG GTT CTT GTC ATG GAT GAG AAC GGG GTA   2047
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val
            610                 615                 620

AGT AGA ATG GTG ACG AAG GGA CTT CTT GTA CAC CTT GGG TGC   2089
Ser Arg Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys
                625                 630

GAA GTG ACC ACG GTG AGT TCA AAC GAG GAG TGT CTC CGA GTT   2131
Glu Val Thr Thr Val Ser Ser Asn Glu Glu Cys Leu Arg Val
635                 640                 645

GTG TCC CAT GAG CAC AAA GTG GTC TTC ATG GAC GTG TGC ATG   2173
Val Ser His Glu His Lys Val Val Phe Met Asp Val Cys Met
    650                 655                 660

CCC GGG GTC GAA AAC TAC CAA ATC GCT CTC CGT ATT CAC GAG   2215
Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg Ile His Glu
        665                 670                 675

AAA TTC ACA AAA CAA CGC CAC CAA CGG CCA CTA CTT GTG GCA   2257
Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val Ala
            680                 685                 690

CTC AGT GGT AAC ACT GAC AAA TCC ACA AAA GAG AAA TGC ATG   2299
Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
                695                 700

AGC TTT GGT CTA GAC GGT GTG TTG CTC AAA CCC GTA TCA CTA   2341
Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
705                 710                 715

GAC AAC ATA AGA GAT GTT CTG TCT GAT CTT CTC GAG CCC CGG   2383
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg
    720                 725                 730

GTA CTG TAC GAG GGC ATG TAAAGGCGAT GGATGCCCCA TGCCCCAGAG  2431
Val Leu Tyr Glu Gly Met
        735

GAGTAATTCC GCTCCCGCCT TCTTCTCCCG TAAAACATCG GAAGCTGATG    2481

TTCTCTGGTT TAATTGTGTA CATATCAGAG ATTGTCGGAG CGTTTTGGAT    2531

GATATCTTAA AACAGAAAGG GAATAACAAA ATAGAAACTC TAAACCGGTA    2581

TGTGTCCGTG GCGATTTCGG TTATAGAGGA ACAAGATGGT GGTGGTATAA    2631

TCATACCATT TCAGATTACA TGTTTGACTA ATGTTGTATC CTTATATATG    2681

TAGTTACATT CTTATAAGAA TTTGGATCGA GTTATGGATG CTTGTTGCGT    2731

GCATGTATGA CATTGATGCA GTATTATGGC GTCAGCTTTG CGCCGCTTAG    2781

TAGAAC                                                    2787
```

FIG. 7D

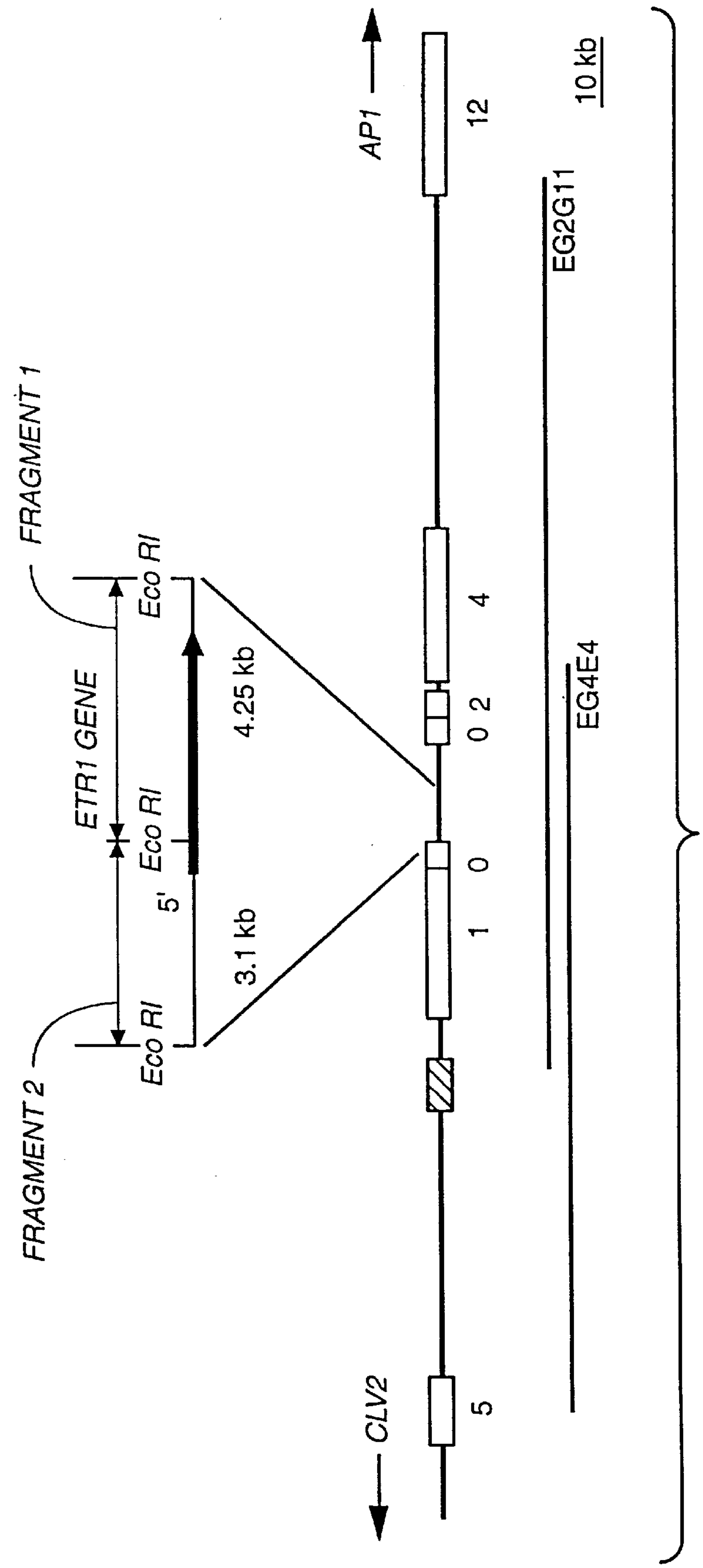
AP1
12
EG2G11
10 kb
FRAGMENT 1
Eco RI
ETR1 GENE
4.25 kb
4
0 2
EG4E4
Eco RI
5'
0
1
3.1 kb
Eco RI
FRAGMENT 2
CLV2
5

FIG. 8

```
                                                   *
ETR1  QNVALDLARREAETAIRARNDFLAV MNHEMRTPM HAIIALSSLLQETELTPEQRL   380
BARA  QNVELDLAKKRAQEAARIKSEFLAN MSHELRTPL NGVIGFTRLTLKTELTPTQRD   329
LEMA  QNIELDLARKEALEASRIKSEFLAN MSHEIRTPL NGILGFTHLLQKSELTPRQFD   311
RPFC          RAVREARHANQAKSRFLAN MSHEFRTPL NGLSGMTEVLATTRLDAEQKE   176

ETR1  MVETILKSSNLLATLMNDVLDLSRLEDGSLQLELGTFNLHTLFREVLNLIKPIAVV   436
BARA  HLNTIERSANNLLAIINDVLDFSKLEAGKLILESIPFPLRSTLDEVVTLLAHSSHD   385
LEMA  YLGTIEKSADNLLSIINEILDFSKIEAGKLVLDNIPFNLRDLLQDTLTILAPAAHA   367
RPFC  CLNTIQASARSLLSLVEEVLDISAIEAGKIRIDRRDFSLREMIGSVNLILQPQARG   232

ETR1  KKLPITLNLAPDLPEFVVGDEKR LMQIILNIVGNA VKFSKQGSI (26) LRVK   510
BARA  KGLELTLNIKSDVPDNVIGDPLR LQQIITNLVGNA IKFTENGNI (15) IEVQ   448
LEMA  KQLELVSLVYRDTPLALSGDPLR LRQILTNLVSNA IKFTREGTI (15) LRIS   430
RPFC  RRLEYGTQVADDVPLLLKGDTAH LRQVLLNLVGNA VKFTEHGHV (16) LRFD   296

ETR1  VKDSGAGIN PQDIPK IFTKF AQTQSLATRSSG GSGLGL AISKRFVNLMEGNI   562
BARA  IRDTGIGIP ERDQSR LFQAF RQADASISRRHG GTGLGL VITQKLVNEMGGDI   500
LEMA  VQDTGIGLS SQDVRA LFQAF SQADNSLSRQPG GTGLGL VISKRLIEQMGGEI   482
RPFC  VEDTGIGVP MDMRPR LFEAF EQADVGLSRRYE GTGLGT TIAKGLVEAMGGSI   348
```

FIG. 9A

```
ETR1  LKVLVM DE NGVSRMVTKGLLVHLGCEVTTVSSNEECLRV   648
BVGS  LRVLVV DD HKPNLMLLRQQLDYLGQRVVAADSGEAALAL  1011
RCSC  MMILVV DD HPINRRLLADQLGSLGYQCKTANDGVDALNV   847
LEMA  PRVLCV DD NPANLLLVQTLLEDMGAEVVAVEGGYAAVNA   695
                    *
ETR1  VSHEH-KVVFM D VCMPGVENYQIALRIH (10) PLLVA   690
BVGS  WHEHAFDVVIT D CNMPGINGYELARRIR (12) CILFG  1056
RCSC  LSKNHIDIVLS D VNMPNMDGYRLTQRIR  (5) LPVIG   885
LEMA  VQQEAFDLVLM D VQMPGMDGRQATEAIR (10) LPIVA   738

ETR1  LSGNTDKSTKEKCMSFGLDGVLL K PVSLDNIRDVLSDLL   729
BVGS  FTASAQMDEAHACRAAGMDDCLF K PIGVDALRQRLNEAA  1095
RCSC  VTANALAEEKQRCLESGMDSCLS K PVTLDVIKQSLTLYA   924
LEMA  LTAHAMANEKRSLLQSGMDDYLT K PISERQLAQVVLKWT   777
```

FIG. 9B

```
                  Met
                           .         .         .         .         .
TOMATO          1 ATGGAATCCTGTGATTGCATTGAGGCTTTACTGCCAACTGGTGACCTGCT 50
                  ||||||  |||  |||| |||||  |   |  |||| | | |||  || |
ARABIDOPSIS   157 ATGGAAGTCTGCAATTGTATTGAACCGCAATGGCCAGCGGATGAATTGTT 206

                           .         .         .         .         .
               51 GGTTAAATACCAATACCTCTCAGATTTCTTCATTGCTGTAGCCTACTTTT 100
                    | ||||||||||||| ||||| ||||||||||||||||  |  || || ||||
              207 AATGAAATACCAATACATCTCCGATTTCTTCATTGCGATTGCGTATTTTT 256

                           .         .         .         .         .
              101 CCATTCCGTTGGAGCTTATTTATTTTGTCCACAAATCTGCATGCTTCCCA 150
                  | |||||  | ||| | ||||| |||||  | ||||| ||    || || 
              257 CGATTCCTCTTGAGTTGATTTACTTTGTGAAGAAATCAGCCGTGTTTCCG 306

                           .         .         .         .         .
              151 TACAGATGGGTCCTCATGCAATTTGGTGCTTTTATTGTGCTCTGCGGAGC 200
                  || ||||||||| ||  | || ||||||||||||||| || || || |||||
              307 TATAGATGGGTACTTGTTCAGTTTGGTGCTTTTATCGTTCTTTGTGGAGC 356

                           .         .         .         .         .
              201 AACACACTTTATTAGCTTGTGGACCTTCTTTATGCACTCTAAGACGGTCG 250
                  ||| ||  |||||| ||| ||||| |||  || ||| || |  || || |
              375 AACTCATCTTATTAACTTATGGACTTTCACTACGCATTCGAGAACCGTGG 406

                           .         .         .         .         .
              251 CTGTGGTTATGACCATATCAAAAATGTTGACAGCTGCCGTGTCCTGTATC 300
                  |  | || ||||| |   | ||  |||| || ||||  || || |||   
              407 CGCTTGTGATGACTACCGCGAAGGTGTTAACCGCTGTTGTCTCGTGTGCT 456

                           .         .         .         .         .
              301 ACAGCTTTGATGCTTGTTCACATTATTCCTGATTTGCTAAGTGTTAAAAC 350
                  || || |||||||||||||| ||||||||||||| |  | |||||||| ||
              457 ACTGCGTTGATGCTTGTTCATATTATTCCTGATCTTTTGAGTGTTAAGAC 506

                           .
              351 GCGAGAGTTGTTCTTGAAA 369
                   || ||| | |||||||||
              507 TCGGGAGCTTTTCTTGAAA 525
                                 Lys
                                 123
```

FIG. 10A

```
                  Ala
                  306
                          .         .         .         .         .
TOMATO           1 GCTCTTTCACATGCTGCAATTTTAGAAGATTCCATGCGAGCCCATGATCA 50
                   ||||| ||||||||||| ||  ||||||| || ||||||||    || | 
ARABIDOPSIS   1072 GCTCTCTCACATGCTGCGATCCTAGAAGAGTCGATGCGAGCTAGGGACCT 1121

                            .         .         .         .         .
                51 GCTCATGGAACAGAATATTGCTTTGGATGTAGCTCGACAAGAAGCAGAGA 100
                    |||||||| |||||| ||||| | ||| ||||| ||| ||||||||| |
              1122 TCTCATGGAGCAGAATGTTGCTCTTGATCTAGCTAGACGAGAAGCAGAAA 1171

                            .         .         .         .         .
               101 TGGCCATCCGTGCACGTAACGACTTCCTTGCTGTGATGAACCATGAAATG 150
                     || |||||||| || || || ||||| || || |||||||||||||||
              1172 CAGCAATCCGTGCCCGCAATGATTTCCTAGCGGTTATGAACCATGAAATG 1221

                            .         .         .         .         .
               151 AGAACGCCCATGCATGCAGTTATTGCTCTGTGCTCTCTGCTTTTAGAAAC 200
                    |||| || ||||||||  ||||||| || |  ||  | ||   ||||||
              1222 CGAACACCGATGCATGCGATTATTGCACTCTCTTCCTTACTCCAAGAAAC 1271

                            .         .         .         .         .
               201 AGACTTAACTCCAGAGCAGAGAGTTATGATTGAGACCATATTGAAGAGCA 250
                    ||  |||| || || || ||| | ||| | || || ||| | || || |
              1272 GGAACTAACCCCTGAACAAAGACTGATGGTGGAAACAATACTTAAAAGTA 1321

                            .         .         .         .
               251 GCAATCTTCTTGCAACACTGATAAATGATGTTCTAGATCTTTCTAG 296
                   | || ||| | ||||| |||| ||||||||  |||||||||| ||
              1322 GTAACCTTTTGGCAACTTTGATGAATGATGTCTTAGATCTTTCAAG 1367

                                                          Ser
                                                          403
```

FIG. 10B

```
                         .         .         .         .         .
     TOMATO   1 MESCDCIEALLPTGDLLVKYQYLSDFFIAVAYFSIPLELIYFVHKSACFP 50
                || |:|||: :|.::||:||||:||||||:|||||||||||||.|||.||
ARABIDOPSIS   1 MEVCNCIEPQWPADELLMKYQYISDFFIAIAYFSIPLELIYFVKKSAVFP 50

                         .         .         .         .         .
             51 YRWVLMQFGAFIVLCGATHFISLWTFFMHSKTVAVVMTISKMLTAAVSCI 100
                |||||:|||||||||||||:|.||||  ||:|||:|||..|:|||.|||
             51 YRWVLVQFGAFIVLCGATHLINLWTFTTHSRTVALVMTTAKVLTAVVSCA 100

                         .         .
            101 TALMLVHIIPDLLSVKTRELFLK 123
                |||||||||||||||||||||||
            101 TALMLVHIIPDLLSVKTRELFLK 123
```

FIG. 11A

```
                         .         .         .         .         .
ARABIDOPSIS 306 ALSHAAILEESMRARDLLMEQNVALDLARREAETAIRARNDFLAVMNHEM 355
                |||||||||:||||:| |||||:|||:||.||| ||||||||||||||||
     TOMATO   1 ALSHAAILEDSMRAHDQLMEQNIALDVARQEAEMAIRARNDFLAVMNHEM 50

                         .         .         .         .
            356 RTPMHAIIALSSLLQETELTPEQRLMVETILKSSNLLATLMNDVLDLS 403
                ||||||:|||:||| ||:||||||:|:|||||||||||||:|||||||
             51 RTPMHAVIALCSLLLETDLTPEQRVMIETILKSSNLLATLINDVLDLS 93
```

FIG. 11B

```
ACTTTTAAAA TTTCTTTATT TCATTGTCAG AAAAAGAGAG CTAATAATAT      50

TATTATTTAA ATGTAACAAG TAGGCCTATA ACACGTGAAC TTCCCTCTTT     100

GCAAAAAAAA AATCATCAAA AACTTTTACC TCTCATTGGT TTCTTCTTTA     150

TCACACTGTT ACGCTTGGAT TCTCATTTCT TCAAGTTCAT AACGCTCGGA     200

TCAATCAGGA AGACGAACTT GAACTTTCTT TTTTTCATCA TTACCCAAAG     250

CTATGAGGCT CACACCACCA ATACGTCCGC CGTCATGAAT CCTTCTCTTC     300

CAGGTACTGT GCCGTCTCGG GATAACAAAC TTTCTATTTA TTCTCTTCTG     350

ATCGGATCTA TCTATCGATG AAGATTGATT TCACTACTTT AGTAACATTT     400

CATCTGATCG ATCTGTGTTG TGTTATCGAG GAATCAATCT CATTTTGTAG     450

ATTCAATTTT CTGGATAGAT TTTGTATCTC TTTTCCATAG CTCTAGTCCA     500

AATCTAGTCT CCACTGATAT CTGAGTTTTG TTGACCAGGT CAACACAAGT     550

CAGAGCTCCA AAA ATG GAG TCA TGC GAT TGT TTT GAG ACG CAT     593
               Met Glu Ser Cys Asp Cys Phe Glu Thr His
                1               5                  10

GTG AAT CAA GAT GAT CTG TTA GTG AAG TAC CAA TAC ATC TCA     635
Val Asn Gln Asp Asp Leu Leu Val Lys Tyr Gln Tyr Ile Ser
                 15                  20

GAT GCG TTG ATT GCT CTT GCA TAC TTC TCA ATC CCA CTC GAG     677
Asp Ala Leu Ile Ala Leu Ala Tyr Phe Ser Ile Pro Leu Glu
25                   30                  35

CTT ATC TAT TTC GTG CAA AAG TCT GCT TTC TTC CCT TAC AAA     719
Leu Ile Tyr Phe Val Gln Lys Ser Ala Phe Phe Pro Tyr Lys
     40                  45                  50

TGG GTG CTT ATG CAG TTT GGA GCC TTT ATC ATT CTC TGT GGA     761
Trp Val Leu Met Gln Phe Gly Ala Phe Ile Ile Leu Cys Gly
         55                  60                  65

GCT ACG CAT TTC ATC AAC CTA TGG ATG TTC TTC ATG CAT TCC     803
Ala Thr His Phe Ile Asn Leu Trp Met Phe Phe Met His Ser
             70                  75                  80

AAA GCC GTT GCC ATT GTC ATG ACT ATT GCT AAA GTC TCT TGC     845
Lys Ala Val Ala Ile Val Met Thr Ile Ala Lys Val Ser Cys
                 85                  90

GCG GTT GTG TCG TGT GCT ACC GCG TTG ATG TTG GTT CAT ATT     887
Ala Val Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile
 95                  100                 105

ATT CCT GAT CTT CTC AGT GTT AAG AAC AGG GAA TTG TTT CTC     929
Ile Pro Asp Leu Leu Ser Val Lys Asn Arg Glu Leu Phe Leu
     110                 115                 120

AAG AAG AAA GCT GAT GAG TTA GAT AGA GAA ATG GGT CTT ATT     971
Lys Lys Lys Ala Asp Glu Leu Asp Arg Glu Met Gly Leu Ile
         125                 130                 135
```

FIG. 12A

```
TTA ACA CAA GAG GAG ACT GGT AGG CAT GTT AGG ATG CTT ACT     1013
Leu Thr Gln Glu Glu Thr Gly Arg His Val Arg Met Leu Thr
            140                 145                 150

CAT GGA ATT AGA AGA ACT CTT GAT AGG CAT ACT ATT TTA AGA     1055
His Gly Ile Arg Arg Thr Leu Asp Arg His Thr Ile Leu Arg
                155                 160

ACC ACT CTT GTT GAG CTT GGT AAA ACT CTT TGT CTT GAG GAA     1097
Thr Thr Leu Val Glu Leu Gly Lys Thr Leu Cys Leu Glu Glu
165                 170                 175

TGT GCG TTG TGG ATG CCT TCT CAA AGT GGT TTA TAT TTG CAG     1139
Cys Ala Leu Trp Met Pro Ser Gln Ser Gly Leu Tyr Leu Gln
    180                 185                 190

CTT TCT CAT ACT TTG AGT CAT AAA ATA CAA GTT GGA AGC AGT     1181
Leu Ser His Thr Leu Ser His Lys Ile Gln Val Gly Ser Ser
        195                 200                 205

GTG CCG ATA AAT CTC CCG ATT ATT AAT GAA CTC TTC AAT AGC     1223
Val Pro Ile Asn Leu Pro Ile Ile Asn Glu Leu Phe Asn Ser
            210                 215                 220

GCT CAA GCT ATG CAC ATA CCT CAT TCT TGT CCT TTG GCT AAG     1265
Ala Gln Ala Met His Ile Pro His Ser Cys Pro Leu Ala Lys
                225                 230

ATT GGG CCT CCG GTT GGG AGA TAT TCA CCT CCT GAG GTT GTT     1307
Ile Gly Pro Pro Val Gly Arg Tyr Ser Pro Pro Glu Val Val
235                 240                 245

TCT GTC CGT GTT CCT CTT TTA CAT CTC TCT AAT TTC CAA GGC     1349
Ser Val Arg Val Pro Leu Leu His Leu Ser Asn Phe Gln Gly
    250                 255                 260

AGT GAC TGG TCG GAT CTC TCT GGC AAA GGT TAC GCT ATC ATG     1391
Ser Asp Trp Ser Asp Leu Ser Gly Lys Gly Tyr Ala Ile Met
        265                 270                 275

GTC CTG ATT CTC CCA ACC GAT GGT GCA AGA AAA TGG AGA GAC     1433
Val Leu Ile Leu Pro Thr Asp Gly Ala Arg Lys Trp Arg Asp
            280                 285                 290

CAT GAG TTA GAG CTT GTA GAA AAC GTG GCG GAT CAG             1469
His Glu Leu Glu Leu Val Glu Asn Val Ala Asp Gln
                295                 300

GTCCATCTCT TTACTTGTAT ATGTTTGGTT GTGTGTCAAG TTGCTTTACC      1519

AGCTTTTAGT GTTTTGTTTT GTCCCCTGAC TCTCACTTCA TTCAG           1564

GTG GCT GTG GCT CTC TCA CAT GCT GCA ATT TTG GAA GAA TCC     1606
Val Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser
        305                 310                 315

ATG CAC GCT CGT GAC CAG CTT ATG GAG CAG AAT TTT GCT TTA     1648
Met His Ala Arg Asp Gln Leu Met Glu Gln Asn Phe Ala Leu
            320                 325                 330

GAC AAG GCT CGT CAA GAG GCT GAG ATG GCA GTA CAT GCT CGA     1690
Asp Lys Ala Arg Gln Glu Ala Glu Met Ala Val His Ala Arg
                335                 340
```

FIG. 12B

```
AAT GAT TTC CTA GCT GTT ATG AAC CAC GAG ATG AGG ACA CCG      1732
Asn Asp Phe Leu Ala Val Met Asn His Glu Met Arg Thr Pro
345                 350                 355

ATG CAT GCC ATC ATC TCT CTT TCT TCT CTT CTC CTT GAG ACT      1774
Met His Ala Ile Ile Ser Leu Ser Ser Leu Leu Leu Glu Thr
    360                 365                 370

GAG CTG TCT CCA GAG CAA AGA GTT ATG ATC GAG ACA ATA CTG      1816
Glu Leu Ser Pro Glu Gln Arg Val Met Ile Glu Thr Ile Leu
        375                 380                 385

AAA AGC AGC AAT CTT GTG GCT ACA CTA ATC AGC GAC GTT CTG      1858
Lys Ser Ser Asn Leu Val Ala Thr Leu Ile Ser Asp Val Leu
            390                 395                 400

GAT CTT TCG AGA TTG GAA GAT GGG AGC TTA CTC TTG GAA AAT      1900
Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Leu Leu Glu Asn
                405                 410

GAA CCA TTC AGT CTA CAA GCG ATC TTT GAA GAG GTAACTAAAT       1943
Glu Pro Phe Ser Leu Gln Ala Ile Phe Glu Glu
415                 420                 425

CCCCCTGATT AACCAGTGAA GTCCATTATA TATGTCTTAC ATGAATAACA       1993

TGGGCGCTTT GAATCTGCAG GTC ATC TCT TTG ATA AAG CCA ATC        2037
                      Val Ile Ser Leu Ile Lys Pro Ile
                                      430

GCA TCA GTG AAG AAA CTA TCA ACG AAT CTG ATT CTG TCT GCA      2079
Ala Ser Val Lys Lys Leu Ser Thr Asn Leu Ile Leu Ser Ala
    435                 440                 445

GAC TTA CCA ACT TAT GCT ATT GGT GAT GAG AAA CGT CTG ATG      2121
Asp Leu Pro Thr Tyr Ala Ile Gly Asp Glu Lys Arg Leu Met
        450                 455                 460

CAA ACA ATT CTT AAC ATC ATG GGC AAC GCT GTG AAA TTT ACT      2163
Gln Thr Ile Leu Asn Ile Met Gly Asn Ala Val Lys Phe Thr
            465                 470                 475

AAG GAA GGC TAC ATC TCC ATA ATA GCC TCT ATC ATG AAA CCC      2205
Lys Glu Gly Tyr Ile Ser Ile Ile Ala Ser Ile Met Lys Pro
                480                 485

GAG TCC TTA CAA GAA TTA CCA TCT CCA GAA TTT TTT CCA GTT      2247
Glu Ser Leu Gln Glu Leu Pro Ser Pro Glu Phe Phe Pro Val
490                 495                 500

CTC AGT GAC AGT CAC TTC TAC CTA TGT GTG CAG GTTAGACCCA       2290
Leu Ser Asp Ser His Phe Tyr Leu Cys Val Gln
    505                 510

ATCTACAAAT TACTAAACTA CAAAGTTAAG CTTCTTACTG TGTTCTTACT       2340

GTTATAATCA TGGTGCAG GTG AAG GAC ACA GGG TGT GGA ATT CAC      2385
                    Val Lys Asp Thr Gly Cys Gly Ile His
                    515                 520

ACA CAA GAC ATT CCT TTG CTC TTT ACC AAA TTT GTA CAG CCT      2427
Thr Gln Asp Ile Pro Leu Leu Phe Thr Lys Phe Val Gln Pro
    525                 530                 535
```

FIG. 12C

```
CGG ACC GGA ACT CAG AGG AAC CAT TCC GGT GGA GGA CTC GGG    2469
Arg Thr Gly Thr Gln Arg Asn His Ser Gly Gly Gly Leu Gly
        540                 545                 550

CTA GCT CTC TGT AAA CGG TAACAACCC AAAAGTATAT ATAAGTTATA   2516
Leu Ala Leu Cys Lys Arg
            555

AGCAGATGGT GTTACAAATA GCTAAAAGGC AAGTTTCTGT TGATGGATGT    2566

CTCTGGTTAG G TTT GTC GGG CTA ATG GGA GGA TAC ATG TGG      2607
             Phe Val Gly Leu Met Gly Gly Tyr Met Trp
                     560                 565

ATA GAA AGT GAA GGC CTA GAG AAA GGC TGC ACA GCT TCG TTC    2649
Ile Glu Ser Glu Gly Leu Glu Lys Gly Cys Thr Ala Ser Phe
        570                 575                 580

ATC ATC AGG CTT GGT ATC TGC AAC GGT CCA AGC AGT AGC AGT    2691
Ile Ile Arg Leu Gly Ile Cys Asn Gly Pro Ser Ser Ser Ser
            585                 590                 595

GGT TCA ATG GCG CTA CAT CTT GCA GCT AAA TCA CAA ACC AGA    2733
Gly Ser Met Ala Leu His Leu Ala Ala Lys Ser Gln Thr Arg
                600                 605

CCG TGG AAC TGG TGATACTTAC GTTGGAAAGA CTTGTATTGA           2775
Pro Trp Asn Trp
610

GGTGAGACTT TTTAACTACA CAGCAGCAAG AGAAAGAAGA AAATACATGA     2825

CCGGACGGTG TGATCTAACT TATTGGATTT TGTTGGATGT AATATGTAAA     2875

ATAAAAATCC TATATACGGG GAGAGGTACC TTATCTGTTC TCACTATATT     2925

TTATTGAACA TTACTTTAGA GAATATGTTT TGGAATTCAC TACTAAATAA     2975

ACGATATAAA TCTTCACGAA AAGAGCAACA TTTT                      3009
```

FIG. 12D

```
AAAAAAATCA TCAAAAACTT TTACCTCTCA TTGGTTTCTT CTTTATCACA       50

CTGTTACGCT TGGATTCTCA TTTCTTCAAG TTCATAACGC TCGGATCAAT      100

CAGGAAGACG AACTTGAACT TTCTTTTTTT CATCATTACC CAAAGCTATG      150

AGGCTCACAC CACCAATACG TCCGCCGTCA TGAATCCTTC TCTTCCAGGT      200

CAACACAAGT CAGAGCTCCA AAA ATG GAG TCA TGC GAT TGT TTT       244
                          Met Glu Ser Cys Asp Cys Phe
                           1               5

GAG ACG CAT GTG AAT CAA GAT GAT CTG TTA GTG AAG TAC CAA     286
Glu Thr His Val Asn Gln Asp Asp Leu Leu Val Lys Tyr Gln
        10                  15                  20

TAC ATC TCA GAT GCG TTG ATT GCT CTT GCA TAC TTC TCA ATC     328
Tyr Ile Ser Asp Ala Leu Ile Ala Leu Ala Tyr Phe Ser Ile
            25                  30                  35

CCA CTC GAG CTT ATC TAT TTC GTG CAA AAG TCT GCT TTC TTC     370
Pro Leu Glu Leu Ile Tyr Phe Val Gln Lys Ser Ala Phe Phe
                40                  45

CCT TAC AAA TGG GTG CTT ATG CAG TTT GGA GCC TTT ATC ATT     412
Pro Tyr Lys Trp Val Leu Met Gln Phe Gly Ala Phe Ile Ile
50                  55                  60

CTC TGT GGA GCT ACG CAT TTC ATC AAC CTA TGG ATG TTC TTC     454
Leu Cys Gly Ala Thr His Phe Ile Asn Leu Trp Met Phe Phe
    65                  70                  75

ATG CAT TCC AAA GCC GTT GCC ATT GTC ATG ACT ATT GCT AAA     496
Met His Ser Lys Ala Val Ala Ile Val Met Thr Ile Ala Lys
        80                  85                  90

GTC TCT TGC GCG GTT GTG TCG TGT GCT ACC GCG TTG ATG TTG     538
Val Ser Cys Ala Val Val Ser Cys Ala Thr Ala Leu Met Leu
            95                  100                 105

GTT CAT ATT ATT CCT GAT CTT CTC AGT GTT AAG AAC AGG GAA     580
Val His Ile Ile Pro Asp Leu Leu Ser Val Lys Asn Arg Glu
                110                 115

TTG TTT CTC AAG AAG AAA GCT GAT GAG TTA GAT AGA GAA ATG     622
Leu Phe Leu Lys Lys Lys Ala Asp Glu Leu Asp Arg Glu Met
120                 125                 130

GGT CTT ATT TTA ACA CAA GAG GAG ACT GGT AGG CAT GTT AGG     664
Gly Leu Ile Leu Thr Gln Glu Glu Thr Gly Arg His Val Arg
    135                 140                 145

ATG CTT ACT CAT GGA ATT AGA AGA ACT CTT GAT AGG CAT ACT     706
Met Leu Thr His Gly Ile Arg Arg Thr Leu Asp Arg His Thr
        150                 155                 160

ATT TTA AGA ACC ACT CTT GTT GAG CTT GGT AAA ACT CTT TGT     748
Ile Leu Arg Thr Thr Leu Val Glu Leu Gly Lys Thr Leu Cys
            165                 170                 175
```

FIG. 13A

```
CTT GAG GAA TGT GCG TTG TGG ATG CCT TCT CAA AGT GGT TTA     790
Leu Glu Glu Cys Ala Leu Trp Met Pro Ser Gln Ser Gly Leu
                180                 185

TAT TTG CAG CTT TCT CAT ACT TTG AGT CAT AAA ATA CAA GTT     832
Tyr Leu Gln Leu Ser His Thr Leu Ser His Lys Ile Gln Val
190                 195                 200

GGA AGC AGT GTG CCG ATA AAT CTC CCG ATT ATT AAT GAA CTC     874
Gly Ser Ser Val Pro Ile Asn Leu Pro Ile Ile Asn Glu Leu
    205                 210                 215

TTC AAT AGC GCT CAA GCT ATG CAC ATA CCT CAT TCT TGT CCT     916
Phe Asn Ser Ala Gln Ala Met His Ile Pro His Ser Cys Pro
        220                 225                 230

TTG GCT AAG ATT GGG CCT CCG GTT GGG AGA TAT TCA CCT CCT     958
Leu Ala Lys Ile Gly Pro Pro Val Gly Arg Tyr Ser Pro Pro
            235                 240                 245

GAG GTT GTT TCT GTC CGT GTT CCT CTT TTA CAT CTC TCT AAT    1000
Glu Val Val Ser Val Arg Val Pro Leu Leu His Leu Ser Asn
                250                 255

TTC CAA GGC AGT GAC TGG TCG GAT CTC TCT GGC AAA GGT TAC    1042
Phe Gln Gly Ser Asp Trp Ser Asp Leu Ser Gly Lys Gly Tyr
260                 265                 270

GCT ATC ATG GTC CTG ATT CTC CCA ACC GAT GGT GCA AGA AAA    1084
Ala Ile Met Val Leu Ile Leu Pro Thr Asp Gly Ala Arg Lys
    275                 280                 285

TGG AGA GAC CAT GAG TTA GAG CTT GTA GAA AAC GTG GCG GAT    1126
Trp Arg Asp His Glu Leu Glu Leu Val Glu Asn Val Ala Asp
        290                 295                 300

CAG GTG GCT GTG GCT CTC TCA CAT GCT GCA ATT TTG GAA GAA    1168
Gln Val Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu
            305                 310                 315

TCC ATG CAC GCT CGT GAC CAG CTT ATG GAG CAG AAT TTT GCT    1210
Ser Met His Ala Arg Asp Gln Leu Met Glu Gln Asn Phe Ala
                320                 325

TTA GAC AAG GCT CGT CAA GAG GCT GAG ATG GCA GTA CAT GCT    1252
Leu Asp Lys Ala Arg Gln Glu Ala Glu Met Ala Val His Ala
330                 335                 340

CGA AAT GAT TTC CTA GCT GTT ATG AAC CAC GAG ATG AGG ACA    1294
Arg Asn Asp Phe Leu Ala Val Met Asn His Glu Met Arg Thr
    345                 350                 355

CCG ATG CAT GCC ATC ATC TCT CTT TCT TCT CTT CTC CTT GAG    1336
Pro Met His Ala Ile Ile Ser Leu Ser Ser Leu Leu Leu Glu
        360                 365                 370

ACT GAG CTG TCT CCA GAG CAA AGA GTT ATG ATC GAG ACA ATA    1378
Thr Glu Leu Ser Pro Glu Gln Arg Val Met Ile Glu Thr Ile
            375                 380                 385
```

FIG. 13B

```
CTG AAA AGC AGC AAT CTT GTG GCT ACA CTA ATC AGC GAC GTT       1420
Leu Lys Ser Ser Asn Leu Val Ala Thr Leu Ile Ser Asp Val
                390                 395

CTG GAT CTT TCG AGA TTG GAA GAT GGG AGC TTA CTC TTG GAA       1462
Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Leu Leu Glu
400                 405                 410

AAT GAA CCA TTC AGT CTA CAA GCG ATC TTT GAA GAG GTC ATC       1504
Asn Glu Pro Phe Ser Leu Gln Ala Ile Phe Glu Glu Val Ile
    415                 420                 425

TCT TTG ATA AAG CCA ATC GCA TCA GTG AAG AAA CTA TCA ACG       1546
Ser Leu Ile Lys Pro Ile Ala Ser Val Lys Lys Leu Ser Thr
        430                 435                 440

AAT CTG ATT CTG TCT GCA GAC TTA CCA ACT TAT GCT ATT GGT       1588
Asn Leu Ile Leu Ser Ala Asp Leu Pro Thr Tyr Ala Ile Gly
            445                 450                 455

GAT GAG AAA CGT CTG ATG CAA ACA ATT CTT AAC ATC ATG GGC       1630
Asp Glu Lys Arg Leu Met Gln Thr Ile Leu Asn Ile Met Gly
                460                 465

AAC GCT GTG AAA TTT ACT AAG GAA GGC TAC ATC TCC ATA ATA       1672
Asn Ala Val Lys Phe Thr Lys Glu Gly Tyr Ile Ser Ile Ile
470                 475                 480

GCC TCT ATC ATG AAA CCC GAG TCC TTA CAA GAA TTA CCA TCT       1714
Ala Ser Ile Met Lys Pro Glu Ser Leu Gln Glu Leu Pro Ser
    485                 490                 495

CCA GAA TTT TTT CCA GTT CTC AGT GAC AGT CAC TTC TAC CTA       1756
Pro Glu Phe Phe Pro Val Leu Ser Asp Ser His Phe Tyr Leu
        500                 505                 510

TGT GTG CAG GTG AAG GAC ACA GGG TGT GGA ATT CAC ACA CAA       1798
Cys Val Gln Val Lys Asp Thr Gly Cys Gly Ile His Thr Gln
            515                 520                 525

GAC ATT CCT TTG CTC TTT ACC AAA TTT GTA CAG CCT CGG ACC       1840
Asp Ile Pro Leu Leu Phe Thr Lys Phe Val Gln Pro Arg Thr
                530                 535

GGA ACT CAG AGG AAC CAT TCC GGT GGA GGA CTC GGG CTA GCT       1882
Gly Thr Gln Arg Asn His Ser Gly Gly Gly Leu Gly Leu Ala
540                 545                 550

CTC TGT AAA CGG TTT GTC GGG CTA ATG GGA GGA TAC ATG TGG       1924
Leu Cys Lys Arg Phe Val Gly Leu Met Gly Gly Tyr Met Trp
    555                 560                 565

ATA GAA AGT GAA GGC CTA GAG AAA GGC TGC ACA GCT TCG TTC       1966
Ile Glu Ser Glu Gly Leu Glu Lys Gly Cys Thr Ala Ser Phe
        570                 575                 580

ATC ATC AGG CTT GGT ATC TGC AAC GGT CCA AGC AGT AGC AGT       2008
Ile Ile Arg Leu Gly Ile Cys Asn Gly Pro Ser Ser Ser Ser
            585                 590                 595
```

FIG. 13C

```
GGT TCA ATG GCG CTA CAT CTT GCA GCT AAA TCA CAA ACC AGA    2050
Gly Ser Met Ala Leu His Leu Ala Ala Lys Ser Gln Thr Arg
                600                 605

CCG TGG AAC TGG TGATACTTAC GTTGGAAAGA CTTGTATTGA           2092
Pro Trp Asn Trp
610

GGTGAGACTT TTTAACTACA CAGCAGCAAG AGAAAGAAGA AAATACATGA     2142

CCGGACGGTG TGATCTAACT TATTGGATTT TGTTGGATGT AATATGTAAA     2192

ATAAAAATCC TATATACGGG GAGAGGTACC TTATCTGTTC TCACTATATT     2242

TTATTGAACA TTACTTTAGA GAATATGTTT TGGAATTCAC TACTAAATAA     2292

ACGATATAAA TCTTCACGAA AA                                   2314
```

FIG. 13D

```
GAATTCGAAC TGCAATGGGA TAAACATTAT ATGCGTTTTA ATAATAGGTT     50
GGTGAAGTTT ATAATTTACA CCATTTGAAA AGCCTTCCAA ATTTAGAAAC    100
TACATTTTTG CAGACCCATG TGAGCTCATA TGAATCAATC ATAGCCTTGA    150
TGTTGTAAAA CAAATTATGA TTATAAAAAT GTGATAGTAT ATTACATGCA    200
TAAAAAATAA AGGAGAGTAA ATGAAAGTCA AATCTGGGTT TTATGAACTG    250
AAAGTTGAAG TTTAGAAGTA GAAGTAGCGA TCAAAGTATG ACCAGTTAAA    300
AGGCCCAATA TCATTTGGAG GTTTGATTTT TGGGTTCGTA AATTTCAAGA    350
GCCAGATTAT GATTTGCTGG GCTTAAAAAT CATGGAAAAA TTGAAATGAC    400
GGTGTTAAAA TATATAACTC AAATTAAAGA TTTTAATTGG GTGTAGTAGG    450
CTGATTTTTT TATAAGAATC TTGTCTATAG ATGCTTCAAG GTTATGCCTT    500
ATAGTACTGG TTGTAAAACA CCACTATCTA ATTTTGAAGC TGGTCAGAAC    550
TATAAGGTAT GTTGTTGTTC GCCTTGTTGC TAATGAAGAT TATAACATTC    600
TGTTGTTGCA TTTTTTTTTT TTTTTTTGTG TTAAATATAT ATATTTTTTT    650
TGCATATTTA TTGTTGCATA TTGTGTTGCA TATTTAGTAA TGGTTACATT    700
CCCTGTTATC GGAGACCAAG ATAATACGGC TCTGTGGCAT GGACTACTAC    750
TCCATGGATT CTTCCAAGTA ATCTTGCTTT GTGTGTCAAT GCAAAGTTTG    800
TTTATCTTAA GGTTCGTCAA CAACACTGGA AAAGTCTACA TTGTTGCTGA    850
ATCTCGGTTG TCATCGCTTC CTAGTGATAA GCCTAAGGCC GGCTTAACTA    900
ATGGAACTTA CTAGTGATAC CATAATGCGA AAGGTGCTAA TTAAGCTTGA    950
CAGTGAAGAG GATTCTTATC AAGTTTTGGA AAATTTTAAT GGAGATTCCT   1000
TGGTTGGGAA GAAGTATGAA CCTTTGTTTG ATTACTTTTA GCGATTTCTC   1050
AAGTGTGACT TTTCGACTAG TAGCAGATGA TTATGTCATG AATGATAGTG   1100
GTACTGGTAT TGTCCATTGT GCTCCTGTCT TTGGTGCAGA TGACTATCGT   1150
GTTTGTCTTG AGAACGAGAT AATTAAGAAG GTTAGATTTG ACAACATCTT   1200
CCTTATATCA CCACCTTTAA CATTAAGTTT ATTTTCTTTC TTGTTTAAGT   1250
TTACAGTATC TTCAAGAACC CATGTTCATG ACACATTTTG TTCATGTGTT   1300
GTTTAGATTG TCAGAGATTT CAAACGTCCA GATGGTTTGA AAGATACAGA   1350
GATTGATGCA GCTGTAGATA GTACATATCT TAATTAAAAA TACCACTTCT   1400
CTATGCTCTA TTGTTGAGGA AACATATAAT ATTTGCATTC GTTCATGGTT   1450
CAGATATGAT GTTATGGTAA TTCTTGATCT ACGAGAAGAT GAATCTTTGA   1500
AAAACGAAGG TGTTGCCCGT GAGGTAAATA AATGTAACCG AAGCGATTAA   1550
TGGTCATATA TAAGTTGTAT ATTTGATATA TGGGTTTCCT TCTCATTGTG   1600
```

FIG. 14A

```
CTCATGCATT GAAAAGCACC CTGTTATGAC TGTGGTTCTA GGAGAACATT    1650
TGCATTTGAC AGTCGGTGAC TAATTGTTAA GCAAGAAGAA CGCATGAGAG    1700
CCTTTTAAAG TGTTTTCTTC TAGATCGTTG CAAAAAGTTA AATGTCTCTT    1750
GAGACTTTGT ACTCATTCTA TAGATAAAGA TGGGATTTAT TACAAAAACA    1800
ACAAGAAACT TTGTTACTTG TGGAAATTCA AAATTATCCG AACTAGCTTC    1850
ACAAAATATG CTCAAGAGTT TCAATGTATT TTTTTTTGTT CTGTAATTGT    1900
ATGACTCCGT TTGAAGCATC AAGATTATGG TTATAGGTAG TGATGCTAAA    1950
ACTCTCTGTT GTTACAGTGA CCACTAAAAA CACCAACAAA AAAAACTTAG    2000
GTAACGTGTC GTCTAAAAAC TTCTAGGTTC AATTTCTTTA GATAGTACTA    2050
TCAATAAATA AAATAAATAT GTACAAAGGC TTTAAACAAT GATGTTTTTC    2100
AAAGATGATT GGTAGATACT AATTAGAGCT TCAATATAAA AGAACACATG    2150
CGATTCTGAC ATTCTGTGGT CTAACATGGT TTCTTCTAGA GTCAAAACCA    2200
TACAATTAAA AGTTAGGAAA GTAATAGCAA TGTGGTTTCA AATATATACT    2250
CATTACTCTT TAGATTCATG TATGGTGAAG GAAACATTAT AATAAAATCA    2300
AAGATCACAG TTTTGTAGGT CCCTCATATT AATCAACATC TTAAGGCGTT    2350
ATACATATCT TCTTTTTGTA AATATTTGAC TAATTAAAAT ATCTAATTAG    2400
AGTATTAGAC TAATCTCATC AAATATCCGA CTACTTGTGT CAGTTCAAAA    2450
CACAGTGATT ACGTTAGATT TTGTGCTCTT TTGTTTATAA ACAAAGCTAA    2500
TTTAAGAAAT ATATGATCTA TTTGCCTCCT TGGTCTTAAT TTTATACTTT    2550
CTTGGAATAA AACACATTTA TTAAAATAAT TTTTAGGGTC CTAGATTCAT    2600
GTCATGTGGC TTGATAGTTT CCAACAATTA TACCAATATT TTACTCATTC    2650
ATATACAAAT AAACAAGCTT TATTCTATTC TTCAGTCTCA TGATATACGG    2700
GATTTTGATA AAATTCAGAG TACCCATTAA TTATTCTATG TTACAGCTTG    2750
TAATAAGTTA AATTTATAAA ACGTACAAGT TGAGGAAATA ACAAATGTTT    2800
TCAATATTAA ATGATTTATT AATACATTAG TGACCAAAAA ATTATTAAGT    2850
GTAAGAAAAA AAACACAACT CAGAAAAAAT TCAAAAGACC GTCTAAGTTC    2900
GGTTCATGTA AGAACAAGTG GGACCTCTTT AAGTTTCTAA ATCAGAGAAT    2950
AAAGAAGAAG AAAAAATCTC AAAACCTTCC TCTAAAACCA ACGGCTCCTA    3000
CCTTTACTTA CACCCTATAC ATACACTTCT CTTTTTATCC TCCATCGGCG    3050
GCTTATGGCG GTTTTCCGGC ACTAATCATC TCCGGCATAT ATAAATAAAC    3100
GTACTTCACG TTTTTTTATA TAACTTCAAA GTAGTTTCAG ATTTGTCTCT    3150
ATCTCTTCAC TTTTAAGTCT TCTGGTTTTG TCATCACCAG CTTTTTTTGT    3200
TCTCTCTCTG TCTCTGTCTC TGTCTTTCTC TTTGTGTATT TTTATTCTCG    3250
```

FIG. 14B

```
TCATCGTTGT TCTTCTATGA GAGGAAGATC GGAATGTCGA AGAGAATTAG      3300

AAGATTCTCG TACATCACTT CGTTGGAATT TCACAGGTCG ATGAGAGATC      3350

TGAGAACTGT TTCATTTTGA TCCAAACTCA TCTCTTTCAG GTATTCCAAA      3400

TTTGTCTTTC TCTGTTCTTT CTACTATTAC CCAAATTAAA GTTTTGATTT      3450

TTATTTCTCA CTCTGTTTCT TGTTTTTCTA ATTGCAGAGT ATAATGGACT      3500

AAGCATTTTT TTTCTCCGAA G ATG GTT AAA GAA ATA GCT TCT TGG     3545
                        Met Val Lys Glu Ile Ala Ser Trp
                         1               5

TTA TTG ATA CTA TCA ATG GTG GTG TTT GTT TCT CCG GTT TTA     3587
Leu Leu Ile Leu Ser Met Val Val Phe Val Ser Pro Val Leu
     10                  15                  20

GCT ATA AAC GGC GGT GGT TAT CCA CGA TGT AAC TGC GAA GAC     3629
Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys Asn Cys Glu Asp
         25                  30                  35

GAA GGA AAC AGT TTC TGG AGT ACA GAG AAC ATT CTA GAA ACT     3671
Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu Glu Thr
             40                  45                  50

CAA AGA GTA AGC GAT TTC TTA ATC GCA GTA GCT TAT TTC TCA     3713
Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser
                 55                  60

ATC CCT ATT GAG TTA CTT TAC TTC GTG AGT TGT TCC AAT GTT     3755
Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val
 65                  70                  75

CCA TTC AAA TGG GTT CTC TTT GAG TTT ATC GCC TTC ATT GTT     3797
Pro Phe Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val
     80                  85                  90

CTT TGT GGT ATG ACT CAT CTT CTT CAT GGT TGG ACT TAC TCT     3839
Leu Cys Gly Met Thr His Leu Leu His Gly Trp Thr Tyr Ser
         95                 100                 105

GCT CAT CCA TTT AGA TTA ATG ATG GCG TTT ACT GTT TTC AAG     3881
Ala His Pro Phe Arg Leu Met Met Ala Phe Thr Val Phe Lys
            110                 115                 120

ATG TTG ACT GCT TTA GTC TCT TGT GCT ACT GCG ATT ACG CTT     3923
Met Leu Thr Ala Leu Val Ser Cys Ala Thr Ala Ile Thr Leu
                125                 130

ATT ACT TTG ATT CCT CTG CTT TTG AAA GTT AAA GTT AGA GAG     3965
Ile Thr Leu Ile Pro Leu Leu Leu Lys Val Lys Val Arg Glu
135                 140                 145

TTT ATG CTT AAG AAG AAA GCT CAT GAG CTT GGT CGT GAA GTT     4007
Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg Glu Val
    150                 155                 160

GGT TTG ATT TTG ATT AAG AAA GAG ACT GGC TTT CAT GTT CGT     4049
Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
        165                 170                 175
```

FIG. 14C

```
ATG CTT ACT CAA GAG ATT CGT AAG TCT TTG GAT CGT CAT ACG     4091
Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr
            180                 185                 190

ATT CTT TAT ACT ACT TTG GTT GAG CTT TCG AAG ACT TTA GGG     4133
Ile Leu Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly
                195                 200

TTG CAG AAT TGT GCG GTT TGG ATG CCG AAT GAC GGT GGA ACG     4175
Leu Gln Asn Cys Ala Val Trp Met Pro Asn Asp Gly Gly Thr
205                 210                 215

GAG ATG GAT TTG ACT CAT GAG TTG AGA GGG AGA GGT GGT TAT     4217
Glu Met Asp Leu Thr His Glu Leu Arg Gly Arg Gly Gly Tyr
    220                 225                 230

GGT GGT TGT TCT GTT TCT ATG GAG GAT TTG GAT GTT GTT AGG     4259
Gly Gly Cys Ser Val Ser Met Glu Asp Leu Asp Val Val Arg
        235                 240                 245

ATT AGG GAG AGT GAT GAA GTG AAT GTG TTG AGT GTT GAC TCG     4301
Ile Arg Glu Ser Asp Glu Val Asn Val Leu Ser Val Asp Ser
            250                 255                 260

TCC ATT GCT CGA GCT AGT GGT GGT GGT GGG GAT GTT AGT GAG     4343
Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val Ser Glu
                265                 270

ATT GGT GCC GTG GCT GCT ATT AGA ATG CCG ATG CTT CGT GTT     4385
Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
275                 280                 285

TCG GAT TTT AAT GGA GAG CTA AGT TAT GCG ATA CTT GTT TGT     4427
Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys
    290                 295                 300

GTT TTA CCG GGC GGG ACC CGT CGG GAT TGG ACT TAT CAG GAG     4469
Val Leu Pro Gly Gly Thr Arg Arg Asp Trp Thr Tyr Gln Glu
        305                 310                 315

ATT GAG ATT GTT AAA GTT GTG GCG GAT CAA GTA ACC GTT GCG     4511
Ile Glu Ile Val Lys Val Val Ala Asp Gln Val Thr Val Ala
            320                 325                 330

TTA GAT CAT GCA GCG GTT CTT GAA GAG TCT CAG CTT ATG AGG     4553
Leu Asp His Ala Ala Val Leu Glu Glu Ser Gln Leu Met Arg
                335                 340

GAG AAG CTG GCG GAA CAG AAC AGG GCG TTG CAG ATG GCG AAG     4595
Glu Lys Leu Ala Glu Gln Asn Arg Ala Leu Gln Met Ala Lys
345                 350                 355

AGA GAC GCG TTG AGA GCG AGC CAA GCG AGG AAT GCG TTT CAG     4637
Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg Asn Ala Phe Gln
    360                 365                 370

AAA ACG ATG AGC GAA GGG ATG AGG CGT CCT ATG CAT TCG ATA     4679
Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His Ser Ile
        375                 380                 385

CTC GGT CTT TTG TCG ATG ATT CAG GAC GAG AAG TTG AGT GAC     4721
Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
            390                 395                 400
```

FIG. 14D

```
GAG CAG AAA ATG ATT GTT GAT ACG ATG GTT AAA ACA GGG AAT    4763
Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn
                405                 410

GTT ATG TCG AAT TTG GTG GGG GAC TCT ATG GAT GTG CCT GAC    4805
Val Met Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp
415                 420                 425

GGT AGA TTT GGT ACG GAG ATG AAA CCG TTT AGT CTG CAT CGT    4847
Gly Arg Phe Gly Thr Glu Met Lys Pro Phe Ser Leu His Arg
    430                 435                 440

ACG ATC CAT GAA GCA GCT TGT ATG GCG AGA TGT TTG TGT CTA    4889
Thr Ile His Glu Ala Ala Cys Met Ala Arg Cys Leu Cys Leu
        445                 450                 455

TGC AAT GGA ATT AGG TTC TTG GTT GAC GCG GAG AAG TCT CTA    4931
Cys Asn Gly Ile Arg Phe Leu Val Asp Ala Glu Lys Ser Leu
            460                 465                 470

CCT GAT AAT GTA GTA GGT GAT GAA AGA AGG GTC TTT CAA GTG    4973
Pro Asp Asn Val Val Gly Asp Glu Arg Arg Val Phe Gln Val
                475                 480

ATA CTT CAT ATG GTT GGT AGT TTA GTA AAG CCT AGA AAA CGT    5015
Ile Leu His Met Val Gly Ser Leu Val Lys Pro Arg Lys Arg
485                 490                 495

CAA GAA GGA TCT TCA TTG ATG TTT AAG GTT TTG AAA GAA AGA    5057
Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
    500                 505                 510

GGA AGC TTG GAT AGG AGT GAT CAT AGA TGG GCT GCT TGG AGA    5099
Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg
        515                 520                 525

TCA CCG GCT TCT TCA GCA GAT GGA GAT GTG TAT ATA AGA TTT    5141
Ser Pro Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe
            530                 535                 540

GAA ATG AAT GTA GAG AAT GAT GAT TCA AGT TCT CAA TCA TTT    5183
Glu Met Asn Val Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe
                545                 550

GCT TCT GTT TCC TCC AGA GAT CAA GAA GTT GGT GAT GTT AGA    5225
Ala Ser Val Ser Ser Arg Asp Gln Glu Val Gly Asp Val Arg
555                 560                 565

TTC TCC GGC GGC TAT GGG TTA GGA CAA GAT CTA AGC TTT GGT    5266
Phe Ser Gly Gly Tyr Gly Leu Gly Gln Asp Leu Ser Phe Gly
    570                 575                 580

GTT TGT AAG AAA GTG GTG CAG GTGAGTTTCC TTACATATCT          5316
Val Cys Lys Lys Val Val Gln
        585

CTTTCTAAAG TTCCTGTCAT TAGTCTGAGT TTCTGTTTAG GAGTTCTTTG     5359
```

FIG. 14E

```
ATAATGTGTG CAG TTG ATT CAT GGG AAT ATC TCG GTG GTC CCT         5401
               Leu Ile His Gly Asn Ile Ser Val Val Pro
               590                 595

GGC TCG GAT GGT TCA CCG GAG ACC ATG TCG TTG CTC CTT CGG        5443
Gly Ser Asp Gly Ser Pro Glu Thr Met Ser Leu Leu Leu Arg
600                 605                 610

TTT CGA CGT AGA CCC TCC ATA TCT GTC CAT GGA TCC AGC GAG        5485
Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly Ser Ser Glu
    615                 620                 625

TCG CCA GCT CCT GAC CAC CAC GCT CAC CCA CAT TCG AAT TCT        5527
Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn Ser
        630                 635                 640

CTG TTA CGT GGC TTA CAA GTT TTA TTG GTA GAC ACC AAC GAT        5569
Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp
            645                 650                 655

TCG AAC CGG GCA GTT ACA CGT AAA CTC TTA GAG AAA CTC GGG        5611
Ser Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly
                660                 665

TGC GAT GTA ACC GCG GTT TCC TCT GGA TTC GAT TGC CTT ACC        5653
Cys Asp Val Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr
670                 675                 680

GCC ATT GCT CCC GGC TCG TCC TCG CCT TCT ACT TCG TTT CAA        5695
Ala Ile Ala Pro Gly Ser Ser Ser Pro Ser Thr Ser Phe Gln
    685                 690                 695

GTG GTG GTG CTT GAT CTT CAA ATG GCA GAG ATG GAC GGT TAT        5737
Val Val Val Leu Asp Leu Gln Met Ala Glu Met Asp Gly Tyr
        700                 705                 710

GAA GTG GCC ATG AGG ATC AGG AGT CGA TCT TGG CCG TTG ATT        5779
Glu Val Ala Met Arg Ile Arg Ser Arg Ser Trp Pro Leu Ile
            715                 720                 725

GTG GCG ACG ACA GTG AGC TTG GAT GAA GAA ATG TGG GAC AAG        5821
Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met Trp Asp Lys
                730                 735

TGT GCA CAG ATT GGA ATC AAT GGA GTT GTG AGA AAG CCA GTG        5863
Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro Val
740                 745                 750

GTG TTA AGA GCT ATG GAG AGT GAG CTC CGA AGA GTA TTG TTG        5905
Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu
    755                 760                 765

CAA GCT GAC CAA CTT CTC TAAGTTGTTA TCTCAACTTC TCTTCTACAT       5953
Gln Ala Asp Gln Leu Leu
        770

TCAAAATTTT TACACCATAG ATTTATGTCA AATATATCAA AATGAAATTT         6003

CGAAATTGTT ATTATATATA CCACCCATAT CTCTATGATT TGTACATCCT         6053

GTTTTTTTTT GTTCTTTTTC TCATTTTGAA CCCCACGAAA TTGCATTGAA         6103

TCTTAGTATT TCGTAGGGTC AAGAAGGAGT CAGTTTCGTA GTTTTTTGTT         6153

TTCTTTATGT TACGAACTTA CGAAACTGAA TATGGCATTA TAGAGTTTT          6202
```

FIG. 14F

```
ATG GTT AAA GAA ATA GCT TCT TGG TTA TTG ATA CTA TCA ATG     42
Met Val Lys Glu Ile Ala Ser Trp Leu Leu Ile Leu Ser Met
 1               5                   10

GTG GTG TTT GTT TCT CCG GTT TTA GCT ATA AAC GGC GGT GGT     84
Val Val Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Gly
15                  20                  25

TAT CCA CGA TGT AAC TGC GAA GAC GAA GGA AAC AGT TTC TGG    126
Tyr Pro Arg Cys Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp
    30                  35                  40

AGT ACA GAG AAC ATT CTA GAA ACT CAA AGA GTA AGC GAT TTC    168
Ser Thr Glu Asn Ile Leu Glu Thr Gln Arg Val Ser Asp Phe
        45                  50                  55

TTA ATC GCA GTA GCT TAT TTC TCA ATC CCT ATT GAG TTA CTT    210
Leu Ile Ala Val Ala Tyr Phe Ser Ile Pro Ile Glu Leu Leu
            60                  65                  70

TAC TTC GTG AGT TGT TCC AAT GTT CCA TTC AAA TGG GTT CTC    252
Tyr Phe Val Ser Cys Ser Asn Val Pro Phe Lys Trp Val Leu
                75                  80

TTT GAG TTT ATC GCC TTC ATT GTT CTT TGT GGT ATG ACT CAT    294
Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met Thr His
85                  90                  95

CTT CTT CAT GGT TGG ACT TAC TCT GCT CAT CCA TTT AGA TTA    336
Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
    100                 105                 110

ATG ATG GCG TTT ACT GTT TTC AAG ATG TTG ACT GCT TTA GTC    378
Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val
        115                 120                 125

TCT TGT GCT ACT GCG ATT ACG CTT ATT ACT TTG ATT CCT CTG    420
Ser Cys Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu
            130                 135                 140

CTT TTG AAA GTT AAA GTT AGA GAG TTT ATG CTT AAG AAG AAA    462
Leu Leu Lys Val Lys Val Arg Glu Phe Met Leu Lys Lys Lys
                145                 150

GCT CAT GAG CTT GGT CGT GAA GTT GGT TTG ATT TTG ATT AAG    504
Ala His Glu Leu Gly Arg Glu Val Gly Leu Ile Leu Ile Lys
155                 160                 165

AAA GAG ACT GGC TTT CAT GTT CGT ATG CTT ACT CAA GAG ATT    546
Lys Glu Thr Gly Phe His Val Arg Met Leu Thr Gln Glu Ile
    170                 175                 180

CGT AAG TCT TTG GAT CGT CAT ACG ATT CTT TAT ACT ACT TTG    588
Arg Lys Ser Leu Asp Arg His Thr Ile Leu Tyr Thr Thr Leu
        185                 190                 195

GTT GAG CTT TCG AAG ACT TTA GGG TTG CAG AAT TGT GCG GTT    630
Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys Ala Val
            200                 205                 210

TGG ATG CCG AAT GAC GGT GGA ACG GAG ATG GAT TTG ACT CAT    672
Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
                215                 220
```

FIG. 15A

```
GAG TTG AGA GGG AGA GGT GGT TAT GGT GGT TGT TCT GTT TCT     714
Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser
225                 230                 235

ATG GAG GAT TTG GAT GTT GTT AGG ATT AGG GAG AGT GAT GAA     756
Met Glu Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu
    240                 245                 250

GTG AAT GTG TTG AGT GTT GAC TCG TCC ATT GCT CGA GCT AGT     798
Val Asn Val Leu Ser Val Asp Ser Ser Ile Ala Arg Ala Ser
        255                 260                 265

GGT GGT GGT GGG GAT GTT AGT GAG ATT GGT GCC GTG GCT GCT     840
Gly Gly Gly Gly Asp Val Ser Glu Ile Gly Ala Val Ala Ala
            270                 275                 280

ATT AGA ATG CCG ATG CTT CGT GTT TCG GAT TTT AAT GGA GAG     882
Ile Arg Met Pro Met Leu Arg Val Ser Asp Phe Asn Gly Glu
                285                 290

CTA AGT TAT GCG ATA CTT GTT TGT GTT TTA CCG GGC GGG ACC     924
Leu Ser Tyr Ala Ile Leu Val Cys Val Leu Pro Gly Gly Thr
295                 300                 305

CGT CGG GAT TGG ACT TAT CAG GAG ATT GAG ATT GTT AAA GTT     966
Arg Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val Lys Val
    310                 315                 320

GTG GCG GAT CAA GTA ACC GTT GCG TTA GAT CAT GCA GCG GTT    1008
Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
        325                 330                 335

CTT GAA GAG TCT CAG CTT ATG AGG GAG AAG CTG GCG GAA CAG    1050
Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln
            340                 345                 350

AAC AGG GCG TTG CAG ATG GCG AAG AGA GAC GCG TTG AGA GCG    1092
Asn Arg Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala
                355                 360

AGC CAA GCG AGG AAT GCG TTT CAG AAA ACG ATG AGC GAA GGG    1134
Ser Gln Ala Arg Asn Ala Phe Gln Lys Thr Met Ser Glu Gly
365                 370                 375

ATG AGG CGT CCT ATG CAT TCG ATA CTC GGT CTT TTG TCG ATG    1176
Met Arg Arg Pro Met His Ser Ile Leu Gly Leu Leu Ser Met
    380                 385                 390

ATT CAG GAC GAG AAG TTG AGT GAC GAG CAG AAA ATG ATT GTT    1218
Ile Gln Asp Glu Lys Leu Ser Asp Glu Gln Lys Met Ile Val
        395                 400                 405

GAT ACG ATG GTT AAA ACA GGG AAT GTT ATG TCG AAT TTG GTG    1260
Asp Thr Met Val Lys Thr Gly Asn Val Met Ser Asn Leu Val
            410                 415                 420

GGG GAC TCT ATG GAT GTG CCT GAC GGT AGA TTT GGT ACG GAG    1302
Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly Thr Glu
                425                 430

ATG AAA CCG TTT AGT CTG CAT CGT ACG ATC CAT GAA GCA GCT    1344
Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
435                 440                 445
```

FIG. 15B

```
TGT ATG GCG AGA TGT TTG TGT CTA TGC AAT GGA ATT AGG TTC     1386
Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe
    450                 455                 460

TTG GTT GAC GCG GAG AAG TCT CTA CCT GAT AAT GTA GTA GGT     1428
Leu Val Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly
        465                 470                 475

GAT GAA AGA AGG GTC TTT CAA GTG ATA CTT CAT ATG GTT GGT     1470
Asp Glu Arg Arg Val Phe Gln Val Ile Leu His Met Val Gly
            480                 485                 490

AGT TTA GTA AAG CCT AGA AAA CGT CAA GAA GGA TCT TCA TTG     1512
Ser Leu Val Lys Pro Arg Lys Arg Gln Glu Gly Ser Ser Leu
                495                 500

ATG TTT AAG GTT TTG AAA GAA AGA GGA AGC TTG GAT AGG AGT     1554
Met Phe Lys Val Leu Lys Glu Arg Gly Ser Leu Asp Arg Ser
505                 510                 515

GAT CAT AGA TGG GCT GCT TGG AGA TCA CCG GCT TCT TCA GCA     1596
Asp His Arg Trp Ala Ala Trp Arg Ser Pro Ala Ser Ser Ala
    520                 525                 530

GAT GGA GAT GTG TAT ATA AGA TTT GAA ATG AAT GTA GAG AAT     1636
Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val Glu Asn
        535                 540                 545

GAT GAT TCA AGT TCT CAA TCA TTT GCT TCT GTT TCC TCC AGA     1680
Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
            550                 555                 560

GAT CAA GAA GTT GGT GAT GTT AGA TTC TCC GGC GGC TAT GGG     1722
Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly
                565                 570

TTA GGA CAA GAT CTA AGC TTT GGT GTT TGT AAG AAA GTG GTG     1764
Leu Gly Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val
575                 580                 585

CAG TTG ATT CAT GGG AAT ATC TCG GTG GTC CCT GGC TCG GAT     1806
Gln Leu Ile His Gly Asn Ile Ser Val Val Pro Gly Ser Asp
    590                 595                 600

GGT TCA CCG GAG ACC ATG TCG TTG CTC CTT CGG TTT CGA CGT     1848
Gly Ser Pro Glu Thr Met Ser Leu Leu Leu Arg Phe Arg Arg
        605                 610                 615

AGA CCC TCC ATA TCT GTC CAT GGA TCC AGC GAG TCG CCA GCT     1890
Arg Pro Ser Ile Ser Val His Gly Ser Ser Glu Ser Pro Ala
            620                 625                 630

CCT GAC CAC CAC GCT CAC CCA CAT TCG AAT TCT CTG TTA CGT     1932
Pro Asp His His Ala His Pro His Ser Asn Ser Leu Leu Arg
                635                 640

GGC TTA CAA GTT TTA TTG GTA GAC ACC AAC GAT TCG AAC CGG     1974
Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser Asn Arg
645                 650                 655

GCA GTT ACA CGT AAA CTC TTA GAG AAA CTC GGG TGC GAT GTA     2016
Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
    660                 665                 670
```

FIG. 15C

```
ACC GCG GTT TCC TCT GGA TTC GAT TGC CTT ACC GCC ATT GCT    2058
Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala
        675                 680                 685

CCC GGC TCG TCC TCG CCT TCT ACT TCG TTT CAA GTG GTG GTG    2100
Pro Gly Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val
            690                 695                 700

CTT GAT CTT CAA ATG GCA GAG ATG GAC GGT TAT GAA GTG GCC    2142
Leu Asp Leu Gln Met Ala Glu Met Asp Gly Tyr Glu Val Ala
                705                 710

ATG AGG ATC AGG AGT CGA TCT TGG CCG TTG ATT GTG GCG ACG    2184
Met Arg Ile Arg Ser Arg Ser Trp Pro Leu Ile Val Ala Thr
715                 720                 725

ACA GTG AGC TTG GAT GAA GAA ATG TGG GAC AAG TGT GCA CAG    2226
Thr Val Ser Leu Asp Glu Glu Met Trp Asp Lys Cys Ala Gln
    730                 735                 740

ATT GGA ATC AAT GGA GTT GTG AGA AAG CCA GTG GTG TTA AGA    2268
Ile Gly Ile Asn Gly Val Val Arg Lys Pro Val Val Leu Arg
        745                 750                 755

GCT ATG GAG AGT GAG CTC CGA AGA GTA TTG TTG CAA GCT GAC    2310
Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln Ala Asp
            760                 765                 770

CAA CTT CTC TAAGTTGTTA TCTCAACTTC TCTTCTACAT TCAAAATTTT    2259
Gln Leu Leu

TACACCATAG ATTTATGTCA AATATATCAA AATGAAATTT CGAAA          2404
```

FIG. 15D

```
TTTTTTTTTT GTCAAAAGCT CGATGTAAAA ATCCGATGGC CACAAGCAAA       50

ACGACAGGTT CCAACTTCAC GGAGATTGTG AAAATGGAGT AGTAGTTCAG      100

TGAAGTAGTA GATACTGAGA TCGCATTCTC CGGCGTCGTT TTTCACATCG      150

AAATAGTCGT GTAAAAAAAT GAAAAAATTG CTGCGAGACA GGTATGTGTC      200

GCAGCAGGAA ATAGCATCTT AAAGGAAGGA AGGAAGGAAA CTCGAAAGTT      250

ACTAAAAATT TTTGATTCTT TGGGACGAAA CGAGATA ATG GAA TCC        296
                                         Met Glu Ser
                                          1

TGT GAT TGC ATT GAG GCT TTA CTG CCA ACT GGT GAC CTG CTG     338
Cys Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu Leu
     5                   10                  15

GTT AAA TAC CAA TAC CTC TCA GAT TTC TTC ATT GCT GTA GCC     380
Val Lys Tyr Gln Tyr Leu Ser Asp Phe Phe Ile Ala Val Ala
         20                  25                  30

TAC TTT TCC ATT CCG TTG GAG CTT ATT TAT TTT GTC CAC AAA     422
Tyr Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val His Lys
             35                  40                  45

TCT GCA TGC TTC CCA TAC AGA TGG GTC CTC ATG CAA TTT GGT     464
Ser Ala Cys Phe Pro Tyr Arg Trp Val Leu Met Gln Phe Gly
                 50                  55

GCT TTT ATT GTG CTC TGT GGA GCA ACA CAC TTT ATT AGC TTG     506
Ala Phe Ile Val Leu Cys Gly Ala Thr His Phe Ile Ser Leu
 60                  65                  70

TGG ACC TTC TTT ATG CAC TCT AAG ACG GTC GCT GTG GTT ATG     548
Trp Thr Phe Phe Met His Ser Lys Thr Val Ala Val Val Met
     75                  80                  85

ACC ATA TCA AAA ATG TTG ACA GCT GCC GTG TCC TGT ATC ACA     590
Thr Ile Ser Lys Met Leu Thr Ala Ala Val Ser Cys Ile Thr
         90                  95                 100

GCT TTG ATG CTT GTT CAC ATT ATT CCT GAT TTG CTA AGT GTT     632
Ala Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val
            105                 110                 115

AAA ACG CGA GAG TTG TTC TTG AAA ACT CGA GCT GAA GAG CTT     674
Lys Thr Arg Glu Leu Phe Leu Lys Thr Arg Ala Glu Glu Leu
                120                 125

GAC AAG GAA ATG GGC CTA ATA ATA AGA CAA GAA GAA ACT GGC     716
Asp Lys Glu Met Gly Leu Ile Ile Arg Gln Glu Glu Thr Gly
130                 135                 140

AGA CAT GTC AGG ATG CTG ACT CAT GAG ATA AGA AGC ACA CTC     758
Arg His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu
    145                 150                 155

GAC AGA CAC ACA ATC TTG AAG ACT ACT CTT GTG GAG CTA GGT     800
Asp Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly
        160                 165                 170
```

FIG. 16A

```
AGG ACC TTA GAC CTG GCA GAA TGT GCT TTG TGG ATG CCA TGC       842
Arg Thr Leu Asp Leu Ala Glu Cys Ala Leu Trp Met Pro Cys
            175                 180                 185

CAA GGA GGC CTG ACT TTG CAA CTT TCC CAT AAT TTA AAC AAT       884
Gln Gly Gly Leu Thr Leu Gln Leu Ser His Asn Leu Asn Asn
                190                 195

CTA ATA CCT CTG GGA TCT ACT GTG CCA ATT AAT CTT CCT ATT       926
Leu Ile Pro Leu Gly Ser Thr Val Pro Ile Asn Leu Pro Ile
200                 205                 210

ATC AAT GAA ATT TTT AGT AGC CCT GAA GCA ATA CAA ATT CCA       968
Ile Asn Glu Ile Phe Ser Ser Pro Glu Ala Ile Gln Ile Pro
    215                 220                 225

CAT ACA AAT CCT TTG GCA AGG ATG AGG AAT ACT GTT GGT AGA      1010
His Thr Asn Pro Leu Ala Arg Met Arg Asn Thr Val Gly Arg
        230                 235                 240

TAT ATT CCA CCA GAA GTA GTT GCT GTT CGT GTA CCG CTT TTA      1052
Tyr Ile Pro Pro Glu Val Val Ala Val Arg Val Pro Leu Leu
            245                 250                 255

CAC CTC TCA AAT TTT ACT AAT GAC TGG GCT GAA CTG TCT ACT      1094
His Leu Ser Asn Phe Thr Asn Asp Trp Ala Glu Leu Ser Thr
                260                 265

AGA AGT TAT GCG GTT ATG GTT CTG GTT CTC CCG ATG AAT GGC      1136
Arg Ser Tyr Ala Val Met Val Leu Val Leu Pro Met Asn Gly
270                 275                 280

TTA AGA AAG TGG CGT GAA CAT GAG TTA GAA CTT GTG CAA GTT      1178
Leu Arg Lys Trp Arg Glu His Glu Leu Glu Leu Val Gln Val
    285                 290                 295

GTC GCA GAT CAG GTT GCT GTC GCT CTT TCA CAT GCT GCA ATT      1220
Val Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile
        300                 305                 310

TTA GAA GAT TCC ATG CGA GCC CAT GAT CAG CTC ATG GAA CAG      1262
Leu Glu Asp Ser Met Arg Ala His Asp Gln Leu Met Glu Gln
            315                 320                 325

AAT ATT GCT TTG GAT GTA GCT CGA CAA GAA GCA GAG ATG GCC      1304
Asn Ile Ala Leu Asp Val Ala Arg Gln Glu Ala Glu Met Ala
                330                 335

ATC CGT GCA CGT AAC GAC TTC CTT GCT GTG ATG AAC CAT GAA      1346
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu
340                 345                 350

ATG AGA ACG CCC ATG CAT GCA GTT ATT GCT CTG TGC TCT CTG      1388
Met Arg Thr Pro Met His Ala Val Ile Ala Leu Cys Ser Leu
    355                 360                 365

CTT TTA GAA ACA GAC TTA ACT CCA GAG CAG AGA GTT ATG ATT      1430
Leu Leu Glu Thr Asp Leu Thr Pro Glu Gln Arg Val Met Ile
        370                 375                 380

GAG ACC ATA TTG AAG AGC AGC AAT CTT CTT GCA ACA CTG ATA      1472
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Ile
            385                 390                 395
```

FIG. 16B

```
AAT GAT GTT CTA GAT CTT TCT AGA CTT GAA GAT GGT ATT CTT    1514
Asn Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ile Leu
                400                 405

GAA CTA GAA AAC GGA ACA TTC AAT CTT CAT GGC ATC TTA AGA    1556
Glu Leu Glu Asn Gly Thr Phe Asn Leu His Gly Ile Leu Arg
410                 415                 420

GAG GCC GTT AAT TTG ATA AAG CCA ATT GCA TCT TTG AAG AAA    1598
Glu Ala Val Asn Leu Ile Lys Pro Ile Ala Ser Leu Lys Lys
    425                 430                 435

TTA TCT ATA ACT CTT GCT TTG GCT CTG GAT TTA CCT ATT CTT    1640
Leu Ser Ile Thr Leu Ala Leu Ala Leu Asp Leu Pro Ile Leu
        440                 445                 450

GCT GTG GGT GAT GCA AAA CGT CTT ATC CAA ACT CTC TTA AAC    1682
Ala Val Gly Asp Ala Lys Arg Leu Ile Gln Thr Leu Leu Asn
            455                 460                 465

GTG GTG GGA AAT GCT GTG AAG TTC ACT AAA GAA GGA CAT ATT    1724
Val Val Gly Asn Ala Val Lys Phe Thr Lys Glu Gly His Ile
                470                 475

TCA ATT GAG GCT TCA GTT GCC AAA CCA GAG TAT GCG AGA GAT    1766
Ser Ile Glu Ala Ser Val Ala Lys Pro Glu Tyr Ala Arg Asp
480                 485                 490

TGT CAT CCT CCT GAA ATG TTC CCT ATG CCA AGT GAT GGC CAG    1808
Cys His Pro Pro Glu Met Phe Pro Met Pro Ser Asp Gly Gln
    495                 500                 505

TTT TAT TTG CGT GTC CAG GTT AGA GAT ACT GGG TGT GGA ATT    1850
Phe Tyr Leu Arg Val Gln Val Arg Asp Thr Gly Cys Gly Ile
        510                 515                 520

AGC CCA CAA GAT ATA CCA CTA GTA TTC ACC AAA TTT GCA GAG    1892
Ser Pro Gln Asp Ile Pro Leu Val Phe Thr Lys Phe Ala Glu
            525                 530                 535

TCA CGG CCT ACG TCA AAT CGA AGT ACT GGA GGG GAA GGT CTA    1934
Ser Arg Pro Thr Ser Asn Arg Ser Thr Gly Gly Glu Gly Leu
                540                 545

GGG CTT GCC ATT TGG AGA CGA TTT ATT CAA CTT ATG AAA GGT    1976
Gly Leu Ala Ile Trp Arg Arg Phe Ile Gln Leu Met Lys Gly
550                 555                 560

AAC ATT TGG ATT GAG AGT GAG GGC CCT GGA AAG GGA ACC ACT    2018
Asn Ile Trp Ile Glu Ser Glu Gly Pro Gly Lys Gly Thr Thr
    565                 570                 575

GTC ACG TTT GTA GTG AAA CTC GGA ATC TGT CAC CAT CCA AAT    2060
Val Thr Phe Val Val Lys Leu Gly Ile Cys His His Pro Asn
        580                 585                 590

GCA TTA CCT CTG CTA CCT ATG CCT CCC AGA GGC AGA TTG AAC    2102
Ala Leu Pro Leu Leu Pro Met Pro Pro Arg Gly Arg Leu Asn
            595                 600                 605

AAA GGT AGC GAT GAT CTC TTC AGG TAT AGA CAG TTC CGT GGA    2144
Lys Gly Ser Asp Asp Leu Phe Arg Tyr Arg Gln Phe Arg Gly
                610                 615
```

FIG. 16C

```
GAT GAT GGT GGG ATG TCT GTG AAT GCT CAA CGC TAT CAA AGA    2186
Asp Asp Gly Gly Met Ser Val Asn Ala Gln Arg Tyr Gln Arg
620                 625                 630

AGT ATG TAA A TGACAAAAGG ACATTGGTGT GACAAAGAAC             2226
Ser Met  *
    635

ATTAAATCAT GACTAGTGAA TTTGAGATTT CTTCACTGTT CTGTACACTC     2276

CAAATGGCAC AGTTTGTCTT GTAACTAACC TAATTCAATG CTCGTAAAGT     2326

GAGTACTGGA GTATCTTGAA AATGTAACTA TCGAATTTAT ACATCGAGCT     2376

TTTGACAAAA AAAAAAAAAA AAAAAAAAA                            2405
```

FIG. 16D

```
                   .         .         .         .         .
Tetr    1 MESCDCIEALLPTGDLLVKYQYLSDFFIAVAYFSIPLELIYFVHKSACFP 50
          || |:|||: :|.::||:||||:||||||:|||||||||||||.|||.||
Etr1    1 MEVCNCIEPQWPADELLMKYQYISDFFIAVAYFSIPLELIYFVKKSAVFP 50

                   .         .         .         .         .
         51 YRWVLMQFGAFIVLCGATHFISLWTFFMHSKTVAVVMTISKMLTAAVSCI 100
            |||||:|||||||||||||:|.||||  ||:|||:|||..|:|||.|||
         51 YRWVLVQFGAFIVLCGATHLINLWTFTTHSRTVALVMTTAKVLTAVVSCA 100

                   .         .         .         .         .
        101 TALMLVHIIPDLLSVKTRELFLKTRAEELDKEMGLIIRQEETGRHVRMLT 150
            |||||||||||||||||||||||.:|.|||:|||||  ||||||||||||
        101 TALMLVHIIPDLLSVKTRELFLKNKAAELDREMGLIRTQEETGRHVRMLT 150

                   .         .         .         .         .
        151 HEIRSTLDRHTILKTTLVELGRTLDLAECALWMPCQGGLTLQLSHNLNNL 200
            ||||||||||||||||||||||||.|.|||||||...||.||||..|.:
        151 HEIRSTLDRHTILKTTLVELGRTLALEECALWMPTRTGLELQLSYTLRHQ 200

                   .         .         .         .         .
        201 IPLGSTVPINLPIINEIFSSPEAIQIPHTNPLARMRNTVGRYIPPEVVAV 250
             |:: ||||.||:||::|:.. |:.|....|:||:| . |:|: .|||||
        201 HPVEYTVPIQLPVINQVFGTSRAVKISPNSPVARLRPVSGKYMLGEVVAV 250

                   .         .         .         .         .
        251 RVPLLHLSNF.TNDWAELSTRSYAVMVLVLPMNGLRKWREHELELVQVVA 299
            |||||||||| .|||:||||:.||:|||:|| :: |.|: ||||||:|||
        251 RVPLLHLSNFQINDWPELSTKRYALMVLMLPSDSARQWHVHELELVEVVA 300

                   .
        300 DQVAVALSHAAILEDS 315
            ||||||||||||||:|
        301 DQVAVALSHAAILEES 316
```

FIG. 17

```
AGATCTGGTA CTACCAAAAG GTATCCAATT AATCCATGCT TGGCCTCCCA        50

TTACAATGCC TGTAAGAAAT AATTGTTCTT TCCACCTCCA CAACTAATTG       100

TCGAACTATT ATATCTATCT TTATTCCCTT AAATGTGAAA CGAATTACAC       150

AGACTATTTG GCGCTACTTT TTTCCTAGAT ATATTGAAGA CCTAGTTTCT       200

TATATTTGTG GGAAGCATTT GGAAGTTCTA TAAGAACTAT ATCATGTTCG       250

AAAACATTCT TATAATTTTC GACAAGATTG CTGAAGGAGT GTCTTATCTT       300

TTATGTATTC TTGACTAGAG GAGTTTAATA AAAAGAAAAT AGAAAGGAAC       350

AAAGAAACGT ACAAGTGTAT AAAAGGAGTT GGGGCAAAGA CATCAGAAAC       400

ATTTAGACCT ACGATTTCAT CCTACATGTT ATGGTTTTAG TTCGTTAGAG       450

GTTTTAACAT ATTAAATCAG CAAAGTTGTG ACATACATAA AGTGCATAAC       500

ATAAAGATGA AATTCACAAT TTGCTGGATC TTTTGGTGCA AGGGAACTAT       550

TTTTTACACT ATAAGTTAGC TGTTAATTTC AATATTGGCT CTTCTACACC       600

TTGTTGTTCT TGAGTATAAT TCTATTTTGC ATCAAACATA TGTCAGAACT       650

TATGCTGCAA TTAAATATAT TCAGGTTGTT TAACTCTTGT ACAGCTTGTT       700

ATTCTTCTGA GGTCTATTTC CTTCTCCTTA TTTGCTAACT TGTGCTGCAG       750

TTATCTTCCA TC GTG GAG TCA TGT AAC TGC ATC ATT GAC CCA        792
              Val Glu Ser Cys Asn Cys Ile Ile Asp Pro
               1               5                  10

CAG TTG CCT GCT GAC GAC TTG CTA ATG AAG TAT CAG TAC ATT      834
Gln Leu Pro Ala Asp Asp Leu Leu Met Lys Tyr Gln Tyr Ile
                15                  20

TCT GAT TTT TTC ATA GCA CTT GCT TAT TTC TCC ATT CCA GTG      876
Ser Asp Phe Phe Ile Ala Leu Ala Tyr Phe Ser Ile Pro Val
 25                 30                  35

GAG TTG ATA TAC TTC GTT AAG AAG TCT GCT GTC TTT CCA TAT      918
Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val Phe Pro Tyr
     40                  45                  50

AGA TGG GTT CTT GTG CAG TTC GGT GCT TTC ATA GTT CTT TGT      960
Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu Cys
         55                  60                  65

GGA GCA ACC CAT CTT ATC AAC TTA TGG ACA TTT AAT ATG CAT     1002
Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Asn Met His
             70                  75                  80

ACA AGG AAT GTG GCA ATA GTA ATG ACT ACT GCA AAG GCC TTG     1044
Thr Arg Asn Val Ala Ile Val Met Thr Thr Ala Lys Ala Leu
                 85                  90

ACT GCA CTG GTG TCA TGT ATA ACT GCT CTC ATG CTT GTC CAC     1086
Thr Ala Leu Val Ser Cys Ile Thr Ala Leu Met Leu Val His
 95                 100                 105
```

FIG. 18A

```
ATC ATT CCT GAT TTA TTA AGT GTC AAA ACT AGA GAA CTG TTC     1128
Ile Ile Pro Asp Leu Leu Ser Val Lys Thr Arg Glu Leu Phe
    110                 115                 120

TTG AAA AAG AAA GCT GCA CAG CTT GAC CGT GAA ATG GGT ATT     1170
Leu Lys Lys Lys Ala Ala Gln Leu Asp Arg Glu Met Gly Ile
        125                 130                 135

ATT CGG ACT CAG GAG GAG ACA GGT AGA CAT GTT AGA ATG CTA     1212
Ile Arg Thr Gln Glu Glu Thr Gly Arg His Val Arg Met Leu
            140                 145                 150

ACT CAT GAA ATC CGA AGC ACT CTT GAT AGA CAT ACT ATT TTA     1254
Thr His Glu Ile Arg Ser Thr Leu Asp Arg His Thr Ile Leu
                155                 160

AAG ACT ACA CTT GTT GAG CTA GGA AGA ACA TTG GCA TTG GAA     1296
Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu Glu
165                 170                 175

GAG TGT GCA TTA TGG ATG CCA ACA CGT ACT GGA CTA GAG CTT     1338
Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu
    180                 185                 190

CAG CTT TCT TAC ACT TTA CGA CAC CAA AAT CCA GTT GGA TTA     1380
Gln Leu Ser Tyr Thr Leu Arg His Gln Asn Pro Val Gly Leu
        195                 200                 205

ACT GTA CCC ATT CAA CTT CCT GTA ATC AAT CAA GTT TTC GGT     1422
Thr Val Pro Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly
            210                 215                 220

ACA AAT CAT GTC GTG AAA ATA TCA CCA AAT TCT CCT GTC GCA     1464
Thr Asn His Val Val Lys Ile Ser Pro Asn Ser Pro Val Ala
                225                 230

AGA CTT CGA CCT GCT GGG AAA TAC ATG CCT GGT GAG GTG GTT     1506
Arg Leu Arg Pro Ala Gly Lys Tyr Met Pro Gly Glu Val Val
235                 240                 245

GCT GTC AGG GTT CCA CTT CTG CAT CTG TCG AAC TTT CAG ATT     1548
Ala Val Arg Val Pro Leu Leu His Leu Ser Asn Phe Gln Ile
    250                 255                 260

AAT GAT TGG CCT GAA CTT TCA ACA AAG CGC TAT GCT TTA ATG     1590
Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg Tyr Ala Leu Met
        265                 270                 275

GTT CTG ATG CTT CCT TCA GAC AGT GCA AGA CAA TGG CAT GTT     1632
Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp His Val
            280                 285                 290

CAT GAG CTG GAG CTT GTT GAA GTG GTA GCT GAT CAG GTT         1671
His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val
                295                 300

TGATTTTTGT TATTGAAAAT TCCTTAATAT AATGTTAAAA TTTCTCTTTT      1721

ATATATTTTT GGGTTGAACA CAACCACGTT GACATACTGA GTTCTGGGTG      1771

TAAAATTAGA CATGGAGAAG ACCAATTACA AAAATCTGAG AATCTGCTAG      1821

CAGAATCACA AGGCTTAGTT GTTCTTAGTA TTATGGTTTT ATCCATTGGA      1871
```

FIG. 18B

```
ATTGCACAGC AGAATTGTTA TTACTGTTAT TTTTTTTTAA AATTTTCAAA    1921

GATAAATCAA AAGCTGAACT ATATGACTTT TTGCATACTT CGTCTGCTGA    1971

TTGCTTTTTG GTGATGGAAT AGTTAGGCTG GGTTGTGGAT GAGTATATCA    2021

TAGTAGATTT TCTGATAGGA TCTTAACTCC TTGGCTTTTG TTTTCTATAG    2071

ATGATCCCTT GTATTAGAAG CACGGGAAAT AGGATCGATG GTATATAGAA    2121

ATATTAGGAA CAGCTTTCTG AATCATTTGA ATATTCCTTT TATGGAACAT    2171

AGAACTCTTG ACGTGTATGT AGTTTTCTTA GTACTTTTAT CATATGAAGT    2221

GAAAATAACG TTTTGCGATA ATGTATTTGA GTGTGTAAAA TTAAATACTA    2271

CTGAGTTTTA CAAAAATAAT TCTTCAACGG AAGCCATTTA TTTTTTTTAC    2321

ATATCTGGCA TCTTACTTCT CCATCAAAGA CTTTAGAGAA CTTTAACTTT    2371

TTCATTCTGT CTCTCGTAGT GTACTGTTCT CTGATGTATG TAATTAGCTC    2421

ACTGGCAAGT AGCACACCTA GTCTTTGTTT GACTTGTTTA AAAATCATGA    2471

TGTATCATCA GTTACGGTGA AGTGTCCAAG TTTTACTGCT TTTTGCTATT    2521

TGCATTGCAG AGTCTTAAAA CATTTCAGTT ATTCCTGGAT TTCTCCTGTT    2571

TATCAATGGA AAATTCAACT ATCAACTATG CCTCAATCAA TAAATGAAAC    2621

CTCTATATCT AACCACTCCA ACTCAGATCC AGAAATCAGA TTTCAAAGAA    2671

ATTCATCATA ACTCAACTAT AGGATTGCTG TTAACCAAGA GTAATCCTCA    2721

TTTGTCCAGA CAGGCGACCA GCTATTATGC TTTCATTATG GGAAAAATTG    2771

ACAATTAATT AAAGGAAGGA ACAACTGAAG AAAAGACATC CTTGTCAGCT    2821

TCCTCTCCCA ACCCTTGCCT GAATAAGACA AAAAGTTTCT TGGAGAAAAC    2871

TCTGAATATT GGTATCCACC TCCTTTCTCC TAATTTAGGA TGCTCTATTT    2921

CTAGACATAT AGGGGAATAC TCTATTCTAG TGGTCGGTGT CTGGTTGCAA    2971

CTAGTTTTAG ATGTTTATAT GTCTTATTTG ATTTAATAAG AGCTATCCTT    3021

GAGTGCCCAA TGTGATTTAA TCTACGCTTC GGCATTTCAG GTT GCT GTT    3070
                                            Val Ala Val
                                                305

GCT CTT TCA CAT GCT GCT ATA TTA GAA GAA TCA ATG AGG GCT    3112
Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala
            310                 315                 320

AGG GAT CTT CTT ATG GAG CAG AAT GTG GCT CTT GAT CTG GCA    3154
Arg Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala
                325                 330

AGA AGA GAA GCA GAA ATG GCT GTT CGT GCA CGT AAT GAT TTC    3196
Arg Arg Glu Ala Glu Met Ala Val Arg Ala Arg Asn Asp Phe
335                 340                 345
```

FIG. 18C

```
TTG GCT GTT ATG AAT CAT GAA ATG AGA ACT CCC ATG CAT GCA   3238
Leu Ala Val Met Asn His Glu Met Arg Thr Pro Met His Ala
    350                 355                 360

ATA ATT GCA CTT TCT TCC TTA CTA CAA GAA ATC GAT CTA ACT   3280
Ile Ile Ala Leu Ser Ser Leu Leu Gln Glu Ile Asp Leu Thr
        365                 370                 375

CCA GAG CAA CGT CTG ATG GTT GAA ACA ATC CTC AAA AGC AGC   3322
Pro Glu Gln Arg Leu Met Val Glu Thr Ile Leu Lys Ser Ser
            380                 385                 390

AAC CTT TTA GCA ACG CTC ATC AAC GAT GTC TTG GAT CTT TCA   3364
Asn Leu Leu Ala Thr Leu Ile Asn Asp Val Leu Asp Leu Ser
                395                 400

AGG CTA GAG GAT GGA AGT CTT CAA CTT GAT ATT GGC ACT TTC   3406
Arg Leu Glu Asp Gly Ser Leu Gln Leu Asp Ile Gly Thr Phe
405                 410                 415

AAT CTC CAT GCT TTA TTT AGA GAG GTG CCCTTCATCA CCCTCTTTTC 3453
Asn Leu His Ala Leu Phe Arg Glu Val
    420                 425

TTTTTTACTT GCAAATTCTA GATTACCTGT CAGAAAAAAA GTGTCATTAC    3503

AGATATTTTG CACTTCAATA TGTTTGCTGG ACCTGCTGAC TGATATATGT    3553

GTCTGCTTAT TCCTGTAG GTC CAT AGC TTA ATC AAG CCT ATT GCA   3598
                    Val His Ser Leu Ile Lys Pro Ile Ala
                            430                 435

TCT GTG AAA AAG TCT GTT GCT CAA CTT AGT TTG TCG TCA GAT   3640
Ser Val Lys Lys Ser Val Ala Gln Leu Ser Leu Ser Ser Asp
            440                 445                 450

TTG CCG GAA TAT GTA ATT GGG GAT GAA AAA CGG TTA ATG CAA   3682
Leu Pro Glu Tyr Val Ile Gly Asp Glu Lys Arg Leu Met Gln
                455                 460

ATT CTC TTA AAC GTT GTT GGC AAT GCT GTA AAG TTC TCA AAG   3724
Ile Leu Leu Asn Val Val Gly Asn Ala Val Lys Phe Ser Lys
465                 470                 475

GAA GGC AAC GTA TCA ATC TCC GCT TTT GTT GCA AAA TCA GAC   3766
Glu Gly Asn Val Ser Ile Ser Ala Phe Val Ala Lys Ser Asp
    480                 485                 490

TCT TTA AGA GAT CCT AGA GCC CCT GAA TTT TTT GCT GTG CCT   3808
Ser Leu Arg Asp Pro Arg Ala Pro Glu Phe Phe Ala Val Pro
        495                 500                 505

AGT GAA AAT CAC TTC TAT TTA CGG GTG CAG                   3838
Ser Glu Asn His Phe Tyr Leu Arg Val Gln
            510                 515

GTATATTTTT ACAAGCTTGA TATACTATCT TCGTAGGTTA AGGATAGTCA    3888

CAAATATGAT ATTTTAGACT TATAACTGTC AGATGTTCTG TTCTTGATAT    3938

TTGTAATATT CTAAGTAATA CTTTCTGTAG                          3968
```

FIG. 18D

```
ATA AAA GAT ACG GGG ATA GGA ATT ACA CCA CAG GAT ATT CCC    4010
Ile Lys Asp Thr Gly Ile Gly Ile Thr Pro Gln Asp Ile Pro
            520                 525                 530

AAC CTG TTT AGC AAG TTT ACA CAA AGC CAA GCG CTA GCA ACT    4052
Asn Leu Phe Ser Lys Phe Thr Gln Ser Gln Ala Leu Ala Thr
                535                 540

ACA AAT TCT GGT GGC ACT GGG CTT GGT CTT GCA ATT TGT AAG    4094
Thr Asn Ser Gly Gly Thr Gly Leu Gly Leu Ala Ile Cys Lys
545                 550                 555

AG GTACGGGTAC CAGTTCCTTA GTGTTCTTTT TCCGACTCTG             4136
Arg

ATTTTCATTC TACGTGAACT TGGTAACTGC TTCATATTCA ATTTCTTTCT     4186

CTTACTGTAT TTACGTATTG ACACATCTCC TGATGGGACA CAAAAAG G      4234

TTT GTG AAT CTT ATG GAA GGA CAT ATT TGG ATT GAA AGT GAA    4276
Phe Val Asn Leu Met Glu Gly His Ile Trp Ile Glu Ser Glu
560                 565                 570

GGT CTT GGC AAG GGG TCT ACT GCT ATA TTT ATC ATT AAA CTT    4318
Gly Leu Gly Lys Gly Ser Thr Ala Ile Phe Ile Ile Lys Leu
    575                 580                 585

GGA CTT CCT GGA CGT GCA AAT GAA TCT AAG CTC CCC TTT GTG    4360
Gly Leu Pro Gly Arg Ala Asn Glu Ser Lys Leu Pro Phe Val
        590                 595                 600

ACC AAA TTG CCA GCA AAT CAC ACG CAG ATG AGT TTT AAG GAT    4402
Thr Lys Leu Pro Ala Asn His Thr Gln Met Ser Phe Lys Asp
            605                 610                 615

TAAAGGTTTT GGTGATGGAT GAGAATGGGT GAGTACTATC TGGACCCCTT     4452

TATCCTCGAC TCTTGTCTTG CCATGCTGTT TAATGATCCA TCTGATTGCG     4502

TGATTTCTCA TCTTATATGT ATTGAGCTGT CTTACTCACT TTACATGAGA     4552

CTACAGTAAT ACTT                                            4566
```

FIG. 18E

```
AAGATAAGAG TGATTCATTA AGGAGTTTGT TC ATC ATG GAT TGT AAC      47
                                   Ile Met Asp Cys Asn
                                    1               5

TGC TTC GAT CCA CTG TTG CCT GCC GAT GAG TTG TTA ATG AAG      89
Cys Phe Asp Pro Leu Leu Pro Ala Asp Glu Leu Leu Met Lys
                 10                  15

TAT CAG TAC ATT TCT GAT TTT TTC ATT GCA GTT GCT TAT TTT     131
Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Val Ala Tyr Phe
 20                  25                  30

TCC ATC CCA ATC GAA CTG GTA TTC TTT GTC CAG AAA TCA GCT     173
Ser Ile Pro Ile Glu Leu Val Phe Phe Val Gln Lys Ser Ala
     35                  40                  45

GTT TTT CCG TAT CGA TGG GTG CTT GTG CAG TTT GGT GCT TTC     215
Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe
         50                  55                  60

ATA GTT CTT TGT GGA GCA ACA CAC CTT ATC AAT TTG TGG ACT     257
Ile Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr
             65                  70                  75

TCT ACT CCT CAT ACA AGG ACT GTG GCA ATG GTG ATG ACT ACG     299
Ser Thr Pro His Thr Arg Thr Val Ala Met Val Met Thr Thr
                 80                  85

GCG AAG TTC TCC ACT GCT GCG GTA TCA TGT GCA ACT GCT GTC     341
Ala Lys Phe Ser Thr Ala Ala Val Ser Cys Ala Thr Ala Val
 90                  95                 100

ATG CTT GTC GCA ATT ATT CCG GAT TTA TTA AGT GTC AAA ACT     383
Met Leu Val Ala Ile Ile Pro Asp Leu Leu Ser Val Lys Thr
    105                 110                 115

AGG GAG CTA TTC TTG AAA AAC AAA GCG GCG GAA CTT GAT CGT     425
Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp Arg
        120                 125                 130

GAA ATG GGT CTT ATT CGG ACA CAG GAG GAG ACG GGT AGA TAT     467
Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg Tyr
            135                 140                 145

GTT AGA ATG CTA ACA CAT GAA ATC AGA AGT ACT CTG GAT AGA     509
Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg
                150                 155

CAT ACT ATT TTG AAG ACT ACA CTT GTT GAA CTT GGA AGA GCA     551
His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Ala
160                 165                 170

TTG CAA CTG GAA GAG TGT GCT TTG TGG ATG CCG ACT CGA ACT     593
Leu Gln Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr
    175                 180                 185

GGA GTG GAG CTT CAA CTT TCT TAC ACT TTA CAT CAT CAA AAT     635
Gly Val Glu Leu Gln Leu Ser Tyr Thr Leu His His Gln Asn
        190                 195                 200

CCA GTT GGA TTT ACA GTA CCT ATA CAA CTC CCT GTA ATT AAT     677
Pro Val Gly Phe Thr Val Pro Ile Gln Leu Pro Val Ile Asn
            201                 210                 215
```

FIG. 19A

```
CAA GTT TTC AGT GCA AAT TGT GCT GTT AAA ATT TCA CCT            716
Gln Val Phe Ser Ala Asn Cys Ala Val Lys Ile Ser Pro
                220                 225

TAATCTGCCG TTGCAAGGCT T                                        737
```

FIG. 19B

```
                    .         .         .         .         .
Tgetr1   1 VESCNCIIDPQLPADDLLMKYQVISDFFIALAYFSIPVELIYFVKKSAVF 50
           :| |||| :||:|||:||||||||||||||:||||||:||||||||||||
  Etr1   1 MEVCNCI.EPQWPADELLMKYQVISDFFIAIAYFSIPLELIYFVKKSAVF 49

                    .         .         .         .         .
        51 PYRWVLVQFGAFIVLCGATHLINLWTFNMHTRNVAIVMTTAKALTALVSC 100
           |||||||||||||||||||||||||||. |.|.||:||||||.|||:|||
        50 PYRWVLVQFGAFIVLCGATHLINLWTFTTHSRTVALVMTTAKVLTAVVSC 99

                    .         .         .         .         .
       101 ITALMLVHIIPDLLSVKTRELFLKKKAAQLDREMGIIRTQEETGRHVRML 150
            |||||||||||||||||||||||.|||:||||||:||||||||||||||
       100 ATALMLVHIIPDLLSVKTRELFLKNKAAELDREMGLIRTQEETGRHVRML 149

                    .         .         .         .         .
       151 THEIRSTLDRHTILKTTLVELGRTLALEECALWMPTRTGLELQLSYTLRH 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       150 THEIRSTLDRHTILKTTLVELGRTLALEECALWMPTRTGLELQLSYTLRH 199

                    .         .         .         .         .
       201 QNPVGLTVPIQLPVINQVFGTNHVVKISPNSPVARLRP.AGKYMPGEVVA 249
           |:||:.|||||||||||||||.:.|||||||||||||| .||||||||||
       200 QHPVEYTVPIQLPVINQVFGTSRAVKISPNSPVARLRPVSGKYMLGEVVA 249

                    .         .         .         .         .
       250 VRVPLLHLSNFQINDWPELSTKRYALMVLMLPSDSARQWHVHELELVEVV 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       250 VRVPLLHLSNFQINDWPELSTKRYALMVLMLPSDSARQWHVHELELVEVV 299

                    .
       300 ADQVAVALSHAAILEES 316
           |||||||||||||||||
       300 ADQVAVALSHAAILEES 316
```

FIG. 20

```
                    .         .         .         .         .
Tgetr2  11 IMDCNCFDPLLPADELLMKYQYISDFFIAVAYFSIPIELVFFVQKSAVFP 60
           :  |||::| :||||||||||||||||||:||||||:||::||.||||||
Etr1     1 MEVCNCIEPQWPADELLMKYQYISDFFIAIAYFSIPLELIYFVKKSAVFP 50

                    .         .         .         .         .
        61 YRWVLVQFGAFIVLCGATHLINLWTSTPHTRTVAMVMTTAKFSTAAVSCA 110
           ||||||||||||||||||||||||| |.|.||||:||||||. ||.||||
        51 YRWVLVQFGAFIVLCGATHLINLWTFTTHSRTVALVMTTAKVLTAVVSCA 100

                    .         .         .         .         .
       111 TAVMLVAIIPDLLSVKTRELFLKNKAAELDREMGLIRTQEETGRYVRMLT 160
           ||:||| |||||||||||||||||||||||||||||||||||||.|||||
       101 TALMLVHIIPDLLSVKTRELFLKNKAAELDREMGLIRTQEETGRHVRMLT 150

                    .         .         .         .         .
       161 HEIRSTLDRHTILKTTLVELGRALQLEECALWMPTRTGVELQLSYTLHHQ 210
           ||||||||||||||||||||||.|.|||||||||||||:||||||||:||
       151 HEIRSTLDRHTILKTTLVELGRTLALEECALWMPTRTGLELQLSYTLRHQ 200

                    .         .         .
       211 NPVGFTVPIQLPVINQVFSANCAVKISP*SAVARL 245
           :||::|||||||||||||:.. |||||| |:||||
       201 HPVEYTVPIQLPVINQVFGTSRAVKISPNSPVARL 235
```

FIG. 21

```
TTTTTTTTTT GTCAAAAGCT CGATGTAAAA ATCCGATGGC CACAAGCAAA      50

ACGACAGGTT CCAACTTCAC GGAGATTGTG AAAATGGAGT AGTAGTTCAG     100

TGAAGTAGTA GATACTGAGA TCGCATTCTC CGGCGTCGTT TTTCACATCG     150

AAATAGTCGT GTAAAAAAAT GAAAAAATTG CTGCGAGACA GGTATGTGTC     200

GCAGCAGGAA ATAGCATCTT AAAGGAAGGA AGGAAGGAAA CTCGAAAGTT     250

ACTAAAAATT TTTGATTCTT TGGGACGAAA CGAGATA ATG GAA TCC TGT   299
                                         Met Glu Ser Cys
                                          1

GAT TGC ATT GAG GCT TTA CTG CCA ACT GGT GAC CTG CTG GTT    341
Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu Leu Val
 5                   10                  15

AAA TAC CAA TAC CTC TCA GAT TTC TTC ATT GCT GTA GCC TAC    383
Lys Tyr Gln Tyr Leu Ser Asp Phe Phe Ile Ala Val Ala Tyr
     20                  25                  30

TTT TCC ATT CTG TTG GAG CTT ATT TAT TTT GTC CAC AAA TCT    425
Phe Ser Ile Leu Leu Glu Leu Ile Tyr Phe Val His Lys Ser
         35                  40                  45

GCA TGC TTC CCA TAC AGA TGG GTC CTC ATG CAA TTT GGT GCT    467
Ala Cys Phe Pro Tyr Arg Trp Val Leu Met Gln Phe Gly Ala
             50                  55                  60

TTT ATT GTG CTC TGT GGA GCA ACA CAC TTT ATT AGC TTG TGG    509
Phe Ile Val Leu Cys Gly Ala Thr His Phe Ile Ser Leu Trp
                 65                  70

ACC TTC TTT ATG CAC TCT AAG ACG GTC GCT GTG GTT ATG ACC    551
Thr Phe Phe Met His Ser Lys Thr Val Ala Val Val Met Thr
 75                  80                  85

ATA TCA AAA ATG TTG ACA GCT GCC GTG TCC TGT ATC ACA GCT    593
Ile Ser Lys Met Leu Thr Ala Ala Val Ser Cys Ile Thr Ala
     90                  95                 100

TTG ATG CTT GTT CAC ATT ATT CCT GAT TTG CTA AGT GTT AAA    635
Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
        105                 110                 115

ACG CGA GAG TTG TTC TTG AAA ACT CGA GCT GAA GAG CTT GAC    677
Thr Arg Glu Leu Phe Leu Lys Thr Arg Ala Glu Glu Leu Asp
            120                 125                 130

AAG GAA ATG GGC CTA ATA ATA AGA CAA GAA GAA ACT GGC AGA    719
Lys Glu Met Gly Leu Ile Ile Arg Gln Glu Glu Thr Gly Arg
                135                 140

CAT GTC AGG ATG CTG ACT CAT GAG ATA AGA AGC ACA CTC GAC    761
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
145                 150                 155

AGA CAC ACA ATC TTG AAG ACT ACT CTT GTG GAG CTA GGT AGG    803
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg
    160                 165                 170
```

FIG. 22A

```
ACC TTA GAC CTG GCA GAA TGT GCT TTG TGG ATG CCA TGC CAA      845
Thr Leu Asp Leu Ala Glu Cys Ala Leu Trp Met Pro Cys Gln
        175                 180                 185

GGA GGC CTG ACT TTG CAA CTT TCC CAT AAT TTA AAC AAT CTA      887
Gly Gly Leu Thr Leu Gln Leu Ser His Asn Leu Asn Asn Leu
            190                 195                 200

ATA CCT CTG GGA TCT ACT GTG CCA ATT AAT CTT CCT ATT ATC      929
Ile Pro Leu Gly Ser Thr Val Pro Ile Asn Leu Pro Ile Ile
                205                 210

AAT GAA ATT TTT AGT AGC CCT GAA GCA ATA CAA ATT CCA CAT      971
Asn Glu Ile Phe Ser Ser Pro Glu Ala Ile Gln Ile Pro His
215                 220                 225

ACA AAT CCT TTG GCA AGG ATG AGG AAT ACT GTT GGT AGA TAT     1013
Thr Asn Pro Leu Ala Arg Met Arg Asn Thr Val Gly Arg Tyr
    230                 235                 240

ATT CCA CCA GAA GTA GTT GCT GTT CGT GTA CCG CTT TTA CAC     1055
Ile Pro Pro Glu Val Val Ala Val Arg Val Pro Leu Leu His
        245                 250                 255

CTC TCA AAT TTT ACT AAT GAC TGG GCT GAA CTG TCT ACT AGA     1097
Leu Ser Asn Phe Thr Asn Asp Trp Ala Glu Leu Ser Thr Arg
            260                 265                 270

AGT TAT GCG GTT ATG GTT CTG GTT CTC CCG ATG AAT GGC TTA     1139
Ser Tyr Ala Val Met Val Leu Val Leu Pro Met Asn Gly Leu
                275                 280

AGA AAG TGG CGT GAA CAT GAG TTA GAA CTT GTG CAA GTT GTC     1181
Arg Lys Trp Arg Glu His Glu Leu Glu Leu Val Gln Val Val
285                 290                 295

GCA GAT CAG GTT GCT GTC GCT CTT TCA CAT GCT GCA ATT TTA     1223
Ala Asp Gln Val Ala Val Ala Leu Ser His Ala Ala Ile Leu
    300                 305                 310

GAA GAT TCC ATG CGA GCC CAT GAT CAG CTC ATG GAA CAG AAT     1265
Glu Asp Ser Met Arg Ala His Asp Gln Leu Met Glu Gln Asn
        315                 320                 325

ATT GCT TTG GAT GTA GCT CGA CAA GAA GCA GAG ATG GCC ATC     1307
Ile Ala Leu Asp Val Ala Arg Gln Glu Ala Glu Met Ala Ile
            330                 335                 340

CGT GCA CGT AAC GAC TTC CTT GCT GTG ATG AAC CAT GAA ATG     1349
Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu Met
                345                 350

AGA ACG CCC ATG CAT GCA GTT ATT GCT CTG TGC TCT CTG CTT     1391
Arg Thr Pro Met His Ala Val Ile Ala Leu Cys Ser Leu Leu
355                 360                 365

TTA GAA ACA GAC TTA ACT CCA GAG CAG AGA GTT ATG ATT GAG     1433
Leu Glu Thr Asp Leu Thr Pro Glu Gln Arg Val Met Ile Glu
    370                 375                 380
```

FIG. 22B

```
ACC ATA TTG AAG AGC AGC AAT CTT CTT GCA ACA CTG ATA AAT    1475
Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Ile Asn
        385                 390                 395

GAT GTT CTA GAT CTT TCT AGA CTT GAA GAT GGT ATT CTT GAA    1517
Asp Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ile Leu Glu
            400                 405                 410

CTA GAA AAC GGA ACA TTC AAT CTT CAT GGC ATC TTA AGA GAG    1559
Leu Glu Asn Gly Thr Phe Asn Leu His Gly Ile Leu Arg Glu
                415                 420

GCC GTT AAT TTG ATA AAG CCA ATT GCA TCT TTG AAG AAA TTA    1601
Ala Val Asn Leu Ile Lys Pro Ile Ala Ser Leu Lys Lys Leu
425                 430                 435

TCT ATA ACT CTT GCT TTG GCT CTG GAT TTA CCT ATT CTT GCT    1643
Ser Ile Thr Leu Ala Leu Ala Leu Asp Leu Pro Ile Leu Ala
    440                 445                 450

GTG GGT GAT GCA AAA CGT CTT ATC CAA ACT CTC TTA AAC GTG    1685
Val Gly Asp Ala Lys Arg Leu Ile Gln Thr Leu Leu Asn Val
        455                 460                 465

GTG GGA AAT GCT GTG AAG TTC ACT AAA GAA GGA CAT ATT TCA    1727
Val Gly Asn Ala Val Lys Phe Thr Lys Glu Gly His Ile Ser
            470                 475                 480

ATT GAG GCT TCA GTT GCC AAA CCA GAG TAT GCG AGA GAT TGT    1769
Ile Glu Ala Ser Val Ala Lys Pro Glu Tyr Ala Arg Asp Cys
                485                 490

CAT CCT CCT GAA ATG TTC CCT ATG CCA AGT GAT GGC CAG TTT    1811
His Pro Pro Glu Met Phe Pro Met Pro Ser Asp Gly Gln Phe
495                 500                 505

TAT TTG CGT GTC CAG GTT AGA GAT ACT GGG TGT GGA ATT AGC    1853
Tyr Leu Arg Val Gln Val Arg Asp Thr Gly Cys Gly Ile Ser
    510                 515                 520

CCA CAA GAT ATA CCA CTA GTA TTC ACC AAA TTT GCA GAG TCA    1895
Pro Gln Asp Ile Pro Leu Val Phe Thr Lys Phe Ala Glu Ser
        525                 530                 535

CGG CCT ACG TCA AAT CGA AGT ACT GGA GGG GAA GGT CTA GGG    1937
Arg Pro Thr Ser Asn Arg Ser Thr Gly Gly Glu Gly Leu Gly
            540                 545                 550

CTT GCC ATT TGG AGA CGA TTT ATT CAA CTT ATG AAA GGT AAC    1979
Leu Ala Ile Trp Arg Arg Phe Ile Gln Leu Met Lys Gly Asn
                555                 560

ATT TGG ATT GAG AGT GAG GGC CCT GGA AAG GGA ACC ACT GTC    2021
Ile Trp Ile Glu Ser Glu Gly Pro Gly Lys Gly Thr Thr Val
565                 570                 575

ACG TTT GTA GTG AAA CTC GGA ATC TGT CAC CAT CCA AAT GCA    2063
Thr Phe Val Val Lys Leu Gly Ile Cys His His Pro Asn Ala
    580                 585                 590
```

FIG. 22C

```
TTA CCT CTG CTA CCT ATG CCT CCC AGA GGC AGA TTG AAC AAA     2105
Leu Pro Leu Leu Pro Met Pro Pro Arg Gly Arg Leu Asn Lys
        595                 600                 605

GGT AGC GAT GAT CTC TTC AGG TAT AGA CAG TTC CGT GGA GAT     2147
Gly Ser Asp Asp Leu Phe Arg Tyr Arg Gln Phe Arg Gly Asp
            610                 615                 620

GAT GGT GGG ATG TCT GTG AAT GCT CAA CGC TAT CAA AGA AGT     2189
Asp Gly Gly Met Ser Val Asn Ala Gln Arg Tyr Gln Arg Ser
                625                 630

ATG TAA A TGACAAAAGG ACATTGGTGT GACAAAGAAC ATTAAATCAT       2236
Met  *
635

GACTAGTGAA TTTGAGATTT CTTCACTGTT CTGTACACTC CAAATGGCAC      2286

AGTTTGTCTT GTAACTAACC TAATTCAATG CTCGTAAAGT GAGTACTGGA      2336

GTATCTTGAA AATGTAACTA TCGAATTTAT ACATCGAGCT TTTGACAAAA      2386

AAAAAAAAAA AAAAAAAAA                                        2405
```

FIG. 22D

PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE BY TRANSFORMATION WITH AN ETR NUCLEIC ACID

This is a continuation of application Ser. No. 08/263,480 filed Jun. 28, 1994, now abandoned which is a continuation-in-part of application Ser. No. 08/086,555 filed Jul. 1, 1993, now abandoned.

The U.S. Government has certain rights in this invention pursuant to Department of Energy Contract No. DE-FG03-88ER13873.

TECHNICAL FIELD OF THE INVENTION

The invention generally relates to modified ETR nucleic acid and plants transformed with such nucleic acid which have a phenotype characterized by a modification in the normal response to ethylene.

BACKGROUND OF THE INVENTION

Ethylene has been recognized as a plant hormone since the turn of the century when its effect on pea seedling development was first described. Neljubow (1901), *Pflanzen Beih. Bot. Zentralb.* 10:128–139. Since then, numerous reports have appeared which demonstrate that ethylene is an endogenous regulator of growth and development in higher plants. For example, ethylene has been implicated in seed dormancy, seedling growth, flower initiation, leaf abscission, senescence and fruit ripening. Ethylene is a plant hormone whose biosynthesis is induced by environmental stress such as oxygen deficiency, wounding, pathogen invasion and flooding.

Recently, genes encoding some of the enzymes involved in ethylene biosynthesis have been cloned. Sato, et al. (1989) *Proc. Natl. Acad. Sci. U.S.A.* 86:6621–6625; Nakajima, et al. (1990) *Plant Cell Phys. Physiol.* 29:989–996; Van Der Straeten, et al. (1990) *Proc. Natl. Acad. Sci U.S.A.* 87:4859–4963; Hamilton, et al. (1991) *Proc. Natl. Acad. Sci. U.S.A.* 88:7434–7437; and Spanu, et al. (1991) *EMBO J.* 10:2007–2013. The pathway for ethylene biosynthesis is shown in FIG. **1**. As can be seen the amino acid methionine is converted to S-adenosyl-methionine (SAM) by SAM synthetase which in turn is converted to 1-aminocyclopropane-1-carboxylic acid (ACC) by ACC synthase. Adams, et al. (1979) *Proc. Natl. Acad. Sci. U.S.A.* 76:170–174. The ACC is then converted to ethylene by way of the enzyme ACC oxidase. Yang, et al. (1984) *Annu. Rev. Plant. Physiol.* 35:155–189.

A number of approaches have been taken in an attempt to control ethylene biosynthesis to thereby control fruit ripening. Oeller, et al. (1991) *Science* 254:437–439 report that expression of an antisense RNA to ACC synthase inhibits fruit ripening in tomato plants. Hamilton, et al. (1990) *Nature* 346:284–287 report the use of an antisense TOM13 (ACC oxidase) gene in transgenic plants. Picton et al. (1993) *Plant Journal* 3:469–481, report altered fruit ripening and leaf senesence in tomatoes expressing an antisense ethylene-forming enzyme.

In a second approach, ethylene biosynthesis was reportedly modulated by expressing an ACC deaminase in plant tissue to lower the level of ACC available for conversion to ethylene. See PCT publication No. WO92/12249 published Jul. 23, 1992, and Klee et al. (1991) *Plant Cell* 3:1187–1193.

While a substantial amount of information has been gathered regarding the biosynthesis of ethylene, very little is known about how ethylene controls plant development. Although several reports indicate that a high affinity binding site for ethylene is present in plant tissues, such receptors have not been identified. Jerie, et al. (1979) *Planta* 144:503; Sisler (1979) *Plant Physiol.* 64:538; Sisler, et al. (1990) *Plant Growth Reg.* 9:157–164, and Sisler (1990) "Ethylene-Binding Component in Plants", *The Plant Hormone Ethylene*, A. K. Mattoo and J. C. Suttle, eds. (Boston) C.R.C. Press, Inc., pp. 81–90. In Arabidopsis, several categories of mutants have been reported. In the first two categories, mutants were reported which produce excess ethylene or reduced ethylene as compared to the wild-type. Guzman, et al. (1990) *The Plant Cell* 2:513–523. In a third category, mutants failed to respond to ethylene. Id.; Bleecker, et al. (1988) *Science* 241:1086–1089, Harpham, et al. (1991) *Ann. of Botany* 68:55–61. The observed insensitivity to ethylene was described as being either a dominant or recessive mutation. Id.

Based upon the foregoing, it is clear that the genetic basis and molecular mechanism of ethylene interaction with plants has not been clearly delineated. Given the wide range of functions regulated by ethylene and the previous attempts to control ethylene function by regulating its synthesis, it would be desirable to have an alternate approach to modulate growth and development in various plant tissues such as fruits, vegetables and flowers by altering the interaction of ethylene with plant tissue.

Accordingly, it is an object of the invention to provide isolated nucleic acids comprising an ethylene response (ETR) nucleic acid.

In addition, it is an object to provide modifications to such ETR nucleic acids to substitute, insert and/or delete one or more nucleotides so as to substitute, insert and/or delete one or more amino acid residues in the protein encoded by the ETR nucleic acid.

Still further, it is an object to provide plant cells transformed with one or more modified ETR nucleic acids. Such transformed plant cells can be used to produce transformed plants wherein the phenotype vis-a-vis the response of one or more tissues of the plant to ethylene is modulated.

SUMMARY OF THE INVENTION

In accordance with the foregoing objects, the invention includes transformed plants having at least one cell transformed with a modified ETR nucleic acid. Such plants have a phenotype characterized by a decrease in the response of at least one transformed plant cell to ethylene as compared to a plant not containing the transformed plant cell.

The invention also includes vectors capable of transforming a plant cell to alter the response to ethylene. In one embodiment, the vector comprises a modified ETR nucleic acid which causes a decrease in cellular response to ethylene. Tissue and/or temporal specificity for expression of the modified ETR nucleic acid is controlled by selecting appropriate expression regulation sequences to target the location and/or time of expression of the transformed nucleic acid.

The invention also includes methods for producing plants having a phenotype characterized by a decrease in the response of at least one transformed plant cell to ethylene as compared to a wild-type plant not containing such a transformed cell. The method comprises transforming at least one plant cell with a modified ETR nucleic acid, regenerating plants from one or more of the transformed plant cells and selecting at least one plant having the desired phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** depicts the biosynthetic pathway for ethylene.

FIGS. **2**A–**2**C depict the genomic nucleic acid sequence (SEQ ID NO:1) for the ETR gene from *Arabidopsis thaliana.*

FIGS. **3**A–**3**D depict the cDNA nucleic acid (SEQ ID NO:2) and deduced amino acid sequence (SEQ ID NO:3) for the ETR gene from *Arabidopsis thaliana.*

FIGS. **4**A, **4**B, **4**C and **4**D depict the cDNA nucleic acid (SEQ ID NO:8) and deduced amino acid sequence (SEQ ID NO:9) of the etr1-3 mutation of the ETR gene from *Arabidopsis thaliana* which confers ethylene insensitivity. The sequences depicted in FIG. **4** differ from the wild-type sequence set forth in FIG. **3** by the substitution of alanine-31 with valine.

FIGS. **5**A, **5**B, **5**C and **5**D depict the cDNA nucleic acid (SEQ ID NO:10) and deduced amino acid sequence (SEQ ID NO:11) of the etr1-4 mutation of the ETR gene from *Arabidopsis thaliana* which confers ethylene insensitivity. The sequences depicted in FIG. **5** differ from the wild-type sequence set forth in FIG. **3** by the substitution of isoleucine-62 with phenylalanine.

FIGS. **6**A, **6**B, **6**C and **6**D depict the cDNA nucleic acid (SEQ ID NO:4) and deduced amino acid sequence (SEQ ID NO:5) of the etr1-1 mutation of the ETR gene from *Arabidopsis thaliana* which confers ethylene insensitivity. The sequences depicted in FIG. **6** differ from the wild-type sequence set forth in FIG. **3** by the substitution of cysteine-65 with tyrosine.

FIGS. **7**A, **7**B, **7**C and **7**D depict the cDNA nucleic acid (SEQ ID NO:6) and deduced amino acid sequence (SEQ ID NO:6) of the etr1-2 mutation of the ETR gene from *Arabidopsis thaliana* which confers ethylene insensitivity. The sequences depicted in FIG. **7** differ from the wild-type sequence set forth in FIG. **3** by the substitution of alanine-102 with threonine.

FIG. **8** depicts the structure of the cosmid insert used to localize the ETR1 gene from *Arabidopsis thaliana*. The starting position for the chromosome walk is indicated by a hatched bar. The open bars give the location and length of DNA segments used as probes to detect recombination break points. The maximum number of break points detected by each probe is shown. The numbers to the right of the ETR1 gene are out of 74 F2 recombinants between etr1-1 and ap-1, and those to the left of the ETR-1 gene are out of 25 F2 recombinants between etr1-1 and clv2. Overlapping YAC clones EG4E4 and EG2G11 are also shown.

FIGS. **9**A–**9**B depict the amino acid sequence alignments of the predicted ETR1 protein and the conserved domains of several bacterial histidine kinases and response regulators. Amino acids are shown in boldface type at positions where there are at least two identities with ETR1. In FIG. **9**A, the deduced ETR1 amino acid sequence (SEQ ID NOs:12 and 27) (residues 326 to 562) aligned with the histidine kinase domains of *E. coli* BarA (SEQ ID NOs:13 and 28), *P. syringae* LemA (SEQ ID NOs:14 and 29) and *X. campestris* RpfC(SEQ ID NOs:15 and 30). Boxes surround the five conserved motifs characteristic of the bacterial histidine kinase domain as compiled by Parkinson and Kofoid (Parkinson et al. (1992) *Annu. Rev. Genet.* 26:71). The conserved histidine residue that is the supposed site of autophosphorylation is indicated by an asterisk. Numbers and positions of amino acids not shown are given in parentheses. In FIG. **9**B, the deduced ETR1 amino acid sequence (residues 610 to 729) (SEQ ID NOs:15 and 31) are aligned with the response regulator domains of *B. parapertussis* BvgS (SEQ ID NOs:17 and 32), *P. syringae* LemA (SEQ ID NOs:19 and 34) and *E. coli* RscC (SEQ ID NOs:18 and 33). Amino acids are shown in boldface type where there are at least two identities with ETR1. Boxes surround the four highly conserved residues in bacterial response regulators. The conserved aspartate residue that is the site of phosphorylation is indicated by an asterisk. Numbers and positions of amino acids not shown are given in parentheses. For alignment purposes, a gap (_) was introduced in the ETR1 sequence.

FIGS. **10**A and **10**B depict specific DNA sequences for ETR nucleic acids from tomato and *Arabidopsis thaliana*. FIG. **10**A compares the DNA sequence encoding amino acid residues 1 through 123 (SEQ ID NOs:20 and 21). FIG. **10**B compares the ETR nucleic acid sequence encoding amino acids 306 through 403 (SEQ ID NOs:22 and 23). The vertical lines in each figure identify homologous nucleotides.

FIGS. **11**A–**11**B compare partial amino acid sequences (using single letter designation) for an ETR protein from tomato and *Arabidopsis thaliana*. FIG. **11**A compares the amino acid sequence for the ETR protein for amino acids 1 through 123 (SEQ ID NOs:24 and 25). FIG. **11**B compares the amino acid sequence for the ETR protein for residues 306 through 403 (SEQ ID NOs:26 and 27). The vertical lines indicate exact sequence homology. Two vertical dots indicate that the amino acid residues are functionally conserved. One dot indicates weak functional conservation as between amino acid residues.

FIGS. **12**A–**12**D depict the genomic nucleic acid sequence (SEQ ID NO:45) and deduced amino acid sequence (SEQ ID NO:46) for the QITR ETR gene from *Arabidopsis thaliana.*

FIGS. **13**A–**13**C depict the cDNA nucleic acid sequence and deduced protein sequence for the QITR ETR gene from *Arabidopsis thaliana.*

FIGS. **14**A–**14**F depict the genomic nucelic acid sequence (SEQ ID NO:41) and deduced amino acid sequence (SEQ ID NO:42) for the Q8 ETR gene from *Arabidopsis thaliana.*

FIGS. **15**A–**15**D depict the cDNA nucleic acid sequence (SEQ ID NO:43) and deduced amino acid sequence (SEQ ID NO:44) for the Q8 ETR gene from *Arabidopsis thaliana.*

FIGS. **16**A–**16**C depict the nucleic acid sequence (SEQ ID NO:35) and deduced amino acid sequence (SEQ ID NO:36) for the TETR nucleic acid from tomato.

FIG. **17** is a comparison of the amino terminal portions of the TETR and ETR1 proteins from tomato and Arabidopsis respectively. The top line is the TETR sequence and extends through amino acid residue 315. The lower line represents the ETR1 protein sequence and extends through amino acid residue 316. The vertical lines and single and double vertical dots have the same meaning as set forth in the description of FIGS. **11**A and **11**B. The percent identity between these sequence portions is 73.33%. The percent similarity is 84.76%.

FIGS. **18**A–**18**E depict the nucleic acid (SEQ ID NO:37) and deduced amino acid sequence (SEQ ID NO:38) for the TGETR1 ETR nucleic acid from tomato.

FIG. **19** depicts the nucleic acid (SEQ ID NO:39) and deduced amino acid sequence (SEQ ID NO:40) for a partial sequence of the TGETR2 ETR nucleic acid from tomato.

FIG. **20** is a comparison of the amino terminal portions for the TGETR1 and ETR1 proteins from tomato and Arabidopsis respectively. The top line is the TGETR1 sequence through amino acid residue 316. The bottom line represents the ETR1 protein sequence through amino acid residue 316. The identity as between these two sequences is 91.75%. The percent similarity is 95.87%. The vertical lines and single and double dots have the same meaning as for FIGS. **11**A and **11**B.

FIG. **21** is a comparison of an amino terminal portion of the TGETR2 protein with the corresponding ETR1 sequence. The top line is the TGETR2 sequence from amino acid residue 11 through amino acid residue 245. The lower line is the ETR1 sequence from amino acid residue 1 through amino acid residue 235. The sequence identity is 85.11% as between these two sequences. The sequence similarity is 92.34%. The vertical lines and single and double dots have the same meaning as for FIGS. **11**A and **11**B.

FIGS. **22**A–**22**C depict the nucleic acid (SEQ ID NO:50) and deduced amino acid sequence (SEQ ID NO:51) for the Nr (Never-ripe) ETR nucleic acid from Never-ripe tomato. The amino acid sequence in FIG. **22** differs from the TETR sequence in FIG. **16** in that the amino acid residue proline at residue 36 is replaced with leucine.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides, in part, plants having cells transformed with a vector comprising an ETR nucleic acid or a modified ETR nucleic acid. Such transformed plant cells have a modulated response to ethylene. In a preferred embodiment, the expression of a modified ETR nucleic acid confers a phenotype on the plant characterized by a decrease in the response to ethylene for at least for those cells expressing the modified ETR nucleic acid as compared to a corresponding non-transformed plant. Thus, for example, when the modified ETR nucleic acid is expressed in fruit such as tomato, the fruit ripening process is retarded thereby reducing spoilage and extending the shelf life and/or harvesting season for the fruit. The invention is similarly useful to prevent spoilage of vegetative tissue and to enhance the longevity of cut flowers.

As used herein, a "plant ETR nucleic acid" refers to nucleic acid encoding all or part of a "plant ETR protein". ETR nucleic acids can initially be identified by homology to the ETR nucleic acid sequences disclosed herein but can also be identified by homology to any identified ETR nucleic acid or amino acid sequence. Examples of ETR nucleic acids include ETR1, QITR and Q8 from Arabidopsis and TETR, TGETR1 and TGETR2 from tomato. ETR nucleic acids, however, are also defined functionally by their ability to confer a modulated ethylene response upon transformation into plant tissue. For example, an antisense construct of an ETR nucleic acid or modified ETR nucleic acid is capable of reducing the ethylene response in plant tissue expressing the antisense or modified ETR nucleic acid. In addition, transformation with an ETR nucleic acid or modified ETR nucleic acid can result in co-suppression of the endogenous ETR alleles which in turn modifies the ethylene response. Furthermore, ETR nucleic acids can be modified as described herein to produce modified ETR nucleic acids which when used to transform plant tissue result in varying degrees of ethylene insensitivity in the tissue expressing such modified ETR nucleic acids. When evaluating a putative ETR nucleic acid for the ability of a modified form of the ETR nucleic acid to confer ethylene insensitivity, it is preferred that a codon or combination of codons encoding the amino acid residues equivalent to Ala-31, Ile-62, Cys-65 or Tyr-102 in the ETR1 protein of *Arabidopsis thaliana* or Pro-36 in the TETR protein in tomato be modified so as to substitute a different amino acid residue such as those disclosed herein for the specified residues.

Plant ETR nucleic acids include genomic DNA, cDNA and oligonucleotides including sense and anti-sense nucleic acids as well as RNA transcripts thereof. The genomic DNA sequence (SEQ ID NO:1) for the ETR1 gene from *Arabidopsis thaliana* is shown in FIG. **2**. The corresponding cDNA sequence (SEQ ID NO:2) and deduced ETR amino acid sequence (SEQ ID NO:3) are shown in FIG. **3**. An amino terminal domain (i.e., resides 1 through about 316) of the predicted ETR protein sequence has no homology to known protein sequences. Approximately midway in the ETR protein (i.e., residues 295 through 313) is a putative transmembrane domain followed by a putative intracellular domain (i.e., residues 314 through 738). A substantial portion of this putative intracellular domain unexpectedly has sequence homology to the two component environmental sensor-regulators known in bacteria. These two families in bacteria form a conserved sensor-regulator system that allows the bacteria to respond to a broad range of environmental fluctuations. It is believed that the amino terminal portion of the ETR protein interacts either directly with ethylene or indirectly (e.g., with an ethylene binding protein or another protein) and that upon such interaction, signal transduction through the intracellular domain occurs.

An ETR nucleic acid or ETR protein can be identified by substantial nucleic acid and/or amino acid sequence homology to a known ETR sequence. Such homology can be based upon the overall nucleic acid or amino acid sequence in which case the overall homology of the protein sequence is preferably greater than about 50%, preferably greater than 60%, still more preferably greater than 75% and most preferably greater than 90% homologous. Notwithstanding overall sequence homology, it is preferred that the unique amino-terminal portion of an ETR protein sequence or the nucleic acid sequence encoding this portion of the molecule (i.e., the 5' terminal portion) be used to identify an ETR protein or ETR nucleic acid. When using this amino terminal sequence portion, it is preferred that the amino acid sequence homology with the known ETR sequence be greater than about 55%, more preferably about 60%, still more preferably about 70%, more preferably greater than 85% and most preferably greater than 95% homologous. Homology based on nucleic acid sequence is commensurate with amino acid homology but takes into account the degeneracy in the genetic code and codon bias in different plants. Accordingly, the nucleic acid sequence homology may be substantially lower than that based on protein sequence. Thus, an ETR protein is any protein which has an amino-terminal portion which is substantially homologous to the amino-terminal domain of a known ETR protein. One such known ETR protein is the ETR1 protein (see FIG. **3**) from *Arabidopsis thaliana*. An ETR nucleic acid by analogy also encodes at least the amino-terminal domain of an ETR protein.

An ETR nucleic acid from a plant species other than *Arabidopsis thaliana* can be readily identified by standard methods utilizing known ETR nucleic acid. For example, labelled probes corresponding to a known ETR nucleic acid or encoding the unique amino-terminal domain can be used for in situ hybridization to detect the presence of an ETR gene in a particular plant species. In addition, such probes can be used to screen genomic or cDNA libraries of a different plant species or to identify one or more bands containing all or part of an ETR gene by hybridization to an electrophoretically separated preparation of genomic DNA digested with one or more restriction endo-nucleases.

The hybridization conditions will vary depending upon the probe used. When a unique nucleotide sequence of an

ETR nucleic acid is used, e.g., an oligonucleotide encoding all or part of the amino terminal domain, relatively high stringency, e.g., about 0.1×SSPE at 65° C. is used. When the hybridization probe covers a region which has a potentially lower sequence homology to known ETR nucleic acids, e.g., a region covering a portion of the unique amino terminal domain and a portion covering a transmembrane domain, the hybridization is preferably carried out under moderate stringency conditions, e.g., about 5×SSPE at 50° C.

For example, using the above criteria, a ripening tomato cDNA library (Stratagene, LaJolla, Calif., Catalog No. 936004) was screened with a labeled probe comprising a nucleic acid sequence encoding an amino terminal portion of the Arabidopsis ETR protein sequence disclosed herein in FIGS. **3**A, B, C and D. Several clones were identified and sequenced by standard techniques. The DNA sequences for this ETR nucleic acid from tomato (TETR) and *Arabidopsis thaliana* (ETR1) encoding amino acid residues 1 through 123 (SEQ ID NOs:20 and 21) and amino acids 306 through 403 (SEQ ID NOs:22 and 23) are set forth in FIGS. **10**A and **10**B, respectively.

The amino acid sequences for the ETR1 protein from *Arabidopsis thaliana* and tomato (TETR) for residues 1 through 123 (SEQ ID NOs:25 and 24) and 306 through 403 (SEQ ID NOs:27 and 26) are set forth in FIGS. **11**A and **11**B, respectively.

The complete ETR nucleic acid (SEQ ID NO:35) and amino acid sequence (SEQ ID NO:36) for TETR is shown in FIG. **16**. A direct comparison of the amino acid sequence between the TETR and ETR1 proteins for the amino terminal 316 amino acid residues is shown in FIG. **17**.

As can be seen, there is substantial homology between these particular Arabidopsis and tomato ETR sequences both on the level of DNA sequence and amino acid sequence. In particular, the homology on the DNA level for the sequence encoding amino acids 1 through 45 is slightly greater than 72%. The homology on the amino acid level for amino acid residues 1 through 123 is approximately 79%. For the amino terminal portion (residues 1 through 316) the overall homology is approximately 73%. In the case of amino acid sequence homology, when the differences between the amino acids at equivalent residues are compared and such differences comprise the substitution of a conserved residue, i.e., amino acid residues which are functionally equivalent, the amino acid sequence similarity rises to about 90% for the first 123 residues. The sequence similarity for the amino terminal 316 amino acids rises to almost 85%. Such sequence similarity was determined using a Best Fit sequence program as described by Devereux et al. (1984) *Nucl. Acids Res.* 12:387–395. Functionally equivalent (i.e., conserved) residues are identified by double and single data in the comparative sequences. Similarly, the nucleic acid sequence homology between Arabidopsis and tomato for the sequence encoding amino acid residues 306 to 403 is approximately 75%. The sequence homology on the amino acid level for identical amino acids is almost 86% whereas the similarity is almost 96%.

In addition to ETR1 from Arabidopsis and TETR (sometimes referred to TXTR) from tomato, a number of other ETR nucleic acids have been identified in Arabidopsis and tomato. In Arabidopsis, the QITR and Q8 ETR nucleic acids and proteins have been identified. See FIGS. **12**, **13**, **14** and **15** and Seq. ID Nos. 41 through 48. For QITR, the overall nucleic acid homology with ETR1 is approximately 69%. With regard to the amino terminal portion between residues 1 and 316, the homology is approximately 71% identical for amino acid sequence and approximately 72% identical in terms of nucleic acid sequence. With regard to Q8, the overall sequence homology to ETR1 from Arabidopsis is approximately 69% for the overall nucleic acid sequence as compared to approximately 81% homology for that portion of the Q8 encoding the amino terminal 316 amino acids. The homology on the amino acid level for the amino terminal portion is between Q8 and ETR1 is approximatley 72%.

The other ETR nucleic acids identified in tomato include TGETR1 (SEQ ID NO:37) and TGETR2 (SEQ ID NO:39). the deduced protein sequence for TGETR1 (SEQ ID NO:38) and TGETR2 (SEQ ID NO:40) are set forth in FIGS. **18** and **19** respectively. The sequence of TGETR2 is incomplete. A comparison of the sequence homology for the first 316 amino acid residues of the TGETR1 protein and the ETR1 protein is shown in FIG. **20**. The sequence identity is just under 92%. The sequence similarity rises to almost 96% between this portion of these two proteins. With regard to TGETR2, FIG. **21** sets forth a comparison of the amino terminal portion of this molecule (through amino acid residue 245) with the corresponding portion of the ETR1 protein. The identity of sequences between these two sequence portions is approximately 85%. The sequence similarity rises to just above 92%.

The cloning and sequencing of the ETR nucleic acids from Arabidopsis is described in the examples herein. However, given the extensive disclosure of the sequences for these ETR nucleic acids, one skilled in the art can readily construct oligonucleotide probes, perform PCR amplification or utilize other standard protocols known to those skilled in the art to isolate the disclosed genes as well as other ETR nucleic acids having homology thereto from other species. When screening the same plant species, relatively moderate to high stringency conditions can be used for hybridization which would vary from between 55° C. to 65° C. in 5×SSPE. When it is desirable to probe for lower homology or in other plant species, lower stringency conditions such as 50° C. at 5×SSPE can be used. Washing conditions however required 0.2×SSPE.

The isolation of the TETR1 ETR nucleic acid from tomato is described in the examples. The isolation of this sequence utilized the amino terminal portion of the ETR1 gene from Arabidopsis. The other tomato ETR nucleic acids disclosed herein (TGETR1 and TGETR2) were identified by probing a tomato genomic library with an ETR1 probe. The genomic library was made from EMBL 3 to which was ligated a partially Sau3A digested genomic DNA extract of tomato. Conditions were 65° C. 5×SSC with washes at 2×SSC.

In reviewing the overall structure of the various ETR nucleic acids and proteins identified to date, it appears that at least one class of ETR protein contains a unique amino terminal portion followed by a histine-kinase domain followed by a response regulatory region. This is the ETR1 protein in Arabidopsis. A second class of ETR protein does not contain the response regulatory region. Examples of such ETR proteins include QITR in Arabidopsis and TETR in tomato. The significance of this is not understood at this time. However, as described hereinafter, mutations in the ETR nucleic acids encoding members from each class can confer a dominate ethylene insensitivity to transgenic plants containing such nucleic acids.

As described hereinafter, substitution of amino acid residues Ala-31, Ile-62, Cys-65 and Tyr-102 with a different amino acid results in modified Arabidopsis ETR nucleic acid which are capable of conferring ethylene insensitivity in a transformed plant. Each of these residues are identical as between the ETR protein of tomato (TETR) and *Arabidopsis thaliana* (ETR1).

Once the ETR nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ETR nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the ETR nucleic acid can be further used as a probe to identify and isolate other ETR nucleic acids. It can also be used as a "precursor" nucleic acid to make modified ETR nucleic acids and proteins.

As used herein, the term "modified ETR nucleic acid" refers to an ETR nucleic acid containing the substitution, insertion or deletion of one or more nucleotides of a precursor ETR nucleic acid. The precursor ETR nucleic acids include naturally-occurring ETR nucleic acids as well as other modified ETR nucleic acids. The naturally-occurring ETR nucleic acid from *Arabidopsis thaliana* can be used as a precursor nucleic acid which can be modified by standard techniques, such as site-directed mutagenesis, cassette mutagenesis and the like, to substitute one or more nucleotides at a codon such as that which encodes alanine at residue 31 in the Arabidopsis ETR nucleic acid. Such in vitro codon modification can result in the generation of a codon at position 31 which encodes any one of the other naturally occurring amino acid residues. Such modification results in a modified ETR nucleic acid.

For example, the mutation responsible for the pheno-type observed in the Never-ripe mutant is disclosed in the examples. As described, a single point mutation changes the proline normally present at residue 36 in the TETR protein to leucine. This single mutation is sufficient to confer a dominant ethylene insensitivity phenotype on the wild-type plant. The transformation of tomato and other plants with this modified ETR nucleic acid is expected to confer the dominant ethylene insensitivity phenotype on such transformed plant cells.

Alternatively, the precursor nucleic acid can be one wherein one or more of the nucleotides of a wild-type ETR nucleic acid have already been modified. Thus, for example, the *Arabidopsis thaliana* ETR nucleic acid can be modified at codon 31 to form a modified nucleic acid containing the substitution of that codon with a codon encoding an amino acid other than alanine, e.g., valine. This modified ETR nucleic acid can also act as a precursor nucleic acid to introduce a second modification. For example, the codon encoding Ala-102 can be modified to encode the substitution of threonine in which case the thus formed modified nucleic acid encodes the substitution of two different amino acids at residues 31 and 102.

Deletions within the ETR nucleic acid are also contemplated. For example, an ETR nucleic acid can be modified to delete that portion encoding the putative transmembrane or intracellular domains. The thus formed modified ETR nucleic acid when expressed within a plant cell produces only an amino-terminal portion of the ETR protein which is potentially capable of binding ethylene, either directly or indirectly, to modulate the effective level of ethylene in plant tissue.

In addition, the modified ETR nucleic acid can be identified and isolated from a mutant plant having a dominant or recessive phenotype characterized by an altered response to ethylene. Such mutant plants can be spontaneously arising or can be induced by well known chemical or radiation mutagenesis techniques followed by the determination of the ethylene response in the progeny of such plants. Examples of such mutant plants which occur spontaneously include the Never ripe mutant of tomato and the ethylene insensitive mutant of carnation. Thus, modified ETR nucleic acids can be obtained by recombinant modification of wild-type ETR nucleic acids or by the identification and isolation of modified ETR alleles from mutant plant species.

It is preferred that the modified ETR nucleic acid encode the substitution, insertion and/or deletion of one or more amino acid residues in the precursor ETR protein. Upon expression of the modified nucleic acid in host plant cells, the modified ETR protein thus produced is capable of modulating at least the host cell's response to ethylene. In connection with the generation of such a phenotype, a number of codons have been identified in the ETR nucleic acid from *Arabidopsis thaliana* which when modified and reintroduced into a wild-type plant result in a decrease in the ethylene response by the transformed plant. These codons encode amino acid residues Ala-31, Ile-62, Cys-65 and Tyr-102 in the ETR protein of *Arabidopsis thaliana*. The ETR gene and each of these particular modified amino acid residues were identified by cloning the wild-type ETR gene from *Arabidopsis thaliana* and chemically modified alleles from four different varieties (etr1-1, etr1-2, etr1-3 and etr1-4) of *Arabidopsis thaliana* (each of which exhibited a dominant phenotype comprising insensitivity to ethylene) and comparing the nucleotide and deduced amino acid sequences. The invention, however, is not limited to modified ETR nucleic acids from *Arabidopsis thaliana* as described in the examples. Rather, the invention includes other readily identifiable modified ETR nucleic acids which modulate ethylene sensitivity.

The above four varieties exhibiting dominant ethylene insensitivity were generated by chemical modification of seedlings of *Arabidopsis thaliana* and identified by observing plant development from such modified seedlings with the addition of exogenous ethylene. Using a similar approach either with or without the addition of exogenous ethylene, the skilled artisan can readily generate other variants of any selected plant species which also have a modulated response to ethylene. Then, using ETR probes based upon the wild-type or modified ETR nucleic acid sequences disclosed herein, other modified ETR nucleic acids can be isolated by probing appropriate genomic or cDNA libraries of the modified selected plant species. The nucleotide and/or encoded amino acid sequence of such newly generated modified ETR nucleic acids is then preferably compared with the wild-type ETR nucleic acid from the selected plant species to determine which modifications, if any, in the ETR nucleic acid are responsible for the observed phenotype. If the wild-type sequence of the selected plant species is not available, the wild-type or modified ETR sequences disclosed herein for *Arabidopsis thaliana* or other ETR sequences which have been identified can be used for comparison. In this manner, other modifications to ETR proteins can be identified which can confer the ethylene insensitivity phenotype. Such modifications include the identification of amino acids other than those disclosed herein which can be substituted at residues equivalent to Ala-31,Ile-62, Cys-65 and Ala-102 in the *Arabidopsis thaliana* ETR protein and the identification of other amino acid residues which can be modified by substitution, insertion and/or deletion of one or more amino acid residues to produce the desired phenotype.

Alternatively, a cloned precursor ETR nucleic acid can be systematically modified such that it encodes the substitution, insertion and/or deletion of one or more amino acid residues and tested to determine the effect of such modification on a plant's ethylene response. Such modifications are preferably made within that portion of the ETR nucleic acid which encodes the amino-terminal portion of the ETR protein. However, modifications to the carboxy-terminal or putative transmembrane domains to modulate signal transduction are also contemplated (e.g., modifications of the conserved histidine of the histidine kinase domain which is the supposed site of autophosphorylation or the conserved aspartate of the response regulator domain which is the supposed site of phosphorylation). One method which may be used for identifying particular amino acid residues involved in the direct or indirect interaction with ethylene is the sequential substitution of the codons of an ETR nucleic acid with codons encoding a scanning amino acid such as glycine or alanine (See, e.g., PCT Publication WO90/04788 published May 3, 1990) followed by transformation of each of the thus formed modified nucleic acids into a plant to determine the effect of such sequential substitution on the ethylene response. Other approaches include random modifications or predetermined targeted modifications of the cloned ETR nucleic (See, e.g., PCT Publication No. WO92/07090 published Apr. 30, 1992) followed by transformation of plant cells and the identification of progeny having an altered ethylene response. The ETR nucleic acid from those plants having the desired phenotype is isolated and sequenced to confirm or identify the modification responsible for the observed phenotype.

Amino acid residues equivalent to those specifically identified in an ETR protein which can be modified to alter the ethylene response can also be readily identified in ETR proteins from other plant species. For example, equivalent amino acid residues to those identified in the ETR protein from*Arabidopsis thaliana* can be readily identified in other FTR proteins. An amino acid residue in a precursor ETR protein is equivalent to a particular residue in the ETR protein of *Arabidopsis thaliana* if it is homologous in position in either primary or tertiary structure to the specified residue of the Arabidopsis ETR protein.

In order to establish homology by way of primary structure, the primary amino acid sequence of a precursor ETR protein is directly compared by alignment with the primary sequence of the ETR protein from *Arabidopsis thaliana*. Such alignment is preferably of the amino-terminal domain and will take into account the potential insertion or deletion of one or more amino acid residues as between the two sequences so as to maximize the amino acid sequence homology. A comparison of a multiplicity of ETR protein sequences with that of *Arabidopsis thaliana* provides for the identification of conserved residues among such sequences which conservation is preferably maintained for further comparison of primary amino acid sequence. Based on the alignment of such sequences, the skilled artisan can readily identify amino acid residues in other ETR proteins which are equivalent to Ala-31, Ile-62, Cys-65, Ala-102 and other residues in *Arabidopsis thaliana* ETR protein. Such equivalent residues are selected for modifications analogous to those of other modified ETR proteins which confer the desired ethylene responsive phenotype. Such modified ETR proteins are preferably made by modifying a precursor ETR nucleic acid to encode the corresponding substitution, insertion and/or deletion at the equivalent amino acid residue.

In addition to homology at the primary sequence level, equivalent residues can be identified based upon homology at the level of tertiary structure. The determination of equivalency at this level will generally require three-dimensional crystal structures for an ETR protein or modified ETR protein from Arabidopsis (or crystal structure of another ETR protein having defined equivalent residues) and the crystal structure of a selected ETR protein. Equivalent residues at the level of tertiary structure are defined as those for which the atomic coordinates of two or more of the main chain atoms of a particular amino acid residue of the selected ETR protein, as compared to the ETR protein from Arabidopsis, are within 0.13 nm and preferably 0.10 nm after alignment. Alignment is achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the ETR proteins in question.

ETR nucleic acids can be derived from any of the higher plants which are responsive to ethylene. Particularly suitable plants include tomato, banana, kiwi fruit, avocado, melon, mango, papaya, apple, peach and other climacteric fruit plants. Non-climacteric species from which ETR nucleic acids can be isolated include strawberry, raspberry, blackberry, blueberry, lettuce, cabbage, cauliflower, onion, broccoli, brussel sprout, cotton, canola, grape, soybean and oil seed rape. In addition, ETR nucleic acids can be isolated from flowering plants within the Division Magnoliophyta which comprise the angiosperms which include dicotyledons (Class Magnoliopsida and Dicotyledoneae) and monocotyledons (Class Liliopsida). Particularly preferred Orders of angiosperm according to "Taxonomy of Flowering Plants", by A. M. Johnson, The Century Co., NY, 1931 include Rosales, Cucurbitales, Rubiales, Campanulatae, Contortae, Tubiflorae, Plantaginales, Ericales, Primulales, Ebenales, Diapensiales, Primulales, Plumbaginales, Opuntiales, Parietales, Myritiflorae, Umbelliflorae, Geraniales, Sapindales, Rhamnales, Malvales, Pandales, Rhoendales, Sarraceniales, Ramales, Centrospermae, Santalales, Euphorbiales, Capparales, Aristolochiales, Julianiales, Juglandales, Fagales, Urticales, Myricales, Polygonales, Batidales, Balanopsidales, Proteales, Salicales, Leitneriales, Garryales, Verticillatae and Piperales. Particularly preferred plants include lily, carnation, chrysanthemum, petunia, rose, geranium, violet, gladioli, orchid, lilac, crabapple, sweetgum, maple, poinsettia, locust, ash and linden tree.

In addition to providing a source for ETR nucleic acids which can be modified or isolated according to the teachings herein, the foregoing plants can be used as recipients of the modified nucleic acid to produce chimeric or transgenic plants which exhibit an ethylene resistance phenotype in one or more tissue types of the transformed plant.

Once a modified ETR nucleic acid has been cloned, it is used to construct vectors for transforming plant cells. The construction of such vectors is facilitated by the use of a shuttle vector which is capable of manipulation and selection in both plant and a convenient cloning host such as a prokaryote. Such shuttle vectors thus can include an antibiotic resistance gene for selection in plant cells (e.g., kanamycin resistance) and an antibiotic resistance gene for selection in a bacterial host (e.g. actinomycin resistance). Such shuttle vectors also contain an origin of replication appropriate for the prokaryotic host used and preferably at least one unique restriction site or a polylinker containing unique restriction sites to facilitate vector construction. Examples of such shuttle vectors include pMON530 (Rogers et al. (1988) *Methods in Enzymology* 153:253–277) and pCGN1547 (McBride et al. (1990) Plant *Molecular Biology* 14:269–276).

In the preferred embodiments, which comprise the best mode for practicing the invention, a promoter is used to drive expression of an ETR or a modified ETR nucleic acid within at least a portion of the tissues of a transformed plant. Expression of an ETR nucleic acid is preferably in the antisense orientation to modulate the ethylene response by reduction in translation of the endogenous ETR RNA transcript. Expression of a modified ETR nucleic acid results in the production of a modified ETR protein which is capable of conferring ethylene insensitivity. Such promoters may be obtained from plants, plant pathogenic bacteria or plant viruses. Constitutive promoters include the 35S and 19S promoters of cauliflower mosaic virus (CaMV35S and CaMV19S), the full-length transcript promoter from the Figwort mosaic virus (FMV35S) (See PCT Publication No. WO92/12249 published Jul. 23, 1992) and promoters associated with Agrobacterium genes such as nopaline, synthase (NOS), mannopine synthase (MOS) or octopine synthase (OCS). Other constitutive promoters include the α-1 and -β1 tubulin promoters (Silflow et al. (1987) *Devel. Genet.* 8:435–460), the histone promoters (Chaubet (1987) *Devl. Genet.* 8:461–473) and the promoters which regulate transcription of ETR nucleic acids.

In some embodiments, tissue and/or temporal-specific promoters can be used to control expression of ETR and modified ETR nucleic acids. Examples of fruit specific promoters include the E8, E4, E17 and J49 promoters from tomato (Lincoln et al. (1988) *Mol. Gen. Genet.* 212:71–75) and the 2A11, Z130 and Z70 promoters from tomato as described in U.S. Pat. Nos. 4,943,674, 5,175,095 and 5,177,307. In addition, preferential expression in rapidly dividing tissue can be obtained utilizing the plant EF-1α promoter as described in U.S. Pat. No. 5,177,011. Examples of floral specific promoters include the leafy promoter and promoters from the apetala, pistillata and agamous genes. A promoter system for targeting expression in the leaves of a transformed plant is a chimeric promoter comprising the CaMV35S promoter ligated to the portion of the ssRUBISCO gene which represses the expression of ssRUBISCO in the absence of light. In addition, pollen-specific promoters can also be used. Such promoters are well known to those skilled in the art and are readily available. A example of such a promoter is Zn13 (Hamilton et al. (1992) *Plant Mol. Biol.* 18:211–218). This promoter was cloned from corn (Monocot) but functions as a strong and pollen-specific promoter when used in tobacco (Dicot).

Examples of inducible promoters which can be used for conditional expression of ETR nucleic acids include those from heat-shock protein genes such as the PHS1 heat-shock protein gene (Takahashi et al. (1989) *Mol. Gen. Genet.* 219:365–372) and light-inducible promoters including the three chlorophyll a/b light harvesting protein promoters (Leutwiler et al. (1986) *Nucl. Acids. Res.* 14:4051–4064) and the pre-ferredoxin promoter (Vorst et al. (1990) *Plant Mol. Biol.* 14:491–499).

In a further embodiment of the invention, the vector used to transform plant cells is constructed to target the insertion of the ETR nucleic acid into an endogenous promoter within a plant cell. One type of vector which can be used to target the integration of a modified ETR nucleic acid to an endogenous promoter comprises a positive-negative selection vector analogous to that set forth by Monsour, et al. *Nature* 336:348–352 (1988) which describes the targeting of exogenous DNA to a predetermined endogenous locus in mammalian ES cells. Similar constructs utilizing positive and negative selection markers functional in plant cells can be readily designed based upon the identification of the endogenous plant promoter and the sequence surrounding it. When such an approach is used, it is preferred that a replacement-type vector be used to minimize the likelihood of reversion to the wild-type genotype.

The vectors of the invention are designed such that the promoter sequence contained in the vector or the promoter sequence targeted in the plant cell genome are operably linked to the nucleic acid encoding the ETR or modified ETR nucleic acid. When the positive strand of the ETR nucleic acid is used, the term "operably linked" means that the promoter sequence is positioned relative to the coding sequence of the ETR nucleic acid such that RNA polymerase is capable of initiating transcription of the ETR nucleic acid from the promoter sequence. In such embodiments it is also preferred to provide appropriate ribosome binding sites, transcription initiation and termination sequences, translation initiation and termination sequences and polyadenylation sequences to produce a functional RNA transcript which can be translated into ETR protein. When an antisense orientation of the ETR nucleic acid is used, all that is required is that the promoter be operably linked to transcribe the ETR antisense strand. Thus, in such embodiments, only transcription start and termination sequences are needed to provide an RNA transcript capable of hybridizing with the mRNA or other RNA transcript from an endogenous ETR gene or modified ETR nucleic acid contained within a transformed plant cell. In addition to promoters, other expression regulation sequences, such as enhancers, can be added to the vector to facilitate the expression of ETR nucleic acid in vivo.

Once a vector is constructed, the transformation of plants can be carried out in accordance with the invention by essentially any of the various transformation methods known to those skilled in the art of plant molecular biology. Such methods are generally described in *Methods and Enzymology*, Vol. 153 ("Recombinant DNA Part D") 1987, Wu and Grossman, Academic Press, eds. As used herein, the term "transformation" means the alteration of the genotype of a plant cell by the introduction of exogenous nucleic acid. Particular methods for transformation of plant cells include the direct microinjection of the nucleic acid into a plant cell by use of micropipettes. Alternatively, the nucleic acid can be transferred into a plant cell by using polyethylene glycol (Paszkowski et al. *EMBO J.* 3:2717–2722 (1984)). Other transformation methods include electroporation of protoplasts (Fromm, et al. Proc. Natl. Acad. Sci. U.S.A. 82:5824 (1985); infection with a plant specific virus, e.g., cauliflower mosaic virus (Hohn et al. "Molecular Biology of Plant Tumors", Academic Press, New York (1982), pp. 549–560) or use of transformation sequences from plant specific bacteria such as Agrobacterium tumefaciens, e.g., a Ti plasmid transmitted to a plant cell upon infection by agrobacterium tumefaciens (Horsch et al. Science 233:496–498 (1984); Fraley et al. *Proc. Natl. Acad. Sci. U.S.A.* 80:4803 (1983)). Alternatively, plant cells can be transformed by introduction of nucleic acid contained within the matrix or on the surface of small beads or particles by way of high velocity ballistic penetration of the plant cell (Klein et al. *Nature* 327:70–73 (1987)).

After the vector is introduced into a plant cell, selection for successful transformation in typically carried out prior to regeneration of a plant. Such selection for transformation is not necessary, but facilitates the selection of regenerated plants having the desired phenotype by reducing wild-type background. Such selection is conveniently based upon the antibiotic resistance and/or herbicide resistance genes which may be incorporated into the transformation vector.

Practically all plants can be regenerated from cultured cells or tissues. As used herein, the term "regeneration" refers to growing a whole plant from a plant cell, a group of plant cells or a plant part. The methods for plant regeneration are well known to those skilled in the art. For example, regeneration from cultured protoplasts is described by Evans et al. "Protoplasts Isolation and Culture", *Handbook of Plant Cell Cultures* 1:124–176 (MacMillan Publishing Co., New York (1983); M. R. Davey, "Recent Developments in the Culture and Regeneration of Plant Protoplasts", *Protoplasts* (1983) *Lecture Proceedings*, pp. 12–29 (Birkhauser, Basil 1983); and H. Binding "Regeneration of Plants", *Plant Protoplasts*, pp. 21–73 (CRC Press, Bocaraton 1985). When transformation is of an organ part, regeneration can be from the plant callus, explants, organs or parts. Such methods for regeneration are also known to those skilled in the art. See, e.g., *Methods in Enzymology*, supra.; *Methods in Enzymology*, Vol. 118; and Klee et al. *Annual Review of Plant Physiology* 38:467–486.

A preferred method for transforming and regenerating petunia with the vectors of the invention is described by Horsch, R. B. et al. (1985) *Science* 227:1229–1231. A preferred method for transforming cotton with the vectors of the invention and regenerating plants therefrom is described by Trolinder et al. (1987) *Plant Cell Reports* 6:231–234.

Tomato plant cells are preferably transformed utilizing Agrobacterium strains by the method as described in McCormick et al., *Plant Cell Reports* 5:81–84 (1986). In particular, cotyledons are obtained from 7–8 day old seedlings. The seeds are surface sterilized for 20 minutes in 30% Clorox bleach and germinated in Plantcons boxes on Davis germination media. Davis germination media is comprised of 4.3 g/l MS salts, 20 g/l sucrose and 10 mls/l Nitsch vitamins, pH 5.8. The Nitsch vitamin solution is comprised of 100 mg/l myo-inositol, 5 mg/l nicotinic acid, 0.5 mg/l pyridoxine HCl, 0.5 mg/l thiamine HCl, 0.05 mg/l folic acid, 0.05 mg/l biotin, 2 mg/l glycine. The seeds are allowed to germinate for 7–8 days in the growth chamber at 25° C., 40% humidity under cool white lights with an intensity of 80 einsteins M^2–s–^{1}. The photoperiod is 16 hours of light and 8 hours of dark.

Once germination occurs, the cotyledons are explanted using a #15 feather blade by cutting away the apical meristem and the hypocotyl to create a rectangular explant. These cuts at the short ends of the germinating cotyledon increase the surface area for infection. The explants are bathed in sterile Davis regeneration liquid to prevent desiccation. Davis regeneration media is composed of 1×MS salts, 3% sucrose, 1× Nitsch vitamins, 2.0 mg/l zeatin, pH 5.8. This solution was autoclaved with 0.8% Noble Agar.

The cotyledons are pre-cultured on "feeder plates" composed of media containing no antibiotics. The media is composed of 4.3 g/l MS salts, 30 g/l sucrose, 0.1 g/l myo-inositol, 0.2 g/l KH_2PO_4, 1.45 mls/l of a 0.9 mg/ml solution of thiamine HCl, 0.2 mls of a 0.5 mg/ml solution of kinetin and 0.1 ml of a 0.2 mg/ml solution of 2,4 D. This solution is adjusted to pH 6.0 with KOH. These plates are overlaid with 1.5–2.0 mls of tobacco suspension cells (TXD's) and a sterile Whitman filter soaked in 2C005K media. 2C005K media is composed of 4.3 g/l Gibco MS salt mixture, 1 ml B5 vitamins (1000× stock), 30 g/l sucrose, 2 mls/l PCPA from 2 mg/ml stock, and 10 μl/l kinetin from 0.5 mg/ml stock. The cotyledons were cultured for 1 day in a growth chamber at 25° C. under cool white lights with a light intensity of 40–50 einsteins m^2s^{-1} with a continuous light photoperiod.

Cotyledons are then inoculated with a log phase solution of Agrobacterium containing the modified or wild type ETR nucleic acid. The concentration of the Agrobacterium is approximately 5×10^8 cells/ml. The cotyledons are allowed to soak in the bacterial solution for six minutes and are then blotted to remove excess solution on sterile Whatman filter disks and subsequently replaced to the original feeder plate where they are allowed to co-culture for 2 days. After the two days, cotyledons are transferred to selection plates containing Davis regeneration media with 2 mg/l zeatin riboside, 500 μg/ml carbenicillin, and 100 μg/ml kanamycin. After 2–3 weeks, cotyledons with callus and/or shoot formation are transferred to fresh Davis regeneration plates containing carbenicillin and kanamycin at the same levels. The experiment is scored for transformants at this time. The callus tissue is subcultured at regular 3 week intervals and any abnormal structures are trimmed so that the developing shoot buds continue to regenerate. Shoots develop within 3–4 months.

Once shoots develop, they are excised cleanly from callus tissue and planted on rooting selection plates. These plates contain 0.5×MSO containing 50 μg/ml kanamycin and 500 μg/ml carbenicillin. These shoots form roots on the selection media within two weeks. If no roots appear after 2 weeks, shoots are trimmed and replanted on the selection media. Shoot cultures are incubated in percivals at a temperature of 22° C. Shoots with roots are then potted when roots were about 2 cm in length. The plants are hardened off in a growth chamber at 21° C. with a photoperiod of 18 hours light and 6 hours dark for 2–3 weeks prior to transfer to a greenhouse. In the greenhouse, the plants are grown at a temperature of 26° C. during the day and 21° C. during the night. The photoperiod is 13 hours light and 11 hours dark and the plants are allowed to mature.

Once plants have been regenerated, one or more plants are selected based upon a change in the ethylene response phenotype. For example, when a modified ETR nucleic acid is used with its native promoter, selection can be based upon an alteration in any of one of the "triple responses" of seedlings from such plants. Guzman et al. (1990) *The Plant Cell* 2:523. Alternatively, or when constitutive promoters are used, various other ethylene responses can be assayed and compared to the wild type plant. Such other ethylene responses include epinasty (which is observed primarily in tomato), epsision, abscission, flower petal senescence and fruit ripening. In addition to overt changes in the ethylene response, the levels of various enzymes can be determined followed by exposure to ethylene to determine the response time for the typical increase or decrease in the level of a particular protein such as an enzyme. Examples of various ethylene responses which can be used to determine whether a particular plant has a decreased response to ethylene are set forth in Chapter 7, The Mechanisms of Ethylene Action in "Ethylene in Plant Biology" 2d Ed. F. B. Abels, P. W. Morgan and M. E. Salveit, Jr., eds., San Diego, Academic Press, Inc. (1992). When a tissue and/or temporal-specific promoter or inducible promoter is used, the determination of a modulation in the ethylene response is determined in the appropriate tissue at the appropriate time and if necessary under the appropriate conditions to activate/inactivate an inducible promoter. In each case, the ethylene response is preferably compared to the same ethylene response from a wild-type plant.

The following are particularly preferred embodiments for modulating the ethylene response in fruit. However, such embodiments can be readily modified to modulate the ethylene response in vegetative tissue and flowers.

In one approach, a modified ETR nucleic acid operably linked to a constitutive promoter of moderate strength is used to reduce the ethylene response. This results in a lengthening of the time for fruit ripening.

In an alternate embodiment, a modified ETR nucleic acid operably linked to a regulatable (inducible) promoter is used so that the condition that turns on the expression of the modified ETR nucleic acid can be maintained to prevent fruit ripening. The condition that turns off the expression of the modified ETR nucleic acid can then be maintained to obtain ripening. For example, a heat-inducible promoter can be used which is active in high (field) temperatures, but not in low temperatures such as during refrigeration. A further example utilizes an auxin or gibberellin-induced promoter such that transformed plants can be treated with commercial auxin analogs such as 2, 4-D or with commercial gibberellin analogs such as Pro-Gibb to prevent early ripening.

Alternatively, a strong constitutive promoter can be operably linked to a modified ETR nucleic acid to prevent fruit ripening. So as to allow eventual fruit ripening, the plant is also transformed with a wild-type ETR nucleic acid operably linked to an inducible promoter. Expression of the wild-type ETR nucleic acid is increased by exposing the plant to the appropriate condition to which the inducible promoter responds. When the wild-type ETR nucleic acid expression is increased, the effect of expression of the modified ETR nucleic acid is reduced such that fruit ripening occurs.

Particular constructs which are desirable for use in transforming plants to confer ethylene insensitivity include the CaMV35S promoter operably linked to any other mutant Arabidopsis ETR genomic or cDNA clones including the corresponding modification at residue 36 to convert proline to leucine. Such constructs are expected to confer a dominant ethylene insensitivity phenotype tp cells and plants transformed with and expressing such constructs.

In addition, a preferred construct includes operably linking the FMV promoter to drive expression of the tomato TETR cDNA which has been engineered to contain a mutation analogous to any of those identified in the ETR genes from Arabidopsis as well as the Nr mutation found in the tomato ETR gene. Such constructs are expected to confer a dominant ethylene insensitivity phenotype to cells and plants which are transformed with and express such constructs.

Other preferred constructs include the operable linking the FMV promoter to ETR antisense cDNAs including TETR and ETR1. Such constructs are expected to confer a dominant ethylene insensitivity phenotype to cells and plants which are transformed with and express such constructs.

The invention can be practiced in a wide variety of plants to obtain useful phenotypes. For example, the invention can be used to delay or prevent floral senescence and abscission during growth or during transport or storage as occurs in flower beds or cotton crops (Hall, et al. (1957) *Physiol. Plant* 10:306–317) and in ornamental flowers (e.g., carnations, roses) that are either cut (Halevy, et al. (1981) *Hort. Rev.* 3:59–143) or not cut. In addition, the invention can be practiced to delay or prevent senescence and abscission of leaves and fruits in cucumber (Jackson, et al. (1972) *Can. J. Bot.* 50:1465–1471), legumes and other crops (Heck, et al. (1962) *Texas Agric. Expt. Sta. Misc. Publ.* MP 613:1–13) and ornamental plants (e.g., holly wreaths) (Curtis et al. (1952) *Proc. Am. Soc. Hort. Sci.* 560:104–108). Other uses include the reduction or prevention of bitter-tasting phenolic compounds (isocoumarins) which are induced by ethylene for example in sweet potatoes (Kitinoja (1978) "Manipulation of Ethylene Responses in Horticulture", Reid, ed., *Acta. Hort.* Vol 201, 377–42) carrots (Coxon et al. (1973) *Phyto. Chem. Istry.* 12:1881–1885), parsnip (Shattuck et al. (1988) *Hort. Sci.* 23:912) and Brassica. Other uses include the prevention of selective damage to reproductive tissues as occurs in oats and canola (Reid et al. (1985) in "Ethylene in Plant Development", Roberts, Tucker, eds. (London), Butterworths, pp. 277–286), the loss of flavor, firmness and/or texture as occurs in stored produce such as apples and watermelons (Risse et al. (1982) *Hort. Sci.* 17:946–948), russet spotting (a post-harvest disorder) which is ethylene induced in crisphead lettuce (Hyodo et al. (1978) *Plant Physiol.* 62:31–35), to promote male flower production (Jaiswal et al. (1985) *Proc. Indian Acad. Sci.* (Plantg Sci. 95:453–459) and to increase plant size, e.g., by delaying the formation of flowers in ornamental bromeliads (Mekers et al. (9183) *Acta Hortic* 137:217–223). Furthermore, a decrease in ethylene response can be used to delay disease developments such as the preventing of lesions and senescence in cucumbers infected with *Colletotrichum lagenarium* and to reduce diseases in plants in which ethylene causes an increase in disease development, e.g., in barley, citrus, Douglas fir seedlings, grapefruit, plum, rose, carnation, strawberry, tobacco, tomato, wheat, watermelon and ornamental plants. In addition, the invention can be used to reduce the effect of ethylene found in the environment and indirectly the effect of various environmental stresses which result in the biosynthesis of ethylene in plant tissue. For example, ethylene exists at biologically detrimental levels in localized atmospheres due to fires, automobile exhaust and industry. See, e.g., Chapter 8, Ethylene in the Environment in "Ethylene in Plant Biology", supra. In addition, the invention can be used to minimize the effect of ethylene synthesized in response to environmental stresses such as flooding, drought, oxygen deficiency, wounding (including pressure and bruising), chilling, pathogen invasion (by viruses, bacteria, fungi, insects, nematodes and the like), chemical exposure (e.g., ozone salt and heavy metal ions) and radiation.

The following is presented by way of example and is not to be construed as a limitation on the scope of the invention. Further, all references referred to herein are expressly incorporated by reference.

EXAMPLE 1

Cloning of the ETR1 Gene

etr1-l plants were crossed with two lines carrying the recessive visible markers ap1 and clv2 respectively. The F_1 progeny were allowed to self-pollinate. Phenotypes were scored in the F_2. The recombination percentages (using the Kosambi mapping function (D. D. Kosambi (1944) *Ann. Eugen.* 12:172)) were determined in centimorgans. The ETR1 locus mapped to the lower portion of chromosome 1 between the visible genetic markers ap1 and clv2 (6.5+/−1.0 cM from AP1 and 2.8+/−1.1 cM from CLV2).

etr1-1 was crossed to tester line W100 (ecotype Landsberg (Koornneef et al. (1987) *Arabidopsis Inf. Serv.* 23:46) and the F_1 plants were allowed to self-pollinate. Linkage of RFLP markers to the ETR1 locus was analyzed in 56 F_2 plants as described in Chang, et al. (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85:6856. Of the RFLP markers that reside in this region of chromosome 1, one marker, 1bAt315, completely cosegregated with the etr1-1 mutant phenotype out of 112 chromosomes. The 1bAt315 clone was therefore used as a probe to initiate a chromosome walk in the ETR1 gene region. Various genomic DNA cosmid libraries were utilized. One library contained subclones of two yeast artificial chromosomes (YACs EG4E4 and EG2G11 (Grill et al.

(1991) *Mol. Gen. Genet.* 226:484)) that hybridized to 1bAt315. To subclone the YACs, total DNA from yeast cells harboring EG4E4 or EG2G11 was partially digested with Sau3AI, and cloned into the BglII site of cosmid vector pCIT30 (Ma et al. (1992) Gene 117:161). Standard cloning and screening methods were used (Sambrook et al, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989)). A library from the etr1-1 mutant was similarly constructed in pCIT30. The wild type library was constructed previously (Yanofsky et al. (1990) *Nature* 346:35). By restriction analysis and sequential hybridization to these libraries, overlapping cosmids (a contig) were obtained that spanned a distance of approximately 230 kb. See FIG. **8**.

The ETR1 gene was localized to a subregion of approximately 47 kb using fine structure RFLP mapping.

To create the fine structure map, meiotic recombinants were isolated based on phenotype from the F2 self-progeny of the above crosses between the etr1-1 mutant (ecotype Columbia) and two lines (both ecotype Landsberg) carrying ap1 and clv2. Recombinants were identified in the F2 progeny as plants that were either wild type at both loci or mutant at both loci. ETR1 was scored in dark grown seedlings (Bleecker et al. (1988) *Science* 241:1086). Seventy-four (74) recombinants between ETR1 and AP1 were obtained, and 25 recombinants between ETR1 and CLV2. The recombination break points were mapped using DNA fragments from the chromosome walk as RFLP probes. Given the number of recombinants isolated, the calculated average distance between break points was roughly 20 kb for each cross. Over the 230 kb contig, the actual density of break points found was consistent with the calculated density on the CLV2 side (with 5 break points in approximately 120 kb). The nearest break points flanking the ETR1 gene defined a DNA segment of approximately 47 kb.

To search for transcripts derived from this 47 kb region, cDNA libraries were screened using DNA fragments. One cDNA clone was designated λC4 and was detected with the 4.25 kb EcoRI fragment 1 shown in FIG. **8**. Because λC4 potentially represented the ETR1 gene, this clone was further characterized.

EXAMPLE 2

ETR Gene Characterization

The nucleotide sequences of the λC4 cDNA and the corresponding genomic DNA (FIG. **2**) (SEQ ID NO:1) was determined using sequenase version 2.0 (United States Biochemical Co., Cleveland, Ohio) and synthetic oligonucleotide primers having a length of 17 nucleotides. The primer sequences were chosen from existing ETR1 sequences in order to extend the sequence until the entire sequence was determined. The initial sequence was obtained using primers that annealed to the cloning vector. Templates were double-stranded plasmids. Both strands of the genomic DNA were sequenced, including 225 bp upstream of the presumed transcriptional start site, and 90 bp downstream of the polyadenylation site. λC4 was sequenced on a single strand.

λC4 was 1812 base pairs long, including a polyA tail of 18 bases. From the DNA sequences and RNA blots (described below), it was determined that λC4 lacked approximately 1000 base pairs of the 5' end.

To obtain longer cDNAs, first strand cDNA was synthesized (RiboClone cDNA Synthesis System, Promega, Madison Wis.) from seedling polyA+RNA using sequence-specific primers internal to λC4. The cDNA was then amplified by PCR (Saiki, R. K. et al. (1985) *Science* 230:1350) using various pairs of primers: 3' PCR primers were chosen to anneal to different exons as deduced from the cDNA and genomic DNA sequences, and 5' PCR primers were chosen to anneal to various 5' portions of genomic DNA sequences. Six different primers at the 5' end were used. The farthest upstream primer which amplified the cDNA was primer Q (5'AGTAAGAACGAAGAAGAAGTG) (SEQ ID NO:26). An overlapping primer, which was shifted twelve bases downstream, also amplified the cDNA. The cDNA could not be amplified using a 5' end primer that was 98 base pairs farther upstream. Genomic DNA templates were used for PCR controls. The longest cDNA was considered to extend to the 5' end of primer Q. The amplified cDNAs were sequenced directly with Sequenase Version 2.0 as follows: after concentrating the PCR reactions by ethanol precipitation, the amplified products were separated by electrophoresis in 0.8% LMP agarose gels. The DNA fragments were excised, and a mixture of 10 μl excised gel (melted at 70° C.), 1 ml 10 mM primer and 1.2 ml 5% Nonidet P-40 was heated at 90° C. for two minutes to denature the DNA. The mixture was then cooled to 37° C. prior to proceeding with sequencing reactions.

The longest cDNA, which was 2786 bases (not including the polyA tail), was consistent with the estimated size of 2800 bases from RNA blots, and was presumed to be close to full length. A potential TATA box (5' ATAATAATAA) (SEQ ID NO:51) lies 33 bp upstream of the 5' end in the genomic sequence. Based on comparison of the cDNA and the genomic DNA sequences, the gene has six introns, one of which is in the 5' untranslated leader. The exons contain a single open reading frame of 738 amino acids. See FIG. **3**.

The determination that this gene is, in fact, ETR1 was established by comparing the nucleotide sequences of the wild type allele and the four mutant alleles. For each mutant allele, an EcoRI size-selected library was constructed in the vector lambda ZAPII (Stratagene, LaJolla, Calif.). Clones of the 4.25 kb EcoRI fragment were isolated by hybridization with the wild type fragment. These clones were converted into plasmids (pBluescript vector) by in vivo excision according to the supplier (Stratagene) and sequenced. Two independent clones were sequenced on a single strand for each mutant allele. The 5' ends (535 bp not contained on the 4.25 kb EcoRI fragment) were amplified by PCR and directly sequenced as previously described. Codon differences were as follows: Codon 65 TGT to TAT in etr1-1 (FIGS. **6**A, B, C and D), Codon 102 GCG to ACG in etr1-2 (FIGS. **7**A, B, C and D), Codon 31 GCG to GTG in etr1-3 (FIGS. **4**A, B, C and D), Codon 62 ATC to TTC in etr1-4 (FIGS. **5**A, B, C and D). All four mutations are clustered in the amino-terminal region of the deduced protein sequence.

The ETR1 message was examined in standard RNA electrophoresis (formaldehyde) gel blots. The 2.8 kb ETR1 transcript was present in all plant parts examined—leaves, roots, stems, flowers and seedlings (data not shown). In addition, no differences were observed between ETR1 transcripts of the wild type and the mutant alleles (data not shown). Treatment with ethylene did not detectably alter the amount of ETR1 mRNA in dark-grown wild type seedlings (data not shown).

When the ETR1 gene was hybridized to Arabidopsis genomic DNA blots at normal stringency (i.e., overnight in 5×SSPE (0.9 M NaCl, 50 mM NaH_2PO_4, 40 mM NaOH, 4.5 mM EDTA, pH 7.4 at 65° C., with the most stringent wash in 0.1×SSPE at 65° C. for 30 minutes), only the expected fragments of the ETR1 locus were observed (data not shown). At reduced stringency (i.e., hybridization in 5×SSPE at 50° C. and washs in 5×SSPE at 50° C.), however, numerous fragments were detected, which suggests that a family of similar genes exists in Arabidopsis.

The predicted amino terminal sequence of ETR1 (residues 1–316) has no similarity to sequences in the GenBank database (version 77.0). The carboxy-terminal portion, however, is highly similar to the conserved domains of both the sensor and the response regulator of the prokaryotic two-component system of signal transduction. In bacteria, the histidine protein kinase domain of the sensor is characterized by five sequence motifs arranged in a specific order with loosely conserved spacing (Parkinson (1992) *Annu. Rev. Genet.* 26:71). The deduced ETR1 sequence contains all five motifs with the same relative order and spacing found in the bacterial proteins (FIG. **9**A). The deduced sequence is most similar to the sequences of *Escherichia coli* Bar A (Nagasawa et al. (1992) *Mol. Microbiol.* 6:3011) and *Pseudomonas syringae* LemA (Harbak et al. (1992) J. Bact. 174:3011); over the entire histidine kinase domain (the 241 amino acids from residues 336 through 566), there are 43% and 41% amino acid identities with BarA and LemA respectively, and 72% and 71% similarities respectively. The function of BarA is unknown, although it was cloned based on its ability to complement a deletion in the *E. coli* osmotic sensor protein, EnvZ (Nagasawa, supra.). LemA is required for pathogenicity of *P. syringae* on bean plants (Hrabak, supra.). Other bacterial proteins with sequences highly similar to this putative ETR1 domain are: *Xanthomonas campestris* RpfC (35% identity) which is possibly involved in host recognition for pathogenicity in cruciferous plants (Tang et al (1991) *Mol. Gen. Genet.* 226:409), *E. coli* RcsC (34% identity) which is involved in regulation of capsule synthesis (Stout et al. (1990) *J. Bacteriol.* 172:659) and *E. coli* ArcB (25% identity) which is responsible for repression of anaerobic enzymes (Luchi et al. (1990) *Mol. Microbiol.* 4:715).

Adjacent to the putative histidine kinase domain, the deduced ETR1 sequence exhibits structural characteristics and conserved residues of bacterial response regulators. Structural characteristics of response regulators are based on the known three-dimensional structure of CheY (the response regulator for chemotaxis) in *Salmonella typhimurium* and *E. coli*, which consists of five parallel β-strands surrounded by five a-helices (Stock et al. (1989) *Nature* 337:745; Volz et al. (1991) *J. Biol. Chem.* 266:15511). Sequences of bacterial response regulators have been aligned to this structure based on residues that are compatible with the hydrophobic core of the CheY (Stock et al. (1989) *Microbiological Rev.* 53:450). The deduced ETR1 sequence can be similarly aligned (data not shown). At four specific positions, response regulators contain highly conserved residues—three aspartates and a lysine (Parkinson et al. (1992) *Annu. Rev. Genet.* 26:71; Stock et al., supra.); the three aspartates form an acidic pocket into which protrudes the side chain of the conserved lysine (Stock et al. (1989) *Nature* 337:745; Volz et al. (1991) J. Biol. Chem. 266:15511) and the third aspartate is the receiver of the phosphate from phosphohistidine (Stock et al. (1989), supra.). Except for the conservative substitution of glutamate for the second aspartate, these conserved amino acids are found in the same positions in the deduced ETR1 sequence (FIG. **9**B). The deduced sequence in this domain (a stretch of 121 amino acids from residues 609 through 729 in ETR1) is most similar to the sequences of *Bordetella parapertussis* BvgS (29% identity, 60% similarity) which controls virulence-associated genes for pathogenicity in humans (Aricò et al. (1991) *Mol. Microbiol.* 5:2481), *E. coli* RcsC (29% identity, 64% similarity), P. syringae LemA (26% identity, 57% similarity), *X. campestris* RpfC (25% identity) and *E. coli* BarA (20% identity). All of the bacterial proteins that are similar to ETR1 in sequence are also structurally similar to ETR1 in that they contain both the histidine kinase domain and the response regulator domain. Although these features are shared, the sensing functions are clearly diverged.

A potential membrane spanning domain (residues 295–313) exists in the deduced ETR1 sequence based on hydropathy analysis (Kyte et al. (1982) *J. Mol. Biol.* 157:105), but it is unclear whether ETR1 is actually a transmembrane protein since there is no clear signal sequence. There are also no N-linked glycosylation sites. While all of the bacterial proteins to which the deduced ETR1 sequence is similar have two potential membrane spanning domains flanking the amino terminal domain, a few bacterial sensors (those which lack the response regulator) do not.

EXAMPLE 3

An etr1 Mutant Gene Confers Ethylene Insensitivity to Wild Type Plants

Dominant ethylene insensitivity was conferred to wild type Arabidopsis plants when the etr1-1 mutant gene was stably introduced using Agrobacterium-mediated transformation. The gene was carried on a 7.3 kb genomic DNA fragment (fragments 1 and 2 in FIG. **8** which included approximately 2.7 kb upstream of the transcription initiation site, and approximately 1 kb downstream of the polyadenylation site). It was cloned into binary transformation vector pCGN1547 obtained from Calgene, Inc., Davis, Calif. The vector also carried a selectable marker for kanamycin resistance in plants.

For the etr1-1 construct, the 4.25 kb EcoRI plasmid clone containing the etr1-1 mutation was linearized by partial EcoRI digestion and ligated with the 3.1 kb EcoRI fragment which was agarose gel-purified from cosmid clone theta8 (a subclone of YAC EG4E4 in the walk). The resulting plasmid, containing the two EcoRI fragments in the correct relative orientation, was linearized at polylinker site Asp718, the ends were filled in using Klenow enzyme, and BamHI linkers were ligated to the blunt ends. Finally, the 7.3 kb insert was removed from the plasmid at the polylinker site BamHI, and ligated into the BamHI site of binary transformation vector pCGN1547 (McBride, K. E. et al. (1990) *Plant Molecular Biology* 14:269). For the control construct, the wild type 7.3 kb fragment was agarose gel-purified from EcoRI partially digested cosmid theta8, and subcloned into the EcoRI site of pBluescript. The fragment was then removed using the BamHI and KpnI sites of the polylinker, and ligated into pCGN1547 that had been digested with BamHI and KpnI. The mutant and wild type constructs were transformed into Agrobacterium (Holsters et al. (1978) *Mol. Gen. Genet.* 163:181) strain ASE (Monsanto) (Rogers et al. (1988) *Meth. Enzymol.* 153:253). Arabidopsis ecotype Nossen was transformed (Valvekens, D. et al. (1988) *Natl. Proc. Acad. Sci. U.S.A.* 85:5536) using root-tissue cultured in liquid rather than on solid medium. Triploid plants having one mutant copy of the ETR1 gene were obtained as the progeny of crosses between the etr1-1 homozygote (diploid) and a tetraploid wild type in ecotype Bensheim which has the same triple response phenotype as ecotype Columbia. Triploid wild type plants were similarly obtained by crossing the diploid wild type to the tetraploid. Ethylene sensitivity was assayed in dark-grown seedlings treated with either ethylene (Bleecker et al., supra.) or 0.5 mM ACC. For ACC treatment, plants were germinated and grown on Murashige and Skoog basal salt mixture (MS, Sigma), pH 5.7, 0.5 mM ACC (Sigma), 1% Bacto-agar (Difco). Kanamycin resistance was measured by the extent of root elongation in one week old seedlings grown on MS pH 5.7 μg/ml Kanamycin, 1% Bacto-agar.

Ten kanamycin resistant plants were produced. Eight of the ten exhibited ethylene insensitive self-progeny as evaluated by the dark-grown seedling response to ethylene. In each line, ethylene insensitivity cosegregated with kanamycin resistance. As a control, transformations were performed using the corresponding 7.3 kb genomic DNA fragment of the wild type from which six kanamycin resistant plants were obtained. These lines gave rise to only ethylene sensitive self-progeny which did not appear to be different from the wild type.

The etr1-1 transformants displayed different levels of ethylene insensitivity. Thus, the wild type gene is capable of attenuating the mutant phenotype and the etr1-1 mutation is not fully dominant in the transformed plants. Of the ten kanamycin resistant lines, six gave completely dominant ethylene insensitivity, indicating the presence of multiple copies of the mutant gene. Two other lines displayed partial dominance, and two lines appeared to be wild type. Reduced ethylene insensitivity was presumably due to low expression levels which can be caused by position effects (e.g., DNA methylation) or possibly by truncation of the transferred DNA.

EXAMPLE 4

Vector Constructs Containing Heterologous Promoter

This example describes the construction of a plant transformation vector containing a heterologous promoter to control expression of wild type and mutant ETR1 nucleic acids.

The cauliflower mosaic virus 35S protein promoter (Guilley et al. (1982) *Cell* 30:763–773; Odell, et al. (1985) *Nature* 313:810–812 and Sanders et al. (1987) *Nucl. Acids Res.* 15:1543–1558) and the 3' end of the Nopaline synthase (NOS) gene were cloned into the pCGN1547 vector to create pCGN18. The 35S promoter, on a HindIII-BamHI fragment of approximately 1.6 kb, was cloned into the unique HindIII-BamHI site of pCGN1547. The 1 kb BamHI-KpnI NOS fragment was cloned into the unique BamHI-KpnI site of pCGN1547.

The 4.25 kb EcoRI fragment of both the wild type and mutant ETR1-1 allele were independently cloned into the unique BamHI site of the above pCGN18 vector using BamHI linkers. This 4.25 kb EcoRI genomic fragment contains the entire coding sequence including five introns and approximately 1 kb genomic DNA downstream of the polyadenylation site. It does not contain the ETR1 promoter which is on the 3.1 EcoRI fragment 2 in FIG. **5**.

These vectors were used to transform root explants as described in Example 3. Kanamycin resistant plants containing the mutant ETR1-1 gene were obtained and demonstrated an ethylene insensitivity phenotype similar to that found in Example 3. Control plants transformed with the wild type ETR1 gene produced only ethylene sensitive self-progeny.

EXAMPLE 5

Vector Construct Utilizing Antisense ETR1

Ethylene insensitivity was- conferred to wild-type Arabidopsis by expression of an ETR1 antisense nucleic acid which was introduced using standard Agrobacterium root transformation procedure. Valvekens et al. (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85:5536. The antisense nucleic acid consisted of a 1.9 kb ETR1 cDNA fragment. Expression of this fragment, which extended from the MscI restriction site at nucleotide 220 to the first SmaI site at nucleotide 2176 in FIGS. **3**A, **3**B, **3**C and **3**D was driven in the reverse orientation by the CaMV 35S promoter. To construct the antisense nucleic acid, BamHI linkers were ligated to the ends of the 1.9 kb MscI-SmaI DNA fragment and the thus formed fragment was ligated into the BamHI site of pCGN 18 transformation vector. Jack et al. (1994) *Cell* 76:703. The construct was transformed into Agrobacterium strain ASE as described above and then into Arabidopsis.

Seedlings derived from this transformation experiment were tested for sensitivity to ethylene as previously described. Seedlings containing the antisense construct were ethylene insensitive.

EXAMPLE 6

Identification of QITR, a Second ETR Nucleic Acid in Arabidopsis

Genomic DNA from *Arabidopsis thaliana* was partially digested with Sau3A and cloned into a λGEM11 (half-site arms) obtained from Promega, Madison, Wis. The genomic digest was partial end filled prior to cloning with λGEM11 and plated on media as suggested by the manufacturer.

The thus cloned library was screened with a ^{32}P-labeled cDNA XbaI fragment extending from nucleotides 993–2308 as set forth in FIGS. **3**B, **3**C and **3**D. Hybridization conditions were 50° C. and 5×SSPE. Washes were made at 50° C. 0.2×SSPE. Several positively hybridizing clones were identified, replated and rescreened. Positively hybridizing clones were digested with SacI (which cleaves within the arms of the cloning phage and within the insert). The multiple fragments obtained therefrom were subcloned into bacterial plasmids for sequencing. The genomic DNA sequence (SEQ ID NO.:45) together with the deduced amino acid sequence (SEQ ID NO.:46 and 48) is set forth in FIG. **12**. This ETR nucleic acid and amino acid sequence is referred to as the QITR nucleic or amino acid sequence respectively. The QITR cDNA sequence (SEQ ID NO.:47) and the QITR amino acid sequence (SEQ ID NOs:46 and 48) are shown in FIG. **13**.

By comparison to the ETR1 Arabidopsis nucleic acid and amino acid sequence (see FIGS. **2** and **3**), the QITR protein appears to contain an amino terminal portion having a relatively high level of homology to the amino terminal portion of the ETR1 protein and a histidine kinase portion with a moderate level of homology to the same sequence in ETR1. The response regulatory region found in ETR1 is not present in the QITR protein. The overall nucleic acid homology is approximately 69%. With regard to the amino terminal portion (i.e., between residues 1 through 316) the homology is approximately 71% identical in terms of amino acid sequence and 72% identical in terms of nucleic acid sequence.

EXAMPLE 7

Modification of QITR Nucleic Acid to Confer Ethylene Insensitivity

An amino acid substitution was made in a 5 kb QITR genomic clone which was analogous to that for the ETR1-4 mutation, namely the substitution of the isoleucine at position 62 with phenylalanine. Compare FIG. **3A** with FIG. **5A** at residue 62. As further indicated at FIGS. **12** and **13**, residue 62 in the QITR protein is also isoleucine as in the ETR1 protein.

The amino acid substitution was made to the QITR nucleic acid using oligonucleotide-directed in vitro mutagenesis. Kunkel et al. (1987) *Methods in Enzymology* 154:367–382. A Muta-gene kit from Bio-Rad Laboratories, Hercules, Calif., was used in connection with this particular mutation. The sequence of the oligonucleotide used was 5' GGA GCC TTT TTC ATT CTC (SEQ ID NO:52). Replacement of nucleotide A with T in the codon ATC changed the amino acid Ile at residue 62 to Phe in the deduced protein sequence.

The QITR nucleic acid spanning approximately 5 kb from the first HindIII site to the second KpnI site contained approximately 2.4 kb of nucleotides upstream from the start codon. This 5 kb fragment was ligated into the pCGN1547 transformation vector (supra.). This construct was then transformed into Agrobacterium strain ASE as described supra and then into Arabidopsis.

Seedlings derived from this transformation experiment were tested for sensitivity to ethylene as previously described. Seedlings containing the QITR nucleic acid containing the modification at residue 62 were ethylene insensitive.

EXAMPLE 8

Identification of Arabidopsis ETR Nucleic Acid Q8

The ETR nucleic acid Q8 (SEQ ID NOs:41 and 43) was identified by direct sequence comparison with the ETR1 nucleic acid from Arabidopsis. The Arabidopsis Q8 nucleic acid was identified in connection with a chromosome walk on chromosome 3 of *Arabidopsis thaliana.*

Briefly, overlapping YAC clones were generated which were thereafter subcloned into plasmids. The genomic inserts in such plasmids were extricated by digesting with restriction endonuclease and hybridized to a cDNA library from Arabidopsis floral tissue.

Positively hybridizing inserts were sequenced to produce the overall genomic sequence (SEQ ID NO.:41) together with the deduced amino acid sequence (SEQ ID NOs:42 and 44) as set forth in FIG. **14**. The cDNA sequence (SEQ ID NO:43) and deduced amino acid sequence (SEQ ID NOs:42 and 44) is set forth in FIG. **15**.

The overall nucleic acid homology as between the Q8 nucleic acid and the ETR1 nucleic acid is approximately 69%. With regard to the amino terminal portion extending from residues 1 through 316, the overall amino sequence homology is approximately 72% whereas the nucleic acid encoding this sequence is approximately has a sequence homology of approximately 71% as between the Q8 and ETR1 nucleic acids.

EXAMPLE 9

Isolation of the TETR cDNA

A ^{32}P-labeled hybridization probe was prepared by random-primer labeling of a 1.3 kb PCR fragment generated by PCR amplification of the Arabidopsis ETR1 gene with the PCR primers "5'BamHI" (CCCGGATCCATAGTGTAAAAAATTCATAATGG) (SEQ ID NO:54) and "3'BamHIB" (CCGGATCCGTTGAAGACTTCCATCTTCTAACC) (SEQ ID NO:54).

This probe was used to screen a cDNA library of red tomato fruit mRNA cloned in the EcoRI site of lambda ZAP II vector from Stratagene, LaJolla, Calif. Twenty (20) positive primary plaques were identified that hybridized to this probe (2×SSC at 65° C. wash conditions) and secondary screens were performed on these to obtain pure plaques. In vivo excision was then performed with resultant recombinant phage and 19 independent plasmid clones were obtained.

Complementary DNAs, from plasmid clones containing the largest fragments that hybridized to the ETR1 probe, were sequenced and the nucleotide sequence and predicted amino acid sequences of the longest tomato cDNA (TETR14, also referred to as TXTR) were compared to the ETR1 and QITR sequences. The nucleotide sequence of TETR14 predicted that the encoded peptide was more similar to the QITR peptide than the ETR1 peptide. This conclusion was based on the fact that the response regulatory domain (which is present in ETR1) is absent in both TETR14 and QITR. The sequence (or partial sequence) of several of the other cDNA clones was determined and they were found to correspond to the same gene.

EXAMPLE 10

Analysis of TETR14 Gene Expression

Northern analysis was performed with mRNA from developing fruits of normal, or mutant tomato (Ripening inhibitor (rin), Non-ripening (nor) or Never-ripe (Nr)) fruit. Stages of developing fruits used were mature green, breaker, breaker plus 7 days, and mature green fruit treated with ethylene. Messenger RNA that hybridized to the TETR14 gene probe was not present at the mature green stage, but was present in breaker, breaker plus 7 days, and ethylene treated mature green fruit. Thus, it was concluded that accumulation of the ETR14 mRNA was regulated by ethylene. Accumulation of the TETR14 mRNA was attenuated in all three ripening mutants, further supporting the finding that mRNA accumulation is ethylene regulated.

EXAMPLE 11

Analysis of the TETR14 Gene from Pearson and Never-ripe DNA

PCR primers were obtained that would specifically amplify the N-terminal region of the TETR14 gene. The amplified portion was between Met1 and Ile214 in FIGS. **16A** and **16B**. The primers were

(CCGGATCCATGGAATCCTGTGATTGCATTG) (SEQ ID NO:55)

and TETR4A (GATAATAGGAAGATTAATTGGC) (SEQ ID NO:56). PCR conditions (Perkin-Elmer Cetus): 1 μg of tomato genomic DNA, 40 picomole of each primer, 1 min 94° C., 2 min 45° C., 2 min 72° C., 35 cycles. PCR products, obtained with these primers, resulting from two independent amplification reactions of pearson and Nr DNA were agarose gel purified and subcloned into either the T/A vector (Invitrogen) or digested with BamHI and XhoI and subcloned into Bluescript KS–that had been linearized with BamHI and SalI. Single stranded template DNA was prepared from the resultant plasmids and sequenced. The sequence of the PCR products from the pearson DNA were identical to the sequence of the TETR14 clone. Sequence analysis revealed that the PCR fragments resulting from PCR of the Nr DNA (TETR14-Nr) were not identical to those obtained from the Pearson DNA. The cytosine nucleotide at position 395 of the TETR14 gene is a thymine in the gene amplified from the Nr DNA. This nucleotide substitution in TETR14-Nr changes the proline at amino acid position 36 of the predicted peptide to a leucine. See FIG. **22** and Seq. ID Nos. 49 and 50 for the overall nucleic acid and amino acid sequence respectively. This Pro-36 of the TETR14 corresponds to the Pro-36 of the ETR1 peptide and to the Pro-36 of the QITR peptide. This results indicates that a mutation in the tomato TETR14 gene confers dominant ethylene-insensitivity. And thus, it is possible to predict that other changes in the TETR14 gene and other tomato ETR1 homologues will result in ethylene insensitivity in tomato.

Having described the preferred embodiments of the invention, it will appear to those of ordinary skill in the art that various modifications may be made to the disclosed embodiments, and that such modifications are intended to be within the scope of the invention.

All references are expressly incorporated herein by reference.

SEQUENCE LISTING

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Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu
    720                 725                 730

tac gag ggc atg taaaggcgat ggatgcccca tgccccagag gagtaattcc         2441
Tyr Glu Gly Met
735

gctcccgcct tcttctcccg taaaacatcg gaagctgatg ttctctggtt taattgtgta   2501

catatcagag attgtcggag cgttttggat gatatcttaa aacagaaagg gaataacaaa   2561

atagaaactc taaaccggta tgtgtccgtg gcgatttcgg ttatagagga acaagatggt   2621

ggtggtataa tcataccatt tcagattaca tgtttgacta atgttgtatc cttatatatg   2681

tagttacatt cttataagaa tttggatcga gttatggatg cttgttgcgt gcatgtatga   2741

cattgatgca gtattatggc gtcagctttg cgccgcttag tagaac                  2787


<210> SEQ ID NO 3
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 3

Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
  1               5                  10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
             20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65                  70                  75                  80
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Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
        115                 120                 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

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

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
            180                 185                 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
        195                 200                 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
    210                 215                 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
225                 230                 235                 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
            260                 265                 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
        275                 280                 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
305                 310                 315                 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
                325                 330                 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
        355                 360                 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
    370                 375                 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
385                 390                 395                 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
                405                 410                 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
            420                 425                 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
        435                 440                 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile
    450                 455                 460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
465                 470                 475                 480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe
                485                 490                 495
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Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys
            500                 505                 510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr
        515                 520                 525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
    530                 535                 540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly
545                 550                 555                 560

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile
                565                 570                 575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
            580                 585                 590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
        595                 600                 605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val
    610                 615                 620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser
625                 630                 635                 640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
                645                 650                 655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
            660                 665                 670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
        675                 680                 685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
    690                 695                 700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
705                 710                 715                 720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu
                725                 730                 735

Gly Met


<210> SEQ ID NO 4
<211> LENGTH: 2787
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (188)..(2401)

<400> SEQUENCE: 4

agtaagaacg aagaagaagt gttaaaccca accaattttg acttgaaaaa aagcttcaac     60

gctccccttt tctccttctc cgtcgctctc cgccgcgtcc caaatcccca attcctcctc    120

ttctccgatc aattcttccc aagtgtgtgt atgtgtgaga gaggaactat agtgtaaaaa    180

attcata atg gaa gtc tgc aat tgt att gaa ccg caa tgg cca gcg gat      229
        Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp
          1               5                  10

gaa ttg tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att      277
Glu Leu Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile
 15                  20                  25                  30

gcg tat ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca      325
Ala Tyr Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
                 35                  40                  45

gcc gtg ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc      373
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile
             50                  55                  60
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gtt ctt tat gga gca act cat ctt att aac tta tgg act ttc act acg       421
Val Leu Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr
         65                  70                  75

cat tcg aga acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc       469
His Ser Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr
     80                  85                  90

gct gtt gtc tcg tgt gct act gcg ttg atg ctt gtt cat att att cct       517
Ala Val Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro
 95                 100                 105                 110

gat ctt ttg agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct       565
Asp Leu Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala
                115                 120                 125

gct gag ctc gat aga gaa atg gga ttg att cga act cag gaa gaa acc       613
Ala Glu Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr
            130                 135                 140

gga agg cat gtg aga atg ttg act cat gag att aga agc act tta gat       661
Gly Arg His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
        145                 150                 155

aga cat act att tta aag act aca ctt gtt gag ctt ggt agg aca tta       709
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu
    160                 165                 170

gct ttg gag gag tgt gca ttg tgg atg cct act aga act ggg tta gag       757
Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu
175                 180                 185                 190

cta cag ctt tct tat aca ctt cgt cat caa cat ccc gtg gag tat acg       805
Leu Gln Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr
                195                 200                 205

gtt cct att caa tta ccg gtg att aac caa gtg ttt ggt act agt agg       853
Val Pro Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg
            210                 215                 220

gct gta aaa ata tct cct aat tct cct gtg gct agg ttg aga cct gtt       901
Ala Val Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val
        225                 230                 235

tct ggg aaa tat atg cta ggg gag gtg gtc gct gtg agg gtt ccg ctt       949
Ser Gly Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu
    240                 245                 250

ctc cac ctt tct aat ttt cag att aat gac tgg cct gag ctt tca aca       997
Leu His Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
255                 260                 265                 270

aag aga tat gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg      1045
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg
                275                 280                 285

caa tgg cat gtc cat gag ttg gaa ctc gtt gaa gtc gtc gct gat cag      1093
Gln Trp His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln
            290                 295                 300

gtg gct gta gct ctc tca cat gct gcg atc cta gaa gag tcg atg cga      1141
Val Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg
        305                 310                 315

gct agg gac ctt ctc atg gag cag aat gtt gct ctt gat cta gct aga      1189
Ala Arg Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg
    320                 325                 330

cga gaa gca gaa aca gca atc cgt gcc cgc aat gat ttc cta gcg gtt      1237
Arg Glu Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val
335                 340                 345                 350

atg aac cat gaa atg cga aca ccg atg cat gcg att att gca ctc tct      1285
Met Asn His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser
                355                 360                 365

tcc tta ctc caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg      1333
Ser Leu Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
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            370                 375                 380

gaa aca ata ctt aaa agt agt aac ctt ttg gca act ttg atg aat gat     1381
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp
        385                 390                 395

gtc tta gat ctt tca agg tta gaa gat gga agt ctt caa ctt gaa ctt     1429
Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu
    400                 405                 410

ggg aca ttc aat ctt cat aca tta ttt aga gag gtc ctc aat ctg ata     1477
Gly Thr Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile
415                 420                 425                 430

aag cct ata gcg gtt gtt aag aaa tta ccc atc aca cta aat ctt gca     1525
Lys Pro Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala
                435                 440                 445

cca gat ttg cca gaa ttt gtt gtt ggg gat gag aaa cgg cta atg cag     1573
Pro Asp Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln
            450                 455                 460

ata ata tta aat ata gtt ggt aat gct gtg aaa ttc tcc aaa caa ggt     1621
Ile Ile Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly
        465                 470                 475

agt atc tcc gta acc gct ctt gtc acc aag tca gac aca cga gct gct     1669
Ser Ile Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
    480                 485                 490

gac ttt ttt gtc gtg cca act ggg agt cat ttc tac ttg aga gtg aag     1717
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys
495                 500                 505                 510

gta aaa gac tct gga gca gga ata aat cct caa gac att cca aag att     1765
Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile
                515                 520                 525

ttc act aaa ttt gct caa aca caa tct tta gcg acg aga agc tcg ggt     1813
Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly
            530                 535                 540

ggt agt ggg ctt ggc ctc gcc atc tcc aag agg ttt gtg aat ctg atg     1861
Gly Ser Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met
        545                 550                 555

gag ggt aac att tgg att gag agc gat ggt ctt gga aaa gga tgc acg     1909
Glu Gly Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr
    560                 565                 570

gct atc ttt gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct     1957
Ala Ile Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser
575                 580                 585                 590

aaa cag tcg ggc ata ccg aaa gtt cca gcc att ccc cga cat tca aat     2005
Lys Gln Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
                595                 600                 605

ttc act gga ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga     2053
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg
            610                 615                 620

atg gtg acg aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg     2101
Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr
        625                 630                 635

gtg agt tca aac gag gag tgt ctc cga gtt gtg tcc cat gag cac aaa     2149
Val Ser Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys
    640                 645                 650

gtg gtc ttc atg gac gtg tgc atg ccc ggg gtc gaa aac tac caa atc     2197
Val Val Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile
655                 660                 665                 670

gct ctc cgt att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca     2245
Ala Leu Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro
                675                 680                 685

cta ctt gtg gca ctc agt ggt aac act gac aaa tcc aca aaa gag aaa     2293
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Leu Leu Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys
            690                 695                 700

tgc atg agc ttt ggt cta gac ggt gtg ttg ctc aaa ccc gta tca cta         2341
Cys Met Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
        705                 710                 715

gac aac ata aga gat gtt ctg tct gat ctt ctc gag ccc cgg gta ctg         2389
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu
    720                 725                 730

tac gag ggc atg taaaggcgat ggatgcccca tgccccagag gagtaattcc         2441
Tyr Glu Gly Met
735

gctcccgcct tcttctcccg taaaacatcg gaagctgatg ttctctggtt taattgtgta   2501

catatcagag attgtcggag cgttttggat gatatcttaa aacagaaagg gaataacaaa   2561

atagaaactc taaaccggta tgtgtccgtg gcgatttcgg ttatagagga acaagatggt   2621

ggtggtataa tcataccatt tcagattaca tgtttgacta atgttgtatc cttatatatg   2681

tagttacatt cttataagaa tttggatcga gttatggatg cttgttgcgt gcatgtatga   2741

cattgatgca gtattatggc gtcagctttg cgccgcttag tagaac                  2787


<210> SEQ ID NO 5
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 5

Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
  1               5                  10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
             20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65                  70                  75                  80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
        115                 120                 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

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

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
            180                 185                 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
        195                 200                 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
    210                 215                 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
225                 230                 235                 240
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Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
            260                 265                 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
        275                 280                 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
305                 310                 315                 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
                325                 330                 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
        355                 360                 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
    370                 375                 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
385                 390                 395                 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
                405                 410                 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
            420                 425                 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
        435                 440                 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile
    450                 455                 460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
465                 470                 475                 480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe
                485                 490                 495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys
            500                 505                 510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr
        515                 520                 525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
    530                 535                 540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly
545                 550                 555                 560

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile
                565                 570                 575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
            580                 585                 590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
        595                 600                 605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val
    610                 615                 620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser
625                 630                 635                 640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
                645                 650                 655
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Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
            660                 665                 670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
        675                 680                 685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
    690                 695                 700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
705                 710                 715                 720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu
                725                 730                 735

Gly Met


<210> SEQ ID NO 6
<211> LENGTH: 2787
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (188)..(2401)

<400> SEQUENCE: 6

agtaagaacg aagaagaagt gttaaaccca accaattttg acttgaaaaa aagcttcaac     60

gctcccсttt tctccttctc cgtcgctctc cgccgcgtcc caaatcccca attcctcctc    120

ttctccgatc aattcttccc aagtgtgtgt atgtgtgaga gaggaactat agtgtaaaaa    180

attcata atg gaa gtc tgc aat tgt att gaa ccg caa tgg cca gcg gat      229
        Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp
          1               5                  10

gaa ttg tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att      277
Glu Leu Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile
 15                  20                  25                  30

gcg tat ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca      325
Ala Tyr Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
                 35                  40                  45

gcc gtg ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc      373
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile
             50                  55                  60

gtt ctt tgt gga gca act cat ctt att aac tta tgg act ttc act acg      421
Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr
         65                  70                  75

cat tcg aga acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc      469
His Ser Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr
     80                  85                  90

gct gtt gtc tcg tgt gct act acg ttg atg ctt gtt cat att att cct      517
Ala Val Val Ser Cys Ala Thr Thr Leu Met Leu Val His Ile Ile Pro
 95                 100                 105                 110

gat ctt ttg agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct      565
Asp Leu Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala
                115                 120                 125

gct gag ctc gat aga gaa atg gga ttg att cga act cag gaa gaa acc      613
Ala Glu Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr
            130                 135                 140

gga agg cat gtg aga atg ttg act cat gag att aga agc act tta gat      661
Gly Arg His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
        145                 150                 155

aga cat act att tta aag act aca ctt gtt gag ctt ggt agg aca tta      709
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu
    160                 165                 170

gct ttg gag gag tgt gca ttg tgg atg cct act aga act ggg tta gag      757
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Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu
175                 180                 185                 190

cta cag ctt tct tat aca ctt cgt cat caa cat ccc gtg gag tat acg       805
Leu Gln Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr
                195                 200                 205

gtt cct att caa tta ccg gtg att aac caa gtg ttt ggt act agt agg       853
Val Pro Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg
            210                 215                 220

gct gta aaa ata tct cct aat tct cct gtg gct agg ttg aga cct gtt       901
Ala Val Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val
        225                 230                 235

tct ggg aaa tat atg cta ggg gag gtg gtc gct gtg agg gtt ccg ctt       949
Ser Gly Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu
    240                 245                 250

ctc cac ctt tct aat ttt cag att aat gac tgg cct gag ctt tca aca       997
Leu His Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
255                 260                 265                 270

aag aga tat gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg      1045
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg
                275                 280                 285

caa tgg cat gtc cat gag ttg gaa ctc gtt gaa gtc gtc gct gat cag      1093
Gln Trp His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln
            290                 295                 300

gtg gct gta gct ctc tca cat gct gcg atc cta gaa gag tcg atg cga      1141
Val Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg
        305                 310                 315

gct agg gac ctt ctc atg gag cag aat gtt gct ctt gat cta gct aga      1189
Ala Arg Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg
    320                 325                 330

cga gaa gca gaa aca gca atc cgt gcc cgc aat gat ttc cta gcg gtt      1237
Arg Glu Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val
335                 340                 345                 350

atg aac cat gaa atg cga aca ccg atg cat gcg att att gca ctc tct      1285
Met Asn His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser
                355                 360                 365

tcc tta ctc caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg      1333
Ser Leu Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
            370                 375                 380

gaa aca ata ctt aaa agt agt aac ctt ttg gca act ttg atg aat gat      1381
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp
        385                 390                 395

gtc tta gat ctt tca agg tta gaa gat gga agt ctt caa ctt gaa ctt      1429
Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu
    400                 405                 410

ggg aca ttc aat ctt cat aca tta ttt aga gag gtc ctc aat ctg ata      1477
Gly Thr Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile
415                 420                 425                 430

aag cct ata gcg gtt gtt aag aaa tta ccc atc aca cta aat ctt gca      1525
Lys Pro Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala
                435                 440                 445

cca gat ttg cca gaa ttt gtt gtt ggg gat gag aaa cgg cta atg cag      1573
Pro Asp Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln
            450                 455                 460

ata ata tta aat ata gtt ggt aat gct gtg aaa ttc tcc aaa caa ggt      1621
Ile Ile Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly
        465                 470                 475

agt atc tcc gta acc gct ctt gtc acc aag tca gac aca cga gct gct      1669
Ser Ile Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
    480                 485                 490
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gac ttt ttt gtc gtg cca act ggg agt cat ttc tac ttg aga gtg aag     1717
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys
495                 500                 505                 510

gta aaa gac tct gga gca gga ata aat cct caa gac att cca aag att     1765
Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile
                515                 520                 525

ttc act aaa ttt gct caa aca caa tct tta gcg acg aga agc tcg ggt     1813
Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly
            530                 535                 540

ggt agt ggg ctt ggc ctc gcc atc tcc aag agg ttt gtg aat ctg atg     1861
Gly Ser Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met
        545                 550                 555

gag ggt aac att tgg att gag agc gat ggt ctt gga aaa gga tgc acg     1909
Glu Gly Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr
    560                 565                 570

gct atc ttt gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct     1957
Ala Ile Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser
575                 580                 585                 590

aaa cag tcg ggc ata ccg aaa gtt cca gcc att ccc cga cat tca aat     2005
Lys Gln Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
                595                 600                 605

ttc act gga ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga     2053
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg
            610                 615                 620

atg gtg acg aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg     2101
Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr
        625                 630                 635

gtg agt tca aac gag gag tgt ctc cga gtt gtg tcc cat gag cac aaa     2149
Val Ser Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys
    640                 645                 650

gtg gtc ttc atg gac gtg tgc atg ccc ggg gtc gaa aac tac caa atc     2197
Val Val Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile
655                 660                 665                 670

gct ctc cgt att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca     2245
Ala Leu Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro
                675                 680                 685

cta ctt gtg gca ctc agt ggt aac act gac aaa tcc aca aaa gag aaa     2293
Leu Leu Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys
            690                 695                 700

tgc atg agc ttt ggt cta gac ggt gtg ttg ctc aaa ccc gta tca cta     2341
Cys Met Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
        705                 710                 715

gac aac ata aga gat gtt ctg tct gat ctt ctc gag ccc cgg gta ctg     2389
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu
    720                 725                 730

tac gag ggc atg taaaggcgat ggatgcccca tgccccagag gagtaattcc         2441
Tyr Glu Gly Met
735

gctcccgcct tcttctcccg taaaacatcg gaagctgatg ttctctggtt taattgtgta   2501

catatcagag attgtcggag cgttttggat gatatcttaa aacagaaagg gaataacaaa   2561

atagaaactc taaaccggta tgtgtccgtg gcgatttcgg ttatagagga acaagatggt   2621

ggtggtataa tcataccatt tcagattaca tgtttgacta atgttgtatc cttatatatg   2681

tagttacatt cttataagaa tttggatcga gttatggatg cttgttgcgt gcatgtatga   2741

cattgatgca gtattatggc gtcagctttg cgccgcttag tagaac                  2787


<210> SEQ ID NO 7
<211> LENGTH: 738
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<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 7

Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
  1               5                  10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
             20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65                  70                  75                  80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Thr Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
        115                 120                 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

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

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
            180                 185                 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
        195                 200                 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
    210                 215                 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
225                 230                 235                 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
            260                 265                 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
        275                 280                 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
305                 310                 315                 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
                325                 330                 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
        355                 360                 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
    370                 375                 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
385                 390                 395                 400
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Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
                405                 410                 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
            420                 425                 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
        435                 440                 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile
    450                 455                 460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
465                 470                 475                 480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe
                485                 490                 495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys
            500                 505                 510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr
        515                 520                 525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
    530                 535                 540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly
545                 550                 555                 560

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile
                565                 570                 575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
            580                 585                 590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
        595                 600                 605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val
    610                 615                 620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser
625                 630                 635                 640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
                645                 650                 655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
            660                 665                 670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
        675                 680                 685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
    690                 695                 700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
705                 710                 715                 720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu
                725                 730                 735

Gly Met


<210> SEQ ID NO 8
<211> LENGTH: 2787
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (188)..(2401)

<400> SEQUENCE: 8

agtaagaacg aagaagaagt gttaaaccca accaattttg acttgaaaaa aagcttcaac     60
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gctccccttt tctccttctc cgtcgctctc cgccgcgtcc caaatcccca attcctcctc    120

ttctccgatc aattcttccc aagtgtgtgt atgtgtgaga gaggaactat agtgtaaaaa    180

attcata atg gaa gtc tgc aat tgt att gaa ccg caa tgg cca gcg gat      229
        Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp
          1               5                  10

gaa ttg tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att      277
Glu Leu Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile
 15                  20                  25                  30

gtg tat ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca      325
Val Tyr Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
                 35                  40                  45

gcc gtg ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc      373
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile
             50                  55                  60

gtt ctt tgt gga gca act cat ctt att aac tta tgg act ttc act acg      421
Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr
         65                  70                  75

cat tcg aga acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc      469
His Ser Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr
     80                  85                  90

gct gtt gtc tcg tgt gct act gcg ttg atg ctt gtt cat att att cct      517
Ala Val Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro
 95                 100                 105                 110

gat ctt ttg agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct      565
Asp Leu Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala
                115                 120                 125

gct gag ctc gat aga gaa atg gga ttg att cga act cag gaa gaa acc      613
Ala Glu Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr
            130                 135                 140

gga agg cat gtg aga atg ttg act cat gag att aga agc act tta gat      661
Gly Arg His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
        145                 150                 155

aga cat act att tta aag act aca ctt gtt gag ctt ggt agg aca tta      709
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu
    160                 165                 170

gct ttg gag gag tgt gca ttg tgg atg cct act aga act ggg tta gag      757
Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu
175                 180                 185                 190

cta cag ctt tct tat aca ctt cgt cat caa cat ccc gtg gag tat acg      805
Leu Gln Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr
                195                 200                 205

gtt cct att caa tta ccg gtg att aac caa gtg ttt ggt act agt agg      853
Val Pro Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg
            210                 215                 220

gct gta aaa ata tct cct aat tct cct gtg gct agg ttg aga cct gtt      901
Ala Val Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val
        225                 230                 235

tct ggg aaa tat atg cta ggg gag gtg gtc gct gtg agg gtt ccg ctt      949
Ser Gly Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu
    240                 245                 250

ctc cac ctt tct aat ttt cag att aat gac tgg cct gag ctt tca aca      997
Leu His Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
255                 260                 265                 270

aag aga tat gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg     1045
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg
                275                 280                 285

caa tgg cat gtc cat gag ttg gaa ctc gtt gaa gtc gtc gct gat cag     1093
Gln Trp His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln
            290                 295                 300
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gtg gct gta gct ctc tca cat gct gcg atc cta gaa gag tcg atg cga     1141
Val Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg
        305                 310                 315

gct agg gac ctt ctc atg gag cag aat gtt gct ctt gat cta gct aga     1189
Ala Arg Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg
    320                 325                 330

cga gaa gca gaa aca gca atc cgt gcc cgc aat gat ttc cta gcg gtt     1237
Arg Glu Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val
335                 340                 345                 350

atg aac cat gaa atg cga aca ccg atg cat gcg att att gca ctc tct     1285
Met Asn His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser
                355                 360                 365

tcc tta ctc caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg     1333
Ser Leu Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
            370                 375                 380

gaa aca ata ctt aaa agt agt aac ctt ttg gca act ttg atg aat gat     1381
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp
        385                 390                 395

gtc tta gat ctt tca agg tta gaa gat gga agt ctt caa ctt gaa ctt     1429
Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu
    400                 405                 410

ggg aca ttc aat ctt cat aca tta ttt aga gag gtc ctc aat ctg ata     1477
Gly Thr Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile
415                 420                 425                 430

aag cct ata gcg gtt gtt aag aaa tta ccc atc aca cta aat ctt gca     1525
Lys Pro Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala
                435                 440                 445

cca gat ttg cca gaa ttt gtt gtt ggg gat gag aaa cgg cta atg cag     1573
Pro Asp Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln
            450                 455                 460

ata ata tta aat ata gtt ggt aat gct gtg aaa ttc tcc aaa caa ggt     1621
Ile Ile Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly
        465                 470                 475

agt atc tcc gta acc gct ctt gtc acc aag tca gac aca cga gct gct     1669
Ser Ile Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
    480                 485                 490

gac ttt ttt gtc gtg cca act ggg agt cat ttc tac ttg aga gtg aag     1717
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys
495                 500                 505                 510

gta aaa gac tct gga gca gga ata aat cct caa gac att cca aag att     1765
Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile
                515                 520                 525

ttc act aaa ttt gct caa aca caa tct tta gcg acg aga agc tcg ggt     1813
Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly
            530                 535                 540

ggt agt ggg ctt ggc ctc gcc atc tcc aag agg ttt gtg aat ctg atg     1861
Gly Ser Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met
        545                 550                 555

gag ggt aac att tgg att gag agc gat ggt ctt gga aaa gga tgc acg     1909
Glu Gly Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr
    560                 565                 570

gct atc ttt gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct     1957
Ala Ile Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser
575                 580                 585                 590

aaa cag tcg ggc ata ccg aaa gtt cca gcc att ccc cga cat tca aat     2005
Lys Gln Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
                595                 600                 605

ttc act gga ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga     2053
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg
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            610                 615                 620

atg gtg acg aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg     2101
Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr
        625                 630                 635

gtg agt tca aac gag gag tgt ctc cga gtt gtg tcc cat gag cac aaa     2149
Val Ser Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys
    640                 645                 650

gtg gtc ttc atg gac gtg tgc atg ccc ggg gtc gaa aac tac caa atc     2197
Val Val Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile
655                 660                 665                 670

gct ctc cgt att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca     2245
Ala Leu Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro
                675                 680                 685

cta ctt gtg gca ctc agt ggt aac act gac aaa tcc aca aaa gag aaa     2293
Leu Leu Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys
            690                 695                 700

tgc atg agc ttt ggt cta gac ggt gtg ttg ctc aaa ccc gta tca cta     2341
Cys Met Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
        705                 710                 715

gac aac ata aga gat gtt ctg tct gat ctt ctc gag ccc cgg gta ctg     2389
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu
    720                 725                 730

tac gag ggc atg taaaggcgat ggatgcccca tgccccagag gagtaattcc         2441
Tyr Glu Gly Met
735

gctcccgcct tcttctcccg taaaacatcg gaagctgatg ttctctggtt taattgtgta   2501

catatcagag attgtcggag cgttttggat gatatcttaa aacagaaagg gaataacaaa   2561

atagaaactc taaaccggta tgtgtccgtg gcgatttcgg ttatagagga acaagatggt   2621

ggtggtataa tcataccatt tcagattaca tgtttgacta atgttgtatc cttatatatg   2681

tagttacatt cttataagaa tttggatcga gttatggatg cttgttgcgt gcatgtatga   2741

cattgatgca gtattatggc gtcagctttg cgccgcttag tagaac                  2787


<210> SEQ ID NO 9
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 9

Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
  1               5                  10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Val Tyr
             20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65                  70                  75                  80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
        115                 120                 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
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    130                 135                 140

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

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
            180                 185                 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
        195                 200                 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
    210                 215                 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
225                 230                 235                 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
            260                 265                 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
        275                 280                 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
305                 310                 315                 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
                325                 330                 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
        355                 360                 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
    370                 375                 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
385                 390                 395                 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
                405                 410                 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
            420                 425                 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
        435                 440                 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile
    450                 455                 460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
465                 470                 475                 480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe
                485                 490                 495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys
            500                 505                 510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr
        515                 520                 525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
    530                 535                 540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly
545                 550                 555                 560
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                                -continued

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile
                565                 570                 575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
            580                 585                 590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
        595                 600                 605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val
    610                 615                 620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser
625                 630                 635                 640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
                645                 650                 655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
            660                 665                 670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
        675                 680                 685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
    690                 695                 700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
705                 710                 715                 720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu
                725                 730                 735

Gly Met


<210> SEQ ID NO 10
<211> LENGTH: 2787
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (188)..(2401)

<400> SEQUENCE: 10

agtaagaacg aagaagaagt gttaaaccca accaattttg acttgaaaaa aagcttcaac     60

gctccccttt tctccttctc cgtcgctctc cgccgcgtcc caaatcccca attcctcctc    120

ttctccgatc aattcttccc aagtgtgtgt atgtgtgaga gaggaactat agtgtaaaaa    180

attcata atg gaa gtc tgc aat tgt att gaa ccg caa tgg cca gcg gat      229
        Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp
          1               5                  10

gaa ttg tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att      277
Glu Leu Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile
 15                  20                  25                  30

gcg tat ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca      325
Ala Tyr Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser
                 35                  40                  45

gcc gtg ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt ttc      373
Ala Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Phe
             50                  55                  60

gtt ctt tgt gga gca act cat ctt att aac tta tgg act ttc act acg      421
Val Leu Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr
         65                  70                  75

cat tcg aga acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc      469
His Ser Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr
     80                  85                  90

gct gtt gtc tcg tgt gct act gcg ttg atg ctt gtt cat att att cct      517
Ala Val Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro
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                                -continued
 95                 100                 105                 110

gat ctt ttg agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct      565
Asp Leu Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala
                115                 120                 125

gct gag ctc gat aga gaa atg gga ttg att cga act cag gaa gaa acc      613
Ala Glu Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr
            130                 135                 140

gga agg cat gtg aga atg ttg act cat gag att aga agc act tta gat      661
Gly Arg His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp
        145                 150                 155

aga cat act att tta aag act aca ctt gtt gag ctt ggt agg aca tta      709
Arg His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu
    160                 165                 170

gct ttg gag gag tgt gca ttg tgg atg cct act aga act ggg tta gag      757
Ala Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu
175                 180                 185                 190

cta cag ctt tct tat aca ctt cgt cat caa cat ccc gtg gag tat acg      805
Leu Gln Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr
                195                 200                 205

gtt cct att caa tta ccg gtg att aac caa gtg ttt ggt act agt agg      853
Val Pro Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg
            210                 215                 220

gct gta aaa ata tct cct aat tct cct gtg gct agg ttg aga cct gtt      901
Ala Val Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val
        225                 230                 235

tct ggg aaa tat atg cta ggg gag gtg gtc gct gtg agg gtt ccg ctt      949
Ser Gly Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu
    240                 245                 250

ctc cac ctt tct aat ttt cag att aat gac tgg cct gag ctt tca aca      997
Leu His Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr
255                 260                 265                 270

aag aga tat gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg     1045
Lys Arg Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg
                275                 280                 285

caa tgg cat gtc cat gag ttg gaa ctc gtt gaa gtc gtc gct gat cag     1093
Gln Trp His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln
            290                 295                 300

gtg gct gta gct ctc tca cat gct gcg atc cta gaa gag tcg atg cga     1141
Val Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg
        305                 310                 315

gct agg gac ctt ctc atg gag cag aat gtt gct ctt gat cta gct aga     1189
Ala Arg Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg
    320                 325                 330

cga gaa gca gaa aca gca atc cgt gcc cgc aat gat ttc cta gcg gtt     1237
Arg Glu Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val
335                 340                 345                 350

atg aac cat gaa atg cga aca ccg atg cat gcg att att gca ctc tct     1285
Met Asn His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser
                355                 360                 365

tcc tta ctc caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg     1333
Ser Leu Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val
            370                 375                 380

gaa aca ata ctt aaa agt agt aac ctt ttg gca act ttg atg aat gat     1381
Glu Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp
        385                 390                 395

gtc tta gat ctt tca agg tta gaa gat gga agt ctt caa ctt gaa ctt     1429
Val Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu
    400                 405                 410

ggg aca ttc aat ctt cat aca tta ttt aga gag gtc ctc aat ctg ata     1477
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Gly Thr Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile
415                 420                 425                 430

aag cct ata gcg gtt gtt aag aaa tta ccc atc aca cta aat ctt gca     1525
Lys Pro Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala
                435                 440                 445

cca gat ttg cca gaa ttt gtt gtt ggg gat gag aaa cgg cta atg cag     1573
Pro Asp Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln
            450                 455                 460

ata ata tta aat ata gtt ggt aat gct gtg aaa ttc tcc aaa caa ggt     1621
Ile Ile Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly
        465                 470                 475

agt atc tcc gta acc gct ctt gtc acc aag tca gac aca cga gct gct     1669
Ser Ile Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala
    480                 485                 490

gac ttt ttt gtc gtg cca act ggg agt cat ttc tac ttg aga gtg aag     1717
Asp Phe Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys
495                 500                 505                 510

gta aaa gac tct gga gca gga ata aat cct caa gac att cca aag att     1765
Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile
                515                 520                 525

ttc act aaa ttt gct caa aca caa tct tta gcg acg aga agc tcg ggt     1813
Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly
            530                 535                 540

ggt agt ggg ctt ggc ctc gcc atc tcc aag agg ttt gtg aat ctg atg     1861
Gly Ser Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met
        545                 550                 555

gag ggt aac att tgg att gag agc gat ggt ctt gga aaa gga tgc acg     1909
Glu Gly Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr
    560                 565                 570

gct atc ttt gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct     1957
Ala Ile Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser
575                 580                 585                 590

aaa cag tcg ggc ata ccg aaa gtt cca gcc att ccc cga cat tca aat     2005
Lys Gln Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn
                595                 600                 605

ttc act gga ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga     2053
Phe Thr Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg
            610                 615                 620

atg gtg acg aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg     2101
Met Val Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr
        625                 630                 635

gtg agt tca aac gag gag tgt ctc cga gtt gtg tcc cat gag cac aaa     2149
Val Ser Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys
    640                 645                 650

gtg gtc ttc atg gac gtg tgc atg ccc ggg gtc gaa aac tac caa atc     2197
Val Val Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile
655                 660                 665                 670

gct ctc cgt att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca     2245
Ala Leu Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro
                675                 680                 685

cta ctt gtg gca ctc agt ggt aac act gac aaa tcc aca aaa gag aaa     2293
Leu Leu Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys
            690                 695                 700

tgc atg agc ttt ggt cta gac ggt gtg ttg ctc aaa ccc gta tca cta     2341
Cys Met Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu
        705                 710                 715

gac aac ata aga gat gtt ctg tct gat ctt ctc gag ccc cgg gta ctg     2389
Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu
    720                 725                 730
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tac gag ggc atg taaaggcgat ggatgcccca tgccccagag gagtaattcc        2441
Tyr Glu Gly Met
735

gctcccgcct tcttctcccg taaaacatcg gaagctgatg ttctctggtt taattgtgta   2501

catatcagag attgtcggag cgttttggat gatatcttaa aacagaaagg gaataacaaa   2561

atagaaactc taaaccggta tgtgtccgtg gcgatttcgg ttatagagga acaagatggt   2621

ggtggtataa tcataccatt tcagattaca tgtttgacta atgttgtatc cttatatatg   2681

tagttacatt cttataagaa tttggatcga gttatggatg cttgttgcgt gcatgtatga   2741

cattgatgca gtattatggc gtcagctttg cgccgcttag tagaac                 2787


<210> SEQ ID NO 11
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 11

Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
  1               5                  10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
             20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
        35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Phe Val Leu
     50                  55                  60

Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65                  70                  75                  80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
        115                 120                 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

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

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
            180                 185                 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
        195                 200                 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
    210                 215                 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
225                 230                 235                 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
            260                 265                 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
        275                 280                 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
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    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
305                 310                 315                 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
                325                 330                 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
        355                 360                 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
    370                 375                 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
385                 390                 395                 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
                405                 410                 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
            420                 425                 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
        435                 440                 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile
    450                 455                 460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
465                 470                 475                 480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe
                485                 490                 495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys
            500                 505                 510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr
        515                 520                 525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
    530                 535                 540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly
545                 550                 555                 560

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile
                565                 570                 575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
            580                 585                 590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
        595                 600                 605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val
    610                 615                 620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser
625                 630                 635                 640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
                645                 650                 655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
            660                 665                 670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
        675                 680                 685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
    690                 695                 700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
705                 710                 715                 720
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Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu
                725                 730                 735

Gly Met


<210> SEQ ID NO 12
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 12

Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala Glu Thr Ala Ile
  1               5                  10                  15

Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu Met Arg Thr
             20                  25                  30

Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu Leu Gln Glu Thr Glu
         35                  40                  45

Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr Ile Leu Lys Ser Ser
     50                  55                  60

Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu Asp Leu Ser Arg Leu
 65                  70                  75                  80

Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr Phe Asn Leu His Thr
                 85                  90                  95

Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro Ile Ala Val Val Lys
            100                 105                 110

Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu Pro Glu Phe Val
        115                 120                 125

Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu Asn Ile Val Gly
    130                 135                 140

Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
145                 150                 155


<210> SEQ ID NO 13
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 13

Gln Asn Val Glu Leu Asp Leu Ala Lys Lys Arg Ala Gln Glu Ala Ala
  1               5                  10                  15

Arg Ile Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Leu Arg Thr
             20                  25                  30

Pro Leu Asn Gly Val Ile Gly Phe Thr Arg Leu Thr Leu Lys Thr Glu
         35                  40                  45

Leu Thr Pro Thr Gln Arg Asp His Leu Asn Thr Ile Glu Arg Ser Ala
     50                  55                  60

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

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

Thr Leu Asp Glu Val Val Thr Leu Leu Ala His Ser Ser His Asp Lys
            100                 105                 110

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

Ile Gly Asp Pro Leu Arg Leu Gln Gln Ile Ile Thr Asn Leu Val Gly
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    130                 135                 140

Asn Ala Ile Lys Phe Thr Glu Asn Gly Asn Ile
145                 150                 155


<210> SEQ ID NO 14
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 14

Gln Asn Ile Glu Leu Asp Leu Ala Arg Lys Glu Ala Leu Glu Ala Ser
  1               5                  10                  15

Arg Ile Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile Arg Thr
             20                  25                  30

Pro Leu Asn Gly Ile Leu Gly Phe Thr His Leu Leu Gln Lys Ser Glu
         35                  40                  45

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

Asp Asn Leu Leu Ser Ile Ile Asn Glu Ile Leu Asp Phe Ser Lys Ile
 65                  70                  75                  80

Glu Ala Gly Lys Leu Val Leu Asp Asn Ile Pro Phe Asn Leu Arg Asp
                 85                  90                  95

Leu Leu Gln Asp Thr Leu Thr Ile Leu Ala Pro Ala Ala His Ala Lys
            100                 105                 110

Gln Leu Glu Leu Val Ser Leu Val Tyr Arg Asp Thr Pro Leu Ala Leu
        115                 120                 125

Ser Gly Asp Pro Leu Arg Leu Arg Gln Ile Leu Thr Asn Leu Val Ser
    130                 135                 140

Asn Ala Ile Lys Phe Thr Arg Glu Gly Thr Ile
145                 150                 155


<210> SEQ ID NO 15
<211> LENGTH: 149
<212> TYPE: PRT
<213> ORGANISM: Xanthomonas campestris

<400> SEQUENCE: 15

Arg Ala Val Arg Glu Ala Arg His Ala Asn Gln Ala Lys Ser Arg Phe
  1               5                  10                  15

Leu Ala Asn Met Ser His Glu Phe Arg Thr Pro Leu Asn Gly Leu Ser
             20                  25                  30

Gly Met Thr Glu Val Leu Ala Thr Thr Arg Leu Asp Ala Glu Gln Lys
         35                  40                  45

Glu Cys Leu Asn Thr Ile Gln Ala Ser Ala Arg Ser Leu Leu Ser Leu
     50                  55                  60

Val Glu Glu Val Leu Asp Ile Ser Ala Ile Glu Ala Gly Lys Ile Arg
 65                  70                  75                  80

Ile Asp Arg Arg Asp Phe Ser Leu Arg Glu Met Ile Gly Ser Val Asn
                 85                  90                  95

Leu Ile Leu Gln Pro Gln Ala Arg Gly Arg Arg Leu Glu Tyr Gly Thr
            100                 105                 110

Gln Val Ala Asp Asp Val Pro Asp Leu Leu Lys Gly Asp Thr Ala His
        115                 120                 125

Leu Arg Gln Val Leu Leu Asn Leu Val Gly Asn Ala Val Lys Phe Thr
    130                 135                 140

Glu His Gly His Val
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145


<210> SEQ ID NO 16
<211> LENGTH: 66
<212> TYPE: PRT
<213> ORGANISM: Xanthomonas campestris

<400> SEQUENCE: 16

Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val Thr
  1               5                  10                  15

Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser Ser
             20                  25                  30

Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val Phe
         35                  40                  45

Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg
     50                  55                  60

Ile His
 65


<210> SEQ ID NO 17
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Bordetella parapertussis

<400> SEQUENCE: 17

Leu Arg Val Leu Val Val Asp Asp His Lys Pro Asn Leu Met Leu Leu
  1               5                  10                  15

Arg Gln Gln Leu Asp Tyr Leu Gly Gln Arg Val Val Ala Ala Asp Ser
             20                  25                  30

Gly Glu Ala Ala Leu Ala Leu Trp His Glu His Ala Phe Asp Val Val
         35                  40                  45

Ile Thr Asp Cys Asn Met Pro Gly Ile Asn Gly Tyr Glu Leu Ala Arg
     50                  55                  60

Arg Ile Arg
 65


<210> SEQ ID NO 18
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 18

Met Met Ile Leu Val Val Asp Asp His Pro Ile Asn Arg Arg Leu Leu
  1               5                  10                  15

Ala Asp Gln Leu Gly Ser Leu Gly Tyr Gln Cys Lys Thr Ala Asn Asp
             20                  25                  30

Gly Val Asp Ala Leu Asn Val Leu Ser Lys Asn His Ile Asp Ile Val
         35                  40                  45

Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg Leu Thr Gln
     50                  55                  60

Arg Ile Arg
 65


<210> SEQ ID NO 19
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 19
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Pro Arg Val Leu Cys Val Asp Asp Asn Pro Ala Asn Leu Leu Leu Val
  1               5                  10                  15

Gln Thr Leu Leu Glu Asp Met Gly Ala Glu Val Val Ala Val Glu Gly
             20                  25                  30

Gly Tyr Ala Ala Val Asn Ala Val Gln Gln Glu Ala Phe Asp Leu Val
         35                  40                  45

Leu Met Asp Val Gln Met Pro Gly Met Asp Gly Arg Gln Ala Thr Glu
     50                  55                  60

Ala Ile Arg
 65
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<210> SEQ ID NO 20
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 20

atggaatcct gtgattgcat tgaggcttta ctgccaactg gtgacctgct ggttaaatac     60

caatacctct cagatttctt cattgctgta gcctactttt ccattccgtt ggagcttatt    120

tattttgtcc acaaatctgc atgcttccca tacagatggg tcctcatgca atttggtgct    180

tttattgtgc tctgcggagc aacacacttt attagcttgt ggaccttctt tatgcactct    240

aagacggtcg ctgtggttat gaccatatca aaaatgttga cagctgccgt gtcctgtatc    300

acagctttga tgcttgttca cattattcct gatttgctaa gtgttaaaac gcgagagttg    360

ttcttgaaa                                                            369
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<210> SEQ ID NO 21
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 21

atggaagtct gcaattgtat tgaaccgcaa tggccagcgg atgaattgtt aatgaaatac     60

caatacatct ccgatttctt cattgcgatt gcgtattttt cgattcctct tgagttgatt    120

tactttgtga agaaatcagc cgtgtttccg tatagatggg tacttgttca gtttggtgct    180

tttatcgttc tttgtggagc aactcatctt attaacttat ggactttcac tacgcattcg    240

agaaccgtgg cgcttgtgat gactaccgcg aaggtgttaa ccgctgttgt ctcgtgtgct    300

actgcgttga tgcttgttca tattattcct gatcttttga gtgttaagac tcgggagctt    360

ttcttgaaa                                                            369
```

```
<210> SEQ ID NO 22
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 22

gctctttcac atgctgcaat tttagaagat tccatgcgag cccatgatca gctcatggaa     60

cagaatattg ctttggatgt agctcgacaa gaagcagaga tggccatccg tgcacgtaac    120

gacttccttg ctgtgatgaa ccatgaaatg agaacgccca tgcatgcagt tattgctctg    180
```

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tgctctctgc ttttagaaac agacttaact ccagagcaga gagttatgat tgagaccata    240

ttgaagagca gcaatcttct tgcaacactg ataaatgatg ttctagatct ttctag        296


<210> SEQ ID NO 23
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 23

gctctctcac atgctgcgat cctagaagag tcgatgcgag ctagggacct tctcatggag     60

cagaatgttg ctcttgatct agctagacga gaagcagaaa cagcaatccg tgcccgcaat    120

gatttcctag cggttatgaa ccatgaaatg cgaacaccga tgcatgcgat tattgcactc    180

tcttccttac tccaagaaac ggaactaacc cctgaacaaa gactgatggt ggaaacaata    240

cttaaaagta gtaacctttt ggcaactttg atgaatgatg tcttagatct ttcaag        296


<210> SEQ ID NO 24
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 24

Met Glu Ser Cys Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu
  1               5                   10                  15

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

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val His Lys Ser Ala Cys
        35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Met Gln Phe Gly Ala Phe Ile Val Leu
    50                  55                  60

Cys Gly Ala Thr His Phe Ile Ser Leu Trp Thr Phe Phe Met His Ser
 65                  70                  75                  80

Lys Thr Val Ala Val Val Met Thr Ile Ser Lys Met Leu Thr Ala Ala
                85                  90                  95

Val Ser Cys Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys
        115                 120


<210> SEQ ID NO 25
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 25

Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu
  1               5                   10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
            20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
        35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
    50                  55                  60

Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65                  70                  75                  80
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Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys
        115                 120


<210> SEQ ID NO 26
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 26

agtaagaacg aagaagaagt g                                               21


<210> SEQ ID NO 27
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 27

Leu Arg Val Lys Val Lys Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp
  1               5                   10                  15

Ile Pro Lys Ile Phe Thr Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr
             20                  25                  30

Arg Ser Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe
         35                  40                  45

Val Asn Leu Met Glu Gly Asn Ile
     50                  55


<210> SEQ ID NO 28
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 28

Ile Glu Val Gln Ile Arg Asp Thr Gly Ile Gly Ile Pro Glu Arg Asp
  1               5                   10                  15

Gln Ser Arg Leu Phe Gln Ala Phe Arg Gln Ala Asp Ala Ser Ile Ser
             20                  25                  30

Arg Arg His Gly Gly Thr Gly Leu Gly Leu Val Ile Thr Gln Lys Leu
         35                  40                  45

Val Asn Glu Met Gly Gly Asp Ile
     50                  55


<210> SEQ ID NO 29
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 29

Leu Arg Ile Ser Val Gln Asp Thr Gly Ile Gly Leu Ser Ser Gln Asp
  1               5                   10                  15

Val Arg Ala Leu Phe Gln Ala Phe Ser Gln Ala Asp Asn Ser Leu Ser
             20                  25                  30

Arg Gln Pro Gly Gly Thr Gly Leu Gly Leu Val Ile Ser Lys Arg Leu
         35                  40                  45

Ile Glu Gln Met Gly Gly Glu Ile
     50                  55
```

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<210> SEQ ID NO 30
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Xanthomonas campestris

<400> SEQUENCE: 30

Leu Arg Phe Asp Val Glu Asp Thr Gly Ile Gly Val Pro Met Asp Met
  1               5                  10                  15

Arg Pro Arg Leu Phe Glu Ala Phe Glu Gln Ala Asp Val Gly Leu Ser
             20                  25                  30

Arg Arg Tyr Glu Gly Thr Gly Leu Gly Thr Thr Ile Ala Lys Gly Leu
         35                  40                  45

Val Glu Ala Met Gly Gly Ser Ile
     50                  55


<210> SEQ ID NO 31
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Xanthomonas campestris

<400> SEQUENCE: 31

Pro Leu Leu Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu
  1               5                  10                  15

Lys Cys Met Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser
             20                  25                  30

Leu Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu
         35                  40


<210> SEQ ID NO 32
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Bordetella parapertussis

<400> SEQUENCE: 32

Cys Ile Leu Phe Gly Phe Thr Ala Ser Ala Gln Met Asp Glu Ala His
  1               5                  10                  15

Ala Cys Arg Ala Ala Gly Met Asp Asp Cys Leu Phe Lys Pro Ile Gly
             20                  25                  30

Val Asp Ala Leu Arg Gln Arg Leu Asn Glu Ala Ala
         35                  40


<210> SEQ ID NO 33
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 33

Leu Pro Val Ile Gly Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln
  1               5                  10                  15

Arg Cys Leu Glu Ser Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr
             20                  25                  30

Leu Asp Val Ile Lys Gln Ser Leu Thr Leu Tyr Ala
         35                  40


<210> SEQ ID NO 34
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae

<400> SEQUENCE: 34
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Leu Pro Ile Val Ala Leu Thr Ala His Ala Met Ala Asn Glu Lys Arg
  1               5                  10                  15

Ser Leu Leu Gln Ser Gly Met Asp Asp Tyr Leu Thr Lys Pro Ile Ser
             20                  25                  30

Glu Arg Gln Leu Ala Gln Val Val Leu Lys Trp Thr
         35                  40


<210> SEQ ID NO 35
<211> LENGTH: 2405
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (288)..(2195)

<400> SEQUENCE: 35

tttttttttt gtcaaaagct cgatgtaaaa atccgatggc cacaagcaaa acgacaggtt     60

ccaacttcac ggagattgtg aaaatggagt agtagttcag tgaagtagta gatactgaga    120

tcgcattctc cggcgtcgtt tttcacatcg aaatagtcgt gtaaaaaaat gaaaaaattg    180

ctgcgagaca ggtatgtgtc gcagcaggaa atagcatctt aaaggaagga aggaaggaaa    240

ctcgaaagtt actaaaaatt tttgattctt tgggacgaaa cgagata atg gaa tcc      296
                                                    Met Glu Ser
                                                      1

tgt gat tgc att gag gct tta ctg cca act ggt gac ctg ctg gtt aaa      344
Cys Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu Leu Val Lys
     5                   10                  15

tac caa tac ctc tca gat ttc ttc att gct gta gcc tac ttt tcc att      392
Tyr Gln Tyr Leu Ser Asp Phe Phe Ile Ala Val Ala Tyr Phe Ser Ile
 20                  25                  30                  35

ccg ttg gag ctt att tat ttt gtc cac aaa tct gca tgc ttc cca tac      440
Pro Leu Glu Leu Ile Tyr Phe Val His Lys Ser Ala Cys Phe Pro Tyr
                 40                  45                  50

aga tgg gtc ctc atg caa ttt ggt gct ttt att gtg ctc tgt gga gca      488
Arg Trp Val Leu Met Gln Phe Gly Ala Phe Ile Val Leu Cys Gly Ala
             55                  60                  65

aca cac ttt att agc ttg tgg acc ttc ttt atg cac tct aag acg gtc      536
Thr His Phe Ile Ser Leu Trp Thr Phe Phe Met His Ser Lys Thr Val
         70                  75                  80

gct gtg gtt atg acc ata tca aaa atg ttg aca gct gcc gtg tcc tgt      584
Ala Val Val Met Thr Ile Ser Lys Met Leu Thr Ala Ala Val Ser Cys
     85                  90                  95

atc aca gct ttg atg ctt gtt cac att att cct gat ttg cta agt gtt      632
Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val
100                 105                 110                 115

aaa acg cga gag ttg ttc ttg aaa act cga gct gaa gag ctt gac aag      680
Lys Thr Arg Glu Leu Phe Leu Lys Thr Arg Ala Glu Glu Leu Asp Lys
                120                 125                 130

gaa atg ggc cta ata ata aga caa gaa gaa act ggc aga cat gtc agg      728
Glu Met Gly Leu Ile Ile Arg Gln Glu Glu Thr Gly Arg His Val Arg
            135                 140                 145

atg ctg act cat gag ata aga agc aca ctc gac aga cac aca atc ttg      776
Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His Thr Ile Leu
        150                 155                 160

aag act act ctt gtg gag cta ggt agg acc tta gac ctg gca gaa tgt      824
Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Asp Leu Ala Glu Cys
    165                 170                 175

gct ttg tgg atg cca tgc caa gga ggc ctg act ttg caa ctt tcc cat      872
Ala Leu Trp Met Pro Cys Gln Gly Gly Leu Thr Leu Gln Leu Ser His
180                 185                 190                 195
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aat tta aac aat cta ata cct ctg gga tct act gtg cca att aat ctt          920
Asn Leu Asn Asn Leu Ile Pro Leu Gly Ser Thr Val Pro Ile Asn Leu
                200                 205                 210

cct att atc aat gaa att ttt agt agc cct gaa gca ata caa att cca          968
Pro Ile Ile Asn Glu Ile Phe Ser Ser Pro Glu Ala Ile Gln Ile Pro
            215                 220                 225

cat aca aat cct ttg gca agg atg agg aat act gtt ggt aga tat att         1016
His Thr Asn Pro Leu Ala Arg Met Arg Asn Thr Val Gly Arg Tyr Ile
        230                 235                 240

cca cca gaa gta gtt gct gtt cgt gta ccg ctt tta cac ctc tca aat         1064
Pro Pro Glu Val Val Ala Val Arg Val Pro Leu Leu His Leu Ser Asn
    245                 250                 255

ttt act aat gac tgg gct gaa ctg tct act aga agt tat gcg gtt atg         1112
Phe Thr Asn Asp Trp Ala Glu Leu Ser Thr Arg Ser Tyr Ala Val Met
260                 265                 270             275

gtt ctg gtt ctc ccg atg aat ggc tta aga aag tgg cgt gaa cat gag         1160
Val Leu Val Leu Pro Met Asn Gly Leu Arg Lys Trp Arg Glu His Glu
                280                 285                 290

tta gaa ctt gtg caa gtt gtc gca gat cag gtt gct gtc gct ctt tca         1208
Leu Glu Leu Val Gln Val Val Ala Asp Gln Val Ala Val Ala Leu Ser
            295                 300                 305

cat gct gca att tta gaa gat tcc atg cga gcc cat gat cag ctc atg         1256
His Ala Ala Ile Leu Glu Asp Ser Met Arg Ala His Asp Gln Leu Met
        310                 315                 320

gaa cag aat att gct ttg gat gta gct cga caa gaa gca gag atg gcc         1304
Glu Gln Asn Ile Ala Leu Asp Val Ala Arg Gln Glu Ala Glu Met Ala
    325                 330                 335

atc cgt gca cgt aac gac ttc ctt gct gtg atg aac cat gaa atg aga         1352
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu Met Arg
340                 345                 350             355

acg ccc atg cat gca gtt att gct ctg tgc tct ctg ctt tta gaa aca         1400
Thr Pro Met His Ala Val Ile Ala Leu Cys Ser Leu Leu Leu Glu Thr
                360                 365                 370

gac tta act cca gag cag aga gtt atg att gag acc ata ttg aag agc         1448
Asp Leu Thr Pro Glu Gln Arg Val Met Ile Glu Thr Ile Leu Lys Ser
            375                 380                 385

agc aat ctt ctt gca aca ctg ata aat gat gtt cta gat ctt tct aga         1496
Ser Asn Leu Leu Ala Thr Leu Ile Asn Asp Val Leu Asp Leu Ser Arg
        390                 395                 400

ctt gaa gat ggt att ctt gaa cta gaa aac gga aca ttc aat ctt cat         1544
Leu Glu Asp Gly Ile Leu Glu Leu Glu Asn Gly Thr Phe Asn Leu His
    405                 410                 415

ggc atc tta aga gag gcc gtt aat ttg ata aag cca att gca tct ttg         1592
Gly Ile Leu Arg Glu Ala Val Asn Leu Ile Lys Pro Ile Ala Ser Leu
420                 425                 430             435

aag aaa tta tct ata act ctt gct ttg gct ctg gat tta cct att ctt         1640
Lys Lys Leu Ser Ile Thr Leu Ala Leu Ala Leu Asp Leu Pro Ile Leu
                440                 445                 450

gct gtg ggt gat gca aaa cgt ctt atc caa act ctc tta aac gtg gtg         1688
Ala Val Gly Asp Ala Lys Arg Leu Ile Gln Thr Leu Leu Asn Val Val
            455                 460                 465

gga aat gct gtg aag ttc act aaa gaa gga cat att tca att gag gct         1736
Gly Asn Ala Val Lys Phe Thr Lys Glu Gly His Ile Ser Ile Glu Ala
        470                 475                 480

tca gtt gcc aaa cca gag tat gcg aga gat tgt cat cct cct gaa atg         1784
Ser Val Ala Lys Pro Glu Tyr Ala Arg Asp Cys His Pro Pro Glu Met
    485                 490                 495

ttc cct atg cca agt gat ggc cag ttt tat ttg cgt gtc cag gtt aga         1832
Phe Pro Met Pro Ser Asp Gly Gln Phe Tyr Leu Arg Val Gln Val Arg
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500                 505                 510                 515

gat act ggg tgt gga att agc cca caa gat ata cca cta gta ttc acc     1880
Asp Thr Gly Cys Gly Ile Ser Pro Gln Asp Ile Pro Leu Val Phe Thr
                520                 525                 530

aaa ttt gca gag tca cgg cct acg tca aat cga agt act gga ggg gaa     1928
Lys Phe Ala Glu Ser Arg Pro Thr Ser Asn Arg Ser Thr Gly Gly Glu
            535                 540                 545

ggt cta ggg ctt gcc att tgg aga cga ttt att caa ctt atg aaa ggt     1976
Gly Leu Gly Leu Ala Ile Trp Arg Arg Phe Ile Gln Leu Met Lys Gly
        550                 555                 560

aac att tgg att gag agt gag ggc cct gga aag gga acc act gtc acg     2024
Asn Ile Trp Ile Glu Ser Glu Gly Pro Gly Lys Gly Thr Thr Val Thr
    565                 570                 575

ttt gta gtg aaa ctc gga atc tgt cac cat cca aat gca tta cct ctg     2072
Phe Val Val Lys Leu Gly Ile Cys His His Pro Asn Ala Leu Pro Leu
580                 585                 590                 595

cta cct atg cct ccc aga ggc aga ttg aac aaa ggt agc gat gat ctc     2120
Leu Pro Met Pro Pro Arg Gly Arg Leu Asn Lys Gly Ser Asp Asp Leu
                600                 605                 610

ttc agg tat aga cag ttc cgt gga gat gat ggt ggg atg tct gtg aat     2168
Phe Arg Tyr Arg Gln Phe Arg Gly Asp Asp Gly Gly Met Ser Val Asn
            615                 620                 625

gct caa cgc tat caa aga agt atg taa atgacaaaag gacattggtg           2215
Ala Gln Arg Tyr Gln Arg Ser Met
        630                 635

tgacaaagaa cattaaatca tgactagtga atttgagatt tcttcactgt tctgtacact   2275

ccaaatggca cagtttgtct tgtaactaac ctaattcaat gctcgtaaag tgagtactgg   2335

agtatcttga aaatgtaact atcgaattta tacatcgagc ttttgacaaa aaaaaaaaaa   2395

aaaaaaaaaa                                                          2405


<210> SEQ ID NO 36
<211> LENGTH: 635
<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 36

Met Glu Ser Cys Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu
  1               5                  10                  15

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

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val His Lys Ser Ala Cys
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Met Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Cys Gly Ala Thr His Phe Ile Ser Leu Trp Thr Phe Phe Met His Ser
 65                  70                  75                  80

Lys Thr Val Ala Val Val Met Thr Ile Ser Lys Met Leu Thr Ala Ala
                 85                  90                  95

Val Ser Cys Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Thr Arg Ala Glu Glu
        115                 120                 125

Leu Asp Lys Glu Met Gly Leu Ile Ile Arg Gln Glu Glu Thr Gly Arg
    130                 135                 140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His
145                 150                 155                 160
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Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Asp Leu
                165                 170                 175

Ala Glu Cys Ala Leu Trp Met Pro Cys Gln Gly Gly Leu Thr Leu Gln
            180                 185                 190

Leu Ser His Asn Leu Asn Asn Leu Ile Pro Leu Gly Ser Thr Val Pro
        195                 200                 205

Ile Asn Leu Pro Ile Ile Asn Glu Ile Phe Ser Ser Pro Glu Ala Ile
    210                 215                 220

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

Arg Tyr Ile Pro Pro Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Thr Asn Asp Trp Ala Glu Leu Ser Thr Arg Ser Tyr
            260                 265                 270

Ala Val Met Val Leu Val Leu Pro Met Asn Gly Leu Arg Lys Trp Arg
        275                 280                 285

Glu His Glu Leu Glu Leu Val Gln Val Val Ala Asp Gln Val Ala Val
    290                 295                 300

Ala Leu Ser His Ala Ala Ile Leu Glu Asp Ser Met Arg Ala His Asp
305                 310                 315                 320

Gln Leu Met Glu Gln Asn Ile Ala Leu Asp Val Ala Arg Gln Glu Ala
                325                 330                 335

Glu Met Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His
            340                 345                 350

Glu Met Arg Thr Pro Met His Ala Val Ile Ala Leu Cys Ser Leu Leu
        355                 360                 365

Leu Glu Thr Asp Leu Thr Pro Glu Gln Arg Val Met Ile Glu Thr Ile
    370                 375                 380

Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Ile Asn Asp Val Leu Asp
385                 390                 395                 400

Leu Ser Arg Leu Glu Asp Gly Ile Leu Glu Leu Glu Asn Gly Thr Phe
                405                 410                 415

Asn Leu His Gly Ile Leu Arg Glu Ala Val Asn Leu Ile Lys Pro Ile
            420                 425                 430

Ala Ser Leu Lys Lys Leu Ser Ile Thr Leu Ala Leu Ala Leu Asp Leu
        435                 440                 445

Pro Ile Leu Ala Val Gly Asp Ala Lys Arg Leu Ile Gln Thr Leu Leu
    450                 455                 460

Asn Val Val Gly Asn Ala Val Lys Phe Thr Lys Glu Gly His Ile Ser
465                 470                 475                 480

Ile Glu Ala Ser Val Ala Lys Pro Glu Tyr Ala Arg Asp Cys His Pro
                485                 490                 495

Pro Glu Met Phe Pro Met Pro Ser Asp Gly Gln Phe Tyr Leu Arg Val
            500                 505                 510

Gln Val Arg Asp Thr Gly Cys Gly Ile Ser Pro Gln Asp Ile Pro Leu
        515                 520                 525

Val Phe Thr Lys Phe Ala Glu Ser Arg Pro Thr Ser Asn Arg Ser Thr
    530                 535                 540

Gly Gly Glu Gly Leu Gly Leu Ala Ile Trp Arg Arg Phe Ile Gln Leu
545                 550                 555                 560

Met Lys Gly Asn Ile Trp Ile Glu Ser Glu Gly Pro Gly Lys Gly Thr
                565                 570                 575
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Thr Val Thr Phe Val Val Lys Leu Gly Ile Cys His His Pro Asn Ala
            580                 585                 590

Leu Pro Leu Leu Pro Met Pro Pro Arg Gly Arg Leu Asn Lys Gly Ser
        595                 600                 605

Asp Asp Leu Phe Arg Tyr Arg Gln Phe Arg Gly Asp Asp Gly Gly Met
    610                 615                 620

Ser Val Asn Ala Gln Arg Tyr Gln Arg Ser Met
625                 630                 635


<210> SEQ ID NO 37
<211> LENGTH: 4567
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (763)..(1671)
<221> NAME/KEY: CDS
<222> LOCATION: (3062)..(3433)
<221> NAME/KEY: CDS
<222> LOCATION: (3572)..(3838)
<221> NAME/KEY: CDS
<222> LOCATION: (3969)..(4097)
<221> NAME/KEY: CDS
<222> LOCATION: (4236)..(4403)
<221> NAME/KEY: misc_feature
<222> LOCATION: (4097)
<223> OTHER INFORMATION: the nucleic acid at position 4097 can be either
      a or g which code for Arginine.

<400> SEQUENCE: 37

agatctggta ctaccaaaag gtatccaatt aatccatgct tggcctccca ttacaatgcc      60

tgtaagaaat aattgttctt tccacctcca caactaattg tcgaactatt atatctatct     120

ttattccctt aaatgtgaaa cgaattacac agactatttg gcgctacttt tttcctagat     180

atattgaaga cctagtttct tatatttgtg ggaagcattt ggaagttcta taagaactat     240

atcatgttcg aaaacattct tataattttc gacaagattg ctgaaggagt gtcttatctt     300

ttatgtattc ttgactagag gagtttaata aaaagaaaat agaaaggaac aaagaaacgt     360

acaagtgtat aaaaggagtt ggggcaaaga catcagaaac atttagacct acgatttcat     420

cctacatgtt atggttttag ttcgttagag gttttaacat attaaatcag caaagttgtg     480

acatacataa agtgcataac ataaagatga aattcacaat ttgctggatc ttttggtgca     540

agggaactat tttttacact ataagttagc tgttaatttc aatattggct cttctacacc     600

ttgttgttct tgagtagaat tctattttgc atcaaacata tgtcagaact tatgctgcaa     660

ttaaatatat tcaggttgtt taactcttgt acagcttgtt attcttctga ggtctatttc     720

cttctcctta tttgctaact tgtgctgcag ttatcttcca tc gtg gag tca tgt       774
                                               Val Glu Ser Cys
                                                 1

aac tgc atc att gac cca cag ttg cct gct gac gac ttg cta atg aag       822
Asn Cys Ile Ile Asp Pro Gln Leu Pro Ala Asp Asp Leu Leu Met Lys
  5                 10                  15                  20

tat cag tac att tct gat ttt ttc ata gca ctt gct tat ttc tcc att       870
Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Leu Ala Tyr Phe Ser Ile
                 25                  30                  35

cca gtg gag ttg ata tac ttc gtt aag aag tct gct gtc ttt cca tat       918
Pro Val Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val Phe Pro Tyr
             40                  45                  50

aga tgg gtt ctt gtg cag ttc ggt gct ttc ata gtt ctt tgt gga gca       966
Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu Cys Gly Ala
         55                  60                  65
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acc cat ctt atc aac tta tgg aca ttt aat atg cat aca agg aat gtg     1014
Thr His Leu Ile Asn Leu Trp Thr Phe Asn Met His Thr Arg Asn Val
     70                  75                  80

gca ata gta atg act act gca aag gcc ttg act gca ctg gtg tca tgt     1062
Ala Ile Val Met Thr Thr Ala Lys Ala Leu Thr Ala Leu Val Ser Cys
 85                  90                  95                 100

ata act gct ctc atg ctt gtc cac atc att cct gat tta tta agt gtc     1110
Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val
                105                 110                 115

aaa act aga gaa ctg ttc ttg aaa aag aaa gct gca cag ctt gac cgt     1158
Lys Thr Arg Glu Leu Phe Leu Lys Lys Lys Ala Ala Gln Leu Asp Arg
            120                 125                 130

gaa atg ggt att att cgg act cag gag gag aca ggt aga cat gtt aga     1206
Glu Met Gly Ile Ile Arg Thr Gln Glu Glu Thr Gly Arg His Val Arg
        135                 140                 145

atg cta act cat gaa atc cga agc act ctt gat aga cat act att tta     1254
Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His Thr Ile Leu
    150                 155                 160

aag act aca ctt gtt gag cta gga aga aca ttg gca ttg gaa gag tgt     1302
Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu Glu Glu Cys
165                 170                 175                 180

gca tta tgg atg cca aca cgt act gga cta gag ctt cag ctt tct tac     1350
Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln Leu Ser Tyr
                185                 190                 195

act tta cga cac caa aat cca gtt gga tta act gta ccc att caa ctt     1398
Thr Leu Arg His Gln Asn Pro Val Gly Leu Thr Val Pro Ile Gln Leu
            200                 205                 210

cct gta atc aat caa gtt ttc ggt aca aat cat gtc gtg aaa ata tca     1446
Pro Val Ile Asn Gln Val Phe Gly Thr Asn His Val Val Lys Ile Ser
        215                 220                 225

cca aat tct cct gtc gca aga ctt cga cct gct ggg aaa tac atg cct     1494
Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Ala Gly Lys Tyr Met Pro
    230                 235                 240

ggt gag gtg gtt gct gtc agg gtt cca ctt ctg cat ctg tcg aac ttt     1542
Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His Leu Ser Asn Phe
245                 250                 255                 260

cag att aat gat tgg cct gaa ctt tca aca aag cgc tat gct tta atg     1590
Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg Tyr Ala Leu Met
                265                 270                 275

gtt ctg atg ctt cct tca gac agt gca aga caa tgg cat gtt cat gag     1638
Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp His Val His Glu
            280                 285                 290

ctg gag ctt gtt gaa gtg gta gct gat cag gtt tgatttttgt tattgaaaat   1691
Leu Glu Leu Val Glu Val Val Ala Asp Gln Val
        295                 300

tccttaatat aatgttaaaa tttctctttt atatattttt gggttgaaca caaccacgtt   1751

gacatactga gttctgggtg taaaattaga catggagaag accaattaca aaaatctgag   1811

aatctgctag cagaatcaca aggcttagtt gttcttagta ttatggtttt atccattgga   1871

attgcacagc agaattgtta ttactgttat tttttttaa aattttcaaa gataaatcaa   1931

aagctgaact atatgacttt ttgcatactt cgtctgctga ttgctttttg gtgatggaat   1991

agttaggctg ggttgtggat gagtatatca tagtagattt tctgatagga tcttaactcc   2051

ttggcttttg ttttctatag atgatccctt gtattagaag cacgggaaat aggatcgatg   2111

gtatatagaa atattaggaa cagctttctg aatcatttga atattccttt tatggaacat   2171

agaactcttg acgtgtatgt agttttctta gtacttttat catatgaagt gaaaataacg   2231

ttttgcgata atgtatttga gtgtgtaaaa ttaaatacta ctgagtttta caaaaataat   2291
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tcttcaacgg aagccattta ttttttttac atatctggca tcttacttct ccatcaaaga   2351

ctttagagaa ctttaacttt ttcattctgt ctctcgtagt gtactgttct ctgatgtatg   2411

taattagctc actggcaagt agcacaccta gtctttgttt gacttgttta aaaatcatga   2471

tgtatcatca gttacggtga agtgtccaag ttttactgct ttttgctatt tgcattgcag   2531

agtcttaaaa catttcagtt attcctggat ttctcctgtt tatcaatgga aaattcaact   2591

atcaactatg cctcaatcaa taaatgaaac ctctatatct aaccactcca actcagatcc   2651

agaaatcaga tttcaaagaa attcatcata actcaactat aggattgctg ttaaccaaga   2711

gtaatcctca tttgtccaga caggcgacca gctattatgc tttcattatg ggaaaaattg   2771

acaattaatt aaaggaagga acaactgaag aaaagacatc cttgtcagct tcctctccca   2831

acccttgcct gaataagaca aaaagtttct tggagaaaac tctgaatatt ggtatccacc   2891

tcctttctcc taatttagga tgctctattt ctagacatat aggggaatac tctattctag   2951

tggtcggtgt ctggttgcaa ctagttttag atgtttatat gtcttatttg atttaataag   3011

agctatcctt gagtgcccaa tgtgatttaa tctacgcttc ggcatttcag gtt gct      3067
                                                       Val Ala
                                                           305

gtt gct ctt tca cat gct gct ata tta gaa gaa tca atg agg gct agg     3115
Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
                310                 315                 320

gat ctt ctt atg gag cag aat gtg gct ctt gat ctg gca aga aga gaa     3163
Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
            325                 330                 335

gca gaa atg gct gtt cgt gca cgt aat gat ttc ttg gct gtt atg aat     3211
Ala Glu Met Ala Val Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
        340                 345                 350

cat gaa atg aga act ccc atg cat gca ata att gca ctt tct tcc tta     3259
His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
    355                 360                 365

cta caa gaa atc gat cta act cca gag caa cgt ctg atg gtt gaa aca     3307
Leu Gln Glu Ile Asp Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
370                 375                 380                 385

atc ctc aaa agc agc aac ctt tta gca acg ctc atc aac gat gtc ttg     3355
Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Ile Asn Asp Val Leu
                390                 395                 400

gat ctt tca agg cta gag gat gga agt ctt caa ctt gat att ggc act     3403
Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Asp Ile Gly Thr
            405                 410                 415

ttc aat ctc cat gct tta ttt aga gag gtg cccttcatca ccctcttttc       3453
Phe Asn Leu His Ala Leu Phe Arg Glu Val
        420                 425

tttttttactt gcaaattcta gattacctgt cagaaaaaaa gtgtcattac agatattttg  3513

cacttcaata tgtttgctgg acctgctgac tgatatatgt gtctgcttat tcctgtag     3571

gtc cat agc tta atc aag cct att gca tct gtg aaa aag tct gtt gct     3619
Val His Ser Leu Ile Lys Pro Ile Ala Ser Val Lys Lys Ser Val Ala
        430                 435                 440

caa ctt agt ttg tcg tca gat ttg ccg gaa tat gta att ggg gat gaa     3667
Gln Leu Ser Leu Ser Ser Asp Leu Pro Glu Tyr Val Ile Gly Asp Glu
    445                 450                 455

aaa cgg tta atg caa att ctc tta aac gtt gtt ggc aat gct gta aag     3715
Lys Arg Leu Met Gln Ile Leu Leu Asn Val Val Gly Asn Ala Val Lys
460                 465                 470                 475

ttc tca aag gaa ggc aac gta tca atc tcc gct ttt gtt gca aaa tca     3763
Phe Ser Lys Glu Gly Asn Val Ser Ile Ser Ala Phe Val Ala Lys Ser
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                480                 485                 490

gac tct tta aga gat cct aga gcc cct gaa ttt ttt gct gtg cct agt     3811
Asp Ser Leu Arg Asp Pro Arg Ala Pro Glu Phe Phe Ala Val Pro Ser
            495                 500                 505

gaa aat cac ttc tat tta cgg gtg cag gtatattttt acaagcttga           3858
Glu Asn His Phe Tyr Leu Arg Val Gln
        510                 515

tatactatct tcgtaggtta aggatagtca caaatatgat attttagact tataactgtc   3918

agatgttctg ttcttgatat ttgtaatatt ctaagtaata ctttctgtag ata aaa     3974
                                                       Ile Lys

gat acg ggg ata gga att aca cca cag gat att ccc aac ctg ttt agc     4022
Asp Thr Gly Ile Gly Ile Thr Pro Gln Asp Ile Pro Asn Leu Phe Ser
    520                 525                 530

aag ttt aca caa agc caa gcg cta gca act aca aat tct ggt ggc act     4070
Lys Phe Thr Gln Ser Gln Ala Leu Ala Thr Thr Asn Ser Gly Gly Thr
535                 540                 545                 550

ggg ctt ggt ctt gca att tgt aag agg gtacgggtac cagttcctta           4117
Gly Leu Gly Leu Ala Ile Cys Lys Arg
                555

gtgttctttt tccgactctg attttcattc tacgtgaact tggtaactgc ttcatattca   4177

atttctttct cttactgtat ttacgtattg acacatctcc tgatgggaca caaaaagg     4235

ttt gtg aat ctt atg gaa gga cat att tgg att gaa agt gaa ggt ctt     4283
Phe Val Asn Leu Met Glu Gly His Ile Trp Ile Glu Ser Glu Gly Leu
560                 565                 570                 575

ggc aag ggg tct act gct ata ttt atc att aaa ctt gga ctt cct gga     4331
Gly Lys Gly Ser Thr Ala Ile Phe Ile Ile Lys Leu Gly Leu Pro Gly
                580                 585                 590

cgt gca aat gaa tct aag ctc ccc ttt gtg acc aaa ttg cca gca aat     4379
Arg Ala Asn Glu Ser Lys Leu Pro Phe Val Thr Lys Leu Pro Ala Asn
            595                 600                 605

cac acg cag atg agt ttt aag gat taaaggtttt ggtgatggat gagaatgggt    4433
His Thr Gln Met Ser Phe Lys Asp
        610                 615

gagtactatc tggacccctt tatcctcgac tcttgtcttg ccatgctgtt taatgatcca   4493

tctgattgcg tgatttctca tcttatatgt attgagctgt cttactcact ttacatgaga   4553

ctacagtaat actt                                                     4567


<210> SEQ ID NO 38
<211> LENGTH: 615
<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 38

Val Glu Ser Cys Asn Cys Ile Ile Asp Pro Gln Leu Pro Ala Asp Asp
  1               5                  10                  15

Leu Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Leu Ala
             20                  25                  30

Tyr Phe Ser Ile Pro Val Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala
         35                  40                  45

Val Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val
     50                  55                  60

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

Thr Arg Asn Val Ala Ile Val Met Thr Thr Ala Lys Ala Leu Thr Ala
                 85                  90                  95
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Leu Val Ser Cys Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp
            100                 105                 110

Leu Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Lys Lys Ala Ala
        115                 120                 125

Gln Leu Asp Arg Glu Met Gly Ile Ile Arg Thr Gln Glu Glu Thr Gly
    130                 135                 140

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

His Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala
                165                 170                 175

Leu Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu
            180                 185                 190

Gln Leu Ser Tyr Thr Leu Arg His Gln Asn Pro Val Gly Leu Thr Val
        195                 200                 205

Pro Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Asn His Val
    210                 215                 220

Val Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Ala Gly
225                 230                 235                 240

Lys Tyr Met Pro Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
            260                 265                 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
        275                 280                 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Val
    290                 295                 300

Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala
305                 310                 315                 320

Arg Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg
                325                 330                 335

Glu Ala Glu Met Ala Val Arg Ala Arg Asn Asp Phe Leu Ala Val Met
            340                 345                 350

Asn His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser
        355                 360                 365

Leu Leu Gln Glu Ile Asp Leu Thr Pro Glu Gln Arg Leu Met Val Glu
    370                 375                 380

Thr Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Ile Asn Asp Val
385                 390                 395                 400

Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Asp Ile Gly
                405                 410                 415

Thr Phe Asn Leu His Ala Leu Phe Arg Glu Val Val His Ser Leu Ile
            420                 425                 430

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

Ser Asp Leu Pro Glu Tyr Val Ile Gly Asp Glu Lys Arg Leu Met Gln
    450                 455                 460

Ile Leu Leu Asn Val Val Gly Asn Ala Val Lys Phe Ser Lys Glu Gly
465                 470                 475                 480

Asn Val Ser Ile Ser Ala Phe Val Ala Lys Ser Asp Ser Leu Arg Asp
                485                 490                 495

Pro Arg Ala Pro Glu Phe Phe Ala Val Pro Ser Glu Asn His Phe Tyr
            500                 505                 510

Leu Arg Val Gln Ile Lys Asp Thr Gly Ile Gly Ile Thr Pro Gln Asp
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        515                 520                 525

Ile Pro Asn Leu Phe Ser Lys Phe Thr Gln Ser Gln Ala Leu Ala Thr
    530                 535                 540

Thr Asn Ser Gly Gly Thr Gly Leu Gly Leu Ala Ile Cys Lys Arg Phe
545                 550                 555                 560

Val Asn Leu Met Glu Gly His Ile Trp Ile Glu Ser Glu Gly Leu Gly
                565                 570                 575

Lys Gly Ser Thr Ala Ile Phe Ile Ile Lys Leu Gly Leu Pro Gly Arg
            580                 585                 590

Ala Asn Glu Ser Lys Leu Pro Phe Val Thr Lys Leu Pro Ala Asn His
        595                 600                 605

Thr Gln Met Ser Phe Lys Asp
    610                 615


<210> SEQ ID NO 39
<211> LENGTH: 737
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (33)..(719)

<400> SEQUENCE: 39

aagataagag tgattcatta aggagtttgt tc atc atg gat tgt aac tgc ttc       53
                                    Ile Met Asp Cys Asn Cys Phe
                                      1               5

gat cca ctg ttg cct gcc gat gag ttg tta atg aag tat cag tac att      101
Asp Pro Leu Leu Pro Ala Asp Glu Leu Leu Met Lys Tyr Gln Tyr Ile
         10                  15                  20

tct gat ttt ttc att gca gtt gct tat ttt tcc atc cca atc gaa ctg      149
Ser Asp Phe Phe Ile Ala Val Ala Tyr Phe Ser Ile Pro Ile Glu Leu
     25                  30                  35

gta ttc ttt gtc cag aaa tca gct gtt ttt ccg tat cga tgg gtg ctt      197
Val Phe Phe Val Gln Lys Ser Ala Val Phe Pro Tyr Arg Trp Val Leu
 40                  45                  50                  55

gtg cag ttt ggt gct ttc ata gtt ctt tgt gga gca aca cac ctt atc      245
Val Gln Phe Gly Ala Phe Ile Val Leu Cys Gly Ala Thr His Leu Ile
                 60                  65                  70

aat ttg tgg act tct act cct cat aca agg act gtg gca atg gtg atg      293
Asn Leu Trp Thr Ser Thr Pro His Thr Arg Thr Val Ala Met Val Met
             75                  80                  85

act acg gcg aag ttc tcc act gct gcg gta tca tgt gca act gct gtc      341
Thr Thr Ala Lys Phe Ser Thr Ala Ala Val Ser Cys Ala Thr Ala Val
         90                  95                 100

atg ctt gtc gca att att ccg gat tta tta agt gtc aaa act agg gag      389
Met Leu Val Ala Ile Ile Pro Asp Leu Leu Ser Val Lys Thr Arg Glu
    105                 110                 115

cta ttc ttg aaa aac aaa gcg gcg gaa ctt gat cgt gaa atg ggt ctt      437
Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu Asp Arg Glu Met Gly Leu
120                 125                 130                 135

att cgg aca cag gag gag acg ggt aga tat gtt aga atg cta aca cat      485
Ile Arg Thr Gln Glu Glu Thr Gly Arg Tyr Val Arg Met Leu Thr His
                140                 145                 150

gaa atc aga agt act ctg gat aga cat act att ttg aag act aca ctt      533
Glu Ile Arg Ser Thr Leu Asp Arg His Thr Ile Leu Lys Thr Thr Leu
            155                 160                 165

gtt gaa ctt gga aga gca ttg caa ctg gaa gag tgt gct ttg tgg atg      581
Val Glu Leu Gly Arg Ala Leu Gln Leu Glu Glu Cys Ala Leu Trp Met
        170                 175                 180
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ccg act cga act gga gtg gag ctt caa ctt tct tac act tta cat cat      629
Pro Thr Arg Thr Gly Val Glu Leu Gln Leu Ser Tyr Thr Leu His His
    185                 190                 195

caa aat cca gtt gga ttt aca gta cct ata caa ctc cct gta att aat      677
Gln Asn Pro Val Gly Phe Thr Val Pro Ile Gln Leu Pro Val Ile Asn
200                 205                 210                 215

caa gtt ttc agt gca aat tgt gct gtt aaa att tca cct taa              719
Gln Val Phe Ser Ala Asn Cys Ala Val Lys Ile Ser Pro
                220                 225

tctgccgttg caaggctt                                                  737


<210> SEQ ID NO 40
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 40

Ile Met Asp Cys Asn Cys Phe Asp Pro Leu Leu Pro Ala Asp Glu Leu
  1               5                  10                  15

Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Val Ala Tyr
             20                  25                  30

Phe Ser Ile Pro Ile Glu Leu Val Phe Phe Val Gln Lys Ser Ala Val
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Cys Gly Ala Thr His Leu Ile Asn Leu Trp Thr Ser Thr Pro His Thr
 65                  70                  75                  80

Arg Thr Val Ala Met Val Met Thr Thr Ala Lys Phe Ser Thr Ala Ala
                 85                  90                  95

Val Ser Cys Ala Thr Ala Val Met Leu Val Ala Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
        115                 120                 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

Tyr Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His
145                 150                 155                 160

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Ala Leu Gln Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Val Glu Leu Gln
            180                 185                 190

Leu Ser Tyr Thr Leu His His Gln Asn Pro Val Gly Phe Thr Val Pro
        195                 200                 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Ser Ala Asn Cys Ala Val
    210                 215                 220

Lys Ile Ser Pro
225


<210> SEQ ID NO 41
<211> LENGTH: 6202
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3522)..(5288)
<221> NAME/KEY: CDS
<222> LOCATION: (5372)..(5926)

<400> SEQUENCE: 41
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gaattcgaac tgcaatggga taaacattat atgcgtttta ataataggtt ggtgaagttt 60

ataatttaca ccatttgaaa agccttccaa atttagaaac tacatttttg cagacccatg 120

tgagctcata tgaatcaatc atagccttga tgttgtaaaa caaattatga ttataaaaat 180

gtgatagtat attacatgca taaaaaataa aggagagtaa atgaaagtca aatctgggtt 240

ttatgaactg aaagttgaag tttagaagta gaagtagcga tcaaagtatg accagttaaa 300

aggcccaata tcatttggag gtttgatttt tgggttcgta aatttcaaga gccagattat 360

gatttgctgg gcttaaaaat catggaaaaa ttgaaatgac ggtgttaaaa tatataactc 420

aaattaaaga ttttaattgg gtgtagtagg ctgatttttt tataagaatc ttgtctatag 480

atgcttcaag gttatgcctt atagtactgg ttgtaaaaca ccactatcta attttgaagc 540

tggtcagaac tataaggtat gttgttgttc gccttgttgc taatgaagat tataacattc 600

tgttgttgca tttttttttt tttttttgtg ttaaatatat atattttttt tgcatattta 660

ttgttgcata ttgtgttgca tatttagtaa tggttacatt ccctgttatc ggagaccaag 720

ataatacggc tctgtggcat ggactactac tccatggatt cttccaagta atcttgcttt 780

gtgtgtcaat gcaaagtttg tttatcttaa ggttcgtcaa caacactgga aaagtctaca 840

ttgttgctga atctcggttg tcatcgcttc ctagtgataa gcctaaggcc ggcttaacta 900

atggaactta ctagtgatac cataatgcga aaggtgctaa ttaagcttga cagtgaagag 960

gattcttatc aagttttgga aaattttaat ggagattcct tggttgggaa gaagtatgaa 1020

cctttgtttg attactttta gcgatttctc aagtgtgact tttcgactag tagcagatga 1080

ttatgtcatg aatgatagtg gtactggtat tgtccattgt gctcctgtct ttggtgcaga 1140

tgactatcgt gtttgtcttg agaacgagat aattaagaag gttagatttg acaacatctt 1200

ccttatatca ccacctttaa cattaagttt attttctttc ttgtttaagt ttacagtatc 1260

ttcaagaacc catgttcatg acacattttg ttcatgtgtt gtttagattg tcagagattt 1320

caaacgtcca gatggtttga aagatacaga gattgatgca gctgtagata gtacatatct 1380

taattaaaaa taccacttct ctatgctcta ttgttgagga aacatataat atttgcattc 1440

gttcatggtt cagatatgat gttatggtaa ttcttgatct acgagaagat gaatctttga 1500

aaaacgaagg tgttgcccgt gaggtaaata aatgtaaccg aagcgattaa tggtcatata 1560

taagttgtat atttgatata tgggtttcct tctcattgtg ctcatgcatt gaaaagcacc 1620

ctgttatgac tgtggttcta ggagaacatt tgcatttgac agtcggtgac taattgttaa 1680

gcaagaagaa cgcatgagag ccttttaaag tgttttcttc tagatcgttg caaaaagtta 1740

aatgtctctt gagactttgt actcattcta tagataaaga tgggatttat tacaaaaaca 1800

acaagaaact ttgttacttg tggaaattca aaattatccg aactagcttc acaaaatatg 1860

ctcaagagtt tcaatgtatt tttttttgtt ctgtaattgt atgactccgt ttgaagcatc 1920

aagattatgg ttataggtag tgatgctaaa actctctgtt gttacagtga ccactaaaaa 1980

caccaacaaa aaaaacttag gtaacgtgtc gtctaaaaac ttctaggttc aatttcttta 2040

gatagtacta tcaataaata aaataaatat gtacaaaggc tttaaacaat gatgtttttc 2100

aaagatgatt ggtagatact aattagagct tcaatataaa agaacacatg cgattctgac 2160

attctgtggt ctaacatggt ttcttctaga gtcaaaacca tacaattaaa agttaggaaa 2220

gtaatagcaa tgtggtttca aatatatact cattactctt tagattcatg tatggtgaag 2280

gaaacattat aataaaatca aagatcacag ttttgtaggt ccctcatatt aatcaacatc 2340

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ttaaggcgtt atacatatct tctttttgta aatatttgac taattaaaat atctaattag   2400

agtattagac taatctcatc aaatatccga ctacttgtgt cagttcaaaa cacagtgatt   2460

acgttagatt ttgtgctctt ttgtttataa acaaagctaa tttaagaaat atatgatcta   2520

tttgcctcct tggtcttaat tttatacttt cttggaataa aacacattta ttaaaataat   2580

ttttagggtc ctagattcat gtcatgtggc ttgatagttt ccaacaatta taccaatatt   2640

ttactcattc atatacaaat aaacaagctt tattctattc ttcagtctca tgatatacgg   2700

gattttgata aaattcagag tacccattaa ttattctatg ttacagcttg taataagtta   2760

aatttataaa acgtacaagt tgaggaaata acaaatgttt tcaatattaa atgatttatt   2820

aatacattag tgaccaaaaa attattaagt gtaagaaaaa aaacacaact cagaaaaaat   2880

tcaaaagacc gtctaagttc ggttcatgta agaacaagtg ggacctcttt aagtttctaa   2940

atcagagaat aaagaagaag aaaaaatctc aaaaccttcc tctaaaacca acggctccta   3000

cctttactta caccctatac atacacttct ctttttatcc tccatcggcg gcttatggcg   3060

gttttccggc actaatcatc tccggcatat ataaataaac gtacttcacg ttttttttata   3120

taacttcaaa gtagtttcag atttgtctct atctcttcac ttttaagtct tctggttttg   3180

tcatcaccag cttttttttgt tctctctctg tctctgtctc tgtctttctc tttgtgtatt   3240

tttattctcg tcatcgttgt tcttctatga gaggaagatc ggaatgtcga agagaattag   3300

aagattctcg tacatcactt cgttggaatt tcacaggtcg atgagagatc tgagaactgt   3360

ttcattttga tccaaactca tctctttcag gtattccaaa tttgtctttc tctgttcttt   3420

ctactattac ccaaattaaa gttttgattt ttatttctca ctctgtttct tgtttttcta   3480

attgcagagt ataatggact aagcattttt tttctccgaa g atg gtt aaa gaa ata   3536
                                              Met Val Lys Glu Ile
                                                1               5

gct tct tgg tta ttg ata cta tca atg gtg gtg ttt gtt tct ccg gtt     3584
Ala Ser Trp Leu Leu Ile Leu Ser Met Val Val Phe Val Ser Pro Val
                 10                  15                  20

tta gct ata aac ggc ggt ggt tat cca cga tgt aac tgc gaa gac gaa     3632
Leu Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys Asn Cys Glu Asp Glu
             25                  30                  35

gga aac agt ttc tgg agt aca gag aac att cta gaa act caa aga gta     3680
Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu Glu Thr Gln Arg Val
         40                  45                  50

agc gat ttc tta atc gca gta gct tat ttc tca atc cct att gag tta     3728
Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser Ile Pro Ile Glu Leu
     55                  60                  65

ctt tac ttc gtg agt tgt tcc aat gtt cca ttc aaa tgg gtt ctc ttt     3776
Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe Lys Trp Val Leu Phe
 70                  75                  80                  85

gag ttt atc gcc ttc att gtt ctt tgt ggt atg act cat ctt ctt cat     3824
Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met Thr His Leu Leu His
                 90                  95                 100

ggt tgg act tac tct gct cat cca ttt aga tta atg atg gcg ttt act     3872
Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu Met Met Ala Phe Thr
            105                 110                 115

gtt ttc aag atg ttg act gct tta gtc tct tgt gct act gcg att acg     3920
Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys Ala Thr Ala Ile Thr
        120                 125                 130

ctt att act ttg att cct ctg ctt ttg aaa gtt aaa gtt aga gag ttt     3968
Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val Lys Val Arg Glu Phe
    135                 140                 145

atg ctt aag aag aaa gct cat gag ctt ggt cgt gaa gtt ggt ttg att     4016
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Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg Glu Val Gly Leu Ile
150                 155                 160                 165

ttg att aag aaa gag act ggc ttt cat gtt cgt atg ctt act caa gag         4064
Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg Met Leu Thr Gln Glu
                170                 175                 180

att cgt aag tct ttg gat cgt cat acg att ctt tat act act ttg gtt         4112
Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu Tyr Thr Thr Leu Val
            185                 190                 195

gag ctt tcg aag act tta ggg ttg cag aat tgt gcg gtt tgg atg ccg         4160
Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys Ala Val Trp Met Pro
        200                 205                 210

aat gac ggt gga acg gag atg gat ttg act cat gag ttg aga ggg aga         4208
Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His Glu Leu Arg Gly Arg
    215                 220                 225

ggt ggt tat ggt ggt tgt tct gtt tct atg gag gat ttg gat gtt gtt         4256
Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu Asp Leu Asp Val Val
230                 235                 240                 245

agg att agg gag agt gat gaa gtg aat gtg ttg agt gtt gac tcg tcc         4304
Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu Ser Val Asp Ser Ser
                250                 255                 260

att gct cga gct agt ggt ggt ggt ggg gat gtt agt gag att ggt gcc         4352
Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val Ser Glu Ile Gly Ala
            265                 270                 275

gtg gct gct att aga atg ccg atg ctt cgt gtt tcg gat ttt aat gga         4400
Val Ala Ala Ile Arg Met Pro Met Leu Arg Val Ser Asp Phe Asn Gly
        280                 285                 290

gag cta agt tat gcg ata ctt gtt tgt gtt tta ccg ggc ggg acc cgt         4448
Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu Pro Gly Gly Thr Arg
    295                 300                 305

cgg gat tgg act tat cag gag att gag att gtt aaa gtt gtg gcg gat         4496
Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val Lys Val Val Ala Asp
310                 315                 320                 325

caa gta acc gtt gcg tta gat cat gca gcg gtt ctt gaa gag tct cag         4544
Gln Val Thr Val Ala Leu Asp His Ala Ala Val Leu Glu Glu Ser Gln
                330                 335                 340

ctt atg agg gag aag ctg gcg gaa cag aac agg gcg ttg cag atg gcg         4592
Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg Ala Leu Gln Met Ala
            345                 350                 355

aag aga gac gcg ttg aga gcg agc caa gcg agg aat gcg ttt cag aaa         4640
Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg Asn Ala Phe Gln Lys
        360                 365                 370

acg atg agc gaa ggg atg agg cgt cct atg cat tcg ata ctc ggt ctt         4688
Thr Met Ser Glu Gly Met Arg Arg Pro Met His Ser Ile Leu Gly Leu
    375                 380                 385

ttg tcg atg att cag gac gag aag ttg agt gac gag cag aaa atg att         4736
Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp Glu Gln Lys Met Ile
390                 395                 400                 405

gtt gat acg atg gtt aaa aca ggg aat gtt atg tcg aat ttg gtg ggg         4784
Val Asp Thr Met Val Lys Thr Gly Asn Val Met Ser Asn Leu Val Gly
                410                 415                 420

gac tct atg gat gtg cct gac ggt aga ttt ggt acg gag atg aaa ccg         4832
Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly Thr Glu Met Lys Pro
            425                 430                 435

ttt agt ctg cat cgt acg atc cat gaa gca gct tgt atg gcg aga tgt         4880
Phe Ser Leu His Arg Thr Ile His Glu Ala Ala Cys Met Ala Arg Cys
        440                 445                 450

ttg tgt cta tgc aat gga att agg ttc ttg gtt gac gcg gag aag tct         4928
Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val Asp Ala Glu Lys Ser
    455                 460                 465
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cta cct gat aat gta gta ggt gat gaa aga agg gtc ttt caa gtg ata     4976
Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg Val Phe Gln Val Ile
470                 475                 480                 485

ctt cat atg gtt ggt agt tta gta aag cct aga aaa cgt caa gaa gga     5024
Leu His Met Val Gly Ser Leu Val Lys Pro Arg Lys Arg Gln Glu Gly
                490                 495                 500

tct tca ttg atg ttt aag gtt ttg aaa gaa aga gga agc ttg gat agg     5072
Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg Gly Ser Leu Asp Arg
            505                 510                 515

agt gat cat aga tgg gct gct tgg aga tca ccg gct tct tca gca gat     5120
Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro Ala Ser Ser Ala Asp
        520                 525                 530

gga gat gtg tat ata aga ttt gaa atg aat gta gag aat gat gat tca     5168
Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val Glu Asn Asp Asp Ser
    535                 540                 545

agt tct caa tca ttt gct tct gtt tcc tcc aga gat caa gaa gtt ggt     5216
Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg Asp Gln Glu Val Gly
550                 555                 560                 565

gat gtt aga ttc tcc ggc ggc tat ggg tta gga caa gat cta agc ttt     5264
Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly Gln Asp Leu Ser Phe
                570                 575                 580

ggt gtt tgt aag aaa gtg gtg cag gtgagtttcc ttacatatct ctttctaaag    5318
Gly Val Cys Lys Lys Val Val Gln
            585

ttcctgtcat tagtctgagt ttctgtttag gagttctttg ataatgtgtg cag ttg      5374
                                                           Leu
                                                           590

att cat ggg aat atc tcg gtg gtc cct ggc tcg gat ggt tca ccg gag     5422
Ile His Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu
                595                 600                 605

acc atg tcg ttg ctc ctt cgg ttt cga cgt aga ccc tcc ata tct gtc     5470
Thr Met Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val
            610                 615                 620

cat gga tcc agc gag tcg cca gct cct gac cac cac gct cac cca cat     5518
His Gly Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His
        625                 630                 635

tcg aat tct ctg tta cgt ggc tta caa gtt tta ttg gta gac acc aac     5566
Ser Asn Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn
    640                 645                 650

gat tcg aac cgg gca gtt aca cgt aaa ctc tta gag aaa ctc ggg tgc     5614
Asp Ser Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys
655                 660                 665                 670

gat gta acc gcg gtt tcc tct gga ttc gat tgc ctt acc gcc att gct     5662
Asp Val Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala
                675                 680                 685

ccc ggc tcg tcc tcg cct tct act tcg ttt caa gtg gtg gtg ctt gat     5710
Pro Gly Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp
            690                 695                 700

ctt caa atg gca gag atg gac ggt tat gaa gtg gcc atg agg atc agg     5758
Leu Gln Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg
        705                 710                 715

agt cga tct tgg ccg ttg att gtg gcg acg aca gtg agc ttg gat gaa     5806
Ser Arg Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu
    720                 725                 730

gaa atg tgg gac aag tgt gca cag att gga atc aat gga gtt gtg aga     5854
Glu Met Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg
735                 740                 745                 750

aag cca gtg gtg tta aga gct atg gag agt gag ctc cga aga gta ttg     5902
Lys Pro Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu
                755                 760                 765
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ttg caa gct gac caa ctt ctc taa gttgttatct caacttctct tctacattca    5956
Leu Gln Ala Asp Gln Leu Leu
            770

aaatttttac accatagatt tatgtcaaat atatcaaaat gaaatttcga aattgttatt   6016

atatatacca cccatatctc tatgatttgt acatcctgtt ttttttgtt ctttttctca    6076

ttttgaaccc cacgaaattg cattgaatct tagtatttcg tagggtcaag aaggagtcag   6136

tttcgtagtt ttttgttttc tttatgttac gaacttacga aactgaatat ggcattatag   6196

agtttt                                                              6202


<210> SEQ ID NO 42
<211> LENGTH: 773
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 42

Met Val Lys Glu Ile Ala Ser Trp Leu Leu Ile Leu Ser Met Val Val
  1               5                  10                  15

Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys
             20                  25                  30

Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu
         35                  40                  45

Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser
     50                  55                  60

Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe
 65                  70                  75                  80

Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met
                 85                  90                  95

Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
            100                 105                 110

Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys
        115                 120                 125

Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val
    130                 135                 140

Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg
145                 150                 155                 160

Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
                165                 170                 175

Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
            180                 185                 190

Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys
        195                 200                 205

Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
    210                 215                 220

Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
225                 230                 235                 240

Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
                245                 250                 255

Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
            260                 265                 270

Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
        275                 280                 285

Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
    290                 295                 300
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Pro Gly Gly Thr Arg Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
305                 310                 315                 320

Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
                325                 330                 335

Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
            340                 345                 350

Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg
        355                 360                 365

Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
    370                 375                 380

Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
385                 390                 395                 400

Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
                405                 410                 415

Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
            420                 425                 430

Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
        435                 440                 445

Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
    450                 455                 460

Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
465                 470                 475                 480

Val Phe Gln Val Ile Leu His Met Val Gly Ser Leu Val Lys Pro Arg
                485                 490                 495

Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
            500                 505                 510

Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
        515                 520                 525

Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
    530                 535                 540

Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
545                 550                 555                 560

Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
                565                 570                 575

Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His
            580                 585                 590

Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met
        595                 600                 605

Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
    610                 615                 620

Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn
625                 630                 635                 640

Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser
                645                 650                 655

Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
            660                 665                 670

Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly
        675                 680                 685

Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln
    690                 695                 700

Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg
705                 710                 715                 720
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Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met
                725                 730                 735

Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro
            740                 745                 750

Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln
        755                 760                 765

Ala Asp Gln Leu Leu
    770


<210> SEQ ID NO 43
<211> LENGTH: 2404
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2322)

<400> SEQUENCE: 43

atg gtt aaa gaa ata gct tct tgg tta ttg ata cta tca atg gtg gtg       48
Met Val Lys Glu Ile Ala Ser Trp Leu Leu Ile Leu Ser Met Val Val
  1               5                  10                  15

ttt gtt tct ccg gtt tta gct ata aac ggc ggt ggt tat cca cga tgt       96
Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys
             20                  25                  30

aac tgc gaa gac gaa gga aac agt ttc tgg agt aca gag aac att cta      144
Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu
         35                  40                  45

gaa act caa aga gta agc gat ttc tta atc gca gta gct tat ttc tca      192
Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser
     50                  55                  60

atc cct att gag tta ctt tac ttc gtg agt tgt tcc aat gtt cca ttc      240
Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe
 65                  70                  75                  80

aaa tgg gtt ctc ttt gag ttt atc gcc ttc att gtt ctt tgt ggt atg      288
Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met
                 85                  90                  95

act cat ctt ctt cat ggt tgg act tac tct gct cat cca ttt aga tta      336
Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
            100                 105                 110

atg atg gcg ttt act gtt ttc aag atg ttg act gct tta gtc tct tgt      384
Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys
        115                 120                 125

gct act gcg att acg ctt att act ttg att cct ctg ctt ttg aaa gtt      432
Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val
    130                 135                 140

aaa gtt aga gag ttt atg ctt aag aag aaa gct cat gag ctt ggt cgt      480
Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg
145                 150                 155                 160

gaa gtt ggt ttg att ttg att aag aaa gag act ggc ttt cat gtt cgt      528
Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
            165                 170                 175

atg ctt act caa gag att cgt aag tct ttg gat cgt cat acg att ctt      576
Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
            180                 185                 190

tat act act ttg gtt gag ctt tcg aag act tta ggg ttg cag aat tgt      624
Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys
        195                 200                 205

gcg gtt tgg atg ccg aat gac ggt gga acg gag atg gat ttg act cat      672
Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
    210                 215                 220
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gag ttg aga ggg aga ggt ggt tat ggt ggt tgt tct gtt tct atg gag      720
Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
225                 230                 235                 240

gat ttg gat gtt gtt agg att agg gag agt gat gaa gtg aat gtg ttg      768
Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
                245                 250                 255

agt gtt gac tcg tcc att gct cga gct agt ggt ggt ggt ggg gat gtt      816
Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
            260                 265                 270

agt gag att ggt gcc gtg gct gct att aga atg ccg atg ctt cgt gtt      864
Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
        275                 280                 285

tcg gat ttt aat gga gag cta agt tat gcg ata ctt gtt tgt gtt tta      912
Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
    290                 295                 300

ccg ggc ggg acc cgt cgg gat tgg act tat cag gag att gag att gtt      960
Pro Gly Gly Thr Arg Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
305                 310                 315                 320

aaa gtt gtg gcg gat caa gta acc gtt gcg tta gat cat gca gcg gtt     1008
Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
                325                 330                 335

ctt gaa gag tct cag ctt atg agg gag aag ctg gcg gaa cag aac agg     1056
Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
            340                 345                 350

gcg ttg cag atg gcg aag aga gac gcg ttg aga gcg agc caa gcg agg     1104
Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg
        355                 360                 365

aat gcg ttt cag aaa acg atg agc gaa ggg atg agg cgt cct atg cat     1152
Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
    370                 375                 380

tcg ata ctc ggt ctt ttg tcg atg att cag gac gag aag ttg agt gac     1200
Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
385                 390                 395                 400

gag cag aaa atg att gtt gat acg atg gtt aaa aca ggg aat gtt atg     1248
Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
                405                 410                 415

tcg aat ttg gtg ggg gac tct atg gat gtg cct gac ggt aga ttt ggt     1296
Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
            420                 425                 430

acg gag atg aaa ccg ttt agt ctg cat cgt acg atc cat gaa gca gct     1344
Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
        435                 440                 445

tgt atg gcg aga tgt ttg tgt cta tgc aat gga att agg ttc ttg gtt     1392
Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
    450                 455                 460

gac gcg gag aag tct cta cct gat aat gta gta ggt gat gaa aga agg     1440
Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
465                 470                 475                 480

gtc ttt caa gtg ata ctt cat atg gtt ggt agt tta gta aag cct aga     1488
Val Phe Gln Val Ile Leu His Met Val Gly Ser Leu Val Lys Pro Arg
                485                 490                 495

aaa cgt caa gaa gga tct tca ttg atg ttt aag gtt ttg aaa gaa aga     1536
Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
            500                 505                 510

gga agc ttg gat agg agt gat cat aga tgg gct gct tgg aga tca ccg     1584
Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
        515                 520                 525

gct tct tca gca gat gga gat gtg tat ata aga ttt gaa atg aat gta     1632
Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
    530                 535                 540
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gag aat gat gat tca agt tct caa tca ttt gct tct gtt tcc tcc aga     1680
Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
545                 550                 555                 560

gat caa gaa gtt ggt gat gtt aga ttc tcc ggc ggc tat ggg tta gga     1728
Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
                565                 570                 575

caa gat cta agc ttt ggt gtt tgt aag aaa gtg gtg cag ttg att cat     1776
Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His
            580                 585                 590

ggg aat atc tcg gtg gtc cct ggc tcg gat ggt tca ccg gag acc atg     1824
Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met
        595                 600                 605

tcg ttg ctc ctt cgg ttt cga cgt aga ccc tcc ata tct gtc cat gga     1872
Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
    610                 615                 620

tcc agc gag tcg cca gct cct gac cac cac gct cac cca cat tcg aat     1920
Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn
625                 630                 635                 640

tct ctg tta cgt ggc tta caa gtt tta ttg gta gac acc aac gat tcg     1968
Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser
                645                 650                 655

aac cgg gca gtt aca cgt aaa ctc tta gag aaa ctc ggg tgc gat gta     2016
Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
            660                 665                 670

acc gcg gtt tcc tct gga ttc gat tgc ctt acc gcc att gct ccc ggc     2064
Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly
        675                 680                 685

tcg tcc tcg cct tct act tcg ttt caa gtg gtg gtg ctt gat ctt caa     2112
Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln
    690                 695                 700

atg gca gag atg gac ggt tat gaa gtg gcc atg agg atc agg agt cga     2160
Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg
705                 710                 715                 720

tct tgg ccg ttg att gtg gcg acg aca gtg agc ttg gat gaa gaa atg     2208
Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met
                725                 730                 735

tgg gac aag tgt gca cag att gga atc aat gga gtt gtg aga aag cca     2256
Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro
            740                 745                 750

gtg gtg tta aga gct atg gag agt gag ctc cga aga gta ttg ttg caa     2304
Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln
        755                 760                 765

gct gac caa ctt ctc taa gttgttatct caacttctct tctacattca            2352
Ala Asp Gln Leu Leu
    770

aaatttttac accatagatt tatgtcaaat atatcaaaat gaaatttcga aa           2404


<210> SEQ ID NO 44
<211> LENGTH: 773
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 44

Met Val Lys Glu Ile Ala Ser Trp Leu Leu Ile Leu Ser Met Val Val
  1               5                  10                  15

Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys
             20                  25                  30

Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu
         35                  40                  45
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Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser
     50                  55                  60

Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe
 65                  70                  75                  80

Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met
                 85                  90                  95

Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
            100                 105                 110

Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys
        115                 120                 125

Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val
    130                 135                 140

Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg
145                 150                 155                 160

Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
                165                 170                 175

Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
            180                 185                 190

Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys
        195                 200                 205

Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
    210                 215                 220

Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
225                 230                 235                 240

Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
                245                 250                 255

Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
            260                 265                 270

Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
        275                 280                 285

Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
    290                 295                 300

Pro Gly Gly Thr Arg Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
305                 310                 315                 320

Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
                325                 330                 335

Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
            340                 345                 350

Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg
        355                 360                 365

Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
    370                 375                 380

Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
385                 390                 395                 400

Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
                405                 410                 415

Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
            420                 425                 430

Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
        435                 440                 445

Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
    450                 455                 460
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Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
465                 470                 475                 480

Val Phe Gln Val Ile Leu His Met Val Gly Ser Leu Val Lys Pro Arg
                485                 490                 495

Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
            500                 505                 510

Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
        515                 520                 525

Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
    530                 535                 540

Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
545                 550                 555                 560

Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
                565                 570                 575

Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His
            580                 585                 590

Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met
        595                 600                 605

Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
    610                 615                 620

Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn
625                 630                 635                 640

Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser
                645                 650                 655

Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
            660                 665                 670

Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly
        675                 680                 685

Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln
    690                 695                 700

Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg
705                 710                 715                 720

Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met
                725                 730                 735

Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro
            740                 745                 750

Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln
        755                 760                 765

Ala Asp Gln Leu Leu
    770


<210> SEQ ID NO 45
<211> LENGTH: 3010
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (564)..(1469)
<221> NAME/KEY: CDS
<222> LOCATION: (1565)..(1933)
<221> NAME/KEY: CDS
<222> LOCATION: (2014)..(2280)
<221> NAME/KEY: CDS
<222> LOCATION: (2359)..(2487)
<221> NAME/KEY: CDS
<222> LOCATION: (2579)..(2749)

<400> SEQUENCE: 45
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acttttaaaa tttctttatt tcattgtcag aaaaagagag ctaataatat tattatttaa      60

atgtaacaag taggcctata acacgtgaac ttccctcttt gcaaaaaaaa aatcatcaaa     120

aacttttacc tctcattggt ttcttcttta tcacactgtt acgcttggat tctcatttct     180

tcaagttcat aacgctcgga tcaatcagga agacgaactt gaactttctt tttttcatca     240

ttacccaaag ctatgaggct cacaccacca atacgtccgc cgtcatgaat ccttctcttc     300

caggtactgt gccgtctcgg gataacaaac tttctattta ttctcttctg atcggatcta     360

tctatcgatg aagattgatt tcactacttt agtaacattt catctgatcg atctgtgttg     420

tgttatcgag gaatcaatct cattttgtag attcaatttt ctggatagat tttgtatctc     480

ttttccatag ctctagtcca aatctagtct ccactgatat ctgagttttg ttgaccaggt     540

caacacaagt cagagctcca aaa atg gag tca tgc gat tgt ttt gag acg cat     593
                          Met Glu Ser Cys Asp Cys Phe Glu Thr His
                            1               5                  10

gtg aat caa gat gat ctg tta gtg aag tac caa tac atc tca gat gcg       641
Val Asn Gln Asp Asp Leu Leu Val Lys Tyr Gln Tyr Ile Ser Asp Ala
                 15                  20                  25

ttg att gct ctt gca tac ttc tca atc cca ctc gag ctt atc tat ttc       689
Leu Ile Ala Leu Ala Tyr Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe
             30                  35                  40

gtg caa aag tct gct ttc ttc cct tac aaa tgg gtg ctt atg cag ttt       737
Val Gln Lys Ser Ala Phe Phe Pro Tyr Lys Trp Val Leu Met Gln Phe
         45                  50                  55

gga gcc ttt atc att ctc tgt gga gct acg cat ttc atc aac cta tgg       785
Gly Ala Phe Ile Ile Leu Cys Gly Ala Thr His Phe Ile Asn Leu Trp
     60                  65                  70

atg ttc ttc atg cat tcc aaa gcc gtt gcc att gtc atg act att gct       833
Met Phe Phe Met His Ser Lys Ala Val Ala Ile Val Met Thr Ile Ala
 75                  80                  85                  90

aaa gtc tct tgc gcg gtt gtg tcg tgt gct acc gcg ttg atg ttg gtt       881
Lys Val Ser Cys Ala Val Val Ser Cys Ala Thr Ala Leu Met Leu Val
                 95                 100                 105

cat att att cct gat ctt ctc agt gtt aag aac agg gaa ttg ttt ctc       929
His Ile Ile Pro Asp Leu Leu Ser Val Lys Asn Arg Glu Leu Phe Leu
            110                 115                 120

aag aag aaa gct gat gag tta gat aga gaa atg ggt ctt att tta aca       977
Lys Lys Lys Ala Asp Glu Leu Asp Arg Glu Met Gly Leu Ile Leu Thr
        125                 130                 135

caa gag gag act ggt agg cat gtt agg atg ctt act cat gga att aga      1025
Gln Glu Glu Thr Gly Arg His Val Arg Met Leu Thr His Gly Ile Arg
    140                 145                 150

aga act ctt gat agg cat act att tta aga acc act ctt gtt gag ctt      1073
Arg Thr Leu Asp Arg His Thr Ile Leu Arg Thr Thr Leu Val Glu Leu
155                 160                 165                 170

ggt aaa act ctt tgt ctt gag gaa tgt gcg ttg tgg atg cct tct caa      1121
Gly Lys Thr Leu Cys Leu Glu Glu Cys Ala Leu Trp Met Pro Ser Gln
                175                 180                 185

agt ggt tta tat ttg cag ctt tct cat act ttg agt cat aaa ata caa      1169
Ser Gly Leu Tyr Leu Gln Leu Ser His Thr Leu Ser His Lys Ile Gln
            190                 195                 200

gtt gga agc agt gtg ccg ata aat ctc ccg att att aat gaa ctc ttc      1217
Val Gly Ser Ser Val Pro Ile Asn Leu Pro Ile Ile Asn Glu Leu Phe
        205                 210                 215

aat agc gct caa gct atg cac ata cct cat tct tgt cct ttg gct aag      1265
Asn Ser Ala Gln Ala Met His Ile Pro His Ser Cys Pro Leu Ala Lys
    220                 225                 230

att ggg cct ccg gtt ggg aga tat tca cct cct gag gtt gtt tct gtc      1313
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Ile Gly Pro Pro Val Gly Arg Tyr Ser Pro Pro Glu Val Val Ser Val
235                 240                 245                 250

cgt gtt cct ctt tta cat ctc tct aat ttc caa ggc agt gac tgg tcg     1361
Arg Val Pro Leu Leu His Leu Ser Asn Phe Gln Gly Ser Asp Trp Ser
                255                 260                 265

gat ctc tct ggc aaa ggt tac gct atc atg gtc ctg att ctc cca acc     1409
Asp Leu Ser Gly Lys Gly Tyr Ala Ile Met Val Leu Ile Leu Pro Thr
            270                 275                 280

gat ggt gca aga aaa tgg aga gac cat gag tta gag ctt gta gaa aac     1457
Asp Gly Ala Arg Lys Trp Arg Asp His Glu Leu Glu Leu Val Glu Asn
        285                 290                 295

gtg gcg gat cag gtccatctct ttacttgtat atgtttggtt gtgtgtcaag         1509
Val Ala Asp Gln
    300

ttgctttacc agcttttagt gttttgtttt gtcccctgac tctcacttca ttcag gtg    1567
                                                             Val

gct gtg gct ctc tca cat gct gca att ttg gaa gaa tcc atg cac gct     1615
Ala Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met His Ala
    305                 310                 315

cgt gac cag ctt atg gag cag aat ttt gct tta gac aag gct cgt caa     1663
Arg Asp Gln Leu Met Glu Gln Asn Phe Ala Leu Asp Lys Ala Arg Gln
320                 325                 330                 335

gag gct gag atg gca gta cat gct cga aat gat ttc cta gct gtt atg     1711
Glu Ala Glu Met Ala Val His Ala Arg Asn Asp Phe Leu Ala Val Met
                340                 345                 350

aac cac gag atg agg aca ccg atg cat gcc atc atc tct ctt tct tct     1759
Asn His Glu Met Arg Thr Pro Met His Ala Ile Ile Ser Leu Ser Ser
            355                 360                 365

ctt ctc ctt gag act gag ctg tct cca gag caa aga gtt atg atc gag     1807
Leu Leu Leu Glu Thr Glu Leu Ser Pro Glu Gln Arg Val Met Ile Glu
        370                 375                 380

aca ata ctg aaa agc agc aat ctt gtg gct aca cta atc agc gac gtt     1855
Thr Ile Leu Lys Ser Ser Asn Leu Val Ala Thr Leu Ile Ser Asp Val
    385                 390                 395

ctg gat ctt tcg aga ttg gaa gat ggg agc tta ctc ttg gaa aat gaa     1903
Leu Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Leu Leu Glu Asn Glu
400                 405                 410                 415

cca ttc agt cta caa gcg atc ttt gaa gag gtaactaaat ccccctgatt       1953
Pro Phe Ser Leu Gln Ala Ile Phe Glu Glu
                420                 425

aaccagtgaa gtccattata tatgtcttac atgaataaca tgggcgcttt gaatctgcag   2013

gtc atc tct ttg ata aag cca atc gca tca gtg aag aaa cta tca acg     2061
Val Ile Ser Leu Ile Lys Pro Ile Ala Ser Val Lys Lys Leu Ser Thr
                430                 435                 440

aat ctg att ctg tct gca gac tta cca act tat gct att ggt gat gag     2109
Asn Leu Ile Leu Ser Ala Asp Leu Pro Thr Tyr Ala Ile Gly Asp Glu
            445                 450                 455

aaa cgt ctg atg caa aca att ctt aac atc atg ggc aac gct gtg aaa     2157
Lys Arg Leu Met Gln Thr Ile Leu Asn Ile Met Gly Asn Ala Val Lys
        460                 465                 470

ttt act aag gaa ggc tac atc tcc ata ata gcc tct atc atg aaa ccc     2205
Phe Thr Lys Glu Gly Tyr Ile Ser Ile Ile Ala Ser Ile Met Lys Pro
    475                 480                 485

gag tcc tta caa gaa tta cca tct cca gaa ttt ttt cca gtt ctc agt     2253
Glu Ser Leu Gln Glu Leu Pro Ser Pro Glu Phe Phe Pro Val Leu Ser
490                 495                 500                 505

gac agt cac ttc tac cta tgt gtg cag gttagaccca atctacaaat           2300
Asp Ser His Phe Tyr Leu Cys Val Gln
                510
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tactaaacta caaagttaag cttcttactg tgttcttact gttataatca tggtgcag     2358

gtg aag gac aca ggg tgt gga att cac aca caa gac att cct ttg ctc     2406
Val Lys Asp Thr Gly Cys Gly Ile His Thr Gln Asp Ile Pro Leu Leu
515                 520                 525                 530

ttt acc aaa ttt gta cag cct cgg acc gga act cag agg aac cat tcc     2454
Phe Thr Lys Phe Val Gln Pro Arg Thr Gly Thr Gln Arg Asn His Ser
                535                 540                 545

ggt gga gga ctc ggg cta gct ctc tgt aaa cga gtaacaaccc aaaagtatat   2507
Gly Gly Gly Leu Gly Leu Ala Leu Cys Lys Arg
            550                 555

ataagttata agcagatggt gttacaaata gctaaaaggc aagtttctgt tgatggatgt   2567

ctctggttag g ttt gtc ggg cta atg gga gga tac atg tgg ata gaa agt    2617
             Phe Val Gly Leu Met Gly Gly Tyr Met Trp Ile Glu Ser
                     560                 565                 570

gaa ggc cta gag aaa ggc tgc aca gct tcg ttc atc atc agg ctt ggt     2665
Glu Gly Leu Glu Lys Gly Cys Thr Ala Ser Phe Ile Ile Arg Leu Gly
                575                 580                 585

atc tgc aac ggt cca agc agt agc agt ggt tca atg gcg cta cat ctt     2713
Ile Cys Asn Gly Pro Ser Ser Ser Ser Gly Ser Met Ala Leu His Leu
            590                 595                 600

gca gct aaa tca caa acc aga ccg tgg aac tgg tga tacttacgtt          2759
Ala Ala Lys Ser Gln Thr Arg Pro Trp Asn Trp
        605                 610

ggaaagactt gtattgaggt gagacttttt aactacacag cagcaagaga aagaagaaaa   2819

tacatgaccg gacggtgtga tctaacttat tggattttgt tggatgtaat atgtaaaata   2879

aaaatcctat atacggggag aggtacctta tctgttctca ctatatttta ttgaacatta   2939

ctttagagaa tatgttttgg aattcactac taaataaacg atataaatct tcacgaaaag   2999

agcaacattt t                                                        3010


<210> SEQ ID NO 46
<211> LENGTH: 613
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 46

Met Glu Ser Cys Asp Cys Phe Glu Thr His Val Asn Gln Asp Asp Leu
  1               5                  10                  15

Leu Val Lys Tyr Gln Tyr Ile Ser Asp Ala Leu Ile Ala Leu Ala Tyr
            20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Gln Lys Ser Ala Phe
         35                  40                  45

Phe Pro Tyr Lys Trp Val Leu Met Gln Phe Gly Ala Phe Ile Ile Leu
     50                  55                  60

Cys Gly Ala Thr His Phe Ile Asn Leu Trp Met Phe Phe Met His Ser
 65                  70                  75                  80

Lys Ala Val Ala Ile Val Met Thr Ile Ala Lys Val Ser Cys Ala Val
                  85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

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

Leu Asp Arg Glu Met Gly Leu Ile Leu Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

His Val Arg Met Leu Thr His Gly Ile Arg Arg Thr Leu Asp Arg His
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145                 150                 155                 160

Thr Ile Leu Arg Thr Thr Leu Val Glu Leu Gly Lys Thr Leu Cys Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Ser Gln Ser Gly Leu Tyr Leu Gln
            180                 185                 190

Leu Ser His Thr Leu Ser His Lys Ile Gln Val Gly Ser Ser Val Pro
        195                 200                 205

Ile Asn Leu Pro Ile Ile Asn Glu Leu Phe Asn Ser Ala Gln Ala Met
    210                 215                 220

His Ile Pro His Ser Cys Pro Leu Ala Lys Ile Gly Pro Pro Val Gly
225                 230                 235                 240

Arg Tyr Ser Pro Pro Glu Val Val Ser Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Gly Ser Asp Trp Ser Asp Leu Ser Gly Lys Gly
            260                 265                 270

Tyr Ala Ile Met Val Leu Ile Leu Pro Thr Asp Gly Ala Arg Lys Trp
        275                 280                 285

Arg Asp His Glu Leu Glu Leu Val Glu Asn Val Ala Asp Gln Val Ala
    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met His Ala Arg
305                 310                 315                 320

Asp Gln Leu Met Glu Gln Asn Phe Ala Leu Asp Lys Ala Arg Gln Glu
                325                 330                 335

Ala Glu Met Ala Val His Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ser Leu Ser Ser Leu
        355                 360                 365

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

Ile Leu Lys Ser Ser Asn Leu Val Ala Thr Leu Ile Ser Asp Val Leu
385                 390                 395                 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Leu Leu Glu Asn Glu Pro
                405                 410                 415

Phe Ser Leu Gln Ala Ile Phe Glu Glu Val Ile Ser Leu Ile Lys Pro
            420                 425                 430

Ile Ala Ser Val Lys Lys Leu Ser Thr Asn Leu Ile Leu Ser Ala Asp
        435                 440                 445

Leu Pro Thr Tyr Ala Ile Gly Asp Glu Lys Arg Leu Met Gln Thr Ile
    450                 455                 460

Leu Asn Ile Met Gly Asn Ala Val Lys Phe Thr Lys Glu Gly Tyr Ile
465                 470                 475                 480

Ser Ile Ile Ala Ser Ile Met Lys Pro Glu Ser Leu Gln Glu Leu Pro
                485                 490                 495

Ser Pro Glu Phe Phe Pro Val Leu Ser Asp Ser His Phe Tyr Leu Cys
            500                 505                 510

Val Gln Val Lys Asp Thr Gly Cys Gly Ile His Thr Gln Asp Ile Pro
        515                 520                 525

Leu Leu Phe Thr Lys Phe Val Gln Pro Arg Thr Gly Thr Gln Arg Asn
    530                 535                 540

His Ser Gly Gly Gly Leu Gly Leu Ala Leu Cys Lys Arg Phe Val Gly
545                 550                 555                 560

Leu Met Gly Gly Tyr Met Trp Ile Glu Ser Glu Gly Leu Glu Lys Gly
                565                 570                 575
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Cys Thr Ala Ser Phe Ile Ile Arg Leu Gly Ile Cys Asn Gly Pro Ser
            580                 585                 590

Ser Ser Ser Gly Ser Met Ala Leu His Leu Ala Ala Lys Ser Gln Thr
        595                 600                 605

Arg Pro Trp Asn Trp
    610


<210> SEQ ID NO 47
<211> LENGTH: 2314
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (224)..(2065)

<400> SEQUENCE: 47

aaaaaaatca tcaaaaactt ttacctctca ttggtttctt ctttatcaca ctgttacgct      60

tggattctca tttcttcaag ttcataacgc tcggatcaat caggaagacg aacttgaact     120

ttcttttttt catcattacc caaagctatg aggctcacac caccaatacg tccgccgtca     180

tgaatccttc tcttccaggt caacacaagt cagagctcca aaa atg gag tca tgc       235
                                                Met Glu Ser Cys
                                                  1

gat tgt ttt gag acg cat gtg aat caa gat gat ctg tta gtg aag tac       283
Asp Cys Phe Glu Thr His Val Asn Gln Asp Asp Leu Leu Val Lys Tyr
  5                  10                  15                  20

caa tac atc tca gat gcg ttg att gct ctt gca tac ttc tca atc cca       331
Gln Tyr Ile Ser Asp Ala Leu Ile Ala Leu Ala Tyr Phe Ser Ile Pro
                 25                  30                  35

ctc gag ctt atc tat ttc gtg caa aag tct gct ttc ttc cct tac aaa       379
Leu Glu Leu Ile Tyr Phe Val Gln Lys Ser Ala Phe Phe Pro Tyr Lys
             40                  45                  50

tgg gtg ctt atg cag ttt gga gcc ttt atc att ctc tgt gga gct acg       427
Trp Val Leu Met Gln Phe Gly Ala Phe Ile Ile Leu Cys Gly Ala Thr
         55                  60                  65

cat ttc atc aac cta tgg atg ttc ttc atg cat tcc aaa gcc gtt gcc       475
His Phe Ile Asn Leu Trp Met Phe Phe Met His Ser Lys Ala Val Ala
     70                  75                  80

att gtc atg act att gct aaa gtc tct tgc gcg gtt gtg tcg tgt gct       523
Ile Val Met Thr Ile Ala Lys Val Ser Cys Ala Val Val Ser Cys Ala
 85                  90                  95                 100

acc gcg ttg atg ttg gtt cat att att cct gat ctt ctc agt gtt aag       571
Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val Lys
                105                 110                 115

aac agg gaa ttg ttt ctc aag aag aaa gct gat gag tta gat aga gaa       619
Asn Arg Glu Leu Phe Leu Lys Lys Lys Ala Asp Glu Leu Asp Arg Glu
            120                 125                 130

atg ggt ctt att tta aca caa gag gag act ggt agg cat gtt agg atg       667
Met Gly Leu Ile Leu Thr Gln Glu Glu Thr Gly Arg His Val Arg Met
        135                 140                 145

ctt act cat gga att aga aga act ctt gat agg cat act att tta aga       715
Leu Thr His Gly Ile Arg Arg Thr Leu Asp Arg His Thr Ile Leu Arg
    150                 155                 160

acc act ctt gtt gag ctt ggt aaa act ctt tgt ctt gag gaa tgt gcg       763
Thr Thr Leu Val Glu Leu Gly Lys Thr Leu Cys Leu Glu Glu Cys Ala
165                 170                 175                 180

ttg tgg atg cct tct caa agt ggt tta tat ttg cag ctt tct cat act       811
Leu Trp Met Pro Ser Gln Ser Gly Leu Tyr Leu Gln Leu Ser His Thr
                185                 190                 195
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ttg agt cat aaa ata caa gtt gga agc agt gtg ccg ata aat ctc ccg      859
Leu Ser His Lys Ile Gln Val Gly Ser Ser Val Pro Ile Asn Leu Pro
            200                 205                 210

att att aat gaa ctc ttc aat agc gct caa gct atg cac ata cct cat      907
Ile Ile Asn Glu Leu Phe Asn Ser Ala Gln Ala Met His Ile Pro His
        215                 220                 225

tct tgt cct ttg gct aag att ggg cct ccg gtt ggg aga tat tca cct      955
Ser Cys Pro Leu Ala Lys Ile Gly Pro Pro Val Gly Arg Tyr Ser Pro
    230                 235                 240

cct gag gtt gtt tct gtc cgt gtt cct ctt tta cat ctc tct aat ttc     1003
Pro Glu Val Val Ser Val Arg Val Pro Leu Leu His Leu Ser Asn Phe
245                 250                 255                 260

caa ggc agt gac tgg tcg gat ctc tct ggc aaa ggt tac gct atc atg     1051
Gln Gly Ser Asp Trp Ser Asp Leu Ser Gly Lys Gly Tyr Ala Ile Met
                265                 270                 275

gtc ctg att ctc cca acc gat ggt gca aga aaa tgg aga gac cat gag     1099
Val Leu Ile Leu Pro Thr Asp Gly Ala Arg Lys Trp Arg Asp His Glu
            280                 285                 290

tta gag ctt gta gaa aac gtg gcg gat cag gtg gct gtg gct ctc tca     1147
Leu Glu Leu Val Glu Asn Val Ala Asp Gln Val Ala Val Ala Leu Ser
        295                 300                 305

cat gct gca att ttg gaa gaa tcc atg cac gct cgt gac cag ctt atg     1195
His Ala Ala Ile Leu Glu Glu Ser Met His Ala Arg Asp Gln Leu Met
    310                 315                 320

gag cag aat ttt gct tta gac aag gct cgt caa gag gct gag atg gca     1243
Glu Gln Asn Phe Ala Leu Asp Lys Ala Arg Gln Glu Ala Glu Met Ala
325                 330                 335                 340

gta cat gct cga aat gat ttc cta gct gtt atg aac cac gag atg agg     1291
Val His Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu Met Arg
                345                 350                 355

aca ccg atg cat gcc atc atc tct ctt tct tct ctt ctc ctt gag act     1339
Thr Pro Met His Ala Ile Ile Ser Leu Ser Ser Leu Leu Leu Glu Thr
            360                 365                 370

gag ctg tct cca gag caa aga gtt atg atc gag aca ata ctg aaa agc     1387
Glu Leu Ser Pro Glu Gln Arg Val Met Ile Glu Thr Ile Leu Lys Ser
        375                 380                 385

agc aat ctt gtg gct aca cta atc agc gac gtt ctg gat ctt tcg aga     1435
Ser Asn Leu Val Ala Thr Leu Ile Ser Asp Val Leu Asp Leu Ser Arg
    390                 395                 400

ttg gaa gat ggg agc tta ctc ttg gaa aat gaa cca ttc agt cta caa     1483
Leu Glu Asp Gly Ser Leu Leu Leu Glu Asn Glu Pro Phe Ser Leu Gln
405                 410                 415                 420

gcg atc ttt gaa gag gtc atc tct ttg ata aag cca atc gca tca gtg     1531
Ala Ile Phe Glu Glu Val Ile Ser Leu Ile Lys Pro Ile Ala Ser Val
                425                 430                 435

aag aaa cta tca acg aat ctg att ctg tct gca gac tta cca act tat     1579
Lys Lys Leu Ser Thr Asn Leu Ile Leu Ser Ala Asp Leu Pro Thr Tyr
            440                 445                 450

gct att ggt gat gag aaa cgt ctg atg caa aca att ctt aac atc atg     1627
Ala Ile Gly Asp Glu Lys Arg Leu Met Gln Thr Ile Leu Asn Ile Met
        455                 460                 465

ggc aac gct gtg aaa ttt act aag gaa ggc tac atc tcc ata ata gcc     1675
Gly Asn Ala Val Lys Phe Thr Lys Glu Gly Tyr Ile Ser Ile Ile Ala
    470                 475                 480

tct atc atg aaa ccc gag tcc tta caa gaa tta cca tct cca gaa ttt     1723
Ser Ile Met Lys Pro Glu Ser Leu Gln Glu Leu Pro Ser Pro Glu Phe
485                 490                 495                 500

ttt cca gtt ctc agt gac agt cac ttc tac cta tgt gtg cag gtg aag     1771
Phe Pro Val Leu Ser Asp Ser His Phe Tyr Leu Cys Val Gln Val Lys
                505                 510                 515
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gac aca ggg tgt gga att cac aca caa gac att cct ttg ctc ttt acc     1819
Asp Thr Gly Cys Gly Ile His Thr Gln Asp Ile Pro Leu Leu Phe Thr
            520                 525                 530

aaa ttt gta cag cct cgg acc gga act cag agg aac cat tcc ggt gga     1867
Lys Phe Val Gln Pro Arg Thr Gly Thr Gln Arg Asn His Ser Gly Gly
        535                 540                 545

gga ctc ggg cta gct ctc tgt aaa cgg ttt gtc ggg cta atg gga gga     1915
Gly Leu Gly Leu Ala Leu Cys Lys Arg Phe Val Gly Leu Met Gly Gly
    550                 555                 560

tac atg tgg ata gaa agt gaa ggc cta gag aaa ggc tgc aca gct tcg     1963
Tyr Met Trp Ile Glu Ser Glu Gly Leu Glu Lys Gly Cys Thr Ala Ser
565                 570                 575                 580

ttc atc atc agg ctt ggt atc tgc aac ggt cca agc agt agc agt ggt     2011
Phe Ile Ile Arg Leu Gly Ile Cys Asn Gly Pro Ser Ser Ser Ser Gly
                585                 590                 595

tca atg gcg cta cat ctt gca gct aaa tca caa acc aga ccg tgg aac     2059
Ser Met Ala Leu His Leu Ala Ala Lys Ser Gln Thr Arg Pro Trp Asn
            600                 605                 610

tgg tga tacttacgtt ggaaagactt gtattgaggt gagacttttt aactacacag      2115
Trp

cagcaagaga aagaagaaaa tacatgaccg gacggtgtga tctaacttat tggattttgt   2175

tggatgtaat atgtaaaata aaaatcctat atacggggag aggtacctta tctgttctca   2235

ctatatttta ttgaacatta ctttagagaa tatgttttgg aattcactac taaataaacg   2295

atataaatct tcacgaaaa                                                2314


<210> SEQ ID NO 48
<211> LENGTH: 613
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 48

Met Glu Ser Cys Asp Cys Phe Glu Thr His Val Asn Gln Asp Asp Leu
  1               5                  10                  15

Leu Val Lys Tyr Gln Tyr Ile Ser Asp Ala Leu Ile Ala Leu Ala Tyr
             20                  25                  30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Gln Lys Ser Ala Phe
         35                  40                  45

Phe Pro Tyr Lys Trp Val Leu Met Gln Phe Gly Ala Phe Ile Ile Leu
     50                  55                  60

Cys Gly Ala Thr His Phe Ile Asn Leu Trp Met Phe Phe Met His Ser
 65                  70                  75                  80

Lys Ala Val Ala Ile Val Met Thr Ile Ala Lys Val Ser Cys Ala Val
                 85                  90                  95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

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

Leu Asp Arg Glu Met Gly Leu Ile Leu Thr Gln Glu Glu Thr Gly Arg
    130                 135                 140

His Val Arg Met Leu Thr His Gly Ile Arg Arg Thr Leu Asp Arg His
145                 150                 155                 160

Thr Ile Leu Arg Thr Thr Leu Val Glu Leu Gly Lys Thr Leu Cys Leu
                165                 170                 175

Glu Glu Cys Ala Leu Trp Met Pro Ser Gln Ser Gly Leu Tyr Leu Gln
            180                 185                 190
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Leu Ser His Thr Leu Ser His Lys Ile Gln Val Gly Ser Ser Val Pro
        195                 200                 205

Ile Asn Leu Pro Ile Ile Asn Glu Leu Phe Asn Ser Ala Gln Ala Met
    210                 215                 220

His Ile Pro His Ser Cys Pro Leu Ala Lys Ile Gly Pro Pro Val Gly
225                 230                 235                 240

Arg Tyr Ser Pro Pro Glu Val Val Ser Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Gln Gly Ser Asp Trp Ser Asp Leu Ser Gly Lys Gly
            260                 265                 270

Tyr Ala Ile Met Val Leu Ile Leu Pro Thr Asp Gly Ala Arg Lys Trp
        275                 280                 285

Arg Asp His Glu Leu Glu Leu Val Glu Asn Val Ala Asp Gln Val Ala
    290                 295                 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met His Ala Arg
305                 310                 315                 320

Asp Gln Leu Met Glu Gln Asn Phe Ala Leu Asp Lys Ala Arg Gln Glu
                325                 330                 335

Ala Glu Met Ala Val His Ala Arg Asn Asp Phe Leu Ala Val Met Asn
            340                 345                 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ser Leu Ser Ser Leu
        355                 360                 365

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

Ile Leu Lys Ser Ser Asn Leu Val Ala Thr Leu Ile Ser Asp Val Leu
385                 390                 395                 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Leu Leu Glu Asn Glu Pro
                405                 410                 415

Phe Ser Leu Gln Ala Ile Phe Glu Glu Val Ile Ser Leu Ile Lys Pro
            420                 425                 430

Ile Ala Ser Val Lys Lys Leu Ser Thr Asn Leu Ile Leu Ser Ala Asp
        435                 440                 445

Leu Pro Thr Tyr Ala Ile Gly Asp Glu Lys Arg Leu Met Gln Thr Ile
    450                 455                 460

Leu Asn Ile Met Gly Asn Ala Val Lys Phe Thr Lys Glu Gly Tyr Ile
465                 470                 475                 480

Ser Ile Ile Ala Ser Ile Met Lys Pro Glu Ser Leu Gln Glu Leu Pro
                485                 490                 495

Ser Pro Glu Phe Phe Pro Val Leu Ser Asp Ser His Phe Tyr Leu Cys
            500                 505                 510

Val Gln Val Lys Asp Thr Gly Cys Gly Ile His Thr Gln Asp Ile Pro
        515                 520                 525

Leu Leu Phe Thr Lys Phe Val Gln Pro Arg Thr Gly Thr Gln Arg Asn
    530                 535                 540

His Ser Gly Gly Gly Leu Gly Leu Ala Leu Cys Lys Arg Phe Val Gly
545                 550                 555                 560

Leu Met Gly Gly Tyr Met Trp Ile Glu Ser Glu Gly Leu Glu Lys Gly
                565                 570                 575

Cys Thr Ala Ser Phe Ile Ile Arg Leu Gly Ile Cys Asn Gly Pro Ser
            580                 585                 590

Ser Ser Ser Gly Ser Met Ala Leu His Leu Ala Ala Lys Ser Gln Thr
        595                 600                 605
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Arg Pro Trp Asn Trp
    610


<210> SEQ ID NO 49
<211> LENGTH: 2405
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (288)..(2195)

<400> SEQUENCE: 49

ttttttttt gtcaaaagct cgatgtaaaa atccgatggc cacaagcaaa acgacaggtt      60

ccaacttcac ggagattgtg aaaatggagt agtagttcag tgaagtagta gatactgaga    120

tcgcattctc cggcgtcgtt tttcacatcg aaatagtcgt gtaaaaaaat gaaaaaattg    180

ctgcgagaca ggtatgtgtc gcagcaggaa atagcatctt aaaggaagga aggaaggaaa    240

ctcgaaagtt actaaaaatt tttgattctt tgggacgaaa cgagata atg gaa tcc      296
                                                    Met Glu Ser
                                                      1

tgt gat tgc att gag gct tta ctg cca act ggt gac ctg ctg gtt aaa      344
Cys Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu Leu Val Lys
      5                  10                  15

tac caa tac ctc tca gat ttc ttc att gct gta gcc tac ttt tcc att      392
Tyr Gln Tyr Leu Ser Asp Phe Phe Ile Ala Val Ala Tyr Phe Ser Ile
 20                  25                  30                  35

ctg ttg gag ctt att tat ttt gtc cac aaa tct gca tgc ttc cca tac      440
Leu Leu Glu Leu Ile Tyr Phe Val His Lys Ser Ala Cys Phe Pro Tyr
                 40                  45                  50

aga tgg gtc ctc atg caa ttt ggt gct ttt att gtg ctc tgt gga gca      488
Arg Trp Val Leu Met Gln Phe Gly Ala Phe Ile Val Leu Cys Gly Ala
             55                  60                  65

aca cac ttt att agc ttg tgg acc ttc ttt atg cac tct aag acg gtc      536
Thr His Phe Ile Ser Leu Trp Thr Phe Phe Met His Ser Lys Thr Val
         70                  75                  80

gct gtg gtt atg acc ata tca aaa atg ttg aca gct gcc gtg tcc tgt      584
Ala Val Val Met Thr Ile Ser Lys Met Leu Thr Ala Ala Val Ser Cys
     85                  90                  95

atc aca gct ttg atg ctt gtt cac att att cct gat ttg cta agt gtt      632
Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu Leu Ser Val
100                 105                 110                 115

aaa acg cga gag ttg ttc ttg aaa act cga gct gaa gag ctt gac aag      680
Lys Thr Arg Glu Leu Phe Leu Lys Thr Arg Ala Glu Glu Leu Asp Lys
                120                 125                 130

gaa atg ggc cta ata ata aga caa gaa gaa act ggc aga cat gtc agg      728
Glu Met Gly Leu Ile Ile Arg Gln Glu Glu Thr Gly Arg His Val Arg
            135                 140                 145

atg ctg act cat gag ata aga agc aca ctc gac aga cac aca atc ttg      776
Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His Thr Ile Leu
        150                 155                 160

aag act act ctt gtg gag cta ggt agg acc tta gac ctg gca gaa tgt      824
Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Asp Leu Ala Glu Cys
    165                 170                 175

gct ttg tgg atg cca tgc caa gga ggc ctg act ttg caa ctt tcc cat      872
Ala Leu Trp Met Pro Cys Gln Gly Gly Leu Thr Leu Gln Leu Ser His
180                 185                 190                 195

aat tta aac aat cta ata cct ctg gga tct act gtg cca att aat ctt      920
Asn Leu Asn Asn Leu Ile Pro Leu Gly Ser Thr Val Pro Ile Asn Leu
                200                 205                 210

cct att atc aat gaa att ttt agt agc cct gaa gca ata caa att cca      968
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Pro Ile Ile Asn Glu Ile Phe Ser Ser Pro Glu Ala Ile Gln Ile Pro
            215                 220                 225

cat aca aat cct ttg gca agg atg agg aat act gtt ggt aga tat att     1016
His Thr Asn Pro Leu Ala Arg Met Arg Asn Thr Val Gly Arg Tyr Ile
        230                 235                 240

cca cca gaa gta gtt gct gtt cgt gta ccg ctt tta cac ctc tca aat     1064
Pro Pro Glu Val Val Ala Val Arg Val Pro Leu Leu His Leu Ser Asn
    245                 250                 255

ttt act aat gac tgg gct gaa ctg tct act aga agt tat gcg gtt atg     1112
Phe Thr Asn Asp Trp Ala Glu Leu Ser Thr Arg Ser Tyr Ala Val Met
260                 265                 270                 275

gtt ctg gtt ctc ccg atg aat ggc tta aga aag tgg cgt gaa cat gag     1160
Val Leu Val Leu Pro Met Asn Gly Leu Arg Lys Trp Arg Glu His Glu
                280                 285                 290

tta gaa ctt gtg caa gtt gtc gca gat cag gtt gct gtc gct ctt tca     1208
Leu Glu Leu Val Gln Val Val Ala Asp Gln Val Ala Val Ala Leu Ser
            295                 300                 305

cat gct gca att tta gaa gat tcc atg cga gcc cat gat cag ctc atg     1256
His Ala Ala Ile Leu Glu Asp Ser Met Arg Ala His Asp Gln Leu Met
        310                 315                 320

gaa cag aat att gct ttg gat gta gct cga caa gaa gca gag atg gcc     1304
Glu Gln Asn Ile Ala Leu Asp Val Ala Arg Gln Glu Ala Glu Met Ala
    325                 330                 335

atc cgt gca cgt aac gac ttc ctt gct gtg atg aac cat gaa atg aga     1352
Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His Glu Met Arg
340                 345                 350                 355

acg ccc atg cat gca gtt att gct ctg tgc tct ctg ctt tta gaa aca     1400
Thr Pro Met His Ala Val Ile Ala Leu Cys Ser Leu Leu Leu Glu Thr
                360                 365                 370

gac tta act cca gag cag aga gtt atg att gag acc ata ttg aag agc     1448
Asp Leu Thr Pro Glu Gln Arg Val Met Ile Glu Thr Ile Leu Lys Ser
            375                 380                 385

agc aat ctt ctt gca aca ctg ata aat gat gtt cta gat ctt tct aga     1496
Ser Asn Leu Leu Ala Thr Leu Ile Asn Asp Val Leu Asp Leu Ser Arg
        390                 395                 400

ctt gaa gat ggt att ctt gaa cta gaa aac gga aca ttc aat ctt cat     1544
Leu Glu Asp Gly Ile Leu Glu Leu Glu Asn Gly Thr Phe Asn Leu His
    405                 410                 415

ggc atc tta aga gag gcc gtt aat ttg ata aag cca att gca tct ttg     1592
Gly Ile Leu Arg Glu Ala Val Asn Leu Ile Lys Pro Ile Ala Ser Leu
420                 425                 430                 435

aag aaa tta tct ata act ctt gct ttg gct ctg gat tta cct att ctt     1640
Lys Lys Leu Ser Ile Thr Leu Ala Leu Ala Leu Asp Leu Pro Ile Leu
                440                 445                 450

gct gtg ggt gat gca aaa cgt ctt atc caa act ctc tta aac gtg gtg     1688
Ala Val Gly Asp Ala Lys Arg Leu Ile Gln Thr Leu Leu Asn Val Val
            455                 460                 465

gga aat gct gtg aag ttc act aaa gaa gga cat att tca att gag gct     1736
Gly Asn Ala Val Lys Phe Thr Lys Glu Gly His Ile Ser Ile Glu Ala
        470                 475                 480

tca gtt gcc aaa cca gag tat gcg aga gat tgt cat cct cct gaa atg     1784
Ser Val Ala Lys Pro Glu Tyr Ala Arg Asp Cys His Pro Pro Glu Met
    485                 490                 495

ttc cct atg cca agt gat ggc cag ttt tat ttg cgt gtc cag gtt aga     1832
Phe Pro Met Pro Ser Asp Gly Gln Phe Tyr Leu Arg Val Gln Val Arg
500                 505                 510                 515

gat act ggg tgt gga att agc cca caa gat ata cca cta gta ttc acc     1880
Asp Thr Gly Cys Gly Ile Ser Pro Gln Asp Ile Pro Leu Val Phe Thr
                520                 525                 530
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aaa ttt gca gag tca cgg cct acg tca aat cga agt act gga ggg gaa     1928
Lys Phe Ala Glu Ser Arg Pro Thr Ser Asn Arg Ser Thr Gly Gly Glu
            535                 540                 545

ggt cta ggg ctt gcc att tgg aga cga ttt att caa ctt atg aaa ggt     1976
Gly Leu Gly Leu Ala Ile Trp Arg Arg Phe Ile Gln Leu Met Lys Gly
        550                 555                 560

aac att tgg att gag agt gag ggc cct gga aag gga acc act gtc acg     2024
Asn Ile Trp Ile Glu Ser Glu Gly Pro Gly Lys Gly Thr Thr Val Thr
    565                 570                 575

ttt gta gtg aaa ctc gga atc tgt cac cat cca aat gca tta cct ctg     2072
Phe Val Val Lys Leu Gly Ile Cys His His Pro Asn Ala Leu Pro Leu
580                 585                 590                 595

cta cct atg cct ccc aga ggc aga ttg aac aaa ggt agc gat gat ctc     2120
Leu Pro Met Pro Pro Arg Gly Arg Leu Asn Lys Gly Ser Asp Asp Leu
                600                 605                 610

ttc agg tat aga cag ttc cgt gga gat gat ggt ggg atg tct gtg aat     2168
Phe Arg Tyr Arg Gln Phe Arg Gly Asp Asp Gly Gly Met Ser Val Asn
            615                 620                 625

gct caa cgc tat caa aga agt atg taa atgacaaaag gacattggtg           2215
Ala Gln Arg Tyr Gln Arg Ser Met
        630                 635

tgacaaagaa cattaaatca tgactagtga atttgagatt tcttcactgt tctgtacact   2275

ccaaatggca cagtttgtct tgtaactaac ctaattcaat gctcgtaaag tgagtactgg   2335

agtatcttga aaatgtaact atcgaattta tacatcgagc ttttgacaaa aaaaaaaaaa   2395

aaaaaaaaaa                                                          2405


<210> SEQ ID NO 50
<211> LENGTH: 635
<212> TYPE: PRT
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 50

Met Glu Ser Cys Asp Cys Ile Glu Ala Leu Leu Pro Thr Gly Asp Leu
  1               5                   10                  15

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

Phe Ser Ile Leu Leu Glu Leu Ile Tyr Phe Val His Lys Ser Ala Cys
         35                  40                  45

Phe Pro Tyr Arg Trp Val Leu Met Gln Phe Gly Ala Phe Ile Val Leu
     50                  55                  60

Cys Gly Ala Thr His Phe Ile Ser Leu Trp Thr Phe Phe Met His Ser
 65                  70                  75                  80

Lys Thr Val Ala Val Val Met Thr Ile Ser Lys Met Leu Thr Ala Ala
                 85                  90                  95

Val Ser Cys Ile Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
            100                 105                 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Thr Arg Ala Glu Glu
        115                 120                 125

Leu Asp Lys Glu Met Gly Leu Ile Ile Arg Gln Glu Glu Thr Gly Arg
    130                 135                 140

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

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Asp Leu
                165                 170                 175

Ala Glu Cys Ala Leu Trp Met Pro Cys Gln Gly Gly Leu Thr Leu Gln
            180                 185                 190
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Leu Ser His Asn Leu Asn Asn Leu Ile Pro Leu Gly Ser Thr Val Pro
        195                 200                 205

Ile Asn Leu Pro Ile Ile Asn Glu Ile Phe Ser Ser Pro Glu Ala Ile
    210                 215                 220

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

Arg Tyr Ile Pro Pro Glu Val Val Ala Val Arg Val Pro Leu Leu His
                245                 250                 255

Leu Ser Asn Phe Thr Asn Asp Trp Ala Glu Leu Ser Thr Arg Ser Tyr
            260                 265                 270

Ala Val Met Val Leu Val Leu Pro Met Asn Gly Leu Arg Lys Trp Arg
        275                 280                 285

Glu His Glu Leu Glu Leu Val Gln Val Val Ala Asp Gln Val Ala Val
    290                 295                 300

Ala Leu Ser His Ala Ala Ile Leu Glu Asp Ser Met Arg Ala His Asp
305                 310                 315                 320

Gln Leu Met Glu Gln Asn Ile Ala Leu Asp Val Ala Arg Gln Glu Ala
                325                 330                 335

Glu Met Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His
            340                 345                 350

Glu Met Arg Thr Pro Met His Ala Val Ile Ala Leu Cys Ser Leu Leu
        355                 360                 365

Leu Glu Thr Asp Leu Thr Pro Glu Gln Arg Val Met Ile Glu Thr Ile
    370                 375                 380

Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Ile Asn Asp Val Leu Asp
385                 390                 395                 400

Leu Ser Arg Leu Glu Asp Gly Ile Leu Glu Leu Glu Asn Gly Thr Phe
                405                 410                 415

Asn Leu His Gly Ile Leu Arg Glu Ala Val Asn Leu Ile Lys Pro Ile
            420                 425                 430

Ala Ser Leu Lys Lys Leu Ser Ile Thr Leu Ala Leu Ala Leu Asp Leu
        435                 440                 445

Pro Ile Leu Ala Val Gly Asp Ala Lys Arg Leu Ile Gln Thr Leu Leu
    450                 455                 460

Asn Val Val Gly Asn Ala Val Lys Phe Thr Lys Glu Gly His Ile Ser
465                 470                 475                 480

Ile Glu Ala Ser Val Ala Lys Pro Glu Tyr Ala Arg Asp Cys His Pro
                485                 490                 495

Pro Glu Met Phe Pro Met Pro Ser Asp Gly Gln Phe Tyr Leu Arg Val
            500                 505                 510

Gln Val Arg Asp Thr Gly Cys Gly Ile Ser Pro Gln Asp Ile Pro Leu
        515                 520                 525

Val Phe Thr Lys Phe Ala Glu Ser Arg Pro Thr Ser Asn Arg Ser Thr
    530                 535                 540

Gly Gly Glu Gly Leu Gly Leu Ala Ile Trp Arg Arg Phe Ile Gln Leu
545                 550                 555                 560

Met Lys Gly Asn Ile Trp Ile Glu Ser Glu Gly Pro Gly Lys Gly Thr
                565                 570                 575

Thr Val Thr Phe Val Val Lys Leu Gly Ile Cys His His Pro Asn Ala
            580                 585                 590

Leu Pro Leu Leu Pro Met Pro Pro Arg Gly Arg Leu Asn Lys Gly Ser
        595                 600                 605
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Asp Asp Leu Phe Arg Tyr Arg Gln Phe Arg Gly Asp Asp Gly Gly Met
    610                 615                 620

Ser Val Asn Ala Gln Arg Tyr Gln Arg Ser Met
625                 630                 635


<210> SEQ ID NO 51
<211> LENGTH: 10
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 51

ataataataa                                                            10


<210> SEQ ID NO 52
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic.

<400> SEQUENCE: 52

ggagcctttt tcattattat c                                               21


<210> SEQ ID NO 53
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 53

cccggatcca tagtgtaaaa aattcataat gg                                   32


<210> SEQ ID NO 54
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 54

ccggatccgt tgaagacttc catcttctaa cc                                   32


<210> SEQ ID NO 55
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 55

ccggatccat ggaatcctgt gattgcattg                                      30


<210> SEQ ID NO 56
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Lycopersicon esculentum

<400> SEQUENCE: 56

gataatagga agattaattg gc                                              22
```

What is claimed is:

1. An isolated nucleic acid comprising a plant ETR nucleic acid encoding an ETR protein, said ETR protein having at least 50% overall similarity to the ETR protein sequence of *Arabidopsis thaliana* as set forth in SEQ ID NO:3, and at least 55% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana*, wherein the expression of said ETR protein encoded by said ETR nucleic acid in a plant cell results in an increased or decreased response to ethylene by said cell.

2. The isolated nucleic acid of claim **1** wherein said ETR protein has at least 70% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana.*

3. The isolated nucleic acid of claim **2** wherein said ETR protein has at least 85% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana.*

4. An isolated nucleic acid comprising a plant ETR nucleic acid encoding an ETR protein, said ETR protein having at least 50% overall similarity to the ETR protein sequence of *Arabidopsis thaliana* as set forth in SEQ ID NO:3, and at least 55% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana*, wherein the expression of said ETR protein encoded by said ETR nucleic acid in a plant cell results in an increased response to ethylene by said cell.

5. An isolated modified plant ETR nucleic acid comprising a precursor ETR nucleic acid which has been modified to encode a modified ETR protein comprising the substitution, insertion or deletion of an amino acid residue in the N-terminal 316 amino acids of the ETR protein encoded by said precursor ETR nucleic acid, wherein said modified ETR protein has at least 50% overall similarity to the ETR protein sequence of *Arabidopsis thaliana* as set forth in SEQ ID NO:3, and at least 55% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana*, wherein the expression of said modified ETR protein encoded by said isolated modified plant ETR nucleic acid in a plant cell results in an increased or decreased response to ethylene by said cell.

6. The isolated modified plant ETR nucleic acid according to claim **5** wherein said modified ETR protein comprises the substitution of a selected amino acid residue in said precursor ETR protein with a different amino acid and wherein said selected amino acid residue in said precursor ETR protein is equivalent to an amino acid residue selected from the group consisting of Ala-31, Pro-36, Ile-62, Cys-65 and Ala-102 in the ETR protein sequence of *Arabidopsis thaliana.*

7. The isolated modified plant ETR nucleic acid of claim **5** wherein said ETR protein has at least 70% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana.*

8. The isolated modified plant ETR nucleic acid of claim **5** wherein said ETR protein has at least 85% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana.*

9. An isolated modified plant ETR nucleic acid comprising a precursor ETR nucleic acid which has been modified to encode a modified ETR protein comprising the substitution or deletion of an amino acid residue in the N-terminal 316 amino acids of the ETR protein encoded by said precursor ETR nucleic acid, wherein said modified ETR protein has at least 50% overall similarity to the ETR protein sequence of *Arabidopsis thaliana* as set forth in SEQ ID NO:3, and at least 55% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana*, wherein the expression of said modified ETR protein encoded by said isolated modified plant ETR nucleic acid in a plant cell results in a decreased response to ethylene by said cell.

10. The isolated modified plant ETR nucleic acid of claim **9** wherein the modified ETR protein has a single amino acid substitution in the N-terminal 316 amino acids.

11. The isolated modified plant ETR nucleic acid of claim **9** wherein the modified ETR protein has a single amino acid deletion in the N-terminal 316 amino acids.

12. A recombinant nucleic acid comprising a promoter operably linked to the modified plant ETR nucleic acid of claim **5**.

13. The recombinant nucleic acid according to claim **12** wherein said promoter is heterologous to said modified plant ETR nucleic acid and causes expression of said modified plant ETR nucleic acid in a plant cell.

14. The recombinant nucleic acid according to claim **13** wherein said promoter is a tissue-specific promoter or temporal-specific promoter.

15. The recombinant nucleic acid according to claim **13** wherein said promoter is inducible.

16. A recombinant nucleic acid comprising a promoter operably linked to an ETR nucleic acid, wherein said ETR nucleic acid hybridizes with a probe having the sequence represented in SEQ ID NO:2 at hybridization conditions of 50° C. in 5×SSPE and washing conditions of 50° C. in 0.2×SSPE, wherein the expression of an ETR protein encoded by said ETR nucleic acid in a plant cell results in an increased or decreased response to ethylene by said cell.

17. A method of producing a plant comprising transformed plant cells having a detectable increased or decreased response to ethylene as compared to untransformed cells of a corresponding wild-type plant, said method comprising the steps of:

a) transforming at least one plant cell with a modified ETR nucleic acid comprising a precursor ETR nucleic acid which has been modified to encode a modified ETR protein comprising the substitution, insertion or deletion of an amino acid residue in the N-terminal 316 amino acids of the ETR protein encoded by said precursor ETR nucleic acid, wherein said modified ETR protein has at least about 50% overall similarity to the ETR protein sequence of *Arabidopsis thaliana* as set forth in SEQ ID NO:3, and at least about 55% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana;*

b) regenerating plants from one or more of the thus transformed plant cells; and

c) selecting a plant comprising said transformed plant cells having a detectable increased or decreased response to ethylene.

18. The method according to claim **17** wherein said modified ETR nucleic acid is operably linked to a tissue-specific promoter.

19. A method of producing a plant comprising transformed plant cells having a detectable decrease in response to ethylene as compared to untransformed cells of a corresponding wild-type plant, said method comprising the steps of:

a) transforming at least one plant cell with a modified ETR nucleic acid comprising a precursor ETR nucleic acid which has been modified to encode a modified ETR protein comprising a substitution, insertion or deletion of an amino acid residue in the N-terminal 316 amino acids of the ETR protein encoded by said precursor ETR nucleic acid, wherein said modified ETR protein has at least about 50% overall similarity to the ETR protein sequence of *Arabidopsis thaliana* as set forth in SEQ ID NO:3, and at least about 55% similarity to the N-terminal 316 amino acids of said ETR protein sequence of *Arabidopsis thaliana;*

b) regenerating plants from one or more of the thus transformed plant cells; and

c) selecting a plant comprising said transformed plant cells having a detectable decrease in response to ethylene.

20. The method of claim **19** wherein the modified ETR protein has a single amino acid substitution in the N-terminal 316 amino acids.

21. The method of claim **19** wherein the modified ETR protein has a single amino acid deletion in the N-terminal 316 amino acids.

22. A plant cell transformed with the recombinant nucleic acid of claim **13**.

23. A plant comprising the plant cell of claim **22**.

24. A plant comprising plant cells transformed with the isolated modified plant ETR nucleic acid of claim **5** wherein said plant cells have an increased or decreased response to ethylene as compared to untransformed cells of a corresponding wild-type plant.

25. The plant according to claim **23** wherein said modified ETR protein comprises the substitution of a selected amino acid residue with a different amino acid, wherein said selected amino acid residue is equivalent to an amino acid residue selected from the group consisting of Ala-31, Pro-36, Ile-62, Cys-65 and Ala-102 in the ETR protein sequence of *Arabidopsis thaliana.*

26. The plant according to claim **24** wherein a tissue-specific promoter is operably linked to said modified ETR nucleic acid.

27. The plant according to claim **26** wherein said plant is fruit-bearing and said tissue specific promoter is a fruit-specific promoter.

28. The plant according to claim **27** wherein said plant has a decrease in the rate of fruit ripening.

29. Fruit from the plant according to claim **28**.

30. The fruit according to claim **29** wherein said fruit is tomato.

31. A plant produced by the method of claim **17**.

32. A plant comprising plant cells transformed with the isolated modified plant ETR nucleic acid of claim **9**, said plant cells having a detectable decrease in response to ethylene as compared too untransformed cells of a corresponding wild-type plant.

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