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(54) **MANIPULATION OF AMMONIUM TRANSPORTERS (AMTS) TO IMPROVE NITROGEN USE EFFICIENCY IN HIGHER PLANTS**

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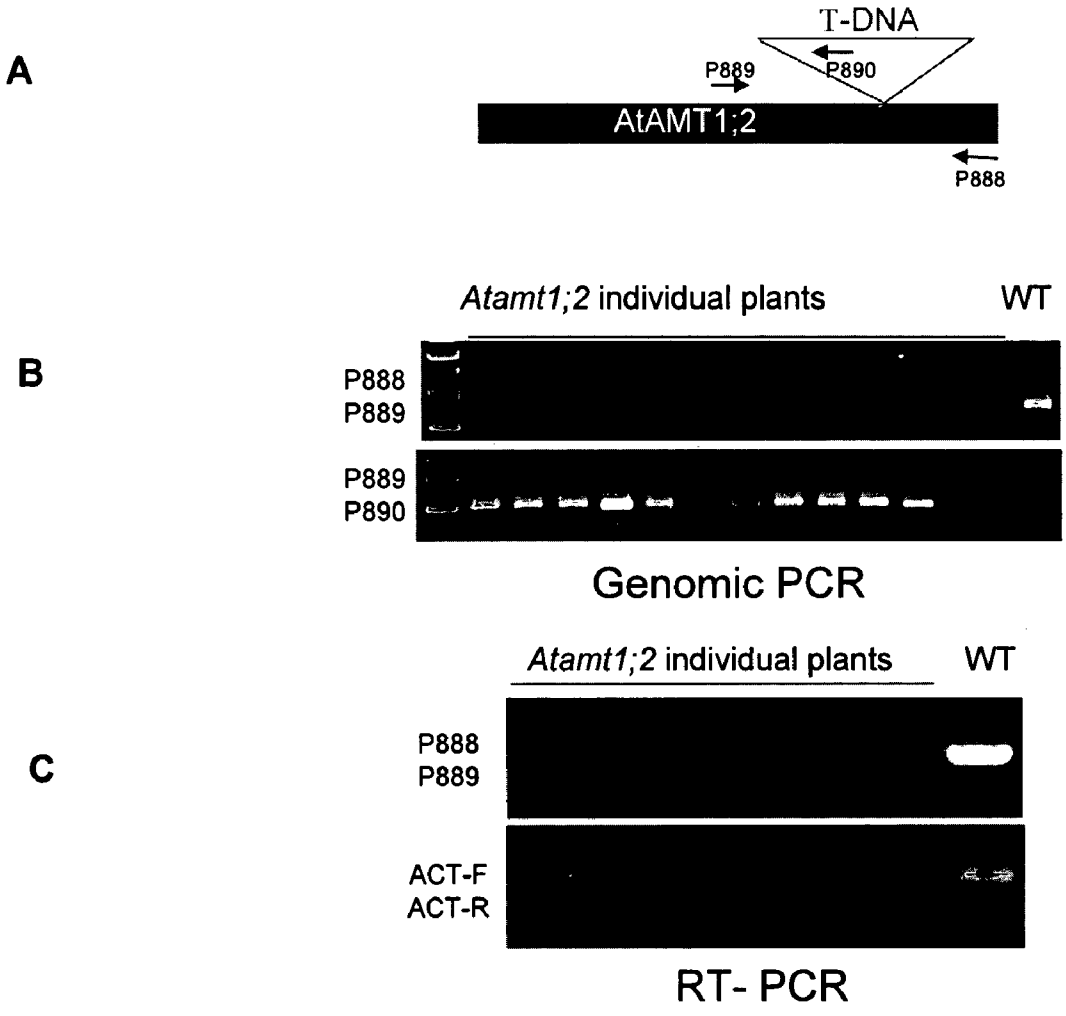
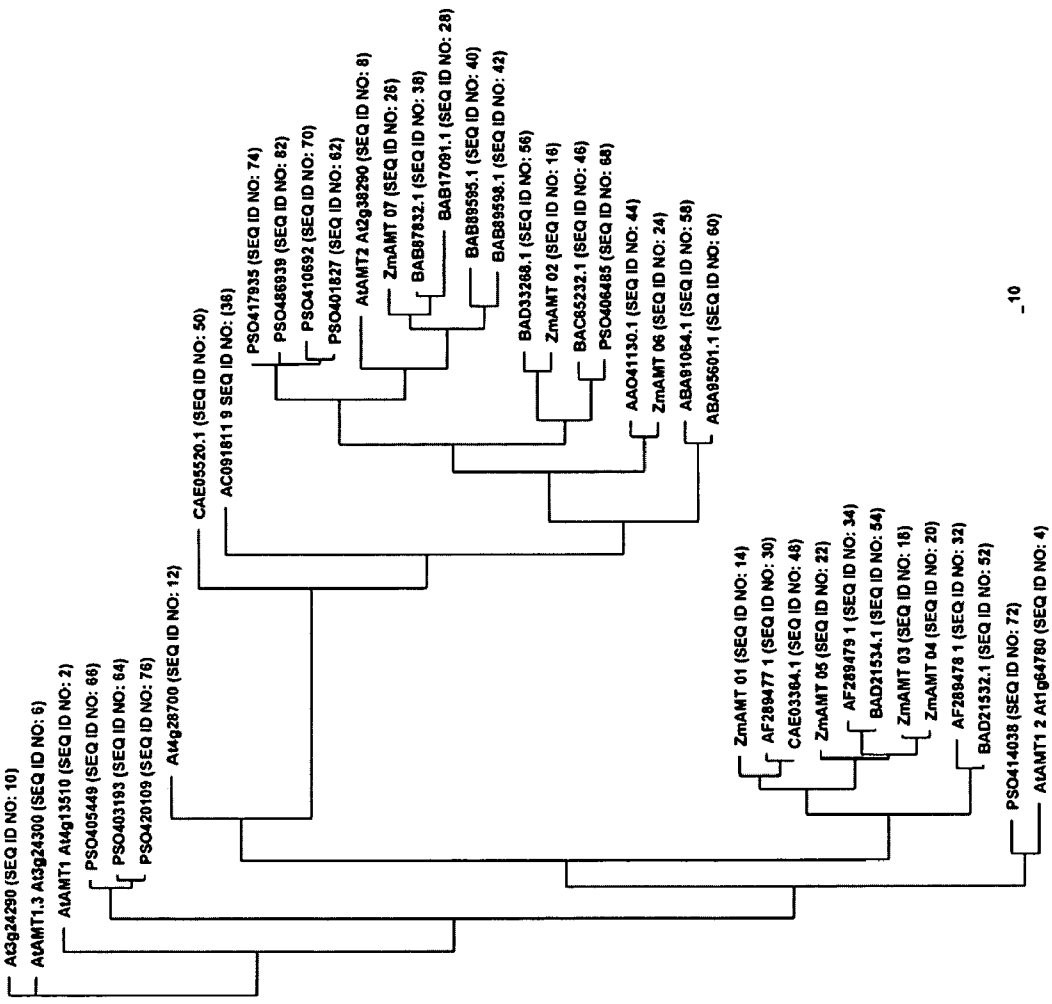
(57) **ABSTRACT**

The present invention provides polynucleotides and related polypeptides of the protein AMT. The invention provides genomic sequence for the AMT gene. AMT is responsible for controlling nitrogen utilization efficiency in plants.

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PSO420109 (SEQ ID NO: 76)
At4g28700 (SEQ ID NO: 12)
CAE05520.1 (SEQ ID NO: 50)
AC091811 9 SEQ ID NO: (36)
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PSO486939 (SEQ ID NO: 82)
PSO410692 (SEQ ID NO: 70)
PSO401827 (SEQ ID NO: 62)
AtAMT2 At2g38290 (SEQ ID NO: 8)
ZmAMT 07 (SEQ ID NO: 26)
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BAB17091.1 (SEQ ID NO: 28)
BAB89595.1 (SEQ ID NO: 40)
BAB89598.1 (SEQ ID NO: 42)
BAD33268.1 (SEQ ID NO: 56)
ZmAMT 02 (SEQ ID NO: 16)
BAC85232.1 (SEQ ID NO: 46)
PSO406485 (SEQ ID NO: 68)
AAO41130.1 (SEQ ID NO: 44)
ZmAMT 06 (SEQ ID NO: 24)
ABA91064.1 (SEQ ID NO: 58)
ABA95601.1 (SEQ ID NO: 60)
ZmAMT 01 (SEQ ID NO: 14)
AF289477 1 (SEQ ID NO: 30)
CAE03364.1 (SEQ ID NO: 48)
ZmAMT 05 (SEQ ID NO: 22)
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BAD21534.1 (SEQ ID NO: 54)
ZmAMT 03 (SEQ ID NO: 18)
ZmAMT 04 (SEQ ID NO: 20)
AF289478 1 (SEQ ID NO: 32)
BAD21532.1 (SEQ ID NO: 52)
PSO414038 (SEQ ID NO: 72)
AtAMT1 2 At1g64780 (SEQ ID NO: 4)
_10

Figure 1

Seq id	Root	Mesocotyl/Coleoptile	Leaf	Stalk	Apical Meristem	Immature Ear	Ovary/R1 Kernel	Embryo	Endosperm	Pericarp	Silk	Tassel Spikelet	Pollen
ZmAMT_01_ins	55.8	0	3892	14.6	0	0.9	0	0	0	0	33	40.5	0
ZmAMT_02_ins	10.6	0	17.6	0.8	0	0	0	0	0	0	0	0.2	0
ZmAMT_04_ins	55.1	0	0.7	0	0	0	0	0	0	0	0	0	0
ZmAMT_05_ins													
ZmAMT_06_ins	0.3	0	0.4	2.4	0	0	0	0	0	3.7	0	0	0
ZmAMT_07_ins	70	0	11.2	15.7	0	0.8	0	0	0	0	84	42.5	0

Figure 2

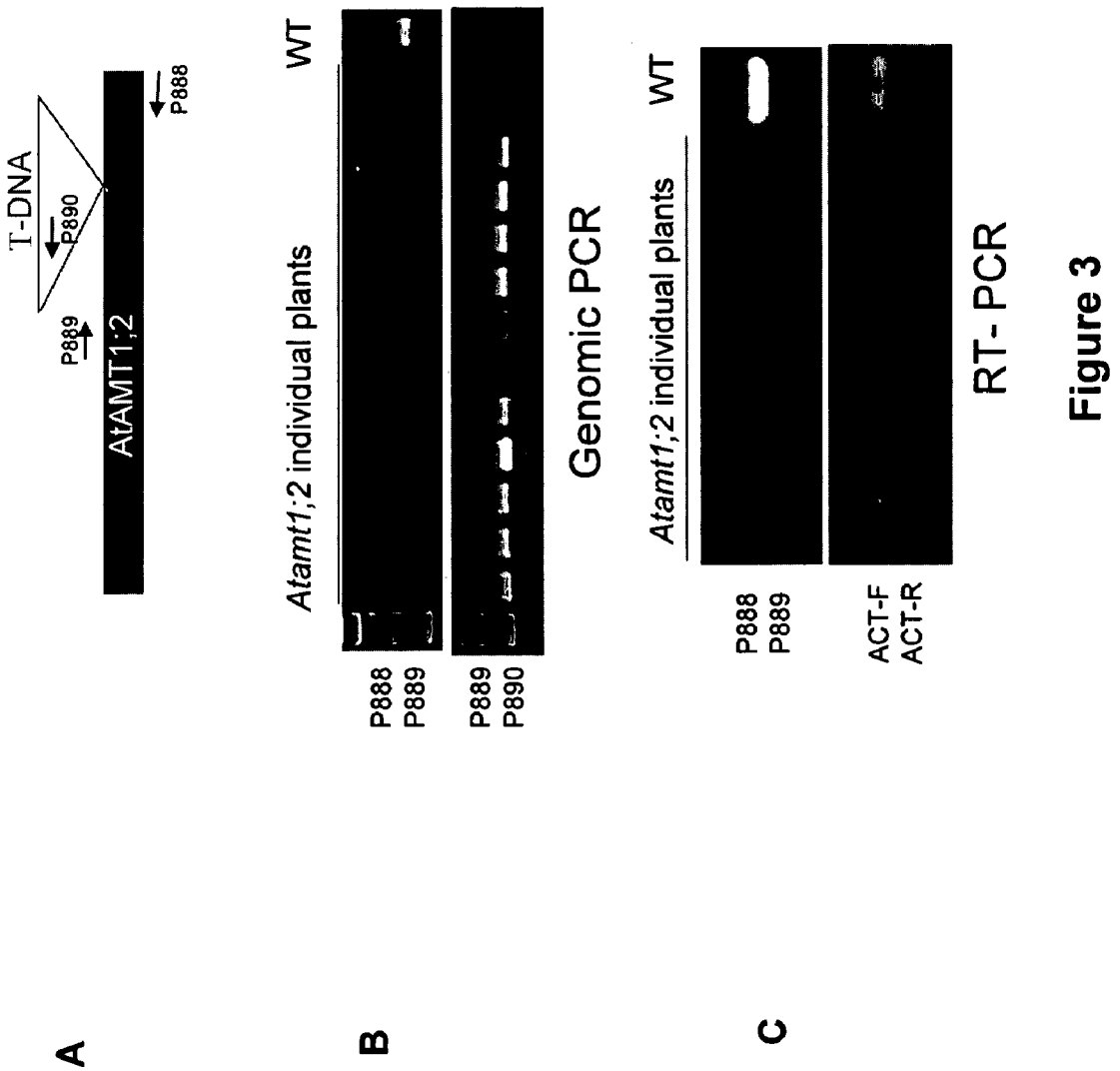
A
T-DNA
P888
P890
P889
AtAMT1;2
B
Atamt1;2 individual plants
WT
P888
P889
P889
P890
Genomic PCR
C
Atamt1;2 individual plants
WT
P888
P889
ACT-F
ACT-R
RT- PCR

Figure 3

A

```
                          151                                                 200
        AtAMT1.2  (151) GTCGACAACACGTATCTCCTCTTCTCCGCCTACCTTGTCTTTGCCATGCA
          AtAMT1  (121) ATAGACAACACTTACCTTCTCTTCTCCGCCTACCTTGTCTTCTCTATGCA
        AtAMT1.3  (133) ATAGACAACACCTACCTCCTCTTCTCTGCCTACCTTGTCTTCGCCATGCA
AtAMT3(At3g24290) (133) ATAGACAACACGTACCTCCTCTTCTCTGCCTATCTTGTCTTTGCGATGCA
AtAMT4(At4g28700) (148) ATCGACAACACTTACCTTCTCTTCTCTGCTTACCTCGTTTTCGCGATGCA
       Consensus  (151) ATAGACAACAC TACCTCCTCTTCTCTGCCTACCTTGTCTTCGC ATGCA
                          201                                                 250
        AtAMT1.2  (201) GCTCGGTTTCGCTATGCTTTGTGCTGGATCAGTCCGAGCCAAGAACACTA
          AtAMT1  (171) GCTTGGCTTCGCTATGCTCTGTGCCGGTTCCGTGAGAGCCAAGAATACTA
        AtAMT1.3  (183) GCTCGGCTTCGCTATGCTTTGTGCTGGTTCTGTTAGAGCCAAGAATACGA
AtAMT3(At3g24290) (183) GCTCGGCTTCGCTATGCTTTGTGCTGGCTCCGTTAGAGCTAAGAACACGA
AtAMT4(At4g28700) (198) GCTCGGTTTCGCCATGCTCTGTGCCGGATCCGTACGTGCAAAAAACACGA
       Consensus  (201) GCTCGGCTTCGCTATGCTTTGTGCTGG TCCGT AGAGCCAAGAACACGA
                          251                                                 300
        AtAMT1.2  (251) TGAACATCATGCTTACCAATGTCCTTGATGCTGCCGCTGGAGCCATCTCT
          AtAMT1  (221) TGAACATCATGCTTACCAACGTCCTTGACGCTGCAGCCGGTGGTCTCTTC
        AtAMT1.3  (233) TGAACATCATGCTTACCAATGTCCTTGACGCTGCAGCCGGAGGACTCTTC
AtAMT3(At3g24290) (233) TGAACATCATGCTCACTAATGTCCTTGATGCTGCAGCCGGAGGACTCTTC
AtAMT4(At4g28700) (248) TGAACATTATGCTCACGAACGTCATCGACGCTGCAGCCGGAGGTCTCTTC
       Consensus  (251) TGAACATCATGCTTACCAATGTCCTTGACGCTGCAGCCGGAGG CTCTTC
                          301                                                 350
        AtAMT1.2  (301) TACTACCTCTTCGGATTCGCATTCGCCTTTGGTACACCTTCCAACGGATT
          AtAMT1  (271) TATTATCTGTTTGGCTACGCCTTTGCCTTTGGATCTCCGTCCAATGGTTT
        AtAMT1.3  (283) TACTATCTCTTTGGTTACGCCTTTGCCTTTGGAGGATCCTCCGAAGGGTT
AtAMT3(At3g24290) (283) TACTACCTCTTTGGTTATGCATTTGCCTTTGGTGAATCCTCCGATGGATT
AtAMT4(At4g28700) (298) TATTATCTCTTCGGTTTCGCTTTTGCTTTTGGATCTCCTTCTAATGGATT
       Consensus  (301) TACTATCTCTTTGGTTACGC TTTGCCTTTGGA CACC TCCAATGGATT
```

B

AtAMT2

acttggtggaataatgacagggttgtttgcacaccctgatctctgcgttttggtacttcctctcccagcgaccagaggagctttctacggtggcaatggcggcggaataatgacagggttgtttgcacaccctgatctctgcgttttggtacttcctctcccagcgaccagaggagctttctacggtggcaatggcggcaaacagcttttgaaacagttggctggagctgccttcattgccgtctggaatgtggtgtcgactactatcattctactcgctattagggtgttcatacattgagaatggctgaggaagag

Figure 4

```
ZmAMT_01_orf  (243) GCTCTTCTACTACCTCTTCGGCTTCGCCTTCGCCTTCGGCACGCCCTCCA
ZmAMT_05_orf  (243) GCTCTTCTACTACCTATTCGGCTTCGCCTTCGCCTACGGCACCCCGTCCA
   Consensus  (243) GCTCTTCTACTACCT TTCGGCTTCGCCTTCGCCT CGGCAC CC TCCA
                    293                                             342
ZmAMT_01_orf  (293) ACGGCTTCATCGGCAAGCAGTTCTTCGGGCTCAAGCACCTGCCCAGGACC
ZmAMT_05_orf  (293) ACGGCTTCATCGGCAAGCACTTCTTCGGCCTCAAGCGCCTGCCCAAGACC
   Consensus  (293) ACGGCTTCATCGGCAAGCA TTCTTCGG CTCAAGC CCTGCCCA GACC
                    343                                             392
ZmAMT_01_orf  (343) GGCTTCGACTACGACTTCTTCCTCTACCAGTGGGCCTTCGCCATCGCCGC
ZmAMT_05_orf  (343) GGCTTCGACTACGACTTCTTCCTATACCAGTGGGCCTTCGCCATCGCCGC
   Consensus  (343) GGCTTCGACTACGACTTCTTCCT TACCAGTGGGCCTTCGCCATCGCCGC
                    393                                             442
ZmAMT_01_orf  (393) CGCGGGCATCACGTCGGGCTCCATCGCCGAGCGGACCCAGTTCGTCGCCT
ZmAMT_05_orf  (393) CGCCGGCATCACGTCCGGCTCCATCGCCGAGAGCACCCAGTTCGTCGCCT
   Consensus  (393) CGC GGCATCACGTC GGCTCCATCGCCGAG G ACCCAGTTCGTCGCCT
                    443                                             492
ZmAMT_01_orf  (443) ACCTCATCTACTCCGCGTTCCTGACGGGGTTCGTCTACCCCGTGGTGTCG
ZmAMT_05_orf  (443) ACCTCATCTACTCCGCCTTCCTCACCGGCTTCGTGTACCCCGTGGCGTCC
   Consensus  (443) ACCTCATCTACTCCGC TTCCT AC GG TTCGT TACCCCGTGG GTC
                    493         507
ZmAMT_01_orf  (493) CACTGGTTCTGGTCC
ZmAMT_05_orf  (493) CACTGGGTCTGGTCC
   Consensus  (493) CACTGG TCTGGTCC


                    241                                             290
ZmAMT_04_orf  (241) CTCTTCTACTACCTATTCGGCTTCGCCTTCGCGTACGGGACCCCGTCCAA
ZmAMT_04_orf  (291) CGGCTTCATCGGCAAGCACTTCTTCGGCCTCAAGCGGCTTCCCCAGGTCG
ZmAMT_04_orf  (341) GGTTCGACTACGACTTCTTCCTCTTCCAGTGGGCTTTCGCCATCGCCGCC
ZmAMT_04_orf  (391) GCCGGGATCACGTCCGGCTCCATCGCCGAGCGCACGCAGTTCGTGGCGTA
ZmAMT_04_orf  (441) CCTCATCTACTCCGCCTTCCTCACCGGCTTCGTGTACCCGGTGGTGTCCC
ZmAMT_04_orf  (491) ACTGGGTCTGGTCCGCCGACGGCTGGGCCTCGCCGTCACGGACGTCGGGG
ZmAMT_04_orf  (541) AAGCTCCTCTTCGGCTCCGGCATCATCGACTTCGCCGGGTCCAGCGTTGT
ZmAMT_03_orf    (1) ----------------------------------------------CGTTGT
   Consensus  (541)                                               CGTTGT
                    591                                             638
ZmAMT_04_orf  (591) CCACATGGTGGGCGGAATCGCCGGCCTCTGGGGCGCCCTCATCGAGGG
ZmAMT_03_orf    (7) CCACATGGTGGGCGGAATCGCCGGCCTCTGGGGCGCCCTCATCGAGGG
   Consensus  (591) CCACATGGTGGGCGGAATCGCCGGCCTCTGGGGCGCCCTCATCGAGGG
```

```
ZmAMT_07_orf   (49) GAGTGGCTGAACAAGGGCGACAACGCGTGGCAGCTGACGGCGGCGACGCT
ZmAMT_02_orf   (46) GACTGGCTGAACAAGGGCGACAATGCGTGGCAGATGACGTCCGCGACGCT
ZmAMT_06_orf   (61) GAGTGGCTGAACAAGGGCGACAACGCGTGGCAGCTGACGGCGGCGACGCT
   Consensus   (65) GAGTGGCTGAACAAGGGCGACAACGCGTGGCAGCTGACGGCGGCGACGCT
                    115                                             164
ZmAMT_07_orf   (99) GGTGGGCATCCAGTCGATGCCGGGGCTGGTGGTGCTGTACGGCAGCATCG
ZmAMT_02_orf   (96) GGTGGGCCTGCAGAGCATGCCCGGGCTGGTGATCCTGTACGGCAGCATCG
ZmAMT_06_orf  (111) GGTGGGGCTGCAGAGCTTCCCGGGTCTGGTGGTCCTGTACGGCGGCGTGG
   Consensus  (115) GGTGGGCCTGCAGAGCATGCCGGGGCTGGTGGTCCTGTACGGCAGCATCG
                    165                                             214
ZmAMT_07_orf  (149) TGAAGAAGAAGTGGGCGGTGAACTCGGCGTTCATGGCGCTGTACGCCTAC
ZmAMT_02_orf  (146) TGAAGAAGAAGTGGGCCATCAACTCGGCGTTCATGGCGCTGTACGCCTTC
ZmAMT_06_orf  (161) TGAAGAAGAAGTGGGCCGTGAACTCGGCCTTCATGGCGCTGTACGCGTTC
   Consensus  (165) TGAAGAAGAAGTGGGCCGTGAACTCGGCGTTCATGGCGCTGTACGCCTTC
                    215                                             264
ZmAMT_07_orf  (199) GCGTCGTCGCTGCTGGTGTGGGTGCTGGCGGGGTTCCGCATGGCGTTCGG
ZmAMT_02_orf  (196) GCCGCCGTCTGGCTCTGCTGGGTGGTGTGGGCCTACAACATGTCGTTCGG
ZmAMT_06_orf  (211) GCGGCGGTGTGGATCTGCTGGGTGACCTGGGCCTACAACATGTCCTTCGG
   Consensus  (215) GCGGCGGTGTGGCTCTGCTGGGTG TGTGGGCCTACAACATGTCGTTCGG
                    265                                             314
ZmAMT_07_orf  (249) GGAGCGGCTGCTCCCGTTCTGGGGCAAGGCCGGGGTGGCGCTCTCCCAGG
ZmAMT_02_orf  (246) CGACCGGCTGCTGCCCTTCTGGGGCAAGGCGAGGCCGGCGCTCGGGCAGC
ZmAMT_06_orf  (261) CGACAGGCTGCTGCCGCTGTGGGGCAAGGCGCGGCCGGCGCTGAGCCAGG
   Consensus  (265) CGACCGGCTGCTGCCGTTCTGGGGCAAGGCG GGCCGGCGCTC GCCAGG
                    315                                             364
ZmAMT_07_orf  (299) GCTACCTGGTCCGGCGCGCCTCGCTCTCGGCGACCGC---GCA-------
ZmAMT_02_orf  (296) GCTTCCTGGTGGCGCAGTCCCAGCTCACGGCCACCGCCGTGCGGTACCGC
ZmAMT_06_orf  (311) GCGGGCTGGTGGGGCAGGCCGGCCTCCCCGCCACGGCGCACCACTTCGCC
   Consensus  (315) GCT CCTGGTGGGGCAGGCC  GCTC CGGCCACCGC   GCA T C  C
                    365                                             414
ZmAMT_07_orf  (339) --CGGGGCC----ACGCCCCG--CACCGAGCCCCTGTACCCGGAGGCGAC
ZmAMT_02_orf  (346) GACGGGTCGCTCGAGGCGGAGATGCTCCACCCCTTCTACCCGGCCGCCAC
ZmAMT_06_orf  (361) AGCGGCGCCCTGGAGACCCCGGCCGCGGAGCCGCTGTACCCGATGGCCAC
   Consensus  (365)   CGGGGCCCT GAGGCCCCG  C CCGAGCCCCTGTACCCGG GGCCAC
                    415                                             464
ZmAMT_07_orf  (381) GCTGGTGCTGTTCCAGTTCGAGTTCGCCGCCATCACGCTGGTGCTCCTGG
ZmAMT_02_orf  (396) CATGGTGTACTTCCAGTGCGTGTTCGCCAGCATCACCGTCATCATCCTCG
ZmAMT_06_orf  (411) GGTGGTGTACTTCCAGTGCGTGTTCGCGGCCATCACCCTGGTGCTGGTCG
   Consensus  (415) G TGGTGTACTTCCAGTGCGTGTTCGCCGCCATCACCCTGGTGCTCCTCG
```

Figure 5

MANIPULATION OF AMMONIUM TRANSPORTERS (AMTS) TO IMPROVE NITROGEN USE EFFICIENCY IN HIGHER PLANTS

CROSS REFERENCE

[0001] This utility application claims the benefit U.S. Provisional Application No. 60/893,901, filed Mar. 9, 2007, which is incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The invention relates generally to the field of molecular biology.

BACKGROUND OF THE INVENTION

[0003] Nitrogen (N) is the most abundant inorganic nutrient taken up from the soil by plants for growth and development. Maize roots absorb most of the N from the soil in the form of nitrate, the majority of which is transported to the leaf for reduction and assimilation. Nitrate is reduced to nitrite by nitrate reductase (NR) in the cytosol and then nitrite is transported into chloroplast where it is reduced by nitrite reductase (NiR) to ammonium. Ammonium is assimilated into glutamine by the glutamine synthase-glutamate synthase system (Crawford and Glass, (1998) *Trends in Plant Science* 3:389-395.). Also, it has long been known that significant amounts of N are lost from the plant aerial parts by volatilization (Glyan'ko, et al., (1980) "Effect of autumn frost and forms of nitrogen on translocation of nitrogen compounds to spring wheat grain", *Agrokhimiya* 8:19-26; Hooker, et al., (1980) "Gaseous N losses from winter wheat", *Agronomy Journal* 72(5):789-792; Silva, et al., (1981) "Nitrogen volatilization from rice leaves. II. Effects of source of applied nitrogen in nutrient culture solution", *Crop Science* 21(6): 913-916; Stutte, et al., (1981) "Nitrogen volatilization from rice leaves. I. Effects of genotype and air temperature", *Crop Science* 21(4):596-600; Foster, et al., (1986) "Glutamine synthetase activity and foliar nitrogen volatilization in response to temperature and inhibitor chemicals" *Annals of Botany* 57(3):305-307; Parton, et al., (1988) "Ammonia volatilization from spring wheat plants" *Agronomy Journal* 80(3):419-425; Kamiji, et al., (1989) "Measurement of ammonium nitrogen volatilization rates from rice leaves during the ripening period." *Japanese Journal of Crop Science* 58(1):140-142; Morgan, et al., (1989) "Characteristics of ammonia volatilization from spring wheat", *Crop Science* 29(3):726-731; O'Deen, (1989) "Wheat volatilized ammonia and resulting nitrogen isotopic fractionation." *Agronomy Journal* 81(6): 980-985; Guindo, et al., (1994) "Nitrogen loss from rice plants during grain fill and oven drying", *Arkansas Farm Research* 43(1):12-13; Heckathorn, et al., (1995) "Ammonia volatilization during drought in perennial C4 grasses of tallgrass prairie." *Oecologia* 101(3):361-365; Cabezas, et al., (1997). "NH3-N volatilization in a maize crop: I Effect of irrigation and partial substitution of urea by ammonium sulphate", *Revista Brasileira de Ciencia do Solo* 21(3):481-487). Experimental evidence supports the loss of N through ammonium and not through N oxides (Hooker, et al., 1980). Treatment with chemicals that inhibit glutamine or glutamate synthase activities led to increased loss of ammonium through volatilization (Foster, et al., 1986). Loss of N is not only limited to C-3 species as C-4 plants have also been reported to lose N through volatilization (Heckathorn, et al., 1995).

[0004] Manipulation of AMTs can be utilized to improve NUE by causing increased dry matter, thereby contributing to an increase in plant yield. Two of the ways to improved dry matter accumulation are: 1) reduce N loss through volatilization and 2) reduce N content of the plant so that more dry matter can be accumulated in the form of low-energy constituents, e.g., starch or cellulose.

[0005] For ammonium to be lost from the leaf, it must first pass through a facilitated channel since it is highly hydrophilic. Ammonium transporters (AMTs) were originally discovered as ammonium transporters but some recent studies have shown that at least in some cases AMTs can act as gas channels (Soupene, et al., (2002) *Proc Natl Acad Sci USA* 99:3926-3931; Kustu and Inwood, (2006) *Transfus Clin Biol* 13:103-110). An amtB knock-out mutant of *Salmonella* grows better on poor N source, apparently because it can sequester more N by keeping it from leaking back out (Soupene, et al., 2002). This application details an invention which is used to manipulate AMTs in higher plants to improve NUE. The inventors identified chloroplast-specific and/or leaf-preferred AMT(s) and knocked them out/down to minimize the loss of ammonium, which resulting in better N assimilation/NUE. In addition, work was not limited only to the chloroplast-localized AMTs but will also down-regulation of the AMTs that are localized to other organelles/membranes.

SUMMARY OF THE INVENTION

[0006] The present invention provides polynucleotides, related polypeptides and all conservatively modified variants of the present AMT sequences. The invention provides sequences for the AMT genes. Six *Arabidopsis,* 7 maize, 17 rice, and 11 soybean AMT genes were identified. Table 1 lists these genes and their seq id numbers.

TABLE 1

SEQUENCE ID NUMBER	IDENTITY
SEQ ID NOS: 1	AtAMT 1 polynucleotide
SEQ ID NOS: 2	AtAMT 1 polypeptide
SEQ ID NO: 3	AtAMT 1;2 polynucleotide
SEQ ID NO: 4	AtAMT 1;2 polypeptide
SEQ ID NO: 5	AtAMT 1;3 polynucleotide
SEQ ID NO: 6	AtAMT 1;3 polypeptide
SEQ ID NO: 7	AtAMT 2 polynucleotide
SEQ ID NO: 8	AtAMT 2 polypeptide
SEQ ID NO: 9	AtAMT 3 polynucleotide
SEQ ID NO: 10	AtAMT 3 polypeptide
SEQ ID NO: 11	AtAMT 4 polynucleotide
SEQ ID NO: 12	AtAMT 4 polypeptide
SEQ ID NO: 13	ZmAMT 1 polynucleotide
SEQ ID NO: 14	ZmAMT 1 polypeptide
SEQ ID NO: 15	ZmAMT 2 polynucleotide
SEQ ID NO: 16	ZmAMT 2 polypeptide
SEQ ID NO: 17	ZmAMT 3 polynucleotide
SEQ ID NO: 18	ZmAMT 3 polypeptide
SEQ ID NO: 19	ZmAMT 4 polynucleotide
SEQ ID NO: 20	ZmAMT 4 polypeptide
SEQ ID NO: 21	ZmAMT 5 polynucleotide
SEQ ID NO: 22	ZmAMT 5 polypeptide
SEQ ID NO: 23	ZmAMT 6 polynucleotide
SEQ ID NO: 24	ZmAMT 6 polypeptide
SEQ ID NO: 25	ZmAMT 7 polynucleotide
SEQ ID NO: 26	ZmAMT 7 polypeptide
SEQ ID NO: 27	OsAMT 1 polynucleotide

TABLE 1-continued

SEQUENCE ID NUMBER	IDENTITY
SEQ ID NO: 28	OsAMT 1 polypeptide
SEQ ID NO: 29	OsAMT 2 polynucleotide
SEQ ID NO: 30	OsAMT 2 polypeptide
SEQ ID NO: 31	OsAMT 3 polynucleotide
SEQ ID NO: 32	OsAMT 3 polypeptide
SEQ ID NO: 33	OsAMT 4 polynucleotide
SEQ ID NO: 34	OsAMT 4 polypeptide
SEQ ID NO: 35	OsAMT 5 polynucleotide
SEQ ID NO: 36	OsAMT 5 polypeptide
SEQ ID NO: 37	OsAMT 6 polynucleotide
SEQ ID NO: 38	OsAMT 6 polypeptide
SEQ ID NO: 39	OsAMT 7 polynucleotide
SEQ ID NO: 40	OsAMT 7 polypeptide
SEQ ID NO: 41	OsAMT 8 polynucleotide
SEQ ID NO: 42	OsAMT 8 polypeptide
SEQ ID NO: 43	OsAMT 9 polynucleotide
SEQ ID NO: 44	OsAMT 9 polypeptide
SEQ ID NO: 45	OsAMT 10 polynucleotide
SEQ ID NO: 46	OsAMT 10 polypeptide
SEQ ID NO: 47	OsAMT 11 polynucleotide
SEQ ID NO: 48	OsAMT 11 polypeptide
SEQ ID NO: 49	OsAMT 12 polynucleotide
SEQ ID NO: 50	OsAMT 12 polypeptide
SEQ ID NO: 51	OsAMT 13 polynucleotide
SEQ ID NO: 52	OsAMT 13 polypeptide
SEQ ID NO: 53	OsAMT 14 polynucleotide
SEQ ID NO: 54	OsAMT 14 polypeptide
SEQ ID NO: 55	OsAMT 15 polynucleotide
SEQ ID NO: 56	OsAMT 15 polypeptide
SEQ ID NO: 57	OsAMT 16 polynucleotide
SEQ ID NO: 58	OsAMT 16 polypeptide
SEQ ID NO: 59	OsAMT 17 polynucleotide
SEQ ID NO: 60	OsAMT 17 polynucleotide
SEQ ID NO: 61	GmAMT 1 polynucleotide
SEQ ID NO: 62	GmAMT 1 polypeptide
SEQ ID NO: 63	GmAMT 2 polynucleotide
SEQ ID NO: 64	GmAMT 2 polypeptide
SEQ ID NO: 65	GmAMT 3 polynucleotide
SEQ ID NO: 66	GmAMT 3 polypeptide
SEQ ID NO: 67	GmAMT 4 polynucleotide
SEQ ID NO: 68	GmAMT 4 polypeptide
SEQ ID NO: 69	GmAMT 5 polynucleotide
SEQ ID NO: 70	GmAMT 5 polypeptide
SEQ ID NO: 71	GmAMT 6 polynucleotide
SEQ ID NO: 72	GmAMT 6 polypeptide
SEQ ID NO: 73	GmAMT 7 polynucleotide
SEQ ID NO: 74	GmAMT 7 polypeptide
SEQ ID NO: 75	GmAMT 8 polynucleotide
SEQ ID NO: 76	GmAMT 8 polypeptide
SEQ ID NO: 77	GmAMT 9 polynucleotide
SEQ ID NO: 78	GmAMT 9 polypeptide
SEQ ID NO: 79	GmAMT 10 polynucleotide
SEQ ID NO: 80	GmAMT 10 polypeptide
SEQ ID NO: 81	GmAMT 11 polynucleotide
SEQ ID NO: 82	GmAMT 11 polypeptide

[0007] Therefore, in one aspect, the present invention relates to an isolated nucleic acid comprising an isolated polynucleotide sequence encoding an AMT protein. One embodiment of the invention is an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81; (b) the nucleotide sequence encoding an amino acid sequence comprising SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80 or 82; and (c) the nucleotide sequence comprising at least 70% sequence identity to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81, wherein said polynucleotide encodes a polypeptide having AMT transporter activity.

[0008] Compositions of the invention include an isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence comprising SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80 or 82; and (b) the amino acid sequence comprising at least 70% sequence identity to SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80 or 82, wherein said polypeptide has AMT transporter activity.

[0009] In another aspect, the present invention relates to a recombinant expression cassette comprising a nucleic acid as described. Additionally, the present invention relates to a vector containing the recombinant expression cassette. Further, the vector containing the recombinant expression cassette can facilitate the transcription and translation of the nucleic acid in a host cell. The present invention also relates to the host cells able to express the polynucleotide of the present invention. A number of host cells could be used, such as but not limited to, microbial, mammalian, plant, or insect.

[0010] In yet another embodiment, the present invention is directed to a transgenic plant or plant cells, containing the nucleic acids of the present invention. Preferred plants containing the polynucleotides of the present invention include but are not limited to maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, tomato, switchgrass, myscanthus, triticale and millet. In another embodiment, the transgenic plant is a maize plant or plant cells. Another embodiment is the transgenic seeds from the transgenic plant. Another embodiment of the invention includes plants comprising an amt polypeptide of the invention operably linked to a promoter that drives expression in the plant. The plants of the invention can have altered AMT as compared to a control plant. In some plants, the AMT is altered in a vegetative tissue, a reproductive tissue, or a vegetative tissue and a reproductive tissue. Plants of the invention can have at least one of the following phenotypes including but not limited to: increased leaf size, increased ear size, increased seed size, increased endosperm size, alterations in the relative size of embryos and endosperms leading to changes in the relative levels of protein, oil, and/or starch in the seeds, absence of tassels, absence of functional pollen bearing tassels, or increased plant size.

[0011] Another embodiment of the invention would be plants that have been genetically modified at a genomic locus, wherein the genomic locus encodes an amt polypeptide of the invention.

[0012] Methods for increasing the activity of an amt polypeptide in a plant are provided. The method can comprise introducing into the plant an amt polynucleotide of the invention. Providing the polypeptide can decrease the number of cells in plant tissue, modulating the tissue growth and size.

[0013] Methods for reducing or eliminating the level of an amt polypeptide in the plant are provided. The level or activity of the polypeptide could also be reduced or eliminated in specific tissues, causing increased AMT in said tissues. Reducing the level and/or activity of the AMT polypeptide increases the number of cells produced in the associated tissue.

[0014] Compositions further include plants and seed having a DNA construct comprising a nucleotide sequence of interest operably linked to a promoter of the current invention. In specific embodiments, the DNA construct is stably integrated into the genome of the plant. The method comprises introducing into a plant a nucleotide sequence of interest operably linked to a promoter of the invention.

BRIEF DESCRIPTION OF THE FIGURES

[0015] FIG. **1**: Phylogentic tree of AMTs from *Arabidopsis*, rice, soybean and maize

[0016] Phylogenetic analyses of all the AMTs from *Arabidopsis*, rice, maize and soybean are shown in FIG. **1**. The length of the line at the base of the figure represents an equivalent of 10 amino acid differences and could be used to approximate the amino acid differences between different ammonium transporter proteins from the individual branch lengths.

[0017] FIG. **2**: Expression analysis of ZM-AMTs

[0018] In order to identify leaf specific/preferred/expressed AMT(s) in maize, Lynx MPSS expression analyses in ~300 libraries reveal that ZmAMT1 (SEQ ID NO: 14), 2, 7 are expressed both in roots and leaves whereas ZmAMT4 (SEQ ID NO: 20) is a root preferred AMT. ZmAMT6 (SEQ ID NO: 24) expresses at very low level in comparison to other Zm-AMTs. In case of ZmAMT5 there was no specific Lynx tag available.

[0019] FIG. **3**: Characterization of atamt1;2 T-DNA knock-out mutant

[0020] In cTP prediction analyses, AtAMT1;2 (SEQ ID NO: 4) posses a putative cTP. For functional analyses of AtAMT1;2 (SEQ ID NO: 4) and to determine it's role in N-assimilation, analyses identified a T-DNA mutant line (SM_3.15680) from the *Arabidopsis* T-DNA mutant data base. In this mutant line T-DNA was inserted in c-terminal of AtAMT1;2 (SEQ ID NO: 4) gene (FIG. **4**A). Genomic PCRs using AtAMT1;2 (SEQ ID NO: 4) gene and T-DNA specific primers show that T-DNA is indeed inserted in the AtAMT1;2 (SEQ ID NO: 4) (FIG. **4**B). AtAMT1;2 (SEQ ID NO: 4) gene specific primers flanking the T-DNA insert couldn't amplify any DNA region in mutant plants where as an expected PCR product was detected in wild type plant (FIG. **4**B, upper panel). Similarly, genomic PCR with AtAMT1;2 (SEQ ID NO: 4) specific forward primer and T-DNA specific reverse primers amplify an expected product in mutant lines and nothing in wild type plants as expected (FIG. **4**B, lower panel). Saturated RT-PCRs (35 cycles) analyses couldn't detect a full length atamt1;2 mRNA in mutant (FIG. **4**C, upper panel) suggesting that AtAMT1;2 (SEQ ID NO: 4) is completely knocked out in this T-DNA mutant. Actin control RT-PCR worked fine in both mutant and wild type plants (FIG. **4**C, lower panel).

[0021] FIG. **4**: Knock-out of multiple AMTs in *Arabidopsis* by single RNAi vector

[0022] Six AMT genes are present in *Arabidopsis* genome. Hence, it is very likely that due to functional redundancy one might need to manipulate the expression of multiple AMTs simultaneously. Analyses of the DNA sequence of all these AMTs was performed which identified the high homology regions among them. There is a stretch of ~200 bp among AtAMT1;2 (SEQ ID NO: 4), AtAMT1 (SEQ ID NO: 2), AMT1;3 (SEQ ID NO: 6), At3g24290 (SEQ ID NO: 10) and At4g28700 (SEQ ID NO: 12) where as AMT2 (SEQ ID NO: 8) stood independent. Amplification of these regions was accomplished (bold and underlined in FIG. **4**) by PCR from AtAMT1;2 (SEQ ID NO: 4) and AtAMT2 (SEQ ID NO: 8) and a multi-way ligation was performed to make an inverted repeat using ADH-intron as a spacer. The RNAi cassette of these hybrid inverted repeats is driven by constitutive or root specific or leaf specific promoter.

[0023] FIG. **5**: Knock-out/down of multiple AMTs in Maize by single RNAi vector

[0024] Detailed analyses of all 7 maize AMTs were performed to identify the DNA regions showing high homology among different ZmAMTs. This analysis reveals that ZmAMT1 (SEQ ID NO: 14) and ZmAMT5 (SEQ ID NO: 22), ZmAMT3 (SEQ ID NO: 18) and ZmAMT4 (SEQ ID NO: 20) and ZmAMT2 (SEQ ID NO: 16), ZmAMT6 (SEQ ID NO: 24) and ZmAMT7 (SEQ ID NO: 26) form three separate groups and there is a very high homology in stretches of DNA sequences with in each group. Three DNA fragments (bold and underlined in FIG. **5**) from ZmAMT 1, 4 and 7 (SEQ ID NOS: 14, 20 and 26) representing each of the different groups were amplified by PCR. Multi-way ligations were performed to make inverted repeats with hybrid of these 3 fragments and ADH intron as a spacer to facilitate the formation of stem-loop structure. This RNAi cassette of 'ZmAMT1 (SEQ ID NO: 14):ZmAMT4 (SEQ ID NO: 20):ZmAMT7 (SEQ ID NO: 26)' inverted repeats was driven by a constitutive (Zm-UBI promoter) or leaf-specific promoter. MOPAT driven by Zm-UBI promoter was used as herbicide resistance marker for selected. In addition to that RFP driven by a pericarp specific promoter LTP2 was also used to sort out the transgenic seeds (red) from there segregating non-transgenic seeds.

DETAILED DESCRIPTION OF THE INVENTION

[0025] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Unless mentioned otherwise, the techniques employed or contemplated herein are standard methodologies well known to one of ordinary skill in the art. The materials, methods and examples are illustrative only and not limiting. The following is presented by way of illustration and is not intended to limit the scope of the invention.

[0026] The present inventions now will be described more fully hereinafter with reference to the accompanying drawings, in which some, but not all embodiments of the invention are shown. Indeed, these inventions may be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will satisfy applicable legal requirements. Like numbers refer to like elements throughout.

[0027] Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

[0028] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of

botany, microbiology, tissue culture, molecular biology, chemistry, biochemistry and recombinant DNA technology, which are within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Langenheim and Thimann, BOTANY: PLANT BIOLOGY AND ITS RELATION TO HUMAN AFFAIRS, John Wiley (1982); CELL CULTURE AND SOMATIC CELL GENETICS OF PLANTS, vol. 1, Vasil, ed. (1984); Stanier, et al., THE MICROBIAL WORLD, 5th ed., Prentice-Hall (1986); Dhringra and Sinclair, BASIC PLANT PATHOLOGY METHODS, CRC Press (1985); Maniatis, et al., MOLECULAR CLONING: A LABORATORY MANUAL (1982); DNA CLONING, vols. I and II, Glover, ed. (1985); OLIGONUCLEOTIDE SYNTHESIS, Gait, ed. (1984); NUCLEIC ACID HYBRIDIZATION, Hames and Higgins, eds. (1984); and the series METHODS IN ENZYMOLOGY, Colowick and Kaplan, eds, Academic Press, Inc., San Diego, Calif.

[0029] Units, prefixes, and symbols may be denoted in their SI accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively. Numeric ranges are inclusive of the numbers defining the range. Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes. The terms defined below are more fully defined by reference to the specification as a whole.

[0030] In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

[0031] By "microbe" is meant any microorganism (including both eukaryotic and prokaryotic microorganisms), such as fungi, yeast, bacteria, actinomycetes, algae and protozoa, as well as other unicellular structures.

[0032] By "amplified" is meant the construction of multiple copies of a nucleic acid sequence or multiple copies complementary to the nucleic acid sequence using at least one of the nucleic acid sequences as a template. Amplification systems include the polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario), Q-Beta Replicase systems, transcription-based amplification system (TAS), and strand displacement amplification (SDA). See, e.g., DIAGNOSTIC MOLECULAR MICROBIOLOGY: PRINCIPLES AND APPLICATIONS, Persing, et al., eds., American Society for Microbiology, Washington, D.C. (1993). The product of amplification is termed an amplicon.

[0033] The term "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refer to those nucleic acids that encode identical or conservatively modified variants of the amino acid sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations" and represent one species of conservatively modified variation. Every nucleic acid sequence herein that encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of ordinary skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine; one exception is *Micrococcus rubens*, for which GTG is the methionine codon (Ishizuka, et al., (1993) *J. Gen. Microbiol.* 139:425-32) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid, which encodes a polypeptide of the present invention, is implicit in each described polypeptide sequence and incorporated herein by reference.

[0034] As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" when the alteration results in the substitution of an amino acid with a chemically similar amino acid. Thus, any number of amino acid residues selected from the group of integers consisting of from 1 to 15 can be so altered. Thus, for example, 1, 2, 3, 4, 5, 7 or 10 alterations can be made. Conservatively modified variants typically provide similar biological activity as the unmodified polypeptide sequence from which they are derived. For example, substrate specificity, enzyme activity, or ligand/receptor binding is generally at least 30%, 40%, 50%, 60%, 70%, 80% or 90%, preferably 60-90% of the native protein for it's native substrate. Conservative substitution tables providing functionally similar amino acids are well known in the art.

[0035] The following six groups each contain amino acids that are conservative substitutions for one another:

[0036] 1) Alanine (A), Serine (S), Threonine (T);

[0037] 2) Aspartic acid (D), Glutamic acid (E);

[0038] 3) Asparagine (N), Glutamine (Q);

[0039] 4) Arginine (R), Lysine (K);

[0040] 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and

[0041] 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

See also, Creighton, PROTEINS, W.H. Freeman and Co. (1984).

[0042] As used herein, "consisting essentially of" means the inclusion of additional sequences to an object polynucleotide where the additional sequences do not selectively hybridize, under stringent hybridization conditions, to the same cDNA as the polynucleotide and where the hybridization conditions include a wash step in 0.1×SSC and 0.1% sodium dodecyl sulfate at 65° C.

[0043] By "encoding" or "encoded," with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequences (e.g., introns) within translated regions of the nucleic acid, or may lack such intervening non-translated sequences (e.g., as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the "universal" genetic code. However, variants of the universal code, such as is present in some plant, animal, and fungal mitochondria, the bacterium *Mycoplasma capricolum* (Yamao, et al., (1985) *Proc. Natl. Acad. Sci. USA* 82:2306-9), or the ciliate Macronucleus, may be used when the nucleic acid is expressed using these organisms.

[0044] When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon prefer-

ences of the intended host where the nucleic acid is to be expressed. For example, although nucleic acid sequences of the present invention may be expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledonous plants or dicotyledonous plants as these preferences have been shown to differ (Murray, et al., (1989) *Nucleic Acids Res.* 17:477-98 and herein incorporated by reference). Thus, the maize preferred codon for a particular amino acid might be derived from known gene sequences from maize. Maize codon usage for 28 genes from maize plants is listed in Table 4 of Murray, et al., supra.

[0045] As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived or, if from the same species, one or both are substantially modified from their original form. A heterologous protein may originate from a foreign species or, if from the same species, is substantially modified from its original form by deliberate human intervention.

[0046] By "host cell" is meant a cell, which comprises a heterologous nucleic acid sequence of the invention, which contains a vector and supports the replication and/or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, plant, amphibian, or mammalian cells. Preferably, host cells are monocotyledonous or dicotyledonous plant cells, including but not limited to maize, sorghum, sunflower, soybean, wheat, alfalfa, rice, cotton, canola, barley, millet, switchgrass, myscanthus, triticale, and tomato. A particularly preferred monocotyledonous host cell is a maize host cell.

[0047] The term "hybridization complex" includes reference to a duplex nucleic acid structure formed by two single-stranded nucleic acid sequences selectively hybridized with each other.

[0048] The term "introduced" in the context of inserting a nucleic acid into a cell, means "transfection" or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

[0049] The terms "isolated" refers to material, such as a nucleic acid or a protein, which is substantially or essentially free from components which normally accompany or interact with it as found in its naturally occurring environment. The isolated material optionally comprises material not found with the material in its natural environment. Nucleic acids, which are "isolated", as defined herein, are also referred to as "heterologous" nucleic acids. Unless otherwise stated, the term "AMT nucleic acid" means a nucleic acid comprising a polynucleotide ("AMT polynucleotide") encoding a full length or partial length AMT polypeptide.

[0050] As used herein, "nucleic acid" includes reference to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (e.g., peptide nucleic acids).

[0051] By "nucleic acid library" is meant a collection of isolated DNA or RNA molecules, which comprise and substantially represent the entire transcribed fraction of a genome of a specified organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, GUIDE TO MOLECULAR CLONING TECHNIQUES, from the series METHODS IN ENZYMOLOGY, vol. 152, Academic Press, Inc., San Diego, Calif. (1987); Sambrook, et al., MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed., vols. 1-3 (1989); and CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Ausubel, et al., eds, Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (1994 Supplement).

[0052] As used herein "operably linked" includes reference to a functional linkage between a first sequence, such as a promoter, and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

[0053] As used herein, the term "plant" includes reference to whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds and plant cells and progeny of same. Plant cell, as used herein includes, without limitation, seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. The class of plants, which can be used in the methods of the invention, is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants including species from the genera: *Cucurbita, Rosa, Vitis, Juglans, Fragaria, Lotus, Medicago, Onobrychis, Trifolium, Trigonella, Vigna, Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Sinapis, Atropa, Capsicum, Datura, Hyoscyamus, Lycopersicon, Nicotiana, Solanum, Petunia, Digitalis, Majorana, Ciahorium, Helianthus, Lactuca, Bromus, Asparagus, Antirrhinum, Heterocallis, Nemesis, Pelargonium, Panieum, Pennisetum, Ranunculus, Senecio, Salpiglossis, Cucumis, Browaalia, Glycine, Pisum, Phaseolus, Lolium, Oryza, Avena, Hordeum, Secale, Allium*, and *Triticum*. A particularly preferred plant is *Zea mays*.

[0054] As used herein, "yield" may include reference to bushels per acre of a grain crop at harvest, as adjusted for grain moisture (15% typically for maize, for example). Grain moisture is measured in the grain at harvest. The adjusted test weight of grain is determined to be the weight in pounds per bushel, adjusted for grain moisture level at harvest.

[0055] As used herein, "polynucleotide" includes reference to a deoxyribopolynucleotide, ribopolynucleotide, or analogs thereof that have the essential nature of a natural ribonucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as naturally occurring nucleotides and/or allow translation into the same amino acid(s) as the naturally occurring nucleotide (s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof.

Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including inter alia, simple and complex cells.

[0056] The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

[0057] As used herein "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. Examples are promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, seeds, fibres, xylem vessels, tracheids, or sclerenchyma. Such promoters are referred to as "tissue preferred." A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" or "regulatable" promoter is a promoter, which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Another type of promoter is a developmentally regulated promoter, for example, a promoter that drives expression during pollen development. Tissue preferred, cell type specific, developmentally regulated, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter, which is active under most environmental conditions.

[0058] The term "AMT polypeptide" refers to one or more amino acid sequences. The term is also inclusive of fragments, variants, homologs, alleles or precursors (e.g., preproproteins or proproteins) thereof. A "AMT protein" comprises an amt polypeptide. Unless otherwise stated, the term "AMT nucleic acid" means a nucleic acid comprising a polynucleotide ("AMT polynucleotide") encoding an amt polypeptide.

[0059] As used herein "recombinant" includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all as a result of deliberate human intervention; or may have reduced or eliminated expression of a native gene. The term "recombinant" as used herein does not encompass the alteration of the cell or vector by naturally occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without deliberate human intervention.

[0060] As used herein, a "recombinant expression cassette" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements, which permit transcription of a particular nucleic acid in a target cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a nucleic acid to be transcribed, and a promoter.

[0061] The term "residue" or "amino acid residue" or "amino acid" are used interchangeably herein to refer to an amino acid that is incorporated into a protein, polypeptide, or peptide (collectively "protein"). The amino acid may be a naturally occurring amino acid and, unless otherwise limited, may encompass known analogs of natural amino acids that can function in a similar manner as naturally occurring amino acids.

[0062] The term "selectively hybridizes" includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least 40% sequence identity, preferably 60-90% sequence identity, and most preferably 100% sequence identity (i.e., complementary) with each other.

[0063] The terms "stringent conditions" or "stringent hybridization conditions" include reference to conditions under which a probe will hybridize to its target sequence, to a detectably greater degree than other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which can be up to 100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Optimally, the probe is approximately 500 nucleotides in length, but can vary greatly in length from less than 500 nucleotides to equal to the entire length of the target sequence.

[0064] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide or Denhardt's. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55 to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60 to 65° C. Specificity is typically the function of post-hybridization washes, the criti-

cal factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, (1984) *Anal. Biochem.,* 138:267-84: T_m=81.5° C.+16.6 (log M)+0.41 (% GC)−0.61 (% form)−500/L; where M is the molarity of monovalent cations, % GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1° C. for each 1% of mismatching; thus, T_m, hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with ≧90% identity are sought, the T_m can be decreased 10° C. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3 or 4° C. lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9 or 10° C. lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15 or 20° C. lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45° C. (aqueous solution) or 32° C. (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY—HYBRIDIZATION WITH NUCLEIC ACID PROBES, part 1, chapter 2, "Overview of principles of hybridization and the strategy of nucleic acid probe assays," Elsevier, N.Y. (1993); and CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, chapter 2, Ausubel, et al., eds, Greene Publishing and Wiley-Interscience, New York (1995). Unless otherwise stated, in the present application high stringency is defined as hybridization in 4×SSC, 5×Denhardt's (5 g Ficoll, 5 g polyvinylpyrrolidone, 5 g bovine serum albumin in 500 ml of water), 0.1 mg/ml boiled salmon sperm DNA, and 25 mM Na phosphate at 65° C., and a wash in 0.1×SSC, 0.1% SDS at 65° C.

[0065] As used herein, "transgenic plant" includes reference to a plant, which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

[0066] As used herein, "vector" includes reference to a nucleic acid used in transfection of a host cell and into which can be inserted a polynucleotide. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

[0067] The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides or polypeptides: (a) "reference sequence," (b) "comparison window," (c) "sequence identity," (d) "percentage of sequence identity," and (e) "substantial identity."

[0068] As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

[0069] As used herein, "comparison window" means includes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100 or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

[0070] Methods of alignment of nucleotide and amino acid sequences for comparison are well known in the art. The local homology algorithm (BESTFIT) of Smith and Waterman, (1981) *Adv. Appl. Math* 2:482, may conduct optimal alignment of sequences for comparison; by the homology alignment algorithm (GAP) of Needleman and Wunsch, (1970) *J. Mol. Biol.* 48:443-53; by the search for similarity method (Tfasta and Fasta) of Pearson and Lipman, (1988) *Proc. Natl. Acad. Sci. USA* 85:2444; by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif., GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG® programs (Accelrys, Inc., San Diego, Calif.).). The CLUSTAL program is well described by Higgins and Sharp, (1988) *Gene* 73:237-44; Higgins and Sharp, (1989) *CABIOS* 5:151-3; Corpet, et al., (1988) *Nucleic Acids Res.* 16:10881-90; Huang, et al., (1992) *Computer Applications in the Biosciences* 8:155-65, and Pearson, et al., (1994) *Meth. Mol. Biol.* 24:307-31. The preferred program to use for optimal global alignment of multiple sequences is PileUp (Feng and Doolittle, (1987) *J. Mol. Evol.,* 25:351-60 which is similar to the method described by Higgins and Sharp, (1989) *CABIOS* 5:151-53 and hereby incorporated by reference). The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide

database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Chapter 19, Ausubel, et al., eds., Greene Publishing and Wiley-Interscience, New York (1995).

[0071] GAP uses the algorithm of Needleman and Wunsch, supra, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package are 8 and 2, respectively. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 100. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50 or greater.

[0072] GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see, Henikoff and Henikoff, (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

[0073] Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters (Altschul, et al., (1997) *Nucleic Acids Res.* 25:3389-402).

[0074] As those of ordinary skill in the art will understand, BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences, which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, (1993) *Comput. Chem.* 17:149-63) and XNU (Claverie and States, (1993) *Comput. Chem.* 17:191-201) low-complexity filters can be employed alone or in combination.

[0075] As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences, which are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences, which differ by such conservative substitutions, are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Meyers and Miller, (1988) *Computer Applic. Biol. Sci.* 4:11-17, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif., USA).

[0076] As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0077] The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has between 50-100% sequence identity, preferably at least 50% sequence identity, preferably at least 60% sequence identity, preferably at least 70%, more preferably at least 80%, more preferably at least 90%, and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of between 55-100%, preferably at least 55%, preferably at least 60%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%.

[0078] Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. The degeneracy of the genetic code allows for many amino acids substitutions that lead to variety in the nucleotide sequence that code for the same amino acid, hence it is possible that the DNA sequence could code for the same polypeptide but not hybridize to each other under stringent conditions. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is that

the polypeptide, which the first nucleic acid encodes, is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

[0079] The terms "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with between 55-100% sequence identity to a reference sequence preferably at least 55% sequence identity, preferably 60% preferably 70%, more preferably 80%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, supra. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. In addition, a peptide can be substantially identical to a second peptide when they differ by a non-conservative change if the epitope that the antibody recognizes is substantially identical. Peptides, which are "substantially similar" share sequences as, noted above except that residue positions, which are not identical, may differ by conservative amino acid changes.

[0080] The invention discloses AMT polynucleotides and polypeptides. The novel nucleotides and proteins of the invention have an expression pattern which indicates that they regulate ammonium transport and thus play an important role in plant development. The polynucleotides are expressed in various plant tissues. The polynucleotides and polypeptides thus provide an opportunity to manipulate plant development to alter seed and vegetative tissue development, timing or composition. This may be used to create a plant with altered N composition in source and sink.

Nucleic Acids

[0081] The present invention provides, inter alia, isolated nucleic acids of RNA, DNA, and analogs and/or chimeras thereof, comprising an amt polynucleotide.

[0082] The present invention also includes polynucleotides optimized for expression in different organisms. For example, for expression of the polynucleotide in a maize plant, the sequence can be altered to account for specific codon preferences and to alter GC content as according to Murray, et al., supra. Maize codon usage for 28 genes from maize plants is listed in Table 4 of Murray et al., supra.

[0083] The AMT nucleic acids of the present invention comprise isolated AMT polynucleotides which are inclusive of:

[0084] (a) a polynucleotide encoding an AMT polypeptide and conservatively modified and polymorphic variants thereof;

[0085] (b) a polynucleotide having at least 70% sequence identity with polynucleotides of (a) or (b);

[0086] (c) complementary sequences of polynucleotides of (a) or (b).

Construction of Nucleic Acids

[0087] The isolated nucleic acids of the present invention can be made using (a) standard recombinant methods, (b) synthetic techniques, or combinations thereof. In some embodiments, the polynucleotides of the present invention will be cloned, amplified, or otherwise constructed from a fungus or bacteria.

[0088] The nucleic acids may conveniently comprise sequences in addition to a polynucleotide of the present invention. For example, a multi-cloning site comprising one or more endonuclease restriction sites may be inserted into the nucleic acid to aid in isolation of the polynucleotide. Also, translatable sequences may be inserted to aid in the isolation of the translated polynucleotide of the present invention. For example, a hexa-histidine marker sequence provides a convenient means to purify the proteins of the present invention. The nucleic acid of the present invention—excluding the polynucleotide sequence—is optionally a vector, adapter, or linker for cloning and/or expression of a polynucleotide of the present invention. Additional sequences may be added to such cloning and/or expression sequences to optimize their function in cloning and/or expression, to aid in isolation of the polynucleotide, or to improve the introduction of the polynucleotide into a cell. Typically, the length of a nucleic acid of the present invention less the length of its polynucleotide of the present invention is less than 20 kilobase pairs, often less than 15 kb, and frequently less than 10 kb. Use of cloning vectors, expression vectors, adapters, and linkers is well known in the art. Exemplary nucleic acids include such vectors as: M13, lambda ZAP Express, lambda ZAP II, lambda gt10, lambda gt11, pBK-CMV, pBK-RSV, pBluescript II, lambda DASH II, lambda EMBL 3, lambda EMBL 4, pWE15, SuperCos 1, SurfZap, Uni-ZAP, pBC, pBS+/−, pSG5, pBK, pCR-Script, pET, pSPUTK, p3'SS, pGEM, pSK+/−, pGEX, pSPORTI and II, pOPRSVI CAT, pOPI3 CAT, pXT1, pSG5, pPbac, pMbac, pMC1neo, pOG44, pOG45, pFRTβGAL, pNEOβGAL, pRS403, pRS404, pRS405, pRS406, pRS413, pRS414, pRS415, pRS416, lambda MOSSlox, and lambda MOSElox. Optional vectors for the present invention, include but are not limited to, lambda ZAP II, and pGEX. For a description of various nucleic acids see, e.g., Stratagene Cloning Systems, Catalogs 1995, 1996, 1997 (La Jolla, Calif.); and, Amersham Life Sciences, Inc, Catalog '97 (Arlington Heights, Ill.).

Synthetic Methods for Constructing Nucleic Acids

[0089] The isolated nucleic acids of the present invention can also be prepared by direct chemical synthesis by methods such as the phosphotriester method of Narang, et al., (1979) *Meth. Enzymol.* 68:90-9; the phosphodiester method of Brown, et al., (1979) *Meth. Enzymol.* 68:109-51; the diethylphosphoramidite method of Beaucage, et al., (1981) *Tetra. Letts.* 22(20):1859-62; the solid phase phosphoramidite triester method described by Beaucage, et al., supra, e.g., using an automated synthesizer, e.g., as described in Needham-VanDevanter, et al., (1984) *Nucleic Acids Res.* 12:6159-68; and, the solid support method of U.S. Pat. No. 4,458,066. Chemical synthesis generally produces a single stranded oligonucleotide. This may be converted into double stranded DNA by hybridization with a complementary sequence or by polymerization with a DNA polymerase using the single strand as a template. One of skill will recognize that while chemical synthesis of DNA is limited to sequences of about 100 bases, longer sequences may be obtained by the ligation of shorter sequences.

UTRs and Codon Preference

[0090] In general, translational efficiency has been found to be regulated by specific sequence elements in the 5' noncoding or untranslated region (5' UTR) of the RNA. Positive

sequence motifs include translational initiation consensus sequences (Kozak, (1987) *Nucleic Acids Res.* 15:8125) and the 5<G> 7 methyl GpppG RNA cap structure (Drummond, et al., (1985) *Nucleic Acids Res.* 13:7375). Negative elements include stable intramolecular 5' UTR stem-loop structures (Muesing, et al., (1987) *Cell* 48:691) and AUG sequences or short open reading frames preceded by an appropriate AUG in the 5' UTR (Kozak, supra, Rao, et al., (1988) *Mol. and Cell. Biol.* 8:284). Accordingly, the present invention provides 5' and/or 3' UTR regions for modulation of translation of heterologous coding sequences.

[0091] Further, the polypeptide-encoding segments of the polynucleotides of the present invention can be modified to alter codon usage. Altered codon usage can be employed to alter translational efficiency and/or to optimize the coding sequence for expression in a desired host or to optimize the codon usage in a heterologous sequence for expression in maize. Codon usage in the coding regions of the polynucleotides of the present invention can be analyzed statistically using commercially available software packages such as "Codon Preference" available from the University of Wisconsin Genetics Computer Group. See, Devereaux, et al., (1984) *Nucleic Acids Res.* 12:387-395; or MacVector 4.1 (Eastman Kodak Co., New Haven, Conn.). Thus, the present invention provides a codon usage frequency characteristic of the coding region of at least one of the polynucleotides of the present invention. The number of polynucleotides (3 nucleotides per amino acid) that can be used to determine a codon usage frequency can be any integer from 3 to the number of polynucleotides of the present invention as provided herein. Optionally, the polynucleotides will be full-length sequences. An exemplary number of sequences for statistical analysis can be at least 1, 5, 10, 20, 50 or 100.

Sequence Shuffling

[0092] The present invention provides methods for sequence shuffling using polynucleotides of the present invention, and compositions resulting therefrom. Sequence shuffling is described in PCT publication No. 96/19256. See also, Zhang, et al., (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-9; and Zhao, et al., (1998) *Nature Biotech* 16:258-61. Generally, sequence shuffling provides a means for generating libraries of polynucleotides having a desired characteristic, which can be selected or screened for. Libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides, which comprise sequence regions, which have substantial sequence identity and can be homologously recombined in vitro or in vivo. The population of sequence-recombined polynucleotides comprises a subpopulation of polynucleotides which possess desired or advantageous characteristics and which can be selected by a suitable selection or screening method. The characteristics can be any property or attribute capable of being selected for or detected in a screening system, and may include properties of: an encoded protein, a transcriptional element, a sequence controlling transcription, RNA processing, RNA stability, chromatin conformation, translation, or other expression property of a gene or transgene, a replicative element, a protein-binding element, or the like, such as any feature which confers a selectable or detectable property. In some embodiments, the selected characteristic will be an altered K_m and/or K_{cat} over the wild-type protein as provided herein. In other embodiments, a protein or polynucleotide generated from sequence shuffling will have a ligand binding affinity greater than the non-shuffled wild-type polynucleotide. In yet other embodiments, a protein or polynucleotide generated from sequence shuffling will have an altered pH optimum as compared to the non-shuffled wild-type polynucleotide. The increase in such properties can be at least 110%, 120%, 130%, 140% or greater than 150% of the wild-type value.

Recombinant Expression Cassettes

[0093] The present invention further provides recombinant expression cassettes comprising a nucleic acid of the present invention. A nucleic acid sequence coding for the desired polynucleotide of the present invention, for example a cDNA or a genomic sequence encoding a polypeptide long enough to code for an active protein of the present invention, can be used to construct a recombinant expression cassette which can be introduced into the desired host cell. A recombinant expression cassette will typically comprise a polynucleotide of the present invention operably linked to transcriptional initiation regulatory sequences which will direct the transcription of the polynucleotide in the intended host cell, such as tissues of a transformed plant.

[0094] For example, plant expression vectors may include (1) a cloned plant gene under the transcriptional control of 5' and 3' regulatory sequences and (2) a dominant selectable marker. Such plant expression vectors may also contain, if desired, a promoter regulatory region (e.g., one conferring inducible or constitutive, environmentally- or developmentally-regulated, or cell- or tissue-specific/selective expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or a polyadenylation signal.

[0095] A plant promoter fragment can be employed which will direct expression of a polynucleotide of the present invention in all tissues of a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the 1'- or 2'-promoter derived from T-DNA of *Agrobacterium tumefaciens*, the Smas promoter, the cinnamyl alcohol dehydrogenase promoter (U.S. Pat. No. 5,683,439), the Nos promoter, the rubisco promoter, the GRP1-8 promoter, the 35S promoter from cauliflower mosaic virus (CaMV), as described in Odell, et al., (1985) *Nature* 313:810-2; rice actin (McElroy, et al., (1990) *Plant Cell* 163-171); ubiquitin (Christensen, et al., (1992) *Plant Mol. Biol.* 12:619-632 and Christensen, et al., (1992) *Plant Mol. Biol.* 18:675-89); PEMU (Last, et al., (1991) *Theor. Appl. Genet.* 81:581-8); MAS (Velten, et al., (1984) *EMBO J.* 3:2723-30); and maize H3 histone (Lepetit, et al., (1992) *Mol. Gen. Genet.* 231:276-85; and Atanassvoa, et al., (1992) *Plant Journal* 2(3):291-300); ALS promoter, as described in PCT Application Number WO 96/30530; and other transcription initiation regions from various plant genes known to those of skill. For the present invention ubiquitin is the preferred promoter for expression in monocot plants.

[0096] Alternatively, the plant promoter can direct expression of a polynucleotide of the present invention in a specific tissue or may be otherwise under more precise environmental or developmental control. Such promoters are referred to here as "inducible" promoters. Environmental conditions that may effect transcription by inducible promoters include pathogen attack, anaerobic conditions, or the presence of light. Examples of inducible promoters are the Adh1 promoter,

which is inducible by hypoxia or cold stress, the Hsp70 promoter, which is inducible by heat stress, and the PPDK promoter, which is inducible by light.

[0097] Examples of promoters under developmental control include promoters that initiate transcription only, or preferentially, in certain tissues, such as leaves, roots, fruit, seeds, or flowers. The operation of a promoter may also vary depending on its location in the genome. Thus, an inducible promoter may become fully or partially constitutive in certain locations.

[0098] If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from a variety of plant genes, or from T-DNA. The 3' end sequence to be added can be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene. Examples of such regulatory elements include, but are not limited to, 3' termination and/or polyadenylation regions such as those of the *Agrobacterium tumefaciens* nopaline synthase (nos) gene (Bevan, et al., (1983) *Nucleic Acids Res.* 12:369-85); the potato proteinase inhibitor II (PINII) gene (Keil, et al., (1986) *Nucleic Acids Res.* 14:5641-50; and An, et al., (1989) *Plant Cell* 1:115-22); and the CaMV 19S gene (Mogen, et al., (1990) *Plant Cell* 2:1261-72).

[0099] An intron sequence can be added to the 5' untranslated region or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold (Buchman and Berg, (1988) *Mol. Cell Biol.* 8:4395-4405; Callis, et al., (1987) *Genes Dev.* 1:1183-200). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. See generally, THE MAIZE HANDBOOK, Chapter 116, Freeling and Walbot, eds., Springer, N.Y. (1994).

[0100] Plant signal sequences, including, but not limited to, signal-peptide encoding DNA/RNA sequences which target proteins to the extracellular matrix of the plant cell (Dratewka-Kos, et al., (1989) *J. Biol. Chem.* 264:4896-900), such as the *Nicotiana plumbaginifolia* extension gene (DeLoose, et al., (1991) *Gene* 99:95-100); signal peptides which target proteins to the vacuole, such as the sweet potato sporamin gene (Matsuka, et al., (1991) *Proc. Natl. Acad. Sci. USA* 88:834) and the barley lectin gene (Wilkins, et al., (1990) *Plant Cell,* 2:301-13); signal peptides which cause proteins to be secreted, such as that of PRIb (Lind, et al., (1992) *Plant Mol. Biol.* 18:47-53) or the barley alpha amylase (BAA) (Rahmatullah, et al., (1989) *Plant Mol. Biol.* 12:119, and hereby incorporated by reference), or signal peptides which target proteins to the plastids such as that of rapeseed enoyl-Acp reductase (Verwaert, et al., (1994) *Plant Mol. Biol.* 26:189-202) are useful in the invention. The barley alpha amylase signal sequence fused to the AMT polynucleotide is the preferred construct for expression in maize for the present invention.

[0101] The vector comprising the sequences from a polynucleotide of the present invention will typically comprise a marker gene, which confers a selectable phenotype on plant cells. Usually, the selectable marker gene will encode antibiotic resistance, with suitable genes including genes coding for resistance to the antibiotic spectinomycin (e.g., the aada gene), the streptomycin phosphotransferase (SPT) gene coding for streptomycin resistance, the neomycin phosphotransferase (NPTII) gene encoding kanamycin or geneticin resistance, the hygromycin phosphotransferase (HPT) gene coding for hygromycin resistance, genes coding for resistance to herbicides which act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-type herbicides (e.g., the acetolactate synthase (ALS) gene containing mutations leading to such resistance in particular the S4 and/or Hra mutations), genes coding for resistance to herbicides which act to inhibit action of glutamine synthase, such as phosphinothricin or basta (e.g., the bar gene), or other such genes known in the art. The bar gene encodes resistance to the herbicide basta, and the ALS gene encodes resistance to the herbicide chlorsulfuron.

[0102] Typical vectors useful for expression of genes in higher plants are well known in the art and include vectors derived from the tumor-inducing (Ti) plasmid of *Agrobacterium tumefaciens* described by Rogers, et al., (1987) *Meth. Enzymol.* 153:253-77. These vectors are plant integrating vectors in that on transformation, the vectors integrate a portion of vector DNA into the genome of the host plant. Exemplary *A. tumefaciens* vectors useful herein are plasmids pKYLX6 and pKYLX7 of Schardl, et al., (1987) *Gene* 61:1-11, and Berger, et al., (1989) *Proc. Natl. Acad. Sci. USA,* 86:8402-6. Another useful vector herein is plasmid pBI101.2 that is available from CLONTECH Laboratories, Inc. (Palo Alto, Calif.).

Expression of Proteins in Host Cells

[0103] Using the nucleic acids of the present invention, one may express a protein of the present invention in a recombinantly engineered cell such as bacteria, yeast, insect, mammalian, or preferably plant cells. The cells produce the protein in a non-natural condition (e.g., in quantity, composition, location, and/or time), because they have been genetically altered through human intervention to do so.

[0104] It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of a nucleic acid encoding a protein of the present invention. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes will be made.

[0105] In brief summary, the expression of isolated nucleic acids encoding a protein of the present invention will typically be achieved by operably linking, for example, the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the DNA encoding a protein of the present invention. To obtain high level expression of a cloned gene, it is desirable to construct expression vectors which contain, at the minimum, a strong promoter, such as ubiquitin, to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Constitutive promoters are classified as providing for a range of constitutive expression. Thus, some are weak constitutive promoters, and others are strong constitutive promoters. Generally, by "weak promoter" is intended a promoter that drives expres-

sion of a coding sequence at a low level. By "low level" is intended at levels of about 1/10,000 transcripts to about 1/100,000 transcripts to about 1/500,000 transcripts. Conversely, a "strong promoter" drives expression of a coding sequence at a "high level," or about 1/10 transcripts to about 1/100 transcripts to about 1/1,000 transcripts.

[0106] One of skill would recognize that modifications could be made to a protein of the present invention without diminishing its biological activity. Some modifications may be made to facilitate the cloning, expression, or incorporation of the targeting molecule into a fusion protein. Such modifications are well known to those of skill in the art and include, for example, a methionine added at the amino terminus to provide an initiation site, or additional amino acids (e.g., poly His) placed on either terminus to create conveniently located restriction sites or termination codons or purification sequences.

Expression in Prokaryotes

[0107] Prokaryotic cells may be used as hosts for expression. Prokaryotes most frequently are represented by various strains of *E. coli*; however, other microbial strains may also be used. Commonly used prokaryotic control sequences which are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences, include such commonly used promoters as the beta lactamase (penicillinase) and lactose (lac) promoter systems (Chang, et al., (1977) *Nature* 198:1056), the tryptophan (trp) promoter system (Goeddel, et al., (1980) *Nucleic Acids Res.* 8:4057) and the lambda derived P L promoter and N-gene ribosome binding site (Shimatake, et al., (1981) *Nature* 292:128). The inclusion of selection markers in DNA vectors transfected in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol.

[0108] The vector is selected to allow introduction of the gene of interest into the appropriate host cell. Bacterial vectors are typically of plasmid or phage origin. Appropriate bacterial cells are infected with phage vector particles or transfected with naked phage vector DNA. If a plasmid vector is used, the bacterial cells are transfected with the plasmid vector DNA. Expression systems for expressing a protein of the present invention are available using *Bacillus* sp. and *Salmonella* (Palva, et al., (1983) *Gene* 22:229-35; Mosbach, et al., (1983) *Nature* 302:543-5). The pGEX-4T-1 plasmid vector from Pharmacia is the preferred *E. coli* expression vector for the present invention.

Expression in Eukaryotes

[0109] A variety of eukaryotic expression systems such as yeast, insect cell lines, plant and mammalian cells, are known to those of skill in the art. As explained briefly below, the present invention can be expressed in these eukaryotic systems. In some embodiments, transformed/transfected plant cells, as discussed infra, are employed as expression systems for production of the proteins of the instant invention.

[0110] Synthesis of heterologous proteins in yeast is well known. Sherman, et al., METHODS IN YEAST GENETICS, Cold Spring Harbor Laboratory (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Two widely utilized yeasts for production of eukaryotic proteins are *Saccharomyces cerevisiae* and *Pichia pastoris*. Vectors, strains, and protocols for expression in *Saccharomyces* and *Pichia* are known in the art and available from commercial suppliers (e.g., Invitrogen). Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or alcohol oxidase, and an origin of replication, termination sequences and the like as desired.

[0111] A protein of the present invention, once expressed, can be isolated from yeast by lysing the cells and applying standard protein isolation techniques to the lysates or the pellets. The monitoring of the purification process can be accomplished by using Western blot techniques or radioimmunoassay of other standard immunoassay techniques.

[0112] The sequences encoding proteins of the present invention can also be ligated to various expression vectors for use in transfecting cell cultures of, for instance, mammalian, insect, or plant origin. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV tk promoter or pgk (phosphoglycerate kinase) promoter), an enhancer (Queen, et al., (1986) *Immunol. Rev.* 89:49), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. Other animal cells useful for production of proteins of the present invention are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7^{th} ed., 1992).

[0113] Appropriate vectors for expressing proteins of the present invention in insect cells are usually derived from the SF9 baculovirus. Suitable insect cell lines include mosquito larvae, silkworm, armyworm, moth, and *Drosophila* cell lines such as a Schneider cell line (see, e.g., Schneider, (1987) *J. Embryol. Exp. Morphol.* 27:353-65).

[0114] As with yeast, when higher animal or plant host cells are employed, polyadenylation or transcription terminator sequences are typically incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, et al., (1983) *J. Virol.* 45:773-81). Additionally, gene sequences to control replication in the host cell may be incorporated into the vector such as those found in bovine papilloma virus type-vectors (Saveria-Campo, "Bovine Papilloma Virus DNA a Eukaryotic Cloning Vector," in DNA CLONING: A PRACTICAL APPROACH, vol. II, Glover, ed., IRL Press, Arlington, Va., pp. 213-38 (1985)).

[0115] In addition, the gene for AMT placed in the appropriate plant expression vector can be used to transform plant cells. The polypeptide can then be isolated from plant callus or the transformed cells can be used to regenerate transgenic plants. Such transgenic plants can be harvested, and the appropriate tissues (seed or leaves, for example) can be subjected to large scale protein extraction and purification techniques.

Plant Transformation Methods

[0116] Numerous methods for introducing foreign genes into plants are known and can be used to insert an amt poly-

nucleotide into a plant host, including biological and physical plant transformation protocols. See, e.g., Miki, et al., "Procedure for Introducing Foreign DNA into Plants," in METHODS IN PLANT MOLECULAR BIOLOGY AND BIOTECHNOLOGY, Glick and Thompson, eds., CRC Press, Inc., Boca Raton, pp. 67-88 (1993). The methods chosen vary with the host plant, and include chemical transfection methods such as calcium phosphate, microorganism-mediated gene transfer such as *Agrobacterium* (Horsch, et al., (1985) *Science* 227:1229-31), electroporation, micro-injection, and biolistic bombardment.

[0117] Expression cassettes and vectors and in vitro culture methods for plant cell or tissue transformation and regeneration of plants are known and available. See, e.g., Gruber, et al., "Vectors for Plant Transformation," in METHODS IN PLANT MOLECULAR BIOLOGY AND BIOTECHNOLOGY, supra, pp. 89-119.

[0118] The isolated polynucleotides or polypeptides may be introduced into the plant by one or more techniques typically used for direct delivery into cells. Such protocols may vary depending on the type of organism, cell, plant or plant cell, i.e. monocot or dicot, targeted for gene modification. Suitable methods of transforming plant cells include microinjection (Crossway, et al., (1986) *Biotechniques* 4:320-334; and U.S. Pat. No. 6,300,543), electroporation (Riggs, et al., (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, direct gene transfer (Paszkowski, et al., (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, Sanford, et al., U.S. Pat. No. 4,945,050; WO 91/10725; and McCabe, et al., (1988) *Biotechnology* 6:923-926). Also see, Tomes, et al., Direct DNA Transfer into Intact Plant Cells Via Microprojectile Bombardment. pp. 197-213 in Plant Cell, Tissue and Organ Culture, Fundamental Methods. eds. O. L. Gamborg & G. C. Phillips. Springer-Verlag Berlin Heidelberg N.Y., 1995; U.S. Pat. No. 5,736,369 (meristem); Weissinger, et al., (1988) *Ann. Rev. Genet.* 22:421-477; Sanford, et al., (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou, et al., (1988) *Plant Physiol.* 87:671-674 (soybean); Datta, et al., (1990) *Biotechnology* 8:736-740 (rice); Klein, et al., (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein, et al., (1988) *Biotechnology* 6:559-563 (maize); WO 91/10725 (maize); Klein, et al., (1988) *Plant Physiol.* 91:440-444 (maize); Fromm, et al., (1990) *Biotechnology* 8:833-839; and Gordon-Kamm, et al., (1990) *Plant Cell* 2:603-618 (maize); Hooydaas-Van Slogteren and Hooykaas (1984) *Nature* (London) 311:763-764; Bytebier, et al., (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet, et al., (1985) *In The Experimental Manipulation of Ovule Tissues*, ed. G. P. Chapman, et al., pp. 197-209 Longman, N.Y. (pollen); Kaeppler, et al., (1990) *Plant Cell Reports* 9:415-418; and Kaeppler, et al., (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); U.S. Pat. No. 5,693,512 (sonication); D'Halluin, et al., (1992) *Plant Cell* 4:1495-1505 (electroporation); Li, et al., (1993) *Plant Cell Reports* 12:250-255; and Christou and Ford (1995) Annals of Botany 75:407-413 (rice); Osjoda, et al., (1996) *Nature Biotech.* 14:745-750; *Agrobacterium* mediated maize transformation (U.S. Pat. No. 5,981,840); silicon carbide whisker methods (Frame, et al., (1994) *Plant J.* 6:941-948); laser methods (Guo, et al., (1995) *Physiologia Plantarum* 93:19-24); sonication methods (Bao, et al., (1997) *Ultrasound in Medicine & Biology* 23:953-959; Finer and Finer (2000) *Lett Appl Microbiol.* 30:406-10; Amoah, et al., (2001) *J Exp Bot* 52:1135-42); polyethylene glycol methods (Krens, et al., (1982) *Nature* 296:72-77); protoplasts of monocot and dicot cells can be transformed using electroporation (Fromm, et al., (1985) *Proc. Natl. Acad. Sci. USA* 82:5824-5828) and microinjection (Crossway, et al., (1986) *Mol. Gen. Genet.* 202:179-185); all of which are herein incorporated by reference.

Agrobacterium-Mediated Transformation

[0119] The most widely utilized method for introducing an expression vector into plants is based on the natural transformation system of *Agrobacterium. A. tumefaciens* and *A. rhizogenes* are plant pathogenic soil bacteria, which genetically transform plant cells. The Ti and Ri plasmids of *A. tumefaciens* and *A. rhizogenes*, respectively, carry genes responsible for genetic transformation of plants. See, e.g., Kado, (1991) *Crit. Rev. Plant Sci.* 10:1. Descriptions of the *Agrobacterium* vector systems and methods for *Agrobacterium*-mediated gene transfer are provided in Gruber, et al., supra; Miki, et al., supra; and Moloney, et al., (1989) *Plant Cell Reports* 8:238.

[0120] Similarly, the gene can be inserted into the T-DNA region of a Ti or Ri plasmid derived from *A. tumefaciens* or *A. rhizogenes*, respectively. Thus, expression cassettes can be constructed as above, using these plasmids. Many control sequences are known which when coupled to a heterologous coding sequence and transformed into a host organism show fidelity in gene expression with respect to tissue/organ specificity of the original coding sequence. See, e.g., Benfey and Chua, (1989) *Science* 244:174-81. Particularly suitable control sequences for use in these plasmids are promoters for constitutive leaf-specific expression of the gene in the various target plants. Other useful control sequences include a promoter and terminator from the nopaline synthase gene (NOS). The NOS promoter and terminator are present in the plasmid pARC2, available from the American Type Culture Collection and designated ATCC 67238. If such a system is used, the virulence (vir) gene from either the Ti or Ri plasmid must also be present, either along with the T-DNA portion, or via a binary system where the vir gene is present on a separate vector. Such systems, vectors for use therein, and methods of transforming plant cells are described in U.S. Pat. No. 4,658,082; US Patent Application Number 913,914, filed Oct. 1, 1986, as referenced in U.S. Pat. No. 5,262,306, issued Nov. 16, 1993; and Simpson, et al., (1986) *Plant Mol. Biol.* 6:403-15 (also referenced in the '306 patent); all incorporated by reference in their entirety.

[0121] Once constructed, these plasmids can be placed into *A. rhizogenes* or *A. tumefaciens* and these vectors used to transform cells of plant species, which are ordinarily susceptible to *Fusarium* or *Alternaria* infection. Several other transgenic plants are also contemplated by the present invention including but not limited to soybean, corn, sorghum, alfalfa, rice, clover, cabbage, banana, coffee, celery, tobacco, cowpea, cotton, melon, switchgrass, myscanthus, triticale and pepper. The selection of either *A. tumefaciens* or *A. rhizogenes* will depend on the plant being transformed thereby. In general *A. tumefaciens* is the preferred organism for transformation. Most dicotyledonous plants, some gymnosperms, and a few monocotyledonous plants (e.g., certain members of the *Liliales* and *Arales*) are susceptible to infection with *A. tumefaciens. A. rhizogenes* also has a wide host range, embracing most dicots and some gymnosperms, which includes members of the Leguminosae, Compositae, and Chenopodiaceae. Monocot plants can now be transformed with some success. EP Patent Application Number 604 662

A1 discloses a method for transforming monocots using *Agrobacterium*. EP Application Number 672 752 A1 discloses a method for transforming monocots with *Agrobacterium* using the scutellum of immature embryos. Ishida, et al., discuss a method for transforming maize by exposing immature embryos to *A. tumefaciens* (*Nature Biotechnology* 14:745-50 (1996)).

[0122] Once transformed, these cells can be used to regenerate transgenic plants. For example, whole plants can be infected with these vectors by wounding the plant and then introducing the vector into the wound site. Any part of the plant can be wounded, including leaves, stems and roots. Alternatively, plant tissue, in the form of an explant, such as cotyledonary tissue or leaf disks, can be inoculated with these vectors, and cultured under conditions, which promote plant regeneration. Roots or shoots transformed by inoculation of plant tissue with *A. rhizogenes* or *A. tumefaciens*, containing the gene coding for the fumonisin degradation enzyme, can be used as a source of plant tissue to regenerate fumonisin-resistant transgenic plants, either via somatic embryogenesis or organogenesis. Examples of such methods for regenerating plant tissue are disclosed in Shahin, (1985) *Theor. Appl. Genet.* 69:235-40; U.S. Pat. No. 4,658,082; Simpson, et al., supra; and US Patent Application Numbers 913,913 and 913, 914, both filed Oct. 1, 1986, as referenced in U.S. Pat. No. 5,262,306, issued Nov. 16, 1993, the entire disclosures therein incorporated herein by reference.

Direct Gene Transfer

[0123] Despite the fact that the host range for *Agrobacterium*-mediated transformation is broad, some major cereal crop species and gymnosperms have generally been recalcitrant to this mode of gene transfer, even though some success has recently been achieved in rice (Hiei, et al., (1994) *The Plant Journal* 6:271-82). Several methods of plant transformation, collectively referred to as direct gene transfer, have been developed as an alternative to *Agrobacterium*-mediated transformation.

[0124] A generally applicable method of plant transformation is microprojectile-mediated transformation, where DNA is carried on the surface of microprojectiles measuring about 1 to 4 μm. The expression vector is introduced into plant tissues with a biolistic device that accelerates the microprojectiles to speeds of 300 to 600 m/s which is sufficient to penetrate the plant cell walls and membranes (Sanford, et al., (1987) *Part. Sci. Technol.* 5:27; Sanford, (1988) *Trends Biotech* 6:299; Sanford, (1990) *Physiol. Plant* 79:206; and Klein, et al., (1992) *Biotechnology* 10:268).

[0125] Another method for physical delivery of DNA to plants is sonication of target cells as described in Zang, et al., (1991) *BioTechnology* 9:996. Alternatively, liposome or spheroplast fusions have been used to introduce expression vectors into plants. See, e.g., Deshayes, et al., (1985) *EMBO J.* 4:2731; and Christou, et al., (1987) *Proc. Natl. Acad. Sci. USA* 84:3962. Direct uptake of DNA into protoplasts using $CaCl_2$ precipitation, polyvinyl alcohol, or poly-L-ornithine has also been reported. See, e.g., Hain, et al., (1985) *Mol. Gen. Genet.* 199:161; and Draper, et al., (1982) *Plant Cell Physiol.* 23:451.

[0126] Electroporation of protoplasts and whole cells and tissues has also been described. See, e.g., Donn, et al., (1990) in *Abstracts of the VIIth Int'l. Congress on Plant Cell and Tissue Culture IAPTC*, A2-38, p. 53; D'Halluin, et al., (1992) *Plant Cell* 4:1495-505; and Spencer, et al., (1994) *Plant Mol. Biol.* 24:51-61.

Increasing the Activity and/or Level of an amt Polypeptide

[0127] Methods are provided to increase the activity and/or level of the AMT polypeptide of the invention. An increase in the level and/or activity of the AMT polypeptide of the invention can be achieved by providing to the plant an amt polypeptide. The AMT polypeptide can be provided by introducing the amino acid sequence encoding the AMT polypeptide into the plant, introducing into the plant a nucleotide sequence encoding an amt polypeptide or alternatively by modifying a genomic locus encoding the AMT polypeptide of the invention.

[0128] As discussed elsewhere herein, many methods are known the art for providing a polypeptide to a plant including, but not limited to, direct introduction of the polypeptide into the plant, introducing into the plant (transiently or stably) a polynucleotide construct encoding a polypeptide having AMT transporter activity. It is also recognized that the methods of the invention may employ a polynucleotide that is not capable of directing, in the transformed plant, the expression of a protein or an RNA. Thus, the level and/or activity of an amt polypeptide may be increased by altering the gene encoding the AMT polypeptide or its promoter. See, e.g., Kmiec, U.S. Pat. No. 5,565,350; Zarling, et al., PCT/US93/03868. Therefore mutagenized plants that carry mutations in AMT genes, where the mutations increase expression of the AMT gene or increase the AMT transporter activity of the encoded AMT polypeptide are provided.

Reducing the Activity and/or Level of an amt Polypeptide

[0129] Methods are provided to reduce or eliminate the activity of an amt polypeptide of the invention by transforming a plant cell with an expression cassette that expresses a polynucleotide that inhibits the expression of the AMT polypeptide. The polynucleotide may inhibit the expression of the AMT polypeptide directly, by preventing transcription or translation of the AMT messenger RNA, or indirectly, by encoding a polypeptide that inhibits the transcription or translation of an amt gene encoding an amt polypeptide. Methods for inhibiting or eliminating the expression of a gene in a plant are well known in the art, and any such method may be used in the present invention to inhibit the expression of an amt polypeptide.

[0130] In accordance with the present invention, the expression of an amt polypeptide is inhibited if the protein level of the AMT polypeptide is less than 70% of the protein level of the same AMT polypeptide in a plant that has not been genetically modified or mutagenized to inhibit the expression of that AMT polypeptide. In particular embodiments of the invention, the protein level of the AMT polypeptide in a modified plant according to the invention is less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5% or less than 2% of the protein level of the same AMT polypeptide in a plant that is not a mutant or that has not been genetically modified to inhibit the expression of that AMT polypeptide. The expression level of the AMT polypeptide may be measured directly, for example, by assaying for the level of AMT polypeptide expressed in the plant cell or plant, or indirectly, for example, by measuring the AMT transporter activity of the AMT polypeptide in the plant cell or plant, or by measuring the AMT in the plant. Methods for performing such assays are described elsewhere herein.

[0131] In other embodiments of the invention, the activity of the AMT polypeptides is reduced or eliminated by transforming a plant cell with an expression cassette comprising a polynucleotide encoding a polypeptide that inhibits the activity of an amt polypeptide. The AMT transporter activity of an amt polypeptide is inhibited according to the present invention if the AMT transporter activity of the AMT polypeptide is less than 70% of the AMT transporter activity of the same AMT polypeptide in a plant that has not been modified to inhibit the AMT transporter activity of that AMT polypeptide. In particular embodiments of the invention, the AMT transporter activity of the AMT polypeptide in a modified plant according to the invention is less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10% or less than 5% of the AMT transporter activity of the same AMT polypeptide in a plant that that has not been modified to inhibit the expression of that AMT polypeptide. The AMT transporter activity of an amt polypeptide is "eliminated" according to the invention when it is not detectable by the assay methods described elsewhere herein. Methods of determining the AMT transporter activity of an amt polypeptide are described elsewhere herein.

[0132] In other embodiments, the activity of an amt polypeptide may be reduced or eliminated by disrupting the gene encoding the AMT polypeptide. The invention encompasses mutagenized plants that carry mutations in AMT genes, where the mutations reduce expression of the AMT gene or inhibit the AMT transporter activity of the encoded AMT polypeptide.

[0133] Thus, many methods may be used to reduce or eliminate the activity of an amt polypeptide. In addition, more than one method may be used to reduce the activity of a single AMT polypeptide. Non-limiting examples of methods of reducing or eliminating the expression of AMT polypeptides are given below.

[0134] 1. Polynucleotide-Based Methods:

[0135] In some embodiments of the present invention, a plant is transformed with an expression cassette that is capable of expressing a polynucleotide that inhibits the expression of an amt polypeptide of the invention. The term "expression" as used herein refers to the biosynthesis of a gene product, including the transcription and/or translation of said gene product. For example, for the purposes of the present invention, an expression cassette capable of expressing a polynucleotide that inhibits the expression of at least one AMT polypeptide is an expression cassette capable of producing an RNA molecule that inhibits the transcription and/or translation of at least one AMT polypeptide of the invention. The "expression" or "production" of a protein or polypeptide from a DNA molecule refers to the transcription and translation of the coding sequence to produce the protein or polypeptide, while the "expression" or "production" of a protein or polypeptide from an RNA molecule refers to the translation of the RNA coding sequence to produce the protein or polypeptide.

[0136] Examples of polynucleotides that inhibit the expression of an amt polypeptide are given below.

[0137] i. Sense Suppression/Cosuppression

[0138] In some embodiments of the invention, inhibition of the expression of an amt polypeptide may be obtained by sense suppression or cosuppression. For cosuppression, an expression cassette is designed to express an RNA molecule corresponding to all or part of a messenger RNA encoding an amt polypeptide in the "sense" orientation. Over expression of the RNA molecule can result in reduced expression of the native gene. Accordingly, multiple plant lines transformed with the cosuppression expression cassette are screened to identify those that show the greatest inhibition of AMT polypeptide expression.

[0139] The polynucleotide used for cosuppression may correspond to all or part of the sequence encoding the AMT polypeptide, all or part of the 5' and/or 3' untranslated region of an amt polypeptide transcript, or all or part of both the coding sequence and the untranslated regions of a transcript encoding an amt polypeptide. In some embodiments where the polynucleotide comprises all or part of the coding region for the AMT polypeptide, the expression cassette is designed to eliminate the start codon of the polynucleotide so that no protein product will be translated.

[0140] Cosuppression may be used to inhibit the expression of plant genes to produce plants having undetectable protein levels for the proteins encoded by these genes. See, for example, Broin, et al., (2002) *Plant Cell* 14:1417-1432. Cosuppression may also be used to inhibit the expression of multiple proteins in the same plant. See, for example, U.S. Pat. No. 5,942,657. Methods for using cosuppression to inhibit the expression of endogenous genes in plants are described in Flavell, et al., (1994) *Proc. Natl. Acad. Sci. USA* 91:3490-3496; Jorgensen, et al., (1996) *Plant Mol. Biol.* 31:957-973; Johansen and Carrington (2001) *Plant Physiol.* 126:930-938; Broin, et al., (2002) *Plant Cell* 14:1417-1432; Stoutjesdijk, et al., (2002) *Plant Physiol.* 129:1723-1731; Yu, et al., (2003) *Phytochemistry* 63:753-763; and U.S. Pat. Nos. 5,034,323, 5,283,184, and 5,942,657; each of which is herein incorporated by reference. The efficiency of cosuppression may be increased by including a poly-dT region in the expression cassette at a position 3' to the sense sequence and 5' of the polyadenylation signal. See, US Patent Application Publication Number 20020048814, herein incorporated by reference. Typically, such a nucleotide sequence has substantial sequence identity to the sequence of the transcript of the endogenous gene, optimally greater than about 65% sequence identity, more optimally greater than about 85% sequence identity, most optimally greater than about 95% sequence identity. See, U.S. Pat. Nos. 5,283,184 and 5,034,323; herein incorporated by reference.

[0141] ii. Antisense Suppression

[0142] In some embodiments of the invention, inhibition of the expression of the AMT polypeptide may be obtained by antisense suppression. For antisense suppression, the expression cassette is designed to express an RNA molecule complementary to all or part of a messenger RNA encoding the AMT polypeptide. Over expression of the antisense RNA molecule can result in reduced expression of the native gene. Accordingly, multiple plant lines transformed with the antisense suppression expression cassette are screened to identify those that show the greatest inhibition of AMT polypeptide expression.

[0143] The polynucleotide for use in antisense suppression may correspond to all or part of the complement of the sequence encoding the AMT polypeptide, all or part of the complement of the 5' and/or 3' untranslated region of the AMT transcript, or all or part of the complement of both the coding sequence and the untranslated regions of a transcript encoding the AMT polypeptide. In addition, the antisense polynucleotide may be fully complementary (i.e., 100% identical to the complement of the target sequence) or partially complementary (i.e., less than 100% identical to the comple-

ment of the target sequence) to the target sequence. Antisense suppression may be used to inhibit the expression of multiple proteins in the same plant. See, for example, U.S. Pat. No. 5,942,657. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides, 100 nucleotides, 200 nucleotides, 300, 400, 450, 500, 550 or greater may be used. Methods for using antisense suppression to inhibit the expression of endogenous genes in plants are described, for example, in Liu, et al., (2002) *Plant Physiol.* 129:1732-1743 and U.S. Pat. Nos. 5,759,829 and 5,942,657, each of which is herein incorporated by reference. Efficiency of antisense suppression may be increased by including a poly-dT region in the expression cassette at a position 3' to the antisense sequence and 5' of the polyadenylation signal. See, US Patent Application Publication Number 20020048814, herein incorporated by reference.

[0144] iii. Double-Stranded RNA Interference

[0145] In some embodiments of the invention, inhibition of the expression of an amt polypeptide may be obtained by double-stranded RNA (dsRNA) interference. For dsRNA interference, a sense RNA molecule like that described above for cosuppression and an antisense RNA molecule that is fully or partially complementary to the sense RNA molecule are expressed in the same cell, resulting in inhibition of the expression of the corresponding endogenous messenger RNA.

[0146] Expression of the sense and antisense molecules can be accomplished by designing the expression cassette to comprise both a sense sequence and an antisense sequence. Alternatively, separate expression cassettes may be used for the sense and antisense sequences. Multiple plant lines transformed with the dsRNA interference expression cassette or expression cassettes are then screened to identify plant lines that show the greatest inhibition of AMT polypeptide expression. Methods for using dsRNA interference to inhibit the expression of endogenous plant genes are described in Waterhouse, et al., (1998) *Proc. Natl. Acad. Sci. USA* 95:13959-13964, Liu, et al., (2002) *Plant Physiol.* 129:1732-1743, and WO 99/49029, WO 99/53050, WO 99/61631, and WO 00/49035; each of which is herein incorporated by reference.

[0147] iv. Hairpin RNA Interference and Intron-Containing Hairpin RNA Interference

[0148] In some embodiments of the invention, inhibition of the expression of an amt polypeptide may be obtained by hairpin RNA (hpRNA) interference or intron-containing hairpin RNA (ihpRNA) interference. These methods are highly efficient at inhibiting the expression of endogenous genes. See, Waterhouse and Helliwell (2003) *Nat. Rev. Genet.* 4:29-38 and the references cited therein.

[0149] For hpRNA interference, the expression cassette is designed to express an RNA molecule that hybridizes with itself to form a hairpin structure that comprises a single-stranded loop region and a base-paired stem. The base-paired stem region comprises a sense sequence corresponding to all or part of the endogenous messenger RNA encoding the gene whose expression is to be inhibited, and an antisense sequence that is fully or partially complementary to the sense sequence. Alternatively, the base-paired stem region may correspond to a portion of a promoter sequence controlling expression of the gene to be inhibited. Thus, the base-paired stem region of the molecule generally determines the specificity of the RNA interference. hpRNA molecules are highly efficient at inhibiting the expression of endogenous genes, and the RNA interference they induce is inherited by subsequent generations of plants. See, for example, Chuang and Meyerowitz (2000) *Proc. Natl. Acad. Sci. USA* 97:4985-4990; Stoutjesdijk, et al., (2002) *Plant Physiol.* 129:1723-1731; and Waterhouse and Helliwell (2003) *Nat. Rev. Genet.* 4:29-38. Methods for using hpRNA interference to inhibit or silence the expression of genes are described, for example, in Chuang and Meyerowitz (2000) *Proc. Natl. Acad. Sci. USA* 97:4985-4990; Stoutjesdijk, et al., (2002) *Plant Physiol.* 129:1723-1731; Waterhouse and Helliwell (2003) *Nat. Rev. Genet.* 4:29-38; Pandolfini, et al., *BMC Biotechnology* 3:7, and US Patent Application Publication Number 20030175965; each of which is herein incorporated by reference. A transient assay for the efficiency of hpRNA constructs to silence gene expression in vivo has been described by Panstruga, et al., (2003) *Mol. Biol. Rep.* 30:135-140, herein incorporated by reference.

[0150] For ihpRNA, the interfering molecules have the same general structure as for hpRNA, but the RNA molecule additionally comprises an intron that is capable of being spliced in the cell in which the ihpRNA is expressed. The use of an intron minimizes the size of the loop in the hairpin RNA molecule following splicing, and this increases the efficiency of interference. See, for example, Smith, et al., (2000) *Nature* 407:319-320. In fact, Smith, et al., show 100% suppression of endogenous gene expression using ihpRNA-mediated interference. Methods for using ihpRNA interference to inhibit the expression of endogenous plant genes are described, for example, in Smith, et al., (2000) *Nature* 407:319-320; Wesley, et al., (2001) *Plant J.* 27:581-590; Wang and Waterhouse (2001) *Curr. Opin. Plant Biol.* 5:146-150; Waterhouse and Helliwell (2003) *Nat. Rev. Genet.* 4:29-38; Helliwell and Waterhouse (2003) *Methods* 30:289-295, and US Patent Application Publication Number 20030180945, each of which is herein incorporated by reference.

[0151] The expression cassette for hpRNA interference may also be designed such that the sense sequence and the antisense sequence do not correspond to an endogenous RNA. In this embodiment, the sense and antisense sequence flank a loop sequence that comprises a nucleotide sequence corresponding to all or part of the endogenous messenger RNA of the target gene. Thus, it is the loop region that determines the specificity of the RNA interference. See, for example, WO 02/00904, Mette, et al., (2000) *EMBO J.* 19:5194-5201; Matzke, et al., (2001) *Curr. Opin. Genet. Devel.* 11:221-227; Scheid, et al., (2002) *Proc. Natl. Acad. Sci.*, USA 99:13659-13662; Aufsaftz, et al., (2002) *Proc. Nat'l. Acad. Sci.* 99(4):16499-16506; Sijen, et al., *Curr. Biol.* (2001) 11:436-440), herein incorporated by reference.

[0152] v. Amplicon-Mediated Interference

[0153] Amplicon expression cassettes comprise a plant virus-derived sequence that contains all or part of the target gene but generally not all of the genes of the native virus. The viral sequences present in the transcription product of the expression cassette allow the transcription product to direct its own replication. The transcripts produced by the amplicon may be either sense or antisense relative to the target sequence (i.e., the messenger RNA for the AMT polypeptide). Methods of using amplicons to inhibit the expression of endogenous plant genes are described, for example, in Angell and Baulcombe (1997) *EMBO J.* 16:3675-3684, Angell and Baulcombe (1999) *Plant J.* 20:357-362, and U.S. Pat. No. 6,646,805, each of which is herein incorporated by reference.

[0154] vi. Ribozymes

[0155] In some embodiments, the polynucleotide expressed by the expression cassette of the invention is catalytic RNA or has ribozyme activity specific for the messenger RNA of the AMT polypeptide. Thus, the polynucleotide causes the degradation of the endogenous messenger RNA, resulting in reduced expression of the AMT polypeptide. This method is described, for example, in U.S. Pat. No. 4,987,071, herein incorporated by reference.

[0156] vii. Small Interfering RNA or Micro RNA

[0157] In some embodiments of the invention, inhibition of the expression of an amt polypeptide may be obtained by RNA interference by expression of a gene encoding a micro RNA (miRNA). miRNAs are regulatory agents consisting of about 22 ribonucleotides. miRNA are highly efficient at inhibiting the expression of endogenous genes. See, for example, Javier, et al., (2003) *Nature* 425:257-263, herein incorporated by reference.

[0158] For miRNA interference, the expression cassette is designed to express an RNA molecule that is modeled on an endogenous miRNA gene. The miRNA gene encodes an RNA that forms a hairpin structure containing a 22-nucleotide sequence that is complementary to another endogenous gene (target sequence). For suppression of AMT expression, the 22-nucleotide sequence is selected from an amt transcript sequence and contains 22 nucleotides of said AMT sequence in sense orientation and 21 nucleotides of a corresponding antisense sequence that is complementary to the sense sequence. miRNA molecules are highly efficient at inhibiting the expression of endogenous genes, and the RNA interference they induce is inherited by subsequent generations of plants.

[0159] 2. Polypeptide-Based Inhibition of Gene Expression

[0160] In one embodiment, the polynucleotide encodes a zinc finger protein that binds to a gene encoding an amt polypeptide, resulting in reduced expression of the gene. In particular embodiments, the zinc finger protein binds to a regulatory region of an amt gene. In other embodiments, the zinc finger protein binds to a messenger RNA encoding an amt polypeptide and prevents its translation. Methods of selecting sites for targeting by zinc finger proteins have been described, for example, in U.S. Pat. No. 6,453,242, and methods for using zinc finger proteins to inhibit the expression of genes in plants are described, for example, in US Patent Application Publication Number 20030037355; each of which is herein incorporated by reference.

[0161] 3. Polypeptide-Based Inhibition of Protein Activity

[0162] In some embodiments of the invention, the polynucleotide encodes an antibody that binds to at least one AMT polypeptide, and reduces the AMT transporter activity of the AMT polypeptide. In another embodiment, the binding of the antibody results in increased turnover of the antibody-AMT complex by cellular quality control mechanisms. The expression of antibodies in plant cells and the inhibition of molecular pathways by expression and binding of antibodies to proteins in plant cells are well known in the art. See, for example, Conrad and Sonnewald (2003) *Nature Biotech.* 21:35-36, incorporated herein by reference.

[0163] 4. Gene Disruption

[0164] In some embodiments of the present invention, the activity of an amt polypeptide is reduced or eliminated by disrupting the gene encoding the AMT polypeptide. The gene encoding the AMT polypeptide may be disrupted by any method known in the art. For example, in one embodiment, the gene is disrupted by transposon tagging. In another embodiment, the gene is disrupted by mutagenizing plants using random or targeted mutagenesis, and selecting for plants that have reduced AMT transporter activity.

[0165] i. Transposon Tagging

[0166] In one embodiment of the invention, transposon tagging is used to reduce or eliminate the AMT activity of one or more AMT polypeptide. Transposon tagging comprises inserting a transposon within an endogenous AMT gene to reduce or eliminate expression of the AMT polypeptide. "AMT gene" is intended to mean the gene that encodes an amt polypeptide according to the invention.

[0167] In this embodiment, the expression of one or more AMT polypeptide is reduced or eliminated by inserting a transposon within a regulatory region or coding region of the gene encoding the AMT polypeptide. A transposon that is within an exon, intron, 5' or 3' untranslated sequence, a promoter, or any other regulatory sequence of an amt gene may be used to reduce or eliminate the expression and/or activity of the encoded AMT polypeptide.

[0168] Methods for the transposon tagging of specific genes in plants are well known in the art. See, for example, Maes, et al., (1999) *Trends Plant Sci.* 4:90-96; Dharmapuri and Sonti (1999) *FEMS Microbiol. Lett.* 179:53-59; Meissner, et al., (2000) *Plant J.* 22:265-274; Phogat, et al., (2000) *J. Biosci.* 25:57-63; Walbot (2000) *Curr. Opin. Plant Biol.* 2:103-107; Gai, et al., (2000) *Nucleic Acids Res.* 28:94-96; Fitzmaurice, et al., (1999) *Genetics* 153:1919-1928). In addition, the TUSC process for selecting Mu insertions in selected genes has been described in Bensen, et al., (1995) *Plant Cell* 7:75-84; Mena, et al., (1996) *Science* 274:1537-1540; and U.S. Pat. No. 5,962,764; each of which is herein incorporated by reference.

[0169] ii. Mutant Plants with Reduced Activity

[0170] Additional methods for decreasing or eliminating the expression of endogenous genes in plants are also known in the art and can be similarly applied to the instant invention. These methods include other forms of mutagenesis, such as ethyl methanesulfonate-induced mutagenesis, deletion mutagenesis, and fast neutron deletion mutagenesis used in a reverse genetics sense (with PCR) to identify plant lines in which the endogenous gene has been deleted. For examples of these methods see, Ohshima, et al., (1998) *Virology* 243: 472-481; Okubara, et al., (1994) *Genetics* 137:867-874; and Quesada, et al., (2000) *Genetics* 154:421-436; each of which is herein incorporated by reference. In addition, a fast and automatable method for screening for chemically induced mutations, TILLING (Targeting Induced Local Lesions In Genomes), using denaturing HPLC or selective endonuclease digestion of selected PCR products is also applicable to the instant invention. See, McCallum, et al., (2000) *Nat. Biotechnol.* 18:455-457, herein incorporated by reference.

[0171] Mutations that impact gene expression or that interfere with the function (AMT transporter activity) of the encoded protein are well known in the art. Insertional mutations in gene exons usually result in null-mutants. Mutations in conserved residues are particularly effective in inhibiting the AMT transporter activity of the encoded protein. Conserved residues of plant AMT polypeptides suitable for mutagenesis with the goal to eliminate AMT transporter activity have been described. Such mutants can be isolated according to well-known procedures, and mutations in dif-

ferent AMT loci can be stacked by genetic crossing. See, for example, Gruis, et al., (2002) *Plant Cell* 14:2863-2882.

[0172] In another embodiment of this invention, dominant mutants can be used to trigger RNA silencing due to gene inversion and recombination of a duplicated gene locus. See, for example, Kusaba, et al., (2003) *Plant Cell* 15:1455-1467.

[0173] The invention encompasses additional methods for reducing or eliminating the activity of one or more AMT polypeptide. Examples of other methods for altering or mutating a genomic nucleotide sequence in a plant are known in the art and include, but are not limited to, the use of RNA:DNA vectors, RNA:DNA mutational vectors, RNA:DNA repair vectors, mixed-duplex oligonucleotides, self-complementary RNA:DNA oligonucleotides, and recombinogenic oligonucleobases. Such vectors and methods of use are known in the art. See, for example, U.S. Pat. Nos. 5,565,350; 5,731,181; 5,756,325; 5,760,012; 5,795,972; and 5,871,984; each of which are herein incorporated by reference. See also, WO 98/49350, WO 99/07865, WO 99/25821, and Beetham, et al., (1999) *Proc. Natl. Acad. Sci. USA* 96:8774-8778; each of which is herein incorporated by reference.

[0174] iii. Modulating AMT Transporter Activity

[0175] In specific methods, the level and/or activity of an amt regulator in a plant is decreased by increasing the level or activity of the AMT polypeptide in the plant. Methods for increasing the level and/or activity of AMT polypeptides in a plant are discussed elsewhere herein. Briefly, such methods comprise providing an amt polypeptide of the invention to a plant and thereby increasing the level and/or activity of the AMT polypeptide. In other embodiments, an amt nucleotide sequence encoding an amt polypeptide can be provided by introducing into the plant a polynucleotide comprising an amt nucleotide sequence of the invention, expressing the AMT sequence, increasing the activity of the AMT polypeptide, and thereby decreasing the ammonium uptake or transport in the plant or plant part. In other embodiments, the AMT nucleotide construct introduced into the plant is stably incorporated into the genome of the plant.

[0176] As discussed above, one of skill will recognize the appropriate promoter to use to modulate the level/activity of an amt transporter in the plant. Exemplary promoters for this embodiment have been disclosed elsewhere herein.

[0177] Accordingly, the present invention further provides plants having a modified number of cells when compared to the number of cells of a control plant tissue. In one embodiment, the plant of the invention has an increased level/activity of the AMT polypeptide of the invention and thus has an increased Ammonium transport in the plant tissue. In other embodiments, the plant of the invention has a reduced or eliminated level of the AMT polypeptide of the invention and thus has an increased NUE in the plant tissue. In other embodiments, such plants have stably incorporated into their genome a nucleic acid molecule comprising an amt nucleotide sequence of the invention operably linked to a promoter that drives expression in the plant cell.

[0178] iv. Modulating Root Development

[0179] Methods for modulating root development in a plant are provided. By "modulating root development" is intended any alteration in the development of the plant root when compared to a control plant. Such alterations in root development include, but are not limited to, alterations in the growth rate of the primary root, the fresh root weight, the extent of lateral and adventitious root formation, the vasculature system, meristem development, or radial expansion.

[0180] Methods for modulating root development in a plant are provided. The methods comprise modulating the level and/or activity of the AMT polypeptide in the plant. In one method, an amt sequence of the invention is provided to the plant. In another method, the AMT nucleotide sequence is provided by introducing into the plant a polynucleotide comprising an amt nucleotide sequence of the invention, expressing the AMT sequence, and thereby modifying root development. In still other methods, the AMT nucleotide construct introduced into the plant is stably incorporated into the genome of the plant.

[0181] In other methods, root development is modulated by altering the level or activity of the AMT polypeptide in the plant. A decrease in AMT activity can result in at least one or more of the following alterations to root development, including, but not limited to, larger root meristems, increased in root growth, enhanced radial expansion, an enhanced vasculature system, increased root branching, more adventitious roots, and/or an increase in fresh root weight when compared to a control plant.

[0182] As used herein, "root growth" encompasses all aspects of growth of the different parts that make up the root system at different stages of its development in both monocotyledonous and dicotyledonous plants. It is to be understood that enhanced root growth can result from enhanced growth of one or more of its parts including the primary root, lateral roots, adventitious roots, etc.

[0183] Methods of measuring such developmental alterations in the root system are known in the art. See, for example, US Patent Application Publication Number 2003/0074698 and Werner, et al., (2001) *PNAS* 18:10487-10492, both of which are herein incorporated by reference.

[0184] As discussed above, one of skill will recognize the appropriate promoter to use to modulate root development in the plant. Exemplary promoters for this embodiment include constitutive promoters and root-preferred promoters. Exemplary root-preferred promoters have been disclosed elsewhere herein.

[0185] Stimulating root growth and increasing root mass by decreasing the activity and/or level of the AMT polypeptide also finds use in improving the standability of a plant. The term "resistance to lodging" or "standability" refers to the ability of a plant to fix itself to the soil. For plants with an erect or semi-erect growth habit, this term also refers to the ability to maintain an upright position under adverse (environmental) conditions. This trait relates to the size, depth and morphology of the root system. In addition, stimulating root growth and increasing root mass by decreasing the level and/or activity of the AMT polypeptide also finds use in promoting in vitro propagation of explants.

[0186] Furthermore, higher root biomass production due to an decreased level and/or activity of AMT activity has a direct effect on the yield and an indirect effect of production of compounds produced by root cells or transgenic root cells or cell cultures of said transgenic root cells. One example of an interesting compound produced in root cultures is shikonin, the yield of which can be advantageously enhanced by said methods.

[0187] Accordingly, the present invention further provides plants having modulated root development when compared to the root development of a control plant. In some embodiments, the plant of the invention has an increased level/activity of the AMT polypeptide of the invention and has enhanced root growth and/or root biomass. In other embodiments, such

plants have stably incorporated into their genome a nucleic acid molecule comprising an amt nucleotide sequence of the invention operably linked to a promoter that drives expression in the plant cell.

[0188] v. Modulating Shoot and Leaf Development

[0189] Methods are also provided for modulating shoot and leaf development in a plant. By "modulating shoot and/or leaf development" is intended any alteration in the development of the plant shoot and/or leaf. Such alterations in shoot and/or leaf development include, but are not limited to, alterations in shoot meristem development, in leaf number, leaf size, leaf and stem vasculature, internode length, and leaf senescence. As used herein, "leaf development" and "shoot development" encompasses all aspects of growth of the different parts that make up the leaf system and the shoot system, respectively, at different stages of their development, both in monocotyledonous and dicotyledonous plants. Methods for measuring such developmental alterations in the shoot and leaf system are known in the art. See, for example, Werner, et al., (2001) *PNAS* 98:10487-10492 and US Patent Application Publication Number 2003/0074698, each of which is herein incorporated by reference.

[0190] The method for modulating shoot and/or leaf development in a plant comprises modulating the activity and/or level of an AMT polypeptide of the invention. In one embodiment, an amt sequence of the invention is provided. In other embodiments, the AMT nucleotide sequence can be provided by introducing into the plant a polynucleotide comprising an amt nucleotide sequence of the invention, expressing the AMT sequence, and thereby modifying shoot and/or leaf development. In other embodiments, the AMT nucleotide construct introduced into the plant is stably incorporated into the genome of the plant.

[0191] In specific embodiments, shoot or leaf development is modulated by increasing the level and/or activity of the AMT polypeptide in the plant. An increase in AMT activity can result in at least one or more of the following alterations in shoot and/or leaf development, including, but not limited to, reduced leaf number, reduced leaf surface, reduced vascular, shorter internodes and stunted growth, and retarded leaf senescence, when compared to a control plant.

[0192] As discussed above, one of skill will recognize the appropriate promoter to use to modulate shoot and leaf development of the plant. Exemplary promoters for this embodiment include constitutive promoters, shoot-preferred promoters, shoot meristem-preferred promoters, and leaf-preferred promoters. Exemplary promoters have been disclosed elsewhere herein.

[0193] Increasing AMT activity and/or level in a plant results in shorter internodes and stunted growth. Thus, the methods of the invention find use in producing dwarf plants. In addition, as discussed above, modulation AMT activity in the plant modulates both root and shoot growth. Thus, the present invention further provides methods for altering the root/shoot ratio. Shoot or leaf development can further be modulated by decreasing the level and/or activity of the AMT polypeptide in the plant.

[0194] Accordingly, the present invention further provides plants having modulated shoot and/or leaf development when compared to a control plant. In some embodiments, the plant of the invention has an increased level/activity of the AMT polypeptide of the invention. In other embodiments, the plant of the invention has a decreased level/activity of the AMT polypeptide of the invention.

[0195] vi Modulating Reproductive Tissue Development

[0196] Methods for modulating reproductive tissue development are provided. In one embodiment, methods are provided to modulate floral development in a plant. By "modulating floral development" is intended any alteration in a structure of a plant's reproductive tissue as compared to a control plant in which the activity or level of the AMT polypeptide has not been modulated. "Modulating floral development" further includes any alteration in the timing of the development of a plant's reproductive tissue (i.e., a delayed or a accelerated timing of floral development) when compared to a control plant in which the activity or level of the AMT polypeptide has not been modulated. Macroscopic alterations may include changes in size, shape, number, or location of reproductive organs, the developmental time period that these structures form, or the ability to maintain or proceed through the flowering process in times of environmental stress. Microscopic alterations may include changes to the types or shapes of cells that make up the reproductive organs.

[0197] The method for modulating floral development in a plant comprises modulating AMT activity in a plant. In one method, an AMT sequence of the invention is provided. AN AMT nucleotide sequence can be provided by introducing into the plant a polynucleotide comprising an amt nucleotide sequence of the invention, expressing the AMT sequence, and thereby modifying floral development. In other embodiments, the AMT nucleotide construct introduced into the plant is stably incorporated into the genome of the plant.

[0198] In specific methods, floral development is modulated by increasing the level or activity of the AMT polypeptide in the plant. An increase in AMT activity can result in at least one or more of the following alterations in floral development, including, but not limited to, retarded flowering, reduced number of flowers, partial male sterility, and reduced seed set, when compared to a control plant. Inducing delayed flowering or inhibiting flowering can be used to enhance yield in forage crops such as alfalfa. Methods for measuring such developmental alterations in floral development are known in the art. See, for example, Mouradov, et al., (2002) *The Plant Cell S*11-S130, herein incorporated by reference.

[0199] As discussed above, one of skill will recognize the appropriate promoter to use to modulate floral development of the plant. Exemplary promoters for this embodiment include constitutive promoters, inducible promoters, shoot-preferred promoters, and inflorescence-preferred promoters.

[0200] In other methods, floral development is modulated by decreasing the level and/or activity of the AMT sequence of the invention. Such methods can comprise introducing an amt nucleotide sequence into the plant and decreasing the activity of the AMT polypeptide. In other methods, the AMT nucleotide construct introduced into the plant is stably incorporated into the genome of the plant. Decreasing expression of the AMT sequence of the invention can modulate floral development during periods of stress. Such methods are described elsewhere herein. Accordingly, the present invention further provides plants having modulated floral development when compared to the floral development of a control plant. Compositions include plants having a decreased level/activity of the AMT polypeptide of the invention and having an altered floral development. Compositions also include plants having a decreased level/activity of the AMT polypeptide of the invention wherein the plant maintains or proceeds through the flowering process in times of stress.

[0201] Methods are also provided for the use of the AMT sequences of the invention to increase nitrogen use efficiency. The method comprises decreasing or increasing the activity of the AMT sequences in a plant or plant part, such as the roots, shoot, epidermal cells, etc.

[0202] As discussed above, one of skill will recognize the appropriate promoter to use to manipulate the expression of AMTs. Exemplary promoters of this embodiment include constitutive promoters, inducible promoters, and root or shoot or leaf preferred promoters.

[0203] vii. Method of Use for AMT Promoter Polynucleotides

[0204] The polynucleotides comprising the AMT promoters disclosed in the present invention, as well as variants and fragments thereof, are useful in the genetic manipulation of any host cell, preferably plant cell, when assembled with a DNA construct such that the promoter sequence is operably linked to a nucleotide sequence comprising a polynucleotide of interest. In this manner, the AMT promoter polynucleotides of the invention are provided in expression cassettes along with a polynucleotide sequence of interest for expression in the host cell of interest. As discussed in Example XX below, the AMT promoter sequences of the invention are expressed in a variety of tissues and thus the promoter sequences can find use in regulating the temporal and/or the spatial expression of polynucleotides of interest.

[0205] Synthetic hybrid promoter regions are known in the art. Such regions comprise upstream promoter elements of one polynucleotide operably linked to the promoter element of another polynucleotide. In an embodiment of the invention, heterologous sequence expression is controlled by a synthetic hybrid promoter comprising the AMT promoter sequences of the invention, or a variant or fragment thereof, operably linked to upstream promoter element(s) from a heterologous promoter. Upstream promoter elements that are involved in the plant defense system have been identified and may be used to generate a synthetic promoter. See, for example, Rushton, et al., (1998) *Curr. Opin. Plant Biol.* 1:311-315. Alternatively, a synthetic AMT promoter sequence may comprise duplications of the upstream promoter elements found within the AMT promoter sequences.

[0206] It is recognized that the promoter sequence of the invention may be used with its native AMT coding sequences. A DNA construct comprising the AMT promoter operably linked with its native AMT gene may be used to transform any plant of interest to bring about a desired phenotypic change, such as, modulating root, shoot, leaf, floral, and embryo development, stress tolerance, and any other phenotype described elsewhere herein.

[0207] The promoter nucleotide sequences and methods disclosed herein are useful in regulating expression of any heterologous nucleotide sequence in a host plant in order to vary the phenotype of a plant. Various changes in phenotype are of interest including modifying the fatty acid composition in a plant, altering the amino acid content of a plant, altering a plant's pathogen defense mechanism, and the like. These results can be achieved by providing expression of heterologous products or increased expression of endogenous products in plants. Alternatively, the results can be achieved by providing for a reduction of expression of one or more endogenous products, particularly enzymes or cofactors in the plant. These changes result in a change in phenotype of the transformed plant.

[0208] Genes of interest are reflective of the commercial markets and interests of those involved in the development of the crop. Crops and markets of interest change, and as developing nations open up world markets, new crops and technologies will emerge also. In addition, as our understanding of agronomic traits and characteristics such as yield and heterosis increase, the choice of genes for transformation will change accordingly. General categories of genes of interest include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include genes encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, and commercial products. Genes of interest include, generally, those involved in oil, starch, carbohydrate, or nutrient metabolism as well as those affecting kernel size, sucrose loading, and the like.

[0209] In certain embodiments the nucleic acid sequences of the present invention can be used in combination ("stacked") with other polynucleotide sequences of interest in order to create plants with a desired phenotype. The combinations generated can include multiple copies of any one or more of the polynucleotides of interest. The polynucleotides of the present invention may be stacked with any gene or combination of genes to produce plants with a variety of desired trait combinations, including but not limited to traits desirable for animal feed such as high oil genes (e.g., U.S. Pat. No. 6,232,529); balanced amino acids (e.g., hordothionins (U.S. Pat. Nos. 5,990,389; 5,885,801; 5,885,802; and 5,703,409); barley high lysine (Williamson, et al., (1987) *Eur. J. Biochem.* 165:99-106; and WO 98/20122); and high methionine proteins (Pedersen, et al., (1986) *J. Biol. Chem.* 261:6279; Kirihara, et al., (1988) *Gene* 71:359; and Musumura, et al., (1989) *Plant Mol. Biol.* 12: 123)); increased digestibility (e.g., modified storage proteins (U.S. patent application Ser. No. 10/053,410, filed Nov. 7, 2001); and thioredoxins (U.S. patent application Ser. No. 10/005,429, filed Dec. 3, 2001)), the disclosures of which are herein incorporated by reference. The polynucleotides of the present invention can also be stacked with traits desirable for insect, disease or herbicide resistance (e.g., *Bacillus thuringiensis* toxic proteins (U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; Geiser, et al., (1986) *Gene* 48:109); lectins (Van Damme, et al., (1994) *Plant Mol. Biol.* 24:825); fumonisin detoxification genes (U.S. Pat. No. 5,792,931); avirulence and disease resistance genes (Jones, et al., (1994) *Science* 266:789; Martin, et al., (1993) *Science* 262:1432; Mindrinos, et al., (1994) *Cell* 78:1089); acetolactate synthase (ALS) mutants that lead to herbicide resistance such as the S4 and/or Hra mutations; inhibitors of glutamine synthase such as phosphinothricin or basta (e.g., bar gene); and glyphosate resistance (EPSPS gene)); and traits desirable for processing or process products such as high oil (e.g., U.S. Pat. No. 6,232,529); modified oils (e.g., fatty acid desaturase genes (U.S. Pat. No. 5,952,544; WO 94/11516)); modified starches (e.g., ADPG pyrophosphorylases (AGPase), starch synthases (SS), starch branching enzymes (SBE) and starch debranching enzymes (SDBE)); and polymers or bioplastics (e.g., U.S. Pat. No. 5,602,321; beta-ketothiolase, polyhydroxybutyrate synthase, and acetoacetyl-CoA reductase (Schubert, et al., (1988) *J. Bacteriol.* 170:5837-5847) facilitate expression of polyhydroxyalkanoates (PHAs)), the disclosures of which are herein incorporated by reference. One could also combine the

polynucleotides of the present invention with polynucleotides affecting agronomic traits such as male sterility (e.g., see, U.S. Pat. No. 5,583,210), stalk strength, flowering time, or transformation technology traits such as cell cycle regulation or gene targeting (e.g., WO 99/61619; WO 00/17364; WO 99/25821), the disclosures of which are herein incorporated by reference.

[0210] In one embodiment, sequences of interest improve plant growth and/or crop yields. For example, sequences of interest include agronomically important genes that result in improved primary or lateral root systems. Such genes include, but are not limited to, nutrient/water transporters and growth induces. Examples of such genes, include but are not limited to, maize plasma membrane H^+-ATPase (MHA2) (Frias, et al., (1996) *Plant Cell* 8:1533-44); AKT1, a component of the potassium uptake apparatus in *Arabidopsis*, (Spalding, et al., (1999) *J Gen Physiol* 113:909-18); RML genes which activate cell division cycle in the root apical cells (Cheng, et al., (1995) *Plant Physiol* 108:881); maize glutamine synthetase genes (Sukanya, et al., (1994) *Plant Mol Biol* 26:1935-46) and hemoglobin (Duff, et al., (1997) *J. Biol. Chem.* 27:16749-16752, Arredondo-Peter, et al., (1997) *Plant Physiol.* 115: 1259-1266; Arredondo-Peter, et al., (1997) *Plant Physiol* 114:493-500 and references sited therein). The sequence of interest may also be useful in expressing antisense nucleotide sequences of genes that that negatively affects root development.

[0211] Additional, agronomically important traits such as oil, starch, and protein content can be genetically altered in addition to using traditional breeding methods. Modifications include increasing content of oleic acid, saturated and unsaturated oils, increasing levels of lysine and sulfur, providing essential amino acids, and also modification of starch. Hordothionin protein modifications are described in U.S. Pat. Nos. 5,703,049, 5,885,801, 5,885,802, and 5,990,389, herein incorporated by reference. Another example is lysine and/or sulfur rich seed protein encoded by the soybean 2S albumin described in U.S. Pat. No. 5,850,016, and the chymotrypsin inhibitor from barley, described in Williamson, et al., (1987) *Eur. J. Biochem.* 165:99-106, the disclosures of which are herein incorporated by reference.

[0212] Derivatives of the coding sequences can be made by site-directed mutagenesis to increase the level of preselected amino acids in the encoded polypeptide. For example, the gene encoding the barley high lysine polypeptide (BHL) is derived from barley chymotrypsin inhibitor, U.S. patent application Ser. No. 08/740,682, filed Nov. 1, 1996, and WO 98/20133, the disclosures of which are herein incorporated by reference. Other proteins include methionine-rich plant proteins such as from sunflower seed (Lilley, et al., (1989) *Proceedings of the World Congress on Vegetable Protein Utilization in Human Foods and Animal Feedstuffs*, ed. Applewhite (American Oil Chemists Society, Champaign, Ill.), pp. 497-502; herein incorporated by reference); corn (Pedersen, et al., (1986) *J. Biol. Chem.* 261:6279; Kirihara, et al., (1988) *Gene* 71:359; both of which are herein incorporated by reference); and rice (Musumura, et al., (1989) *Plant Mol. Biol.* 12:123, herein incorporated by reference). Other agronomically important genes encode latex, Floury 2, growth factors, seed storage factors, and transcription factors.

[0213] Insect resistance genes may encode resistance to pests that have great yield drag such as rootworm, cutworm, European Corn Borer, and the like. Such genes include, for example, *Bacillus thuringiensis* toxic protein genes (U.S. Pat. Nos. 5,366,892; 5,747,450; 5,736,514; 5,723,756; 5,593,881; and Geiser, et al., (1986) *Gene* 48:109); and the like.

[0214] Genes encoding disease resistance traits include detoxification genes, such as against fumonosin (U.S. Pat. No. 5,792,931); avirulence (avr) and disease resistance (R) genes (Jones, et al., (1994) *Science* 266:789; Martin, et al., (1993) *Science* 262:1432; and Mindrinos, et al., (1994) *Cell* 78:1089); and the like.

[0215] Herbicide resistance traits may include genes coding for resistance to herbicides that act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-type herbicides (e.g., the acetolactate synthase (ALS) gene containing mutations leading to such resistance, in particular the S4 and/or Hra mutations), genes coding for resistance to herbicides that act to inhibit action of glutamine synthase, such as phosphinothricin or basta (e.g., the bar gene), or other such genes known in the art. The bar gene encodes resistance to the herbicide basta, the nptII gene encodes resistance to the antibiotics kanamycin and geneticin, and the ALS-gene mutants encode resistance to the herbicide chlorsulfuron.

[0216] Sterility genes can also be encoded in an expression cassette and provide an alternative to physical detasseling. Examples of genes used in such ways include male tissue-preferred genes and genes with male sterility phenotypes such as QM, described in U.S. Pat. No. 5,583,210. Other genes include kinases and those encoding compounds toxic to either male or female gametophytic development.

[0217] The quality of grain is reflected in traits such as levels and types of oils, saturated and unsaturated, quality and quantity of essential amino acids, and levels of cellulose. In corn, modified hordothionin proteins are described in U.S. Pat. Nos. 5,703,049, 5,885,801, 5,885,802 and 5,990,389.

[0218] Commercial traits can also be encoded on a gene or genes that could increase for example, starch for ethanol production, or provide expression of proteins. Another important commercial use of transformed plants is the production of polymers and bioplastics such as described in U.S. Pat. No. 5,602,321. Genes such as β-Ketothiolase, PHBase (polyhydroxyburyrate synthase), and acetoacetyl-CoA reductase (see, Schubert, et al., (1988) *J. Bacteriol.* 170:5837-5847) facilitate expression of polyhyroxyalkanoates (PHAs).

[0219] Exogenous products include plant enzymes and products as well as those from other sources including procaryotes and other eukaryotes. Such products include enzymes, cofactors, hormones, and the like. The level of proteins, particularly modified proteins having improved amino acid distribution to improve the nutrient value of the plant, can be increased. This is achieved by the expression of such proteins having enhanced amino acid content.

[0220] This invention can be better understood by reference to the following non-limiting examples. It will be appreciated by those skilled in the art that other embodiments of the invention may be practiced without departing from the spirit and the scope of the invention as herein disclosed and claimed.

EXAMPLES

Example 1

Isolation of AMT Sequences

[0221] A routine for identifying all members of a given species' ammonium transporter (AMT) gene family was employed. First, a diverse set of all the known available members of the gene family as protein sequences was pre-

pared from public and proprietary sources. This data could include orthologous sequences from other species besides these four. Then, as in the example of maize, these protein query sequences were BLAST algorithm searched against a combination of proprietary and public maize, genomic or transcript, nucleotide sequence datasets, and a non-redundant set of candidate AMTs or 'hits' was identified. These sequences were combined with any existing maize gene family sequences, and then curated and edited to arrive at a new working set of unique maize AMT gene or transcript sequences and their translations. This search for gene family members was repeated. If there were recovered new sequences whose nucleotide sequences were unique (not same-gene matches), the process repeated until completion, that is until no new and distinct nucleotide sequences were found. In this way it was determined that the maize AMT family of genes consisted of at least seven members. Eleven distinct soybean sequences were found. Without the complete genome sequences of maize or soybean available, researchers were less certain of the exact gene family size, than they were for *Arabidopsis* (6 members) and rice (17 members). The availability of complete genome sequences for *Arabidopsis* and rice simplified the search, aided also by availability of fairly mature gene models and annotations for these species.

Example 2

Transformation and Regeneration of Transgenic Plants

[0222] Immature maize embryos from greenhouse donor plants are bombarded with a plasmid containing the AMT sequence operably linked to the drought-inducible promoter RAB17 promoter (Vilardell, et al., (1990) *Plant Mol Biol* 14:423-432) and the selectable marker gene PAT, which confers resistance to the herbicide Bialaphos. Alternatively, the selectable marker gene is provided on a separate plasmid. Transformation is performed as follows. Media recipes follow below.

[0223] Preparation of Target Tissue:

[0224] The ears are husked and surface sterilized in 30% Clorox bleach plus 0.5% Micro detergent for 20 minutes, and rinsed two times with sterile water. The immature embryos are excised and placed embryo axis side down (scutellum side up), 25 embryos per plate, on 560Y medium for 4 hours and then aligned within the 2.5-cm target zone in preparation for bombardment.

[0225] Preparation of DNA:

[0226] A plasmid vector comprising the AMT sequence operably linked to an ubiquitin promoter is made. This plasmid DNA plus plasmid DNA containing a PAT selectable marker is precipitated onto 1.1 μm (average diameter) tungsten pellets using a $CaCl_2$ precipitation procedure as follows:

[0227] 100 μl prepared tungsten particles in water

[0228] 10 μl (1 μg) DNA in Tris EDTA buffer (1 μg total DNA)

[0229] 100 μl 2.5 M $CaC1_2$

[0230] 10 μl 0.1 M spermidine

[0231] Each reagent is added sequentially to the tungsten particle suspension, while maintained on the multitube vortexer. The final mixture is sonicated briefly and allowed to incubate under constant vortexing for 10 minutes. After the precipitation period, the tubes are centrifuged briefly, liquid removed, washed with 500 ml 100% ethanol, and centrifuged for 30 seconds. Again the liquid is removed, and 105 μl 100% ethanol is added to the final tungsten particle pellet. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated and 10 μl spotted onto the center of each macrocarrier and allowed to dry about 2 minutes before bombardment.

[0232] Particle Gun Treatment:

[0233] The sample plates are bombarded at level #4 in particle gun #HE34-1 or #HE34-2. All samples receive a single shot at 650 PSI, with a total of ten aliquots taken from each tube of prepared particles/DNA.

[0234] Subsequent Treatment:

[0235] Following bombardment, the embryos are kept on 560Y medium for 2 days, then transferred to 560R selection medium containing 3 mg/liter Bialaphos, and subcultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to medium for germination and transferred to the lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V hormone-free medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to classic 600 pots (1.6 gallon) and grown to maturity. Plants are monitored and scored for increased drought tolerance. Assays to measure improved drought tolerance are routine in the art and include, for example, increased kernel-earring capacity yields under drought conditions when compared to control maize plants under identical environmental conditions. Alternatively, the transformed plants can be monitored for a modulation in meristem development (i.e., a decrease in spikelet formation on the ear). See, for example, Bruce, et al., (2002) *Journal of Experimental Botany* 53:1-13.

[0236] Bombardment and Culture Media:

[0237] Bombardment medium (560Y) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000×SIGMA-1511), 0.5 mg/l thiamine HCl, 120.0 g/l sucrose, 1.0 mg/l 2,4-D, and 2.88 g/l L-proline (brought to volume with D-1 H_2O following adjustment to pH 5.8 with KOH); 2.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 8.5 mg/l silver nitrate (added after sterilizing the medium and cooling to room temperature). Selection medium (560R) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000×SIGMA-1511), 0.5 mg/l thiamine HCl, 30.0 g/l sucrose, and 2.0 mg/l 2,4-D (brought to volume with D-I H_2O following adjustment to pH 5.8 with KOH); 3.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 0.85 mg/l silver nitrate and 3.0 mg/l bialaphos (both added after sterilizing the medium and cooling to room temperature).

[0238] Plant regeneration medium (288J) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g nicotinic acid, 0.02 g/l thiamine HCL, 0.10 g/l pyridoxine HCL, and 0.40 g/l glycine brought to volume with polished D-I H_2O) (Murashige and Skoog (1962) *Physiol. Plant.* 15:473), 100 mg/l myo-inositol, 0.5 mg/l zeatin, 60 g/l sucrose, and 1.0 ml/l of 0.1 mM abscisic acid (brought to volume with polished D-I H_2O after adjusting to pH 5.6); 3.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 1.0 mg/l indoleacetic acid and 3.0 mg/l bialaphos (added after sterilizing the medium and cooling to 60°

C.). Hormone-free medium (272V) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g/l nicotinic acid, 0.02 g/l thiamine HCL, 0.10 g/l pyridoxine HCL, and 0.40 g/l glycine brought to volume with polished D-I H_2O), 0.1 g/l myo-inositol, and 40.0 g/l sucrose (brought to volume with polished D-I H_2O after adjusting pH to 5.6); and 6 g/l bacto-agar (added after bringing to volume with polished D-I H_2O), sterilized and cooled to 60° C.

Example 3

Agrobacterium-Mediated Transformation

[0239] For *Agrobacterium*-mediated transformation of maize with an antisense sequence of the AMT sequence of the present invention, preferably the method of Zhao is employed (U.S. Pat. No. 5,981,840, and PCT patent publication WO98/32326; the contents of which are hereby incorporated by reference). Briefly, immature embryos are isolated from maize and the embryos contacted with a suspension of *Agrobacterium*, where the bacteria are capable of transferring the antisense AMT sequences to at least one cell of at least one of the immature embryos (step 1: the infection step). In this step the immature embryos are preferably immersed in an *Agrobacterium* suspension for the initiation of inoculation. The embryos are co-cultured for a time with the *Agrobacterium* (step 2: the co-cultivation step). Preferably the immature embryos are cultured on solid medium following the infection step. Following this co-cultivation period an optional "resting" step is contemplated. In this resting step, the embryos are incubated in the presence of at least one antibiotic known to inhibit the growth of *Agrobacterium* without the addition of a selective agent for plant transformants (step 3: resting step). Preferably the immature embryos are cultured on solid medium with antibiotic, but without a selecting agent, for elimination of *Agrobacterium* and for a resting phase for the infected cells. Next, inoculated embryos are cultured on medium containing a selective agent and growing transformed callus is recovered (step 4: the selection step). Preferably, the immature embryos are cultured on solid medium with a selective agent resulting in the selective growth of transformed cells. The callus is then regenerated into plants (step 5: the regeneration step), and preferably calli grown on selective medium are cultured on solid medium to regenerate the plants. Plants are monitored and scored for a modulation in tissue development.

Example 4

Soybean Embryo Transformation

[0240] Soybean embryos are bombarded with a plasmid containing an antisense AMT sequences operably linked to an ubiquitin promoter as follows. To induce somatic embryos, cotyledons, 3-5 mm in length dissected from surface-sterilized, immature seeds of the soybean cultivar A2872, are cultured in the light or dark at 26° C. on an appropriate agar medium for six to ten weeks. Somatic embryos producing secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos that multiplied as early, globular-staged embryos, the suspensions are maintained as described below.

[0241] Soybean embryogenic suspension cultures can be maintained in 35 ml liquid media on a rotary shaker, 150 rpm, at 26° C. with florescent lights on a 16:8 hour day/night schedule. Cultures are subcultured every two weeks by inoculating approximately 35 mg of tissue into 35 ml of liquid medium.

[0242] Soybean embryogenic suspension cultures may then be transformed by the method of particle gun bombardment (Klein, et al., (1987) *Nature* (London) 327:70-73, U.S. Pat. No. 4,945,050). A Du Pont Biolistic PDS1000/HE instrument (helium retrofit) can be used for these transformations.

[0243] A selectable marker gene that can be used to facilitate soybean transformation is a transgene composed of the 35S promoter from Cauliflower Mosaic Virus (Odell, et al., (1985) *Nature* 313:810-812), the hygromycin phosphotransferase gene from plasmid pJR225 (from *E. coli*; Gritz, et al., (1983) *Gene* 25:179-188), and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*. The expression cassette comprising an antisense AMT sequence operably linked to the ubiquitin promoter can be isolated as a restriction fragment. This fragment can then be inserted into a unique restriction site of the vector carrying the marker gene.

[0244] To 50 μl of a 60 mg/ml 1 μm gold particle suspension is added (in order): 5 μl DNA (1 μg/μl), 20 μl spermidine (0.1 M), and 50 μl $CaCl_2$ (2.5 M). The particle preparation is then agitated for three minutes, spun in a microfuge for 10 seconds and the supernatant removed. The DNA-coated particles are then washed once in 400 μl 70% ethanol and resuspended in 40 μl of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five microliters of the DNA-coated gold particles are then loaded on each macro carrier disk.

[0245] Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty 60×15 mm petri dish and the residual liquid removed from the tissue with a pipette. For each transformation experiment, approximately 5-10 plates of tissue are normally bombarded. Membrane rupture pressure is set at 1100 psi, and the chamber is evacuated to a vacuum of 28 inches mercury. The tissue is placed approximately 3.5 inches away from the retaining screen and bombarded three times. Following bombardment, the tissue can be divided in half and placed back into liquid and cultured as described above.

[0246] Five to seven days post bombardment, the liquid media may be exchanged with fresh media, and eleven to twelve days post-bombardment with fresh media containing 50 mg/ml hygromycin. This selective media can be refreshed weekly. Seven to eight weeks post-bombardment, green, transformed tissue may be observed growing from untransformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated as an independent transformation event. These suspensions can then be subcultured and maintained as clusters of immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

Example 5

Sunflower Meristem Tissue Transformation

[0247] Sunflower meristem tissues are transformed with an expression cassette containing an antisense AMT sequences operably linked to a ubiquitin promoter as follows (see also, European Patent Number EP 0 486233, herein incorporated by reference, and Malone-Schoneberg, et al., (1994) *Plant*

Science 103:199-207). Mature sunflower seed (*Helianthus annuus* L.) are dehulled using a single wheat-head thresher. Seeds are surface sterilized for 30 minutes in a 20% Clorox bleach solution with the addition of two drops of Tween 20 per 50 ml of solution. The seeds are rinsed twice with sterile distilled water.

[0248] Split embryonic axis explants are prepared by a modification of procedures described by Schrammeijer, et al. (Schrammeijer, et al., (1990) *Plant Cell Rep.* 9:55-60). Seeds are imbibed in distilled water for 60 minutes following the surface sterilization procedure. The cotyledons of each seed are then broken off, producing a clean fracture at the plane of the embryonic axis. Following excision of the root tip, the explants are bisected longitudinally between the primordial leaves. The two halves are placed, cut surface up, on GBA medium consisting of Murashige and Skoog mineral elements (Murashige, et al., (1962) *Physiol. Plant.,* 15:473-497), Shepard's vitamin additions (Shepard (1980) in *Emergent Techniques for the Genetic Improvement of Crops* (University of Minnesota Press, St. Paul, Minn.), 40 mg/l adenine sulfate, 30 g/l sucrose, 0.5 mg/l 6-benzyl-aminopurine (BAP), 0.25 mg/l indole-3-acetic acid (IAA), 0.1 mg/l gibberellic acid (GA_3), pH 5.6, and 8 g/l Phytagar.

[0249] The explants are subjected to microprojectile bombardment prior to *Agrobacterium* treatment (Bidney, et al., (1992) *Plant Mol. Biol.* 18:301-313). Thirty to forty explants are placed in a circle at the center of a 60×20 mm plate for this treatment. Approximately 4.7 mg of 1.8 mm tungsten microprojectiles are resuspended in 25 ml of sterile TE buffer (10 mM Tris HCl, 1 mM EDTA, pH 8.0) and 1.5 ml aliquots are used per bombardment. Each plate is bombarded twice through a 150 mm nytex screen placed 2 cm above the samples in a PDS 1000® particle acceleration device.

[0250] Disarmed *Agrobacterium tumefaciens* strain EHA105 is used in all transformation experiments. A binary plasmid vector comprising the expression cassette that contains the AMT gene operably linked to the ubiquitin promoter is introduced into *Agrobacterium* strain EHA105 via freeze-thawing as described by Holsters, et al., (1978) *Mol. Gen. Genet.* 163:181-187. This plasmid further comprises a kanamycin selectable marker gene (i.e., nptII). Bacteria for plant transformation experiments are grown overnight (28° C. and 100 RPM continuous agitation) in liquid YEP medium (10 gm/l yeast extract, 10 gm/l Bactopeptone, and 5 gm/l NaCl, pH 7.0) with the appropriate antibiotics required for bacterial strain and binary plasmid maintenance. The suspension is used when it reaches an OD_{600} of about 0.4 to 0.8. The *Agrobacterium* cells are pelleted and resuspended at a final OD_{600} of 0.5 in an inoculation medium comprised of 12.5 mM MES pH 5.7, 1 gm/l NH_4Cl, and 0.3 gm/l $MgSO_4$.

[0251] Freshly bombarded explants are placed in an *Agrobacterium* suspension, mixed, and left undisturbed for 30 minutes. The explants are then transferred to GBA medium and co-cultivated, cut surface down, at 26° C. and 18-hour days. After three days of co-cultivation, the explants are transferred to 374B (GBA medium lacking growth regulators and a reduced sucrose level of 1%) supplemented with 250 mg/l cefotaxime and 50 mg/l kanamycin sulfate. The explants are cultured for two to five weeks on selection and then transferred to fresh 374B medium lacking kanamycin for one to two weeks of continued development. Explants with differentiating, antibiotic-resistant areas of growth that have not produced shoots suitable for excision are transferred to GBA medium containing 250 mg/l cefotaxime for a second 3-day phytohormone treatment. Leaf samples from green, kanamycin-resistant shoots are assayed for the presence of NPTII by ELISA and for the presence of transgene expression by assaying for a modulation in meristem development (i.e., an alteration of size and appearance of shoot and floral meristems).

[0252] NPTII-positive shoots are grafted to Pioneer® hybrid 6440 in vitro-grown sunflower seedling rootstock. Surface sterilized seeds are germinated in 48-0 medium (half-strength Murashige and Skoog salts, 0.5% sucrose, 0.3% gelrite, pH 5.6) and grown under conditions described for explant culture. The upper portion of the seedling is removed, a 1 cm vertical slice is made in the hypocotyl, and the transformed shoot inserted into the cut. The entire area is wrapped with parafilm to secure the shoot. Grafted plants can be transferred to soil following one week of in vitro culture. Grafts in soil are maintained under high humidity conditions followed by a slow acclimatization to the greenhouse environment. Transformed sectors of T_0 plants (parental generation) maturing in the greenhouse are identified by NPTII ELISA and/or by AMT activity analysis of leaf extracts while transgenic seeds harvested from NPTII-positive T_0 plants are identified by AMT activity analysis of small portions of dry seed cotyledon.

[0253] An alternative sunflower transformation protocol allows the recovery of transgenic progeny without the use of chemical selection pressure. Seeds are dehulled and surface-sterilized for 20 minutes in a 20% Clorox bleach solution with the addition of two to three drops of Tween 20 per 100 ml of solution, then rinsed three times with distilled water. Sterilized seeds are imbibed in the dark at 26° C. for 20 hours on filter paper moistened with water. The cotyledons and root radical are removed, and the meristem explants are cultured on 374E (GBA medium consisting of MS salts, Shepard vitamins, 40 mg/l adenine sulfate, 3% sucrose, 0.5 mg/l 6-BAP, 0.25 mg/l IAA, 0.1 mg/l GA, and 0.8% Phytagar at pH 5.6) for 24 hours under the dark. The primary leaves are removed to expose the apical meristem, around 40 explants are placed with the apical dome facing upward in a 2 cm circle in the center of 374M (GBA medium with 1.2% Phytagar), and then cultured on the medium for 24 hours in the dark.

[0254] Approximately 18.8 mg of 1.8 μm tungsten particles are resuspended in 150 μl absolute ethanol. After sonication, 8 μl of it is dropped on the center of the surface of macrocarrier. Each plate is bombarded twice with 650 psi rupture discs in the first shelf at 26 mm of Hg helium gun vacuum.

[0255] The plasmid of interest is introduced into *Agrobacterium tumefaciens* strain EHA105 via freeze thawing as described previously. The pellet of overnight-grown bacteria at 28° C. in a liquid YEP medium (10 g/l yeast extract, 10 g/l Bactopeptone, and 5 g/l NaCl, pH 7.0) in the presence of 50 μg/l kanamycin is resuspended in an inoculation medium (12.5 mM 2-mM 2-(N-morpholino) ethanesulfonic acid, MES, 1 g/l NH_4Cl and 0.3 g/l $MgSO_4$ at pH 5.7) to reach a final concentration of 4.0 at OD 600. Particle-bombarded explants are transferred to GBA medium (374E), and a droplet of bacteria suspension is placed directly onto the top of the meristem. The explants are co-cultivated on the medium for 4 days, after which the explants are transferred to 374C medium (GBA with 1% sucrose and no BAP, IAA, GA3 and supplemented with 250 μg/ml cefotaxime). The plantlets are cultured on the medium for about two weeks under 16-hour day and 26° C. incubation conditions.

[0256] Explants (around 2 cm long) from two weeks of culture in 374C medium are screened for a modulation in

meristem development (i.e., an alteration of size and appearance of shoot and floral meristems). After positive (i.e., a decrease in AMT expression) explants are identified, those shoots that fail to exhibit a decrease in AMT activity are discarded, and every positive explant is subdivided into nodal explants. One nodal explant contains at least one potential node. The nodal segments are cultured on GBA medium for three to four days to promote the formation of auxiliary buds from each node. Then they are transferred to 374C medium and allowed to develop for an additional four weeks. Developing buds are separated and cultured for an additional four weeks on 374C medium. Pooled leaf samples from each newly recovered shoot are screened again by the appropriate protein activity assay. At this time, the positive shoots recovered from a single node will generally have been enriched in the transgenic sector detected in the initial assay prior to nodal culture.

[0257] Recovered shoots positive for a decreased AMT expression are grafted to Pioneer hybrid 6440 in vitro-grown sunflower seedling rootstock. The rootstocks are prepared in the following manner. Seeds are dehulled and surface-sterilized for 20 minutes in a 20% Clorox bleach solution with the addition of two to three drops of Tween 20 per 100 ml of solution, and are rinsed three times with distilled water. The sterilized seeds are germinated on the filter moistened with water for three days, then they are transferred into 48 medium (half-strength MS salt, 0.5% sucrose, 0.3% gelrite pH 5.0) and grown at 26° C. under the dark for three days, then incubated at 16-hour-day culture conditions. The upper portion of selected seedling is removed, a vertical slice is made in each hypocotyl, and a transformed shoot is inserted into a V-cut. The cut area is wrapped with parafilm. After one week of culture on the medium, grafted plants are transferred to soil. In the first two weeks, they are maintained under high humidity conditions to acclimatize to a greenhouse environment.

Example 6

Identification, Phylogenetic Analysis and Chloroplast Targeting Peptide (cTP) Predictions of AMTs in *Arabidopsis*, Rice, Soybean and Maize

[0258] Taking a 'genomic' approach AMTs were identified in several higher plants. In *Arabidopsis* 6 AMTs have been identified, and phylogenetic analyses reveals that AtAMT1 (SEQ ID NO: 2) AtAMT1;2 (SEQ ID NO: 4), AtAMT1;3 (SEQ ID NO: 6) and At3g24290 (SEQ ID NO: 10) cluster in one group where as AtAMT2 (SEQ ID NO: 8) and At4g28700 (SEQ ID NO: 12) are independent. Chloroplast targeting peptide (cTP) prediction by ChloroP program reveals that AtAMT1;2 (SEQ ID NO: 4) have a putative cTP (with 55% probability) where as all other AtAMTs did not contain any predicted cTP In rice, soybean and maize, 17, 11, 7 AMTs have been identified, respectively. cTP prediction in AMTs proteins from maize and soybean didn't identify any AMT candidate with a putative cTP, however in rice one AMT has putative cTP with more than 50% probability. Phylogenetic analyses of all the AMTs from *Arabidopsis*, rice, maize and soybean are shown in FIG. **1**.

Example 7

Expression Analysis of AMTs in Maize

[0259] In order to identify leaf specific/preferred/expressed AMT(s) in maize, Lynx MPSS expression analyses in ~300 libraries reveal that ZmAMT1 (SEQ ID NO: 14), 2, 7 are expressed both in roots and leaves (FIG. **2**) whereas ZmAMT4 (SEQ ID NO: 20) is a root preferred AMT. ZmAMT6 (SEQ ID NO: 24) expresses at very low level in comparison to other ZmAMTs. In case of ZmAMT5 there was no specific Lynx tag available. Researchers also performed RT-PCR on leaf and roots of B73 maize and the results confirm Lynx analysis results that there is no leaf specific AMT in maize, although ZmAMT1, 2, 7 (SEQ ID NOS: 14, 16 and 26) are expressed in leaves and roots.

Example 8

CTP Predictions in Chloroplast Outer Envelope Proteins

[0260] Initial cTP prediction couldn't detect a putative cTP in most of the higher plant AMTs analyzed. The chloroplast localized AMT (if any) has to be in the outer envelope of the chloroplast. In order to determine whether proteins localized in outer envelop of the chloroplast have any predicted cTP, researchers searched the NCBI database using 'chloroplast outer envelop/membrane' as keyword and identified the 14, 14, and 5 proteins from *Arabidopsis*, rice and maize, respectively that are suppose to be localized in outer envelop of chloroplast. Some of these are well characterized proteins and known to be localized in the outer membrane of chloroplast. ChloroP program was used to identify putative cTP in these 33 candidate proteins and interestingly none of these proteins show any putative cTP with high probability. These observations suggest that either a cTP is not required or not identified/characterized for these proteins so far. This also suggests that although most of the AMTs don't have a predicted cTP but some of them might be localized in the chloroplast outer membrane.

Example 9

Isolation and Characterization of AtAMT1;2 (SEQ ID NO: 4) T-DNA Mutant

[0261] In cTP prediction analyses, AtAMT1;2 (SEQ ID NO: 4) posses a putative cTP. For functional analyses of AtAMT1;2 (SEQ ID NO: 4) and to determine it's role in N-assimilation, researchers identified a T-DNA mutant line (SM_3.15680) from the *Arabidopsis* T-DNA mutant data base. The T-DNA mutant line was ordered from ABRC and the homozygous plants were subjected to molecular analyses. In this mutant line T-DNA was inserted in c-terminal of AtAMT1;2 (SEQ ID NO: 4) gene (FIG. **3**A). Genomic PCRs using AtAMT1;2 (SEQ ID NO: 4) gene and T-DNA specific primers show that T-DNA is indeed inserted in the AtAMT1;2 (SEQ ID NO: 4) (FIG. **3**B). AtAMT1;2 (SEQ ID NO: 4) gene specific primers flanking the T-DNA insert couldn't amplify any DNA region in mutant plants where as an expected PCR product was detected in wild type plant (FIG. **4**B, upper panel). Similarly, genomic PCR with AtAMT1;2 (SEQ ID NO: 4) specific forward primer and T-DNA specific reverse primers amplify an expected product in mutant lines and nothing in wild type plants as expected (FIG. **4**B, lower panel). Saturated RT-PCRs (35 cycles) analyses couldn't detect a full length atamt1;2 mRNA in mutant (FIG. **4**C, upper panel) suggesting that AtAMT1;2 (SEQ ID NO: 4) is

completely knocked out in this T-DNA mutant. Actin control RT-PCR worked fine in both mutant and wild type plants (FIG. **3**C, lower panel).

Example 10

Generation and Molecular Characterization of AtAMT1;2 (SEQ ID NO: 4) RNAi Lines

[0262] In addition to T-DNA mutant, another parallel approach was also undertaken for functional analysis of AtAMT1;2 (SEQ ID NO: 4). A RNAi vector containing ZM-UBI promoter driven RNAi cassette consisting of inverted repeats of AtAMT1;2 (SEQ ID NO: 4) specific DNA regions and ADH intron as a spacer was constructed. Wild type *Arabidopsis* (Columbia-0) was transformed with this RNAi vector by *Agrobacterium* mediated 'floral-dip' method. Several transgenic lines were identified by selecting the T0 seeds for herbicide resistance in soil. Molecular characterization of these transgenic lines were performed by RT-PCR for Actin, AtAMT1;2 (SEQ ID NO: 4) RNAi cassette, endogenous AtAMT1;2 (SEQ ID NO: 4) and presence of gDNA in RNA preparations. Several lines with a significant reduced levels of AtAMT1;2 (SEQ ID NO: 4) were identified after molecular analysis.

Example 11

Sub-Cellular Localization and Regulation of Expression of AtAMT1;2 (SEQ ID NO: 4)

[0263] cTP prediction analyses indicate that AtAMT1;2 (SEQ ID NO: 4) contains a putative predicted cTP (but with only 55% probability). The objectives of the experiments described in this example are to determine sub-cellular localization and regulation of expression the endogenous AtAMT1;2 (SEQ ID NO: 4). The coding sequence of AtAMT1;2 (SEQ ID NO: 4) was tagged with green fluorescent protein (GFP) as an in-frame C-terminal fusion under the control of AtAMT1;2 (SEQ ID NO: 4) native promoter and a strong constitutive (ZM-UBI) promoter. *Arabidopsis* transgenic lines were generated and analyzed for GFP expression by confocal microscopy. Analyses show that AtAMT1;2:GFP is localized in the plasma membrane of endodermis and the cortex in roots.

Example 12

Knock-Out/Knock-Down of Zm-AMTs in Maize

[0264] ESTs corresponding to all seven maize AMTs were identified and annotated and full length cDNA clones were obtained. Experiments to knock-out/knock-down of all these individual ZmAMTs by RNAi are in progress. TUSC screening experiments were used to identify knock-out mutants for three leaf expressed ZmAMT1 (SEQ ID NO: 14), ZmAMT2 (SEQ ID NO: 16) and ZmAMT7 (SEQ ID NO: 26).

Example 13

Knock-Out/Knock-Down of Multiple AtAMTs with Single RNAi Vector in *Arabidopsis*

[0265] Six AMT genes are present in *Arabidopsis* genome. Hence, it is very likely that due to functional redundancy one might need to manipulate the expression of multiple AMTs simultaneously. The DNA sequence of all these AMTs was analyzed and identified the high homology regions among them. For example there is such a stretch of ~200 bp among AtAMT1;2 (SEQ ID NO: 4), AtAMT1 (SEQ ID NO: 2), AMT1;3 (SEQ ID NO: 6), At3g24290 (SEQ ID NO: 10) and At4g28700 (SEQ ID NO: 12) where as AMT2 (SEQ ID NO: 8) stood independent (FIG. **4**). These regions were amplified (bold and underlined in FIG. **4**) by PCR from AtAMT1;2 (SEQ ID NO: 4) and AtAMT2 (SEQ ID NO: 8) and performed a multi-way ligation to make an inverted repeat using ADH-intron as a spacer. The RNAi cassette of these hybrid inverted repeats is driven by a constitutive or root-specific or leaf-specific promoter. Several transgenic *Arabidopsis* lines were generated for these three constructs. Molecular analyses of these lines were performed by genomic and RT-PCR. Several lines were identified that expressed significantly reduced levels of multiple AtAMTs. These transgenic lines show a methyl ammonium (ammonium analog toxic to plants) tolerant/better growth phenotype as compared to wild type control when grown on MS media supplemented with 10-30 mM of methyl ammonium. These results indicate multiple AMTs were knocked-down in these lines, resulting in reduced uptake of methyl ammonium.

Example 14

Knock-Out/Knock-Down of Multiple ZmAMTs in Maize by Single RNAi Vector

[0266] In maize at least 7 AMT like genes were identified and at least 3 of them are expressed both in leaf and root (see, Example 2). For improving NUE by reducing loss of ammonia by volatilization, one might have to knock-out/knock-down multiple AMTs. Detailed analyses of all 7 maize AMTs were performed to identify the DNA regions showing high homology among different ZmAMTs. This analysis reveals that ZmAMT1 (SEQ ID NO: 14) and ZmAMT5 (SEQ ID NO: 22), ZmAMT3 (SEQ ID NO: 18) and ZmAMT4 (SEQ ID NO: 20) and ZmAMT2 (SEQ ID NO: 16), ZmAMT6 (SEQ ID NO: 24) and ZmAMT7 (SEQ ID NO: 26) form three separate groups and there is a very high homology in stretches of DNA sequences with in each group (FIG. **5**). Three DNA fragments (bold and underlined in FIG. **5**) from ZmAMT 1, 4 and 7 (SEQ ID NOS: 14, 20 and 26) representing each of the different groups were amplified by PCR. Multi-way ligations were performed to make inverted repeats with hybrid of these 3 fragments and ADH intron as a spacer to facilitate the formation of stem-loop structure. This hybrid RNAi cassette of 'ZmAMT1 (SEQ ID NO: 14):ZmAMT4 (SEQ ID NO: 20):ZmAMT7 (SEQ ID NO: 26)' inverted repeats was driven by Zm-UBI promoter and a leaf-specific promoter. MOPAT driven by Zm-UBI promoter was used as herbicide resistance marker for selected. In addition to that RFP driven by a pericarp specific promoter LTP2 was also used to sort out the transgenic seeds (red) from there segregating non-transgenic seeds. Transgenic lines for the constructs were generated, with molecular analyses of the T0 events performed by genomic and RT-PCR. Several lines with significantly reduced expression of individual/multiple ZmAMTs have been identified and characterized.

Example 15

Variants of AMT Sequences

[0267] A. Variant Nucleotide Sequences of AMT that do not Alter the Encoded Amino Acid Sequence

[0268] The AMT nucleotide sequences are used to generate variant nucleotide sequences having the nucleotide sequence

of the open reading frame with about 70%, 75%, 80%, 85%, 90% and 95% nucleotide sequence identity when compared to the starting unaltered ORF nucleotide sequence of the corresponding SEQ ID NO. These functional variants are generated using a standard codon table. While the nucleotide sequence of the variants are altered, the amino acid sequence encoded by the open reading frames do not change.

[0269] B. Variant Amino Acid Sequences of AMT Polypeptides

[0270] Variant amino acid sequences of the AMT polypeptides are generated. In this example, one amino acid is altered. Specifically, the open reading frames are reviewed to determine the appropriate amino acid alteration. The selection of the amino acid to change is made by consulting the protein alignment (with the other orthologs and other gene family members from various species). An amino acid is selected that is deemed not to be under high selection pressure (not highly conserved) and which is rather easily substituted by an amino acid with similar chemical characteristics (i.e., similar functional side-chain). Using the protein alignment set forth in FIG. **2**, an appropriate amino acid can be changed. Once the targeted amino acid is identified, the procedure outlined in the following section C is followed. Variants having about 70%, 75%, 80%, 85%, 90% and 95% nucleic acid sequence identity are generated using this method.

[0271] C. Additional Variant Amino Acid Sequences of AMT Polypeptides

[0272] In this example, artificial protein sequences are created having 80%, 85%, 90% and 95% identity relative to the reference protein sequence. This latter effort requires identifying conserved and variable regions from the alignment set forth in FIG. **2** and then the judicious application of an amino acid substitutions table. These parts will be discussed in more detail below.

[0273] Largely, the determination of which amino acid sequences are altered is made based on the conserved regions among AMT protein or among the other AMT polypeptides. Based on the sequence alignment, the various regions of the AMT polypeptide that can likely be altered are represented in lower case letters, while the conserved regions are represented by capital letters. It is recognized that conservative substitutions can be made in the conserved regions below without altering function. In addition, one of skill will understand that functional variants of the AMT sequence of the invention can have minor non-conserved amino acid alterations in the conserved domain.

[0274] Artificial protein sequences are then created that are different from the original in the intervals of 80-85%, 85-90%, 90-95% and 95-100% identity. Midpoints of these intervals are targeted, with liberal latitude of plus or minus 1%, for example. The amino acids substitutions will be effected by a custom Perl script. The substitution table is provided below in Table 2.

TABLE 2

Substitution Table

Amino Acid	Strongly Similar and Optimal Substitution	Rank of Order to Change	Comment
I	L, V	1	50:50 substitution
L	I, V	2	50:50 substitution
V	I, L	3	50:50 substitution
A	G	4	
G	A	5	
D	E	6	
E	D	7	
W	Y	8	
Y	W	9	
S	T	10	
T	S	11	
K	R	12	
R	K	13	
N	Q	14	
Q	N	15	
F	Y	16	
M	L	17	First methionine cannot change
H		Na	No good substitutes
C		Na	No good substitutes
P		Na	No good substitutes

[0275] First, any conserved amino acids in the protein that should not be changed is identified and "marked off" for insulation from the substitution. The start methionine will of course be added to this list automatically. Next, the changes are made. H, C, and P are not changed in any circumstance. The changes will occur with isoleucine first, sweeping N-terminal to C-terminal. Then leucine, and so on down the list until the desired target it reached. Interim number substitutions can be made so as not to cause reversal of changes. The list is ordered 1-17, so start with as many isoleucine changes as needed before leucine, and so on down to methionine. Clearly many amino acids will in this manner not need to be changed. L, I and V will involve a 50:50 substitution of the two alternate optimal substitutions.

[0276] The variant amino acid sequences are written as output. Perl script is used to calculate the percent identities. Using this procedure, variants of the AMT polypeptides are generating having about 80%, 85%, 90%, and 95% amino acid identity to the starting unaltered ORF nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81.

Example 16

Over-Expression of AMTs in Plants to Improve NUE

[0277] The over-expression of AMTs has been demonstrated with strong constitutively or organ-specific (e.g. in roots) expression which improves ammonium uptake (especially in low ammonium soils in anaerobic conditions typical of rice field conditions) leading to improved nitrogen use efficiency. In other plants, such as maize, typically most of the N is absorbed by roots in the form of nitrate, the available source in most soil, however there is still a considerable proportion of N available as ammonium. Over-expression of AMTs in these conditions leads to improved nitrogen utilization. Since nitrate needs to be reduced to ammonium by an energy expensive reaction before it is assimilated, ammonium is a preferable source of N when available to the plant.

[0278] All publications and patent applications in this specification are indicative of the level of ordinary skill in the

art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated by reference.

[0279] The invention has been described with reference to various specific and preferred embodiments and techniques. However, it should be understood that many variations and modifications may be made while remaining within the spirit and scope of the invention.

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cttggttatc gctctgttgt ggacagatag tgtggaactg ttaacaataa catgatcagt 1800

atgtcttttt aattaaagtg aacgtttggt atcaaaatta aacattggaa tttgagcggt 1860

<210> SEQ ID NO 4
<211> LENGTH: 514
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 4

Met Asp Thr Ala Thr Thr Thr Cys Ser Ala Val Asp Leu Ser Ala Leu
1 5 10 15

Leu Ser Ser Ser Ser Asn Ser Thr Ser Ser Leu Ala Ala Ala Thr Phe
20 25 30

Leu Cys Ser Gln Ile Ser Asn Ile Ser Asn Lys Leu Ser Asp Thr Thr
35 40 45

Tyr Ala Val Asp Asn Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe
50 55 60

Ala Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala
65 70 75 80

Lys Asn Thr Met Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Ala
85 90 95

Gly Ala Ile Ser Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Thr
100 105 110

Pro Ser Asn Gly Phe Ile Gly Arg His His Ser Phe Phe Ala Leu Ser
115 120 125

Ser Tyr Pro Glu Arg Pro Gly Ser Asp Phe Ser Phe Phe Leu Tyr Gln
130 135 140

Trp Ala Phe Ala Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala
145 150 155 160

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

Gly Phe Val Tyr Pro Thr Val Ser His Trp Phe Trp Ser Ser Asp Gly
180 185 190

Trp Ala Ser Ala Ser Arg Ser Asp Asn Asn Leu Leu Phe Gly Ser Gly
195 200 205

Ala Ile Asp Phe Ala Gly Ser Gly Val Val His Met Val Gly Gly Ile
210 215 220

Ala Gly Leu Cys Gly Ala Leu Val Glu Gly Pro Arg Ile Gly Arg Phe
225 230 235 240

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Asp Arg Ser Gly Arg Ser Val Ala Leu Arg Gly His Ser Ala Ser Leu
245                 250                 255

Val Val Leu Gly Thr Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn
260                 265                 270

Pro Gly Ser Phe Leu Thr Ile Leu Lys Gly Tyr Asp Lys Ser Arg Pro
275                 280                 285

Tyr Tyr Gly Gln Trp Ser Ala Val Gly Arg Thr Ala Val Thr Thr Thr
290                 295                 300

Leu Ser Gly Cys Thr Ala Ala Leu Thr Thr Leu Phe Ser Lys Arg Leu
305                 310                 315                 320

Leu Ala Gly His Trp Asn Val Ile Asp Val Cys Asn Gly Leu Leu Gly
325                 330                 335

Gly Phe Ala Ala Ile Thr Ser Gly Cys Ala Val Val Glu Pro Trp Ala
340                 345                 350

Ala Ile Val Cys Gly Phe Val Ala Ser Trp Val Leu Ile Gly Phe Asn
355                 360                 365

Leu Leu Ala Lys Lys Leu Lys Tyr Asp Asp Pro Leu Glu Ala Ala Gln
370                 375                 380

Leu His Gly Gly Cys Gly Ala Trp Gly Leu Ile Phe Thr Gly Leu Phe
385                 390                 395                 400

Ala Arg Lys Glu Tyr Val Asn Glu Ile Tyr Ser Gly Asp Arg Pro Tyr
405                 410                 415

Gly Leu Phe Met Gly Gly Gly Gly Lys Leu Leu Ala Ala Gln Ile Val
420                 425                 430

Gln Ile Ile Val Ile Val Gly Trp Val Thr Val Thr Met Gly Pro Leu
435                 440                 445

Phe Tyr Gly Leu His Lys Met Asn Leu Leu Arg Ile Ser Ala Glu Asp
450                 455                 460

Glu Met Ala Gly Met Asp Met Thr Arg His Gly Gly Phe Ala Tyr Ala
465                 470                 475                 480

Tyr Asn Asp Glu Asp Asp Val Ser Thr Lys Pro Trp Gly His Phe Ala
485                 490                 495

Gly Arg Val Glu Pro Thr Ser Arg Ser Ser Thr Pro Thr Pro Thr Leu
500                 505                 510

Thr Val


<210> SEQ ID NO 5
<211> LENGTH: 1758
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 5

gtatctctct ttctctctct cagctctctc aaacatgtca ggagcaataa catgctctgc     60

ggccgatctc gccaccctac ttggccccaa cgccacggcg gcggccgact acatttgcgg    120

ccaattaggc accgttaaca acaagttcac cgatgcagcc ttcgccatag acaacaccta    180

cctcctcttc tctgcctacc ttgtcttcgc catgcagctc ggcttcgcta tgctttgtgc    240

tggttctgtt agagccaaga atacgatgaa catcatgctt accaatgtcc ttgacgctgc    300

agccggagga ctcttctact atctctttgg ttacgccttt gcctttggag gatcctccga    360

agggttcatt ggaagacaca actttgctct tagagacttt ccgactccca cagctgatta    420

ctctttcttc ctctaccaat gggcgttcgc aatcgcggcc gctggaatca caagtggttc    480
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gatcgcagag aggactcagt tcgtggctta cttgatatac tcttctttct taaccggatt    540

tgtttacccg gttgtctctc actggttttg gtccccggat ggatgggcca gtccctttcg    600

ttcagcggat gatcgtttgt ttagcaccgg agccattgac tttgctggct ccggtgttgt    660

tcacatggtt ggtggcatag caggtttatg gggtgctctt attgaaggtc ctcgtcgtgg    720

tcggttcgag aaaggtggtc gcgctattgc tctgcgcggc cactctgcct cgctagtagt    780

cttaggaacc ttcctcctat ggtttggatg gtatggtttc aaccccggtt ccttcactaa    840

gatactcgtt ccgtataatt ctggttccaa ctacggccaa tggagcggaa tcggccgtac    900

agcggttaac accacactct caggatgcac agcagctcta accacactct ttggtaaacg    960

tctcctatca ggccactgga acgtaacgga cgtttgcaac gggttactcg gtgggtttgc   1020

ggccataacc gcaggttgct ccgtcgtaga gccatgggca gcgattgtgt gcggcttcat   1080

ggcttctgtc gtccttatcg gatgcaacaa gctcgcggag cttgtacaat atgatgatcc   1140

actcgaggca gcccaactac atggagggtg tggcgcgtgg gggttgatat tcgtaggatt   1200

gtttgccaaa gagaagtatc taaacgaggt ttatggcgcc accccgggaa ggccatatgg   1260

actatttatg ggcggaggag ggaagctgtt gggagcacaa ttggttcaaa tacttgtgat   1320

tgtaggatgg gttagtgcca caatgggaac actcttcttc atcctcaaaa ggctcaatct   1380

gcttaggatc tcggagcagc atgaaatgca agggatggat atgacacgtc acggtggctt   1440

tgcttatatc taccatgata atgatgatga gtctcataga gtggatcctg gatctccttt   1500

ccctcgatca gctactcctc ctcgcgttta attttcaact ttttggtaat ttattaccgt   1560

ttaagtattg tttgggtttt ggttttgaaa tataaatatt tggatgtttt ggtttgtttt   1620

aagtgaccta tcgtcttttt gtgtttataa gtgttttagt ttatgttttt ttttttttc   1680

ttgaatttta attttacatg cctcggctaa tgtttatgct atttcttaga aatttatata   1740

tacaactttt ggtgatcc                                                1758
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<210> SEQ ID NO 6
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 6

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Met Ser Gly Ala Ile Thr Cys Ser Ala Ala Asp Leu Ala Thr Leu Leu
1               5                  10                  15

Gly Pro Asn Ala Thr Ala Ala Ala Asp Tyr Ile Cys Gly Gln Leu Gly
20                  25                  30

Thr Val Asn Asn Lys Phe Thr Asp Ala Ala Phe Ala Ile Asp Asn Thr
35                  40                  45

Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala Met Gln Leu Gly Phe
50                  55                  60

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

Met Leu Thr Asn Val Leu Asp Ala Ala Ala Gly Gly Leu Phe Tyr Tyr
85                  90                  95

Leu Phe Gly Tyr Ala Phe Ala Phe Gly Gly Ser Ser Glu Gly Phe Ile
100                 105                 110

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

Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe Val Ala Tyr Leu
145                 150                 155                 160

Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Val Val Ser His
165                 170                 175

Trp Phe Trp Ser Pro Asp Gly Trp Ala Ser Pro Phe Arg Ser Ala Asp
180                 185                 190

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

Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile Glu
210                 215                 220

Gly Pro Arg Arg Gly Arg Phe Glu Lys Gly Gly Arg Ala Ile Ala Leu
225                 230                 235                 240

Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu Trp
245                 250                 255

Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Thr Lys Ile Leu Val
260                 265                 270

Pro Tyr Asn Ser Gly Ser Asn Tyr Gly Gln Trp Ser Gly Ile Gly Arg
275                 280                 285

Thr Ala Val Asn Thr Thr Leu Ser Gly Cys Thr Ala Ala Leu Thr Thr
290                 295                 300

Leu Phe Gly Lys Arg Leu Leu Ser Gly His Trp Asn Val Thr Asp Val
305                 310                 315                 320

Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ala Gly Cys Ser
325                 330                 335

Val Val Glu Pro Trp Ala Ala Ile Val Cys Gly Phe Met Ala Ser Val
340                 345                 350

Val Leu Ile Gly Cys Asn Lys Leu Ala Glu Leu Val Gln Tyr Asp Asp
355                 360                 365

Pro Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Ala Trp Gly Leu
370                 375                 380

Ile Phe Val Gly Leu Phe Ala Lys Glu Lys Tyr Leu Asn Glu Val Tyr
385                 390                 395                 400

Gly Ala Thr Pro Gly Arg Pro Tyr Gly Leu Phe Met Gly Gly Gly Gly
405                 410                 415

Lys Leu Leu Gly Ala Gln Leu Val Gln Ile Leu Val Ile Val Gly Trp
420                 425                 430

Val Ser Ala Thr Met Gly Thr Leu Phe Phe Ile Leu Lys Arg Leu Asn
435                 440                 445

Leu Leu Arg Ile Ser Glu Gln His Glu Met Gln Gly Met Asp Met Thr
450                 455                 460

Arg His Gly Gly Phe Ala Tyr Ile Tyr His Asp Asn Asp Asp Glu Ser
465                 470                 475                 480

His Arg Val Asp Pro Gly Ser Pro Phe Pro Arg Ser Ala Thr Pro Pro
485                 490                 495

Arg Val


<210> SEQ ID NO 7
<211> LENGTH: 1428
<212> TYPE: DNA
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<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 7

atggccggag cttacgatcc aagcttgccg gaggttcctg aatggctcaa caaaggagac 60

aacgcgtggc agctcacggc agcgactctg gttggtctac agagtatgcc aggtcttgtt 120

atcctctatg cctccatcgt caagaagaaa tgggctgtga attcagcttt tatggctctt 180

tacgctttcg ccgccgttct tctctgttgg gttctcctct gttacaaaat ggcttttgga 240

gaagagcttt tgccgttttg gggcaaaggt ggtccagctt tcgaccaagg ataccttaag 300

ggacaagcaa agatcccaaa tagtaatgtg gcggcgccgt attttccgat ggcgacgttg 360

gtgtattttc agttcacatt cgcggcgata acgacgatac ttgtggcggg atctgtgttg 420

gggaggatga atattaaagc atggatggct tttgtgccat tgtggttgat ctttagctac 480

acagttggag cttatagtat atggggaggt gggtttctgt atcagtgggg agttattgat 540

tattccggcg gttatgttat tcatctctcc tccggtgttg ccggtttcgt cgctgcttac 600

tgggtaggac caaggcctaa ggctgacaga gagagattcc caccgaacaa tgttcttcta 660

atgcttgctg gagctggact tttatggatg ggatggtccg gttttaacgg tggtgctcct 720

tacgcggcca acttaacctc ctctatcgcc gtgttaaaca ccaacctctc ggccgccaca 780

agcctccttg tatggactac acttgatgtc atcttctttg gcaaaccttc tgtcatcgga 840

gcaattcaag gcatggttac tggcttagcc ggcgtcactc ccggagcagg tttgatccaa 900

acatgggcag ctataataat tggagtagtc tcaggaacag ctccatgggc ctctatgatg 960

atcattcaca agaaatccgc tctccttcaa aaggtggatg atacattagc ggtgttttac 1020

acacacgccg tggctggttt acttggtgga ataatgacag ggttgtttgc acaccctgat 1080

ctctgcgttt tggtacttcc tctcccagcg accagaggag ctttctacgg tggcaatggc 1140

ggcaaacagc ttttgaaaca gttggctgga gctgccttca ttgccgtctg gaatgtggtg 1200

tcgactacta tcattctact cgctattagg gtgttcatac cattgagaat ggctgaggaa 1260

gagctcggga ttggagacga cgcagcacat ggggaagaag cttatgctct ttggggagat 1320

ggagagaagt ttgatgctac aaggcatgtg caacagtttg agagagatca agaagctgct 1380

catccttctt atgttcatgg tgctagaggt gtcaccattg ttctatga 1428

<210> SEQ ID NO 8
<211> LENGTH: 475
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 8

Met Ala Gly Ala Tyr Asp Pro Ser Leu Pro Glu Val Pro Glu Trp Leu
1 5 10 15

Asn Lys Gly Asp Asn Ala Trp Gln Leu Thr Ala Ala Thr Leu Val Gly
20 25 30

Leu Gln Ser Met Pro Gly Leu Val Ile Leu Tyr Ala Ser Ile Val Lys
35 40 45

Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala Leu Tyr Ala Phe Ala
50 55 60

Ala Val Leu Leu Cys Trp Val Leu Leu Cys Tyr Lys Met Ala Phe Gly
65 70 75 80

Glu Glu Leu Leu Pro Phe Trp Gly Lys Gly Gly Pro Ala Phe Asp Gln

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85                  90                  95

Gly Tyr Leu Lys Gly Gln Ala Lys Ile Pro Asn Ser Asn Val Ala Ala
100                 105                 110

Pro Tyr Phe Pro Met Ala Thr Leu Val Tyr Phe Gln Phe Thr Phe Ala
115                 120                 125

Ala Ile Thr Thr Ile Leu Val Ala Gly Ser Val Leu Gly Arg Met Asn
130                 135                 140

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

Thr Val Gly Ala Tyr Ser Ile Trp Gly Gly Gly Phe Leu Tyr Gln Trp
165                 170                 175

Gly Val Ile Asp Tyr Ser Gly Gly Tyr Val Ile His Leu Ser Ser Gly
180                 185                 190

Val Ala Gly Phe Val Ala Ala Tyr Trp Val Gly Pro Arg Pro Lys Ala
195                 200                 205

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

Ala Gly Leu Leu Trp Met Gly Trp Ser Gly Phe Asn Gly Gly Ala Pro
225                 230                 235                 240

Tyr Ala Ala Asn Leu Thr Ser Ser Ile Ala Val Leu Asn Thr Asn Leu
245                 250                 255

Ser Ala Ala Thr Ser Leu Leu Val Trp Thr Thr Leu Asp Val Ile Phe
260                 265                 270

Phe Gly Lys Pro Ser Val Ile Gly Ala Ile Gln Gly Met Val Thr Gly
275                 280                 285

Leu Ala Gly Val Thr Pro Gly Ala Gly Leu Ile Gln Thr Trp Ala Ala
290                 295                 300

Ile Ile Ile Gly Val Val Ser Gly Thr Ala Pro Trp Ala Ser Met Met
305                 310                 315                 320

Ile Ile His Lys Lys Ser Ala Leu Leu Gln Lys Val Asp Asp Thr Leu
325                 330                 335

Ala Val Phe Tyr Thr His Ala Val Ala Gly Leu Leu Gly Gly Ile Met
340                 345                 350

Thr Gly Leu Phe Ala His Pro Asp Leu Cys Val Leu Val Leu Pro Leu
355                 360                 365

Pro Ala Thr Arg Gly Ala Phe Tyr Gly Gly Asn Gly Gly Lys Gln Leu
370                 375                 380

Leu Lys Gln Leu Ala Gly Ala Ala Phe Ile Ala Val Trp Asn Val Val
385                 390                 395                 400

Ser Thr Thr Ile Ile Leu Leu Ala Ile Arg Val Phe Ile Pro Leu Arg
405                 410                 415

Met Ala Glu Glu Glu Leu Gly Ile Gly Asp Asp Ala Ala His Gly Glu
420                 425                 430

Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu Lys Phe Asp Ala Thr Arg
435                 440                 445

His Val Gln Gln Phe Glu Arg Asp Gln Glu Ala Ala His Pro Ser Tyr
450                 455                 460

Val His Gly Ala Arg Gly Val Thr Ile Val Leu
465                 470                 475
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<210> SEQ ID NO 9

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<211> LENGTH: 1491
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 9

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acggcagcgg ctgactacat ttgcggccag ttgggttccg ttaacaacaa gtttaccgat 120

gcagcctacg ctatagacaa cacgtacctc ctcttctctg cctatcttgt ctttgcgatg 180

cagctcggct tcgctatgct ttgtgctggc tccgttagag ctaagaacac gatgaacatc 240

atgctcacta atgtccttga tgctgcagcc ggaggactct tctactacct ctttggttat 300

gcatttgcct ttggtgaatc ctccgatgga ttcattggaa gacacaactt tggtcttcaa 360

aactttccga ctctcacctc ggattactcc ttcttcctct accaatgggc gtttgcaatc 420

gcagccgctg gaatcaccag cggctccatt gccgagagga ctaagttcgt ggcgtatttg 480

atatactctt ctttttgac cgggtttgtt tacccagttg tctctcactg gttctggtct 540

ccggatggat gggctagtcc cttccgttca gaagaccgtt tgtttggcac tggagccatc 600

gactttgctg ggtcaggtgt tgttcacatg gttggtggta tcgcaggatt atggggtgcc 660

cttattgaag gccctcggat tggtcggttt cctgatgggg gtcatgctat tgctctgcga 720

ggccactctg cctcactcgt cgtcttaggg accttccttc tctggtttgg ttggtacggg 780

ttcaaccctg gttccttcac caagatactc attccctaca attctggttc caactatggc 840

caatggagtg gaataggccg caccgcggtt acaactacac tctcgggatg cacagcggct 900

ctaaccacac tcttcggaaa acgtctccta tcaggccact ggaacgtaac tgacgtttgc 960

aacgggttac tcggagggtt tgcggccata acggcaggtt gctctgtggt tgatccatgg 1020

gcagcgatcg tatgtggctt cgtggcttcc ctcgtcctta tcggatgcaa caagctcgca 1080

gagctcttaa aatatgacga tccacttgag gccgcacaac tacacggagg gtgtggtgct 1140

tggggtttga tatttgtagg actgtttgca aaagagaagt atataaatga ggtttacggc 1200

gcgagcccag gaaggcacta cgggctattt atgggcggag gagggaagct attgggagca 1260

caactggttc aaataattgt gattgttgga tgggttagtg ccacaatggg aacactcttc 1320

ttcatcctca aaaagctcaa tttgcttagg atctcggagc agcatgaaat gcgaggaatg 1380

gatttagcag gtcatggtgg ttttgcttat atctaccatg ataatgatga tgattccatt 1440

ggagtgcctg gatctccagt acctcgtgcg cctaaccctc cagccgtttg a 1491

<210> SEQ ID NO 10
<211> LENGTH: 496
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 10

Met Ser Gly Ala Ile Thr Cys Ser Ala Ala Asp Leu Ser Ala Leu Leu
1 5 10 15

Gly Pro Asn Ala Thr Ala Ala Ala Asp Tyr Ile Cys Gly Gln Leu Gly
20 25 30

Ser Val Asn Asn Lys Phe Thr Asp Ala Ala Tyr Ala Ile Asp Asn Thr
35 40 45

Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala Met Gln Leu Gly Phe
50 55 60

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

Met Leu Thr Asn Val Leu Asp Ala Ala Ala Gly Gly Leu Phe Tyr Tyr
85                  90                  95

Leu Phe Gly Tyr Ala Phe Ala Phe Gly Glu Ser Ser Asp Gly Phe Ile
100                 105                 110

Gly Arg His Asn Phe Gly Leu Gln Asn Phe Pro Thr Leu Thr Ser Asp
115                 120                 125

Tyr Ser Phe Phe Leu Tyr Gln Trp Ala Phe Ala Ile Ala Ala Ala Gly
130                 135                 140

Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Lys Phe Val Ala Tyr Leu
145                 150                 155                 160

Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Val Val Ser His
165                 170                 175

Trp Phe Trp Ser Pro Asp Gly Trp Ala Ser Pro Phe Arg Ser Glu Asp
180                 185                 190

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

His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile Glu Gly
210                 215                 220

Pro Arg Ile Gly Arg Phe Pro Asp Gly Gly His Ala Ile Ala Leu Arg
225                 230                 235                 240

Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu Trp Phe
245                 250                 255

Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Thr Lys Ile Leu Ile Pro
260                 265                 270

Tyr Asn Ser Gly Ser Asn Tyr Gly Gln Trp Ser Gly Ile Gly Arg Thr
275                 280                 285

Ala Val Thr Thr Thr Leu Ser Gly Cys Thr Ala Ala Leu Thr Thr Leu
290                 295                 300

Phe Gly Lys Arg Leu Leu Ser Gly His Trp Asn Val Thr Asp Val Cys
305                 310                 315                 320

Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ala Gly Cys Ser Val
325                 330                 335

Val Asp Pro Trp Ala Ala Ile Val Cys Gly Phe Val Ala Ser Leu Val
340                 345                 350

Leu Ile Gly Cys Asn Lys Leu Ala Glu Leu Leu Lys Tyr Asp Asp Pro
355                 360                 365

Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Ala Trp Gly Leu Ile
370                 375                 380

Phe Val Gly Leu Phe Ala Lys Glu Lys Tyr Ile Asn Glu Val Tyr Gly
385                 390                 395                 400

Ala Ser Pro Gly Arg His Tyr Gly Leu Phe Met Gly Gly Gly Gly Lys
405                 410                 415

Leu Leu Gly Ala Gln Leu Val Gln Ile Ile Val Ile Val Gly Trp Val
420                 425                 430

Ser Ala Thr Met Gly Thr Leu Phe Phe Ile Leu Lys Lys Leu Asn Leu
435                 440                 445

Leu Arg Ile Ser Glu Gln His Glu Met Arg Gly Met Asp Leu Ala Gly
450                 455                 460

His Gly Gly Phe Ala Tyr Ile Tyr His Asp Asn Asp Asp Asp Ser Ile
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465                 470                 475                 480

Gly Val Pro Gly Ser Pro Val Pro Arg Ala Pro Asn Pro Pro Ala Val
485                 490                 495


<210> SEQ ID NO 11
<211> LENGTH: 1515
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 11

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aacgccaccg cagcagcagc cgccgctgaa tacatctgcg ggagattcga cacagtcgcc    120

gggaaattca ctgatgcggc ttacgcaatc gacaacactt accttctctt ctctgcttac    180

ctcgttttcg cgatgcagct cggtttcgcc atgctctgtg ccggatccgt acgtgcaaaa    240

aacacgatga acattatgct cacgaacgtc atcgacgctg cagccggagg tctcttctat    300

tatctcttcg gtttcgcttt tgcttttgga tctccttcta atggattcat cggaaaacat    360

ttctttggaa tgtatgattt tcctcaacct acgtttgatt atccttattt tctatatcaa    420

tggactttcg ctatcgccgc cgctggaatc acgagtggtt cgatagcgga gaggactcag    480

ttcgttgcgt atttgatcta ttcttctttc ttgacgggtc ttgtttaccc gattgtgtcg    540

cattggtttt ggtcttctga tggttgggcg tctccggcta gatctgagaa ccttctgttt    600

caatcaggtg tgattgattt cgctggctct ggtgttgttc atatggttgg tggtattgct    660

ggtttatggg gagctttaat tgaaggacct aggattggtc ggtttggagt tgggggtaaa    720

ccggttacgt tgcgtggtca tagtgctacg ttggttgttc ttggaacgtt tttgttatgg    780

ttcggatggt acgggtttaa cccgggctcg tttgcaacta tttttaaggc gtatggggag    840

actccaggga gctcgtttta cggacaatgg agcgcagttg ggagaaccgc ggtaacaact    900

acgttagctg gttgcacggc ggcgttaacg actctgtttg ggaaaagact tattgatggg    960

tattggaatg taactgatgt ttgcaatggt ttgttaggcg ggtttgcggc tataactagc   1020

ggatgttcgg ttgtggaacc gtgggctgcg cttgtatgtg ggtttgtagc cgcatgggtg   1080

ctgatgggat gcaatagact agcggaaaag ctccaatttg atgatccgtt ggaagcggct   1140

cagcttcacg gtggttgtgg tgcgtggggg attattttca ccgggttgtt cgcggagaaa   1200

agatacattg ccgagatctt tggaggcgac ccgaataggc ctttcggatt gctaatggga   1260

ggaggaggta ggttgcttgc ggcgcacgtc gttcagattt tggtgattac gggttgggtt   1320

agtgtgacaa tggggactct gtttttttatt ttgcataagc tgaaactgtt gaggataccg   1380

gcggaggatg agatagctgg ggtggatccg acgagtcacg gagggttggc ttatatgtac   1440

acagaagatg agattaggaa tgggatcatg gttaggagag tgggtggtga taatgatccc   1500

aatgtaggtg tttga                                                    1515


<210> SEQ ID NO 12
<211> LENGTH: 504
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 12

Met Ala Ser Ala Leu Ser Cys Ser Ala Ser Asp Leu Ile Pro Leu Leu
1               5                  10                  15
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Ser Gly Gly Ala Asn Ala Thr Ala Ala Ala Ala Ala Ala Glu Tyr Ile
20                  25                  30

Cys Gly Arg Phe Asp Thr Val Ala Gly Lys Phe Thr Asp Ala Ala Tyr
35                  40                  45

Ala Ile Asp Asn Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
50                  55                  60

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
65                  70                  75                  80

Asn Thr Met Asn Ile Met Leu Thr Asn Val Ile Asp Ala Ala Ala Gly
85                  90                  95

Gly Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ser Pro
100                 105                 110

Ser Asn Gly Phe Ile Gly Lys His Phe Phe Gly Met Tyr Asp Phe Pro
115                 120                 125

Gln Pro Thr Phe Asp Tyr Pro Tyr Phe Leu Tyr Gln Trp Thr Phe Ala
130                 135                 140

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln
145                 150                 155                 160

Phe Val Ala Tyr Leu Ile Tyr Ser Ser Phe Leu Thr Gly Leu Val Tyr
165                 170                 175

Pro Ile Val Ser His Trp Phe Trp Ser Ser Asp Gly Trp Ala Ser Pro
180                 185                 190

Ala Arg Ser Glu Asn Leu Leu Phe Gln Ser Gly Val Ile Asp Phe Ala
195                 200                 205

Gly Ser Gly Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly
210                 215                 220

Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Gly Val Gly Gly Lys
225                 230                 235                 240

Pro Val Thr Leu Arg Gly His Ser Ala Thr Leu Val Val Leu Gly Thr
245                 250                 255

Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Ala
260                 265                 270

Thr Ile Phe Lys Ala Tyr Gly Glu Thr Pro Gly Ser Ser Phe Tyr Gly
275                 280                 285

Gln Trp Ser Ala Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly
290                 295                 300

Cys Thr Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Ile Asp Gly
305                 310                 315                 320

Tyr Trp Asn Val Thr Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala
325                 330                 335

Ala Ile Thr Ser Gly Cys Ser Val Val Glu Pro Trp Ala Ala Leu Val
340                 345                 350

Cys Gly Phe Val Ala Ala Trp Val Leu Met Gly Cys Asn Arg Leu Ala
355                 360                 365

Glu Lys Leu Gln Phe Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly
370                 375                 380

Gly Cys Gly Ala Trp Gly Ile Ile Phe Thr Gly Leu Phe Ala Glu Lys
385                 390                 395                 400

Arg Tyr Ile Ala Glu Ile Phe Gly Gly Asp Pro Asn Arg Pro Phe Gly
405                 410                 415

Leu Leu Met Gly Gly Gly Gly Arg Leu Leu Ala Ala His Val Val Gln
```

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420                 425                 430

Ile Leu Val Ile Thr Gly Trp Val Ser Val Thr Met Gly Thr Leu Phe
435                 440                 445

Phe Ile Leu His Lys Leu Lys Leu Leu Arg Ile Pro Ala Glu Asp Glu
450                 455                 460

Ile Ala Gly Val Asp Pro Thr Ser His Gly Gly Leu Ala Tyr Met Tyr
465                 470                 475                 480

Thr Glu Asp Glu Ile Arg Asn Gly Ile Met Val Arg Arg Val Gly Gly
485                 490                 495

Asp Asn Asp Pro Asn Val Gly Val
500
```

<210> SEQ ID NO 13
<211> LENGTH: 2073
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 13

```
atccgcgcca caccctccca atcccctccc cctcgcgtat ccacactttt cacacgcgac     60

gccggagaga cagagcgcgc gcgcgcccga aagatgtcga cgtgcgcggc ggacctggcg    120

ccgctgctcg gcccggcggc ggcgaacgcc acggactacc tgtgcgggca gttcgcggac    180

acggcctccg cggtggacgc cacgtacctg ctcttctcgg cctacctcgt gttcgccatg    240

cagctcggct tcgccatgct gtgcgccggc tccgtccgcg ccaagaacac catgaacatc    300

atgctcacca acgtgctcga cgccgccgcg ggggcgctct tctactacct cttcggcttc    360

gccttcgcct tcggcacgcc ctccaacggc ttcatcggca agcagttctt cgggctcaag    420

cacctgccca ggaccggctt cgactacgac ttcttcctct accagtgggc cttcgccatc    480

gccgccgcgg gcatcacgtc gggctccatc gccgagcgga cccagttcgt cgcctacctc    540

atctactccg cgttcctgac ggggttcgtc taccccgtgg tgtcgcactg gttctggtcc    600

gccgacggct gggccggcgc cagccgcacg tccggcccgc tgctcttcgg gtccggcgtc    660

atcgacttcg ccggctccgg cgtcgtccac atggtcggcg gcatcgcggg gctgtggggc    720

gcgctcatcg agggcccccg catcgggcgc ttcgaccacg ccggccgctc cgtggcgctc    780

aagggccaca gcgcgtcgct cgtggtgctc ggcaccttcc tgctgtggtt cggctggtac    840

gggttcaacc ccgggtcctt caccaccatc ctcaagtcgt acggccccgc cgggaccgtc    900

cacgggcagt ggtcggccgt gggccgcacc gccgtcacca ccaccctcgc cggcagcgtc    960

gccgcgctca ccacgctgtt cgggaagcgg ctccagacgg gccactggaa cgtggtggac   1020

gtctgcaacg gcctcctcgg cgggttcgcg gccatcacgg ccgggtgcag cgtggtggag   1080

ccgtgggcgg ccgtcatctg cgggttcgtg tccgcgtggg tgctcatcgg cgccaacgcc   1140

ctcgcggcgc gcttcaggtt cgacgacccg ctggaggcgg cgcagctgca cggcgggtgt   1200

ggcgcctggg gcgtcctctt cacggggctc ttcgcgaggc gaaagtacgt ggaggagatc   1260

tacggcgccg ggaggcccta cgggctgttc atgggcggcg gcgggaagct cctcgccgcg   1320

cagatcatcc agatcctggt gatcgccggg tgggtgagct gcaccatggg cccgctcttc   1380

tacgcgctca agaagctggg cctgctgcgc atctcggccg acgacgagat gtccggcatg   1440

gacctgaccc ggcacggcgg cttcgcctac gtctaccacg acgaggaccc tggcgacaag   1500

gccggggttg gtgggttcat gctcaagtcc gcgcagaacc gtgtcgagcc ggcggcggcg   1560
```

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gtggcggcgg cgaccagcag ccaggtgtaa aaaaaaaatc aggagcaaat tgaaaccgag 1620

ctgaagttac gtgcttgcct ttttcagtat gttgtcgcgt atcacgtttg aggtggatcg 1680

tatctgccgg tcagtacgca gtgtttgggc aaatacttgg ctacttggga gtcgcaagaa 1740

attgtgtaaa ttatatagag gaggatggcg acgaagcacg catgtgttac gtagttgggg 1800

tttgtgtgca catggtggtg ggcaggggct aggagagggt ttatctttag gttattttcg 1860

tagtggaatg aatcttatga tcggatatcc atcgtcggaa ggtgtggcgg gctgctggtc 1920

aagataggtg gcttctatga ctatgagggt tgaaacaaca agtggacgat tctgtcctgt 1980

ggtcactgct catcatccaa tctagcggct ttgacggtcg tgccttttta gtatcaataa 2040

tattattcca agtttaaaaa aaaaaaaaaa aaa 2073

<210> SEQ ID NO 14
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 14

Met Ser Thr Cys Ala Ala Asp Leu Ala Pro Leu Leu Gly Pro Ala Ala
1 5 10 15

Ala Asn Ala Thr Asp Tyr Leu Cys Gly Gln Phe Ala Asp Thr Ala Ser
20 25 30

Ala Val Asp Ala Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
35 40 45

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
50 55 60

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

Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Thr Pro
85 90 95

Ser Asn Gly Phe Ile Gly Lys Gln Phe Phe Gly Leu Lys His Leu Pro
100 105 110

Arg Thr Gly Phe Asp Tyr Asp Phe Phe Leu Tyr Gln Trp Ala Phe Ala
115 120 125

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln
130 135 140

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

Pro Val Val Ser His Trp Phe Trp Ser Ala Asp Gly Trp Ala Gly Ala
165 170 175

Ser Arg Thr Ser Gly Pro Leu Leu Phe Gly Ser Gly Val Ile Asp Phe
180 185 190

Ala Gly Ser Gly Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp
195 200 205

Gly Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly
210 215 220

Arg Ser Val Ala Leu Lys Gly His Ser Ala Ser Leu Val Val Leu Gly
225 230 235 240

Thr Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe
245 250 255

Thr Thr Ile Leu Lys Ser Tyr Gly Pro Ala Gly Thr Val His Gly Gln

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260                 265                 270

Trp Ser Ala Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser
275                 280                 285

Val Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His
290                 295                 300

Trp Asn Val Val Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala
305                 310                 315                 320

Ile Thr Ala Gly Cys Ser Val Val Glu Pro Trp Ala Ala Val Ile Cys
325                 330                 335

Gly Phe Val Ser Ala Trp Val Leu Ile Gly Ala Asn Ala Leu Ala Ala
340                 345                 350

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

Cys Gly Ala Trp Gly Val Leu Phe Thr Gly Leu Phe Ala Arg Arg Lys
370                 375                 380

Tyr Val Glu Glu Ile Tyr Gly Ala Gly Arg Pro Tyr Gly Leu Phe Met
385                 390                 395                 400

Gly Gly Gly Gly Lys Leu Leu Ala Ala Gln Ile Ile Gln Ile Leu Val
405                 410                 415

Ile Ala Gly Trp Val Ser Cys Thr Met Gly Pro Leu Phe Tyr Ala Leu
420                 425                 430

Lys Lys Leu Gly Leu Leu Arg Ile Ser Ala Asp Asp Glu Met Ser Gly
435                 440                 445

Met Asp Leu Thr Arg His Gly Gly Phe Ala Tyr Val Tyr His Asp Glu
450                 455                 460

Asp Pro Gly Asp Lys Ala Gly Val Gly Gly Phe Met Leu Lys Ser Ala
465                 470                 475                 480

Gln Asn Arg Val Glu Pro Ala Ala Ala Val Ala Ala Ala Thr Ser Ser
485                 490                 495

Gln Val
```

<210> SEQ ID NO 15
<211> LENGTH: 1597
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 15

```
tttgctagcg aagtccagta gtgcaactca ccccttcctg gtcctgctgc tccgccctct     60

ccacctagct accactccct tagagcgcca ctgccaagcc atggcgggag gaggggcggc    120

ctaccagagc tcgtcggcgt cgccggactg gctgaacaag ggcgacaatg cgtggcagat    180

gacgtccgcg acgctggtgg gcctgcagag catgcccggg ctggtgatcc tgtacggcag    240

catcgtgaag aagaagtggg ccatcaactc ggcgttcatg gcgctgtacg ccttcgccgc    300

cgtctggctc tgctgggtgg tgtgggccta caacatgtcg ttcggcgacc ggctgctgcc    360

cttctggggc aaggcgaggc cggcgctcgg gcagcgcttc ctggtggcgc agtcccagct    420

cacggccacc gccgtgcggt accgcgacgg gtcgctcgag gcggagatgc tccacccctt    480

ctacccggcc gccaccatgg tgtacttcca gtgcgtgttc gccagcatca ccgtcatcat    540

cctcgccggc tcgctgctgg gccgcatgga catcaaggcc tggatggcct tcgtcccgct    600

ctggatcacc ttctcctaca ccgtctccgc cttctcgctc tggggcggcg gcttcctctt    660
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ccagtggggc gtcatcgact actccggcgg ctacgtcatc cacctctcct cgggaatcgc    720

cggcctcacc gccgcttact gggtagggcc aaggtcggcg tcggacaggg agcggttccc    780

tcccaacaac atactgctgg tgctggcggg ggcaggcctg ctgtggctcg gatggactgg    840

cttcaacggc ggcgacccgt actcggccaa catcgactcg tccatggcgg tgctcaacac    900

gcacatctgc gcctccacca gcctcctcat gtggaccctc cttgacgtct tcttcttcgg    960

gaagccgtcg gtgatcggtg ctgtgcaggg catgatcacc ggccttgtgt gcatcacgcc   1020

tggcgcaggc ctggtgcaag ggtgggcagc cattgtcatg ggaattctct caggtagcat   1080

cccctggtac actatgatgg tactgcacaa gaaatggtcc ttcatgcaga ggatcgacga   1140

caccctcggc gtattccaca cccatgcggt cgctgggctc ctcggcggcg ccactactgg   1200

actctttgct gagcctgtcc tctgcaacct cttcctcgcc atcccggact ccagaggtgc   1260

attttatggt ggtggtggat cacagtttgg gaagcagatc gctggcgcac tcttcgtcat   1320

tggctggaac attgttatca cttccataat ctgtgttctt attggcctag tcctgcccct   1380

ccgaattcct gatgcacagc tgcttatcgg ggatgatgct gtacatggtg aggaggcgta   1440

tgctatatgg gcagaaggcg agctcaacga tgtaacccgc caagatgaaa gcaggcatgg   1500

cagcgtcgct gtaggagtca cacaatgttt gagcatagtt cttgtaaggt tgaaagaaag   1560

aaaaatacaa gtgcatttgt ttgctaattg ctattaa                            1597
```

<210> SEQ ID NO 16
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 16

```
Met Ala Gly Gly Gly Ala Ala Tyr Gln Ser Ser Ser Ala Ser Pro Asp
1               5                  10                  15

Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Met Thr Ser Ala Thr Leu
20                  25                  30

Val Gly Leu Gln Ser Met Pro Gly Leu Val Ile Leu Tyr Gly Ser Ile
35                  40                  45

Val Lys Lys Lys Trp Ala Ile Asn Ser Ala Phe Met Ala Leu Tyr Ala
50                  55                  60

Phe Ala Ala Val Trp Leu Cys Trp Val Val Trp Ala Tyr Asn Met Ser
65                  70                  75                  80

Phe Gly Asp Arg Leu Leu Pro Phe Trp Gly Lys Ala Arg Pro Ala Leu
85                  90                  95

Gly Gln Arg Phe Leu Val Ala Gln Ser Gln Leu Thr Ala Thr Ala Val
100                 105                 110

Arg Tyr Arg Asp Gly Ser Leu Glu Ala Glu Met Leu His Pro Phe Tyr
115                 120                 125

Pro Ala Ala Thr Met Val Tyr Phe Gln Cys Val Phe Ala Ser Ile Thr
130                 135                 140

Val Ile Ile Leu Ala Gly Ser Leu Leu Gly Arg Met Asp Ile Lys Ala
145                 150                 155                 160

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

Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu Phe Gln Trp Gly Val Ile
180                 185                 190
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Asp Tyr Ser Gly Gly Tyr Val Ile His Leu Ser Ser Gly Ile Ala Gly
195                 200                 205

Leu Thr Ala Ala Tyr Trp Val Gly Pro Arg Ser Ala Ser Asp Arg Glu
210                 215                 220

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

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

Asn Ile Asp Ser Ser Met Ala Val Leu Asn Thr His Ile Cys Ala Ser
260                 265                 270

Thr Ser Leu Leu Met Trp Thr Leu Leu Asp Val Phe Phe Phe Gly Lys
275                 280                 285

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

Ile Thr Pro Gly Ala Gly Leu Val Gln Gly Trp Ala Ala Ile Val Met
305                 310                 315                 320

Gly Ile Leu Ser Gly Ser Ile Pro Trp Tyr Thr Met Met Val Leu His
325                 330                 335

Lys Lys Trp Ser Phe Met Gln Arg Ile Asp Asp Thr Leu Gly Val Phe
340                 345                 350

His Thr His Ala Val Ala Gly Leu Leu Gly Gly Ala Thr Thr Gly Leu
355                 360                 365

Phe Ala Glu Pro Val Leu Cys Asn Leu Phe Leu Ala Ile Pro Asp Ser
370                 375                 380

Arg Gly Ala Phe Tyr Gly Gly Gly Gly Ser Gln Phe Gly Lys Gln Ile
385                 390                 395                 400

Ala Gly Ala Leu Phe Val Ile Gly Trp Asn Ile Val Ile Thr Ser Ile
405                 410                 415

Ile Cys Val Leu Ile Gly Leu Val Leu Pro Leu Arg Ile Pro Asp Ala
420                 425                 430

Gln Leu Leu Ile Gly Asp Asp Ala Val His Gly Glu Glu Ala Tyr Ala
435                 440                 445

Ile Trp Ala Glu Gly Glu Leu Asn Asp Val Thr Arg Gln Asp Glu Ser
450                 455                 460

Arg His Gly Ser Val Ala Val Gly Val Thr Gln Cys Leu Ser Ile Val
465                 470                 475                 480

Leu Val Arg Leu Lys Glu Arg Lys Ile Gln Val His Leu Phe Ala Asn
485                 490                 495

Cys Tyr


<210> SEQ ID NO 17
<211> LENGTH: 964
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 17

cgttgtccac atggtgggcg gaatcgccgg cctctggggc gccctcatcg agggcccccg     60

cattggccgg ttcgaccacg ccggccgctc ggtggcgctg cgcggccaca gcgcgtcgct    120

cgtcgtgctc ggcactttcc tgctgtggtt cggctggttc gggttcaacc ccgggtcgtt    180

cctcaccatc ctcaagagct acggcccggc cggcagcatc cacgggcagt ggtcggccgt    240

gggccgcacg gccgtgacca ccaccctcgc cggcagcacg gcggcgctca cgacgctctt    300
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cgggaagagg ctccagacgg ggcactggaa cgtggtcgac gtctgcaacg gcctcctcgg 360

cggcttcgcg gcgatcaccg cgggctgctc cgtggtcgac ccctgggcgg ccatcatatg 420

cgggttcgtg tcggcgtggg tgctcatcgg gctcaacgcg ctggccgcga ggctccggtt 480

cgacgacccg ctggaggccg cgcagttgca cggtgggtgc ggcgcgtggg gggtcctctt 540

cacgggcctg ttcgcgcgca gggagtacgt ggagcagatc tacggcacgc cggggcggcc 600

gtacggcctg ttcatgggcg gcggcgggag gctgctggcc gcgaacgtgg tgatgatcct 660

ggtgatcgcc gcgtgggtta gcgtcaccat ggctccgctg ttcctggcgc tcaacaagat 720

ggggctgctc cgagtctcgg ccgaggacga gatggccggc atggaccaga cgcggcacgg 780

cgggttcgcg tacgcgtacc acgacgacga cttgagcttg agcagcaggc ccaaggggat 840

gcagagcacg cagatcgcgg acgcggccag cggcgagttc tagtgtgttg gatcacaaat 900

ctcagtatgc tagtcctaca tcatgattgt caatagggcc attttaaaac cccttctttt 960

gggt 964

<210> SEQ ID NO 18
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 18

Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile
1 5 10 15

Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly Arg Ser Val Ala
20 25 30

Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu
35 40 45

Trp Phe Gly Trp Phe Gly Phe Asn Pro Gly Ser Phe Leu Thr Ile Leu
50 55 60

Lys Ser Tyr Gly Pro Ala Gly Ser Ile His Gly Gln Trp Ser Ala Val
65 70 75 80

Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser Thr Ala Ala Leu
85 90 95

Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His Trp Asn Val Val
100 105 110

Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ala Gly
115 120 125

Cys Ser Val Val Asp Pro Trp Ala Ala Ile Ile Cys Gly Phe Val Ser
130 135 140

Ala Trp Val Leu Ile Gly Leu Asn Ala Leu Ala Ala Arg Leu Arg Phe
145 150 155 160

Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Ala Trp
165 170 175

Gly Val Leu Phe Thr Gly Leu Phe Ala Arg Arg Glu Tyr Val Glu Gln
180 185 190

Ile Tyr Gly Thr Pro Gly Arg Pro Tyr Gly Leu Phe Met Gly Gly Gly
195 200 205

Gly Arg Leu Leu Ala Ala Asn Val Val Met Ile Leu Val Ile Ala Ala
210 215 220

Trp Val Ser Val Thr Met Ala Pro Leu Phe Leu Ala Leu Asn Lys Met

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225 230 235 240

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

Thr Arg His Gly Gly Phe Ala Tyr Ala Tyr His Asp Asp Asp Leu Ser
260 265 270

Leu Ser Ser Arg Pro Lys Gly Met Gln Ser Thr Gln Ile Ala Asp Ala
275 280 285

Ala Ser Gly Glu Phe
290

<210> SEQ ID NO 19
<211> LENGTH: 1587
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 19

atggcgacgt gcgctacgac cctcgcacct cttctgggcc cggcggcaaa cgcgacggag 60

taccttttgca accaattcgc ggacaccacg tcggcggtgg actcgacgta cctgctcttc 120

tcggcctacc tcgtcttcgc catgcagctc gggttcgcca tgctctgcgc gggctccgtc 180

cgcgccaaga acaccatgaa catcatgctc accaacgtgc tcgacgccgc cgccggcgcg 240

ctcttctact acctattcgg cttcgccttc gcgtacggga ccccgtccaa cggcttcatc 300

ggcaagcact tcttcggcct caagcggctt ccccaggtcg ggttcgacta cgacttcttc 360

ctcttccagt gggctttcgc catcgccgcc gccgggatca cgtccggctc catcgccgag 420

cgcacgcagt tcgtggcgta cctcatctac tccgccttcc tcaccggctt cgtgtacccg 480

gtggtgtccc actgggtctg gtccgccgac ggctgggcct cgccgtcacg gacgtcgggg 540

aagctcctct tcggctccgg catcatcgac ttcgccgggt ccagcgttgt ccacatggtg 600

ggcggaatcg ccggcctctg gggcgccctc atcgagggcc cccgcattgg ccggttcgac 660

cacgccggcc gctcggtggc gctgcgcggc cacagcgcgt cgctcgtcgt gctcggcact 720

ttcctgctgt ggttcggctg gttcgggttc aaccccgggt cgttcctcac catcctcaag 780

agctacggcc cggccggcag catccacggg cagtggtcgg ccgtgggccg cacggccgtg 840

accaccaccc tcgccggcag cacggcggcg ctcacgacgc tcttcgggaa gaggctccag 900

acggggcact ggaacgtggt cgacgtctgc aacggcctcc tcggcggctt cgcggcgatc 960

accgcgggct gctccgtggt cgacccctgg gcggccatca tatgcgggtt cgtgtcggcg 1020

tgggtgctca tcgggctcaa cctggccgcg aggctccggt tcgacgaccc ccgggaggcc 1080

gcgcagttgc acggtgggtg cggcgcgtgg ggggtcctct tcacgggcct gttcgcgcgc 1140

agggagtacg tggagcagag cacgccgggg cggccgtacg gcctgttcat gggcggcggc 1200

aggctgctgg ccgcgaacgt ggtgatgatc ctggtgatcg ccgcgtgggt tagcgtcacc 1260

atggctccgc tgttcctggc gctcaacaag atggggctgc tccgagtctc ggccgaggac 1320

gagatggccg gcatggacca gacgcggcac ggcgggttcg cgtacgcgta ccacgacgac 1380

gacttgagct tgagcagcag gcccaagggg atgcgagcac gcagatcgcg gacgcggcca 1440

gcggcgagtt ctagtgtgtt ggatcacaaa tctcagtatg ctagtcctac atcatgattg 1500

tacaataaca accatgagta tactcccttc gttctaagga ttactttgac gaagtatcta 1560

gttaatttaa agataaagaa aatttaa 1587

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<210> SEQ ID NO 20
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 20

Met Ala Thr Cys Ala Thr Thr Leu Ala Pro Leu Leu Gly Pro Ala Ala
1 5 10 15

Asn Ala Thr Glu Tyr Leu Cys Asn Gln Phe Ala Asp Thr Thr Ser Ala
20 25 30

Val Asp Ser Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala Met
35 40 45

Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys Asn
50 55 60

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

Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Tyr Gly Thr Pro Ser
85 90 95

Asn Gly Phe Ile Gly Lys His Phe Phe Gly Leu Lys Arg Leu Pro Gln
100 105 110

Val Gly Phe Asp Tyr Asp Phe Phe Leu Phe Gln Trp Ala Phe Ala Ile
115 120 125

Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe
130 135 140

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

Val Val Ser His Trp Val Trp Ser Ala Asp Gly Trp Ala Ser Pro Ser
165 170 175

Arg Thr Ser Gly Lys Leu Leu Phe Gly Ser Gly Ile Ile Asp Phe Ala
180 185 190

Gly Ser Ser Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly
195 200 205

Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly Arg
210 215 220

Ser Val Ala Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr
225 230 235 240

Phe Leu Leu Trp Phe Gly Trp Phe Gly Phe Asn Pro Gly Ser Phe Leu
245 250 255

Thr Ile Leu Lys Ser Tyr Gly Pro Ala Gly Ser Ile His Gly Gln Trp
260 265 270

Ser Ala Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser Thr
275 280 285

Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His Trp
290 295 300

Asn Val Val Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile
305 310 315 320

Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ala Ile Ile Cys Gly
325 330 335

Phe Val Ser Ala Trp Val Leu Ile Gly Leu Asn Leu Ala Ala Arg Leu
340 345 350

Arg Phe Asp Asp Pro Arg Glu Ala Ala Gln Leu His Gly Gly Cys Gly
355 360 365

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```
Ala Trp Gly Val Leu Phe Thr Gly Leu Phe Ala Arg Arg Glu Tyr Val
370                 375                 380

Glu Gln Ser Thr Pro Gly Arg Pro Tyr Gly Leu Phe Met Gly Gly Gly
385                 390                 395                 400

Arg Leu Leu Ala Ala Asn Val Val Met Ile Leu Val Ile Ala Ala Trp
405                 410                 415

Val Ser Val Thr Met Ala Pro Leu Phe Leu Ala Leu Asn Lys Met Gly
420                 425                 430

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

Arg His Gly Gly Phe Ala Tyr Ala Tyr His Asp Asp Asp Leu Ser Leu
450                 455                 460

Ser Ser Arg Pro Lys Gly Met Arg Ala Arg Arg Ser Arg Thr Arg Pro
465                 470                 475                 480

Ala Ala Ser Ser Ser Val Leu Asp His Lys Ser Gln Tyr Ala Ser Pro
485                 490                 495

Thr Ser
```

<210> SEQ ID NO 21
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 715
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 21

```
tcccaatccc ctccccctcg cgtatccaca cttttcacac gcgacgccgg agagacagag     60

cgcgcgcgcg cccgaaagat ggcgacgtgc gcgacggacc tggcgccgct gctcggcccg    120

gcggcggcaa acgccacgga ctacctctgc aaccaattcg cggacaccac ctccgcggtg    180

gacgccacgt acctgctctt ctcggcctac ctcgtcttcg ccatgcagct cggcttcgcc    240

atgctctgcg ccggctccgt ccgcgccaag aacaccatga acatcatgct caccaacgtg    300

ctcgacgccg ccgccggcgc gctcttctac tacctattcg gcttcgcctt cgcctacggc    360

accccgtcca acggcttcat cggcaagcac ttcttcggcc tcaagcgcct gcccaagacc    420

ggcttcgact acgacttctt cctataccag tgggccttcg ccatcgccgc cgccggcatc    480

acgtccggct ccatcgccga gagcacccag ttcgtcgcct acctcatcta ctccgccttc    540

ctcaccggct tcgtgtaccc cgtggcgtcc cactgggtct ggtccgccga cggctgggcc    600

gccgccggcc gcacgtccgg cccgctgctc ttcgggtccg gcgccatcga cttcgccggc    660

tccggcgtgg tccacatggt cggcggcatc gcggggttct ggggcgcgct cgtcnagggc    720

ccccgtatcg ggcgcttcga ccac                                           744
```

<210> SEQ ID NO 22
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 213
<223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 22

-continued

```
Met Ala Thr Cys Ala Thr Asp Leu Ala Pro Leu Leu Gly Pro Ala Ala
1               5                  10                  15

Ala Asn Ala Thr Asp Tyr Leu Cys Asn Gln Phe Ala Asp Thr Thr Ser
20                  25                  30

Ala Val Asp Ala Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
35                  40                  45

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
50                  55                  60

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

Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Tyr Gly Thr Pro
85                  90                  95

Ser Asn Gly Phe Ile Gly Lys His Phe Phe Gly Leu Lys Arg Leu Pro
100                 105                 110

Lys Thr Gly Phe Asp Tyr Asp Phe Phe Leu Tyr Gln Trp Ala Phe Ala
115                 120                 125

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Ser Thr Gln
130                 135                 140

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

Pro Val Ala Ser His Trp Val Trp Ser Ala Asp Gly Trp Ala Ala Ala
165                 170                 175

Gly Arg Thr Ser Gly Pro Leu Leu Phe Gly Ser Gly Ala Ile Asp Phe
180                 185                 190

Ala Gly Ser Gly Val Val His Met Val Gly Gly Ile Ala Gly Phe Trp
195                 200                 205

Gly Ala Leu Val Xaa Gly Pro Arg Ile Gly Arg Phe Asp His
210                 215                 220


<210> SEQ ID NO 23
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 23

gaggtcgtcg tctctagcta gctgctaaga gagagagaga gagagaggta tacgtaggac     60

cgccggcaac tagctaacta acatgtcgtc gtcgtccggg acgacgatgc cgctggcgta    120

ccagacgtcg gcgtcgtctc ccgagtggct gaacaagggc gacaacgcgt ggcagctgac    180

ggcggcgacg ctggtggggc tgcagagctt cccgggtctg gtggtcctgt acggcggcgt    240

ggtgaagaag aagtgggccg tgaactcggc cttcatggcg ctgtacgcgt tcgcggcggt    300

gtggatctgc tgggtgacct gggcctacaa catgtccttc ggcgacaggc tgctgccgct    360

gtggggcaag gcgcggccgg cgctgagcca gggcgggctg gtggggcagg ccggcctccc    420

cgccacggcg caccacttcg ccagcggcgc cctggagacc ccggccgcgg agccgctgta    480

cccgatggcc acggtggtgt acttccagtg cgtgttcgcg gccatcaccc tggtgctggt    540

cgccgggtcg ctgctgggcc ggatgagctt cgccgcgtgg atgctgttcg tgccgctctg    600

gctcaccttc tcctacaccg tcggcgcctt ctccgtatgg ggcggcgggt tcctcttcca    660

gtggggcgtc atcgactact gcggcggcta cgtcatccac ctctccgctg gcttcgccgg    720

gttcacggca gcctactggg tggggccccg ggcgcagaag gacagggaga ggttcccgcc    780
```

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gaacaacatc ctgttcacgc tcaccggcgc gggcctgctg tggatggggt gggccggctt 840

caacggcggc gggccgtacg ccgccaacgt ggtggcgtcc atgtcggtgc tcaacaccaa 900

catctgcacc gccatgagcc tcctcgtctg gacctgcctc gacgtcgtct tcttcaagaa 960

gccctccgtc gtgggcgccg tccagggcat gatcaccgga ctcgtctgca tcacgcccgc 1020

cgca 1024

<210> SEQ ID NO 24
<211> LENGTH: 314
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 24

Met Ser Ser Ser Ser Gly Thr Thr Met Pro Leu Ala Tyr Gln Thr Ser
1 5 10 15

Ala Ser Ser Pro Glu Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu
20 25 30

Thr Ala Ala Thr Leu Val Gly Leu Gln Ser Phe Pro Gly Leu Val Val
35 40 45

Leu Tyr Gly Gly Val Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe
50 55 60

Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Thr Trp
65 70 75 80

Ala Tyr Asn Met Ser Phe Gly Asp Arg Leu Leu Pro Leu Trp Gly Lys
85 90 95

Ala Arg Pro Ala Leu Ser Gln Gly Gly Leu Val Gly Gln Ala Gly Leu
100 105 110

Pro Ala Thr Ala His His Phe Ala Ser Gly Ala Leu Glu Thr Pro Ala
115 120 125

Ala Glu Pro Leu Tyr Pro Met Ala Thr Val Val Tyr Phe Gln Cys Val
130 135 140

Phe Ala Ala Ile Thr Leu Val Leu Val Ala Gly Ser Leu Leu Gly Arg
145 150 155 160

Met Ser Phe Ala Ala Trp Met Leu Phe Val Pro Leu Trp Leu Thr Phe
165 170 175

Ser Tyr Thr Val Gly Ala Phe Ser Val Trp Gly Gly Gly Phe Leu Phe
180 185 190

Gln Trp Gly Val Ile Asp Tyr Cys Gly Gly Tyr Val Ile His Leu Ser
195 200 205

Ala Gly Phe Ala Gly Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg Ala
210 215 220

Gln Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Phe Thr Leu
225 230 235 240

Thr Gly Ala Gly Leu Leu Trp Met Gly Trp Ala Gly Phe Asn Gly Gly
245 250 255

Gly Pro Tyr Ala Ala Asn Val Val Ala Ser Met Ser Val Leu Asn Thr
260 265 270

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

Val Phe Phe Lys Lys Pro Ser Val Val Gly Ala Val Gln Gly Met Ile
290 295 300

-continued

Thr Gly Leu Val Cys Ile Thr Pro Ala Ala
305 310

<210> SEQ ID NO 25
<211> LENGTH: 1798
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 25

ttatgatcca cttggttaac tagcataatt aatcgcagat gaagcagcag ttcatgaagg 60

caggaagcag ctaaatcacc catataaatg gtcgcgcgcg ctagcatagc atagtagcga 120

tagccaccac cgatcgaagc atgatggcgg cgtcgggcgc gtacgcggcg caactcccgg 180

cggtgccgga gtggctgaac aagggcgaca acgcgtggca gctgacggcg gcgacgctgg 240

tgggcatcca gtcgatgccg gggctggtgg tgctgtacgg cagcatcgtg aagaagaagt 300

gggcggtgaa ctcggcgttc atggcgctgt acgcctacgc gtcgtcgctg ctggtgtggg 360

tgctggcggg gttccgcatg gcgttcgggg agcggctgct cccgttctgg ggcaaggccg 420

gggtggcgct ctcccagggc tacctggtcc ggcgcgcctc gctctcggcg accgcgcacg 480

gggccacgcc ccgcaccgag cccctgtacc cggaggcgac gctggtgctg ttccagttcg 540

agttcgccgc catcacgctg gtgctcctgg ccggctccgt gcttggccgc atgaacatca 600

aggcctggat ggccttcacc ccgctctggc tcctcttctc ctacaccgtc ggcgccttca 660

gcatctgggg cggcggcttc ctctaccact ggggcgtcat cgactactcc ggcggatacg 720

tcatccacct ctcctccggc atcgccggct tcaccgccgc atactgggtg ggcccgaggc 780

tgaagagcga ccgggagcgc ttctccccga acaacatcct gctgatgatc gcgggcggcg 840

ggctgctgtg gatgggctgg gccgggttca acggcggcgc gccctacgcc gccaacatcg 900

cggcgtccgt ggccgtgctc aacaccaacg tctccgccgc caccagcctc ctcacctgga 960

cctgcctcga cgtcatcttc ttcggcaagc cgtccgtgat cggcgccgtg cagggcatga 1020

tgacggggct cgtctgcatc acccccggag cagggctggt gcagacctgg gcggcggtga 1080

tcatgggcgt gttcgcgggc agcgtgccgt ggttcaccat gatgatcctg cacaagaagg 1140

tggcgctgct gacgagggtg gacgacacgc tgggcgtctt ccacacgcac gccgtcgcgg 1200

gcctgctggg cggcgtcctc acggggctgc tggccacgcc ggagctgctg gagatcgagt 1260

cccccgtgcc gggcctccgc ggcgcgttct acggcggagg gatccgccag gtcggcaagc 1320

agctggcggg ggccgccttc gtggtggcgt ggaacgtcgt ggtcacgtcg ctcatcctgc 1380

tggccatcgg cctgctggtg cccctgcgga tgcccgagga ccagctcatg atcggcgacg 1440

acgccgcgca cggggaggag gcctacgcgc tctggggcga cggggagaag ttcgatgcca 1500

ccaggcacga cgcggtcagg gtcgccggcg tcatggatag agaagggtcc gcggagcagc 1560

ggctatcagg gggcgtcacc attcagctgt aggcgcacgc ccgacggtcc ataagacacg 1620

acttttagc ggacattttt ttttcatggg agaagagcag tgttttaggc tttttattat 1680

tagcatgaaa ggttgtccat gtatcatatt tggcccagag cacgtagtct ctgctagttt 1740

ataaagaaat taggtcatgt atttttcctc ttaatctagt ctacccgcaa catgtact 1798

<210> SEQ ID NO 26
<211> LENGTH: 483
<212> TYPE: PRT
<213> ORGANISM: Zea mays

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<400> SEQUENCE: 26

```
Met Met Ala Ala Ser Gly Ala Tyr Ala Ala Gln Leu Pro Ala Val Pro
1               5                  10                  15

Glu Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu Thr Ala Ala Thr
20                  25                  30

Leu Val Gly Ile Gln Ser Met Pro Gly Leu Val Val Leu Tyr Gly Ser
35                  40                  45

Ile Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala Leu Tyr
50                  55                  60

Ala Tyr Ala Ser Ser Leu Leu Val Trp Val Leu Ala Gly Phe Arg Met
65                  70                  75                  80

Ala Phe Gly Glu Arg Leu Leu Pro Phe Trp Gly Lys Ala Gly Val Ala
85                  90                  95

Leu Ser Gln Gly Tyr Leu Val Arg Arg Ala Ser Leu Ser Ala Thr Ala
100                 105                 110

His Gly Ala Thr Pro Arg Thr Glu Pro Leu Tyr Pro Glu Ala Thr Leu
115                 120                 125

Val Leu Phe Gln Phe Glu Phe Ala Ala Ile Thr Leu Val Leu Leu Ala
130                 135                 140

Gly Ser Val Leu Gly Arg Met Asn Ile Lys Ala Trp Met Ala Phe Thr
145                 150                 155                 160

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

Gly Gly Gly Phe Leu Tyr His Trp Gly Val Ile Asp Tyr Ser Gly Gly
180                 185                 190

Tyr Val Ile His Leu Ser Ser Gly Ile Ala Gly Phe Thr Ala Ala Tyr
195                 200                 205

Trp Val Gly Pro Arg Leu Lys Ser Asp Arg Glu Arg Phe Ser Pro Asn
210                 215                 220

Asn Ile Leu Leu Met Ile Ala Gly Gly Gly Leu Leu Trp Met Gly Trp
225                 230                 235                 240

Ala Gly Phe Asn Gly Gly Ala Pro Tyr Ala Ala Asn Ile Ala Ala Ser
245                 250                 255

Val Ala Val Leu Asn Thr Asn Val Ser Ala Ala Thr Ser Leu Leu Thr
260                 265                 270

Trp Thr Cys Leu Asp Val Ile Phe Phe Gly Lys Pro Ser Val Ile Gly
275                 280                 285

Ala Val Gln Gly Met Met Thr Gly Leu Val Cys Ile Thr Pro Gly Ala
290                 295                 300

Gly Leu Val Gln Thr Trp Ala Ala Val Ile Met Gly Val Phe Ala Gly
305                 310                 315                 320

Ser Val Pro Trp Phe Thr Met Met Ile Leu His Lys Lys Val Ala Leu
325                 330                 335

Leu Thr Arg Val Asp Asp Thr Leu Gly Val Phe His Thr His Ala Val
340                 345                 350

Ala Gly Leu Leu Gly Gly Val Leu Thr Gly Leu Leu Ala Thr Pro Glu
355                 360                 365

Leu Leu Glu Ile Glu Ser Pro Val Pro Gly Leu Arg Gly Ala Phe Tyr
370                 375                 380

Gly Gly Gly Ile Arg Gln Val Gly Lys Gln Leu Ala Gly Ala Ala Phe
```

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```
385                 390                 395                 400

Val Val Ala Trp Asn Val Val Val Thr Ser Leu Ile Leu Leu Ala Ile
405                 410                 415

Gly Leu Leu Val Pro Leu Arg Met Pro Glu Asp Gln Leu Met Ile Gly
420                 425                 430

Asp Asp Ala Ala His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly
435                 440                 445

Glu Lys Phe Asp Ala Thr Arg His Asp Ala Val Arg Val Ala Gly Val
450                 455                 460

Met Asp Arg Glu Gly Ser Ala Glu Gln Arg Leu Ser Gly Gly Val Thr
465                 470                 475                 480

Ile Gln Leu
```

<210> SEQ ID NO 27
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 27

```
atggtgccgg gactccgcgg cgcgttctac ggcggcggca tcaagcagat cagcaagcag     60

ctcggcggcg ctgcgtttgt gatcgcgtgg aacctcgtgg tcaccacggc catcctcctt    120

ggcatcggcc tgttcatccc gctgcggatg cccgacgagc agctcatgat cggcgacgac    180

gcggcgcacg gcgaggaggc ctacgcgttg tggggcgacg gcgagaagtt caacgcgaca    240

cagcacgacc tatcgagggg tggcggcggc ggcgacaggg acggccccga gcggctctcc    300

atcctaggcg ccaggggcgt caccatctag                                     330
```

<210> SEQ ID NO 28
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 28

```
Met Thr Pro Pro Arg Gly Pro Ser Pro Ser Thr Asn Ala Ala Arg Arg
1               5                  10                  15

Cys Arg Leu Thr Lys His Arg His Gly Arg Ala Thr Pro Ser Pro Pro
20                  25                  30

Ile Thr Cys Ala Ser Ser Arg Arg Pro Pro Arg Glu Thr Thr Leu Pro
35                  40                  45

His Pro Arg Cys Gly Gly Ala Pro Arg Arg His Pro His Gly Pro Pro
50                  55                  60

Gly His Pro Gly Ala Leu Leu Pro Arg Gly Leu Glu Ser Met Val Pro
65                  70                  75                  80

Gly Leu Arg Gly Ala Phe Tyr Gly Gly Gly Ile Lys Gln Ile Ser Lys
85                  90                  95

Gln Leu Gly Gly Ala Ala Phe Val Ile Ala Trp Asn Leu Val Val Thr
100                 105                 110

Thr Ala Ile Leu Leu Gly Ile Gly Leu Phe Ile Pro Leu Arg Met Pro
115                 120                 125

Asp Glu Gln Leu Met Ile Gly Asp Asp Ala Ala His Gly Glu Glu Ala
130                 135                 140

Tyr Ala Leu Trp Gly Asp Gly Glu Lys Phe Asn Ala Thr Gln His Asp
145                 150                 155                 160
```

-continued

Leu Ser Arg Gly Gly Gly Gly Gly Asp Arg Asp Gly Pro Glu Arg Leu
165 170 175

Ser Ile Leu Gly Ala Arg Gly Val Thr Ile
180 185

<210> SEQ ID NO 29
<211> LENGTH: 4123
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 29

gataaccaaa tcggacgctg accttgctgg gcgaactggg tgatcatcga tggcgatgcg 60

agacatcacc caactgcgtc gggtctccac aggagggagt tgcttgtgct tggtccgttt 120

ggggatcgtt aacttaaaca cttttacggc gacctcgaca cagctaaacc ctaaactaat 180

tgcgagttag aggcttatct cgatctcttc tatgcagatg tttgacaact tgggagtagt 240

ttactgctgg tttggagtat cttctcaact tgcaatttga ttatgtttaa acggggagtg 300

catgattggt gttcgcatgg ttttaaatca gattttataa actgatgctc gtcaagagac 360

gacaaggggc cagattaggg cagcagagta cgtgcttgct tgaattctga agcatgtacg 420

aaataaatac gatagaaatt tcttaagaaa ttaggtattt ttctgaccct ccaataagat 480

cgcgtggttg ccagtattgc acgtcgacta ctacatatct gaattcagaa caatccaaaa 540

gagaagttac tgttgatatt tctacgtata aaaaaaacat caaaatgctt tgtatattac 600

gaaaacagag cgagttccct tattgaccag agcaaaaagg ttgagcctga ttaaacaaag 660

tctatgagct tgcaggatgc gtctcttccc aaatttattc acaccaaagt cctcttcgat 720

gacatcgccc tatttgaatc ttatcgttga cattgctcat tttgctcttt agttaatctg 780

ggcaaatgat tggcggtggt acttcgtgat gtggaacagt gaaactgttt gtcaatctgt 840

gcgctcgagg tacaaccagg tcggttcctt tgctgtttta ttaataaaag gagcataaat 900

tagcgccaaa actcaagttt taccacaaaa aaacagtcag ttttaataaa gattaagcaa 960

acccttgaat tgcactctgt aaaatgtttg tttcccctca aaagctgata aggacggacg 1020

ccgatgtgaa acgaaacctg ctatttcaac catgtacata tataatcaag aatttcctac 1080

acgacttcca ttttttgtgt gttgactagt ttctctcctt cctggaggtg ttaaaagagt 1140

tccgattctg tcaaaacttc catacagata aatccaacct gtcaaactac cagctgttta 1200

attattcctt ttcccatttt gttatggtac acaaaggcac ataaccattt acacggagca 1260

gaacagaata ggatatgtat taaaaaaaca gaatggaaga aaaatcctga gtcacaagca 1320

cgaaaaatga aggcgagatt aattcgaaac catacacatc atcatccaca tctcgtcgtt 1380

tgtctcacag gacatgacac agggagcgaa aaccacatca ttaatcgcgg cctacagcta 1440

cacatccaga ttctcccggg atccccgaaa cggctcccac cccgcaaccg ccgcaagccg 1500

acccagccaa aggagatccc cctccaccac ggaagattca ctgcgcggtg ggccccgccg 1560

ccaaaaacca aaacgacgaa accattccgc gtcatctctc ccgcacggcg agcgagcgag 1620

cgagcgacct gacctcctcc tcctataaat ccggcgccag cgtatctccc caacctccca 1680

cgcccaatcc tgccgccgtt tcagcagctc tagtttgaac gagggatcgt agagaggagg 1740

gtttggtgag ggagggagga agatggcgac gtgcgcggcg gacctggcgc cgctgctggg 1800

gccggtggcg gcgaacgcga cggactacct gtgcaaccgg ttcgccgaca cgacgtcggc 1860

-continued

ggtggacgcg acgtacctgc tcttctcggc gtacctcgtg ttcgccatgc agctcgggtt 1920

cgcgatgctc tgcgccgggt cggtgcgggc caagaacacg atgaacatca tgctcaccaa 1980

cgtgctcgac gccgcggccg gggcgctctt ctactacctc ttcggcttcg ccttcgcctt 2040

cggcacgccg tccaacggct tcatcgggaa gcagttcttc ggcctcaagc acatgccgca 2100

gaccgggttc gactacgact tcttcctctt ccagtgggcc ttcgccatcg ccgccgccgg 2160

gatcacgtcg ggctccatcg ccgagaggac gcagttcgtc gcctacctca tctactccgc 2220

cttcctcacc gggttcgtct acccggtggt gtcccactgg atctggtccg ccgatgggtg 2280

ggcctctgcc tcccgcacgt ccggacctct gctgttcggc tccggtgtca tcgacttcgc 2340

cggctccggc gtcgtccaca tggtcggcgg tgtcgccggg ctctggggcg cgctcatcga 2400

gggcccccgc atcgggaggt tcgaccacgc cggccgatcg gtggcgctca agggccacag 2460

cgcgtcgctc gtcgtgcttg gcaccttcct gctgtggttc ggctggtacg gattcaaccc 2520

cgggtcgttc accaccatcc tcaagacgta cggcccggcc ggcggcatca acgggcagtg 2580

gtccggagtc ggccgcaccg ccgtgacgac gaccctggcc ggcagcgtgg cggcgctcac 2640

cacgctgttc gggaagcggc tccagacggg gcactggaac gtggtcgacg tctgcaacgg 2700

cctcctcggc gggttcgccg ccatcaccgc cgggtgcagc gtcgtcgacc cgtgggccgc 2760

gatcatctgc gggttcgtct cggcgtgggt gctcatcggc ctcaacgcgc tcgccgcgcg 2820

cctcaagttc gacgacccgc tcgaggccgc ccagctccac ggcgggtgcg gcgcgtgggg 2880

gatcctcttc accgcgctct tcgcgaggca gaagtacgtc gaggagatct acggcgccgg 2940

ccggccgtac ggcctgttca tgggcggcgg cggcaagctg ctcgccgcgc acgtcatcca 3000

gatcctggtc atcttcgggt gggtcagctg caccatggga cctctcttct acgggctcaa 3060

gaagctcggc ctgctccgca tctccgccga ggacgagacg tccggcatgg acctgacacg 3120

gcacggcggg ttcgcgtacg tctaccacga cgaggacgag cacgacaagt ctggggttgg 3180

tgggttcatg ctccggtccg cgcagacccg cgtcgagccg gcggcggccg gctgcctcca 3240

acagcaacaa ccaagtgtaa ccaatccaga acgaacgacg tcacagcgaa ggaagaaatc 3300

acgggtttct ctccctctcc gatctcgatc gtcacgtcat aaatttgatc cccatatttg 3360

attgccagtt tctgtttggg ccaaatgctt ttgccgctct ctctggtgtt gcaagactgt 3420

aaaaacactg taggatggac gagtgtcttt cacttttgct gggcttctct tgtgtacagg 3480

catgcgtacg tgtcttagaa tgtgtggtgt gaaggtggga agaatcagag gttagggttt 3540

aattttcttt tgcacaatgg ttactgctat tattgtttta ttttgtggtc gaattttatc 3600

gtcataaggg tgtggtggaa tggtggtcaa gataggtggc tgtgcagggc tcaaagactt 3660

tgcgtgggtc cttttgtcct gcagtgctct acctctctat caaaactttg gcttatttcc 3720

tggaatctag tggtttgaga gtgtttgttt tatactcagt tctgcattat gtttacgata 3780

tatttttttt tttaccaaaa gcatttcatt taaactctac cgagagtact tgtttatgct 3840

gaatcagtac atctacactg agtgatattt agagccttat actaattgaa gattaaatag 3900

tcaaagtcca tgtgcacatt tctactcgcc agttagtctg aaagaaaaga ttcctgtgtg 3960

caattgtgca tatcagcata tgccacctgg cgataaagta aacatactat agttgtgaac 4020

tgtgcgatga caacgaccaa attaagcagc ctgatcttta caacgaccgc tgtatagaga 4080

acagactata tcaaggtttt gggtccgtgg tcttcttttt ggg 4123

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<210> SEQ ID NO 30
<211> LENGTH: 532
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 30

Met Ala Thr Cys Ala Ala Asp Leu Ala Pro Leu Leu Gly Pro Val Ala
1 5 10 15

Ala Asn Ala Thr Asp Tyr Leu Cys Asn Arg Phe Ala Asp Thr Thr Ser
20 25 30

Ala Val Asp Ala Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
35 40 45

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
50 55 60

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

Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Thr Pro
85 90 95

Ser Asn Gly Phe Ile Gly Lys Gln Phe Phe Gly Leu Lys His Met Pro
100 105 110

Gln Thr Gly Phe Asp Tyr Asp Phe Phe Leu Phe Gln Trp Ala Phe Ala
115 120 125

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln
130 135 140

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

Pro Val Val Ser His Trp Ile Trp Ser Ala Asp Gly Trp Ala Ser Ala
165 170 175

Ser Arg Thr Ser Gly Pro Leu Leu Phe Gly Ser Gly Val Ile Asp Phe
180 185 190

Ala Gly Ser Gly Val Val His Met Val Gly Gly Val Ala Gly Leu Trp
195 200 205

Gly Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly
210 215 220

Arg Ser Val Ala Leu Lys Gly His Ser Ala Ser Leu Val Val Leu Gly
225 230 235 240

Thr Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe
245 250 255

Thr Thr Ile Leu Lys Thr Tyr Gly Pro Ala Gly Gly Ile Asn Gly Gln
260 265 270

Trp Ser Gly Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser
275 280 285

Val Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His
290 295 300

Trp Asn Val Val Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala
305 310 315 320

Ile Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ala Ile Ile Cys
325 330 335

Gly Phe Val Ser Ala Trp Val Leu Ile Gly Leu Asn Ala Leu Ala Ala
340 345 350

Arg Leu Lys Phe Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly

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355                 360                 365

Cys Gly Ala Trp Gly Ile Leu Phe Thr Ala Leu Phe Ala Arg Gln Lys
370                 375                 380

Tyr Val Glu Glu Ile Tyr Gly Ala Gly Arg Pro Tyr Gly Leu Phe Met
385                 390                 395                 400

Gly Gly Gly Gly Lys Leu Leu Ala Ala His Val Ile Gln Ile Leu Val
405                 410                 415

Ile Phe Gly Trp Val Ser Cys Thr Met Gly Pro Leu Phe Tyr Gly Leu
420                 425                 430

Lys Lys Leu Gly Leu Leu Arg Ile Ser Ala Glu Asp Glu Thr Ser Gly
435                 440                 445

Met Asp Leu Thr Arg His Gly Gly Phe Ala Tyr Val Tyr His Asp Glu
450                 455                 460

Asp Glu His Asp Lys Ser Gly Val Gly Gly Phe Met Leu Arg Ser Ala
465                 470                 475                 480

Gln Thr Arg Val Glu Pro Ala Ala Ala Gly Cys Leu Gln Gln Gln Gln
485                 490                 495

Pro Ser Val Thr Asn Pro Glu Arg Thr Thr Ser Gln Arg Arg Lys Lys
500                 505                 510

Ser Arg Val Ser Leu Pro Leu Arg Ser Arg Ser Ser Arg His Lys Phe
515                 520                 525

Asp Pro His Ile
530


<210> SEQ ID NO 31
<211> LENGTH: 4654
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 31

gagctccact cagctaccgg atcttgaccg ggaacctgtt tgtctacgta ctccaacgcc     60

ttgaatgatg ccgccgtgca gccaatttta accagctgct gcgcaaccgg ccaaccgccc    120

agccgtgcag ctgtggtgga gtgaccacgg ccacgactcc gtgcgcgcgg gtggacgtaa    180

gcgttgggcc ctcggctcgc gcgcgcggcc gcatccggcg atgcatcggt cgcgttcgcg    240

gtttgtggct tcgcgtcatc gccgatgcga acagaggctg ctttgcgttg tcgtcatcgg    300

cttgttgacg tccacgagtt ggcgagttgc tctgttcctc tctcgcgcgc gccgcagata    360

tccgaggtgg aaaaaatata ctacatatga acagatgtgg cccagctgtg agcaagacgc    420

caagaccaaa gataagtgca gttcaaatgg gcctgaaatt ggccttcatc aattacaaag    480

cccgtgaaaa gtttcagaaa agcattacaa agcttcagat aagttcaggg gtgactgaaa    540

tacacataca acaagtaacg tagagagatc cccaaatcag ctgcggcaga aggcagaaac    600

cgtgactagt acatctcata aacttaacga gcagtacaat ttctgtacat tggtttatca    660

ataagtcaag agtagcattt gggtaagaag agaaaaaaaa tcttttacgg tggcgtttat    720

tgacatttga tccctggagc cgagaagact agtttatctc atccgtgaaa actatttgtc    780

actagacatc aacgtctcgc tgaggacacc cggtttgcaa tttgctaata agaaacactc    840

gtttccgtcc aatggcgatt cgtttactag agatccgtcc attctctgaa cttctgaagg    900

tcaaccttct gatatgcata caggtgtggt agcaggcacg acaaaagtat aaaacaatag    960

gtatttaatc gcatcagcgt gatctatctc cagagtgtaa aaattagata cgcagcatct   1020
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gcaagtcata cttgcaagga agaagcaatt gcgtccctat ccaccacatc ttatccagtc 1080

ttgtcagagt tttgacctaa ggaattgctt catcatctga atttattcta ctggaagaaa 1140

ttacctactg ctatgccaag aagtaagaat acatggttaa tctatgttga caccctcatt 1200

tctgaagaca aacaacataa atttgcagtg agttaaaaca tatagtttca gtgaaaatat 1260

cgtacaggtt aatgtagcca gaccaacaca gagatctgat tgacaattac agagtactca 1320

gtagtcagca agcaggttta gcatggacta cctgttgatt acatggtttc agtcagacac 1380

gagttcttca gggaggcaaa ttaatcacaa ggttcttcca agacagaagc cgccggtaag 1440

gtatggaagc aaatgggttt atctccgttt gtgccaataa ccttatcgaa tatctaattg 1500

ttcgctaagt acgcattgca cacatcatat accatctcga ttgatgagtt ttgtcgccat 1560

gttctgctag gtacgaccta tccgctgctg ggtttacatg catgcctgaa gaacttaaac 1620

agttaatcaa caaagtcaat ggatattacg catacaagta tatggttgta tatatgcaac 1680

ttcatgacac aacagtatgc gtatagtcgg acgtgacgac aagcaactac ctcgtgcaag 1740

gatgcgagga gataccagat taaaacctgt aatacttgaa gttgacaaaa tgcgattctt 1800

cagacgatat aataacaaga acatttctga atcttccttt aaaaaatgtt gaatgcataa 1860

aagaatctta gctgtgatgg caacaacacg actttctgat agtgacattg gatcttagtt 1920

gaatctggca tcttgcgtat gcgaccttgc ttggatctgt cggatactcc caacccagca 1980

taaattactg atgtctgaaa ctttctgagc aaagcgggaa ctcaggctag ttgagtcgct 2040

catcatcaaa agtcaagaca atacttaagt aaaaacaaaa caaatatcac tgtcgcaaaa 2100

ccagtgtaaa cctattggga taattttaac agtcttacaa caccagcgcc gagacgtcta 2160

ggtaacaaat taaatcatca ctgacaatat ttgaagataa gtgaatcaca tgtctttctc 2220

aatgaactta aatttatgaa tgaaccaacc tatacatgca actaaatatg atatcaagat 2280

cagttaaaaa tcttgttttg tgaaatttca aaacaaaaaa ataaaattgc agcgtacctt 2340

tatttcaaga gaaatttaat tcactaaaaa aaagtaattg tatgtgccaa attttacatt 2400

aaaaaatggt atctgcaatg tattcttaag gatgataaaa ttatctcagt aatattcaat 2460

cattcattaa tagaggtgaa ctgctcgttc ttttactcat cacacctgtt ggatgaaaag 2520

attggttgct gccactaaaa aaattaatca actcattgca gttggcaaaa aagaaaaaaa 2580

aaggttttca ggcactagta tatgtgatgt tagaaggaat ccaaaacagt atacatgcat 2640

ccacgcgcac ctcggttttg catttcccgc tgtctgtgat catgaatcat ccaattaaaa 2700

acaaccatca accatggatt ccaatgtgtt ctgcccctat aaatagtcca gcatctcatt 2760

ctctcgtcta cttcaaagaa tcacacacca aaacctccat tagttcctaa accctagcaa 2820

gaagcagcac aaaaccttgc cacacttggc tagtgacact gagacacacc atggcgacgt 2880

gcttggacag cctcgggccg cttctcggcg gcgcggcgaa ctccaccgac gcggccaact 2940

acatctgcaa caggttcacg gacacctcct ccgcggtgga cgcgacgtac ctgctcttct 3000

cggcctacct cgtgttcgcc atgcagctcg ggttcgccat gctctgcgcg ggctccgtcc 3060

gcgccaagaa ctcaatgaac atcatgctca ccaacgtgtt cgacgccgcc gccggcgcgc 3120

tcttctacta cctcttcggc ttcgcttcgc gtcggacgcc gtccaagggc ttcatcggga 3180

agcagttctt cgggctgaag cacatgccgc agacagggta cgactacgac ttcttcctct 3240

tccagtgggc cttcgccatc gccgccgccg gcatcacgtc cggttccatc gccgaacgga 3300

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tgtcgcactg gttctggtcc accgacgggt gggcttcggc cggccggctg acgggtccgt 3420

tgctgttcaa gtcgggcgtc atcgacttcg ccggctccgg cgtcgtccat ctggtcggtg 3480

gcattgctgg cctgtggggt gccttcatcg agggcccccg catcgggcgc ttcgacgccg 3540

ccggccgcac ggtggcgatg aaagggcaca gcgcctcact ggtcgtgctc ggcaccttcc 3600

tgctgtggtt cgggtggttc ggcttcaacc cggggtcctt caccaccatc tccaagatct 3660

acggcgagtc gggcacgatc gacgggcagt ggtcggcggt gggccgcacc gccgtgacga 3720

cgtcgctggc gggcagcgtc gccgcgctta accacgctgt acggcaagag atggctgacg 3780

gggcactgga acgtgaccga cgtctgcaac ggtctcctcg gcgggttcgc gcgatcaccg 3840

cgggctgctc cgtggtcgac ccgtgggcgt cggtgatctg cgggttcgtg tcggcgtggg 3900

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cgcagctgca cggcgggtgc ggcgcgtggg ggatcatctt caccgcgctg ttcgcgcgca 4020

aggagtacgt cgagctgatc tacggggtgc cggggaggcc gtacgggctg ttcatgggcg 4080

gcggcgggag gcttctcgcg gcgcacatcg tgcagatcct ggtgatcgtc gggtgggtca 4140

gcgccaccat ggggacgctc ttctacgtgc tgcacaggtt cgggctgctc cgcgtctcga 4200

cctcgacaga gatggaaggc atggacccgt cgtgccacgg cgggttcggg tacgtggacg 4260

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ccagaaagtc gccggagcaa gccgcggcgg gccagttggt gtagtaggat catatcgatc 4380

gtgtccgttc ggggaaagtg ttttgtgaag tgtgcatata taagctgagg cagtcagtcg 4440

tgtgggcgtg gtggcacttc agcccatggt ggttgtggct ttcttttgat atttgcttcc 4500

tttcttctct gcatttgcat ctgtatggat ttttgtggct ttcaatcttt tatgcttttc 4560

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gtatttaggt cattatgatg ttaacgtgga gctc 4654

<210> SEQ ID NO 32
<211> LENGTH: 497
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 32

Met Ala Thr Cys Leu Asp Ser Leu Gly Pro Leu Leu Gly Gly Ala Ala
1 5 10 15

Asn Ser Thr Asp Ala Ala Asn Tyr Ile Cys Asn Arg Phe Thr Asp Thr
20 25 30

Ser Ser Ala Val Asp Ala Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val
35 40 45

Phe Ala Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg
50 55 60

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

Ala Gly Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Ser Arg Arg Thr
85 90 95

Pro Ser Lys Gly Phe Ile Gly Lys Gln Phe Phe Gly Leu Lys His Met
100 105 110

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Pro Gln Thr Gly Tyr Asp Tyr Asp Phe Phe Leu Phe Gln Trp Ala Phe
115                 120                 125

Ala Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr
130                 135                 140

Arg Phe Ser Ala Tyr Leu Ile Tyr Ser Ala Phe Leu Thr Gly Phe Val
145                 150                 155                 160

Tyr Pro Val Val Ser His Trp Phe Trp Ser Thr Asp Gly Trp Ala Ser
165                 170                 175

Ala Gly Arg Leu Thr Gly Pro Leu Leu Phe Lys Ser Gly Val Ile Asp
180                 185                 190

Phe Ala Gly Ser Gly Val Val His Leu Val Gly Gly Ile Ala Gly Leu
195                 200                 205

Trp Gly Ala Phe Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp Ala Ala
210                 215                 220

Gly Arg Thr Val Ala Met Lys Gly His Ser Ala Ser Leu Val Val Leu
225                 230                 235                 240

Gly Thr Phe Leu Leu Trp Phe Gly Trp Phe Gly Phe Asn Pro Gly Ser
245                 250                 255

Phe Thr Thr Ile Ser Lys Ile Tyr Gly Glu Ser Gly Thr Ile Asp Gly
260                 265                 270

Gln Trp Ser Ala Val Gly Arg Thr Ala Val Thr Thr Ser Leu Ala Gly
275                 280                 285

Ser Val Ala Ala Leu Asn His Ala Val Arg Gln Glu Met Ala Asp Gly
290                 295                 300

Ala Leu Glu Arg Asp Arg Arg Leu Gln Arg Ser Pro Arg Arg Val Arg
305                 310                 315                 320

Ala Ile Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ser Val Ile
325                 330                 335

Cys Gly Phe Val Ser Ala Trp Val Leu Ile Gly Cys Asn Lys Leu Ala
340                 345                 350

Leu Met Leu Lys Phe Asp Asp Pro Leu Glu Ala Thr Gln Leu His Gly
355                 360                 365

Gly Cys Gly Ala Trp Gly Ile Ile Phe Thr Ala Leu Phe Ala Arg Lys
370                 375                 380

Glu Tyr Val Glu Leu Ile Tyr Gly Val Pro Gly Arg Pro Tyr Gly Leu
385                 390                 395                 400

Phe Met Gly Gly Gly Gly Arg Leu Leu Ala Ala His Ile Val Gln Ile
405                 410                 415

Leu Val Ile Val Gly Trp Val Ser Ala Thr Met Gly Thr Leu Phe Tyr
420                 425                 430

Val Leu His Arg Phe Gly Leu Leu Arg Val Ser Thr Ser Thr Glu Met
435                 440                 445

Glu Gly Met Asp Pro Ser Cys His Gly Gly Phe Gly Tyr Val Asp Glu
450                 455                 460

Asp Glu Gly Gln Arg Arg Val Arg Ala Lys Ser Ala Ala Glu Thr Ala
465                 470                 475                 480

Arg Val Glu Pro Arg Lys Ser Pro Glu Gln Ala Ala Ala Gly Gln Leu
485                 490                 495

Val
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<210> SEQ ID NO 33

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<211> LENGTH: 2987
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 212
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 33

attatctcca atgatttcat agctaatcca tatgctggaa gggttaggaa ttcaagccat 60

ttcaaattcc aaaaaattac ctatactaaa gtaaaaaaaa acctatgacc taccctcaat 120

gtttgttaac caatttaggc cttgtttgat tccacttaga attattataa tcctgattat 180

tattaggagt aagctgaaac aaacagataa cntattatga tagattatta taatctataa 240

gccagattac tataatctgg taatccactc taaaggtgct ttttttaatt attggatagc 300

taataactag caaacagcta ataatccaga taaacaaaca gctaacaact tattctatat 360

cggcttatta taatcttatt ataatccaat ttatagtaat ctagctcaat aatatatatt 420

ataataatct taaactgaaa caaacagggc tttagaaatt catatgtttt gaaatggaga 480

tagtaccact cagaaagctt gaaggatttc atgtgttttg gttaacatat tcatgtgtgt 540

cttttcgtgc aaccaaaatt ttctttagaa acatggtgaa ccaattagat ttagaaatta 600

taaaatattt ccaagtgtta caagtggaaa tataataaaa ataatattgt taaaaaagta 660

aagaaagttt aagtacaaac tgaggaggaa atataacaag tgcttcacta tagacaaata 720

tagaggtgga cgaaatgtac aaacagtcgt ttttaaaaat acaaaccacc gtattgcgac 780

tcaggccttg tttagatccc aaaaaatttt agccaaaaat atcacatcaa atgtttggac 840

acatgcatag gatattaaat atggggaaaa aaaatcaatt acacagtttg caggtaaatt 900

gcgagacaaa tctttttagt ctaattacgt catgatttga ccatgtgatg ctatagtaaa 960

catttactaa tgacagattg attaggctta ataaattcat ctcgcaattt acaaacagaa 1020

tctataattt attttattat tagtctatat ttaatatttt aaatatatat ccgtgtagtt 1080

caaaaacttt atatcaaaag aactaaacac agcctccagg ccgcagccta cagtaggcct 1140

atagagagat tccacgggat tcgatgaact acgaccacga acaggagggg gacaaatcaa 1200

caagcaaatc ataggggtcg cacatttcag aggtagccaa agattcactg gcaggtgggc 1260

ccttcacact ttgaaggaat caacaacgac acccccccaag tcatggattc cttctcgctc 1320

cctctccacg tcgcctataa atccgacgcg ggccgctccc cactccaccc acagcccaca 1380

cttccattgc tcctcccctc tcctctacag tctgtgttga gcgcgcgtcg agcggcgagg 1440

atggcaacgt gcgcggatac cctcggcccg ctgctgggca cggcggcggc gaacgcgacg 1500

gactacctgt gcaaccagtt cgcggacacc acgtcggccg tggactcgac gtacctgctc 1560

ttctcggcgt acctcgtgtt cgccatgcag ctcggcttcg ccatgctctg cgccgggtcc 1620

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ttcctcttcc agtgggcctt cgccatcgcc gccgcgggca tcacgtccgg ctccatcgcc 1860

gagcggaccc agttcgtggc gtacctcatc tactccgcct tcctcaccgg cttcgtctac 1920

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gggtcgctgc tcttcgggtc cggcgtcatc gacttcgccg ggtcaggggt tgtccacatg 2040

gtggcggcgt gccggactct ggggcgccct catcgagggc ccccgcattg gcggttcgac 2100

cacgccggcc gctcggtggc gctgcgcggc cacagcgcgt cgctcgtcgt gctcggcagc 2160

ttcctgctgt ggttcgggtg gtacgggttt aaccccggct cgttcctcac catcctcaaa 2220

tcctacggcc cgcccggtag catccacggg cagtggtcgg cggtgggacg caccgccgtg 2280

accaccaccc tcgccggcag cacggcggcg ctcacgacgc tcttcgggaa gaggctccag 2340

acggggcact ggaacgtgat cgacgtctgc aacggcctcc tcggcggctt cgcggcgatc 2400

accgccggtt gctccgtcgt cgacccgtgg gccgcgatca tctgcgggtt cgtctcggcg 2460

tgggtgctca tcggcctcaa cgcgctggcg gcgaggctca agttcgacga cccgctcgag 2520

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gtgagcttca ccatggcgcc gctgttcctg gtgctcaaca agctgggatt gctgcgcatc 2760

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tcggcgcacg gcacgcaggt cgccgccgag atgggaggcc atgtctagtg gaaccggagg 2940

agctgagcta gtagtacata catgcagcat catcgatcct cgagctc 2987

<210> SEQ ID NO 34
<211> LENGTH: 495
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 34

Met Ala Thr Cys Ala Asp Thr Leu Gly Pro Leu Leu Gly Thr Ala Ala
1 5 10 15

Ala Asn Ala Thr Asp Tyr Leu Cys Asn Gln Phe Ala Asp Thr Thr Ser
20 25 30

Ala Val Asp Ser Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
35 40 45

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
50 55 60

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

Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ala Pro
85 90 95

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

Gln Val Gly Phe Asp Tyr Ser Phe Phe Leu Phe Gln Trp Ala Phe Ala
115 120 125

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln
130 135 140

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

Pro Val Val Ser His Trp Ile Trp Ser Ala Asp Gly Trp Ala Ser Ala
165 170 175

Ser Arg Thr Ser Gly Ser Leu Leu Phe Gly Ser Gly Val Ile Asp Phe

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180                 185                 190

Ala Gly Ser Gly Val Val His Met Val Ala Ala Cys Arg Thr Leu Gly
195                 200                 205

Arg Pro His Arg Gly Pro Pro His Trp Arg Phe Asp His Ala Gly Arg
210                 215                 220

Ser Val Ala Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Ser
225                 230                 235                 240

Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Leu
245                 250                 255

Thr Ile Leu Lys Ser Tyr Gly Pro Pro Gly Ser Ile His Gly Gln Trp
260                 265                 270

Ser Ala Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser Thr
275                 280                 285

Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His Trp
290                 295                 300

Asn Val Ile Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile
305                 310                 315                 320

Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ala Ile Ile Cys Gly
325                 330                 335

Phe Val Ser Ala Trp Val Leu Ile Gly Leu Asn Ala Leu Ala Ala Arg
340                 345                 350

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

Gly Ala Trp Gly Val Ile Phe Thr Ala Leu Phe Ala Arg Lys Glu Tyr
370                 375                 380

Val Asp Gln Ile Phe Gly Gln Pro Gly Arg Pro Tyr Gly Leu Phe Met
385                 390                 395                 400

Gly Gly Gly Gly Arg Leu Leu Gly Ala His Ile Val Val Ile Leu Val
405                 410                 415

Ile Ala Ala Trp Val Ser Phe Thr Met Ala Pro Leu Phe Leu Val Leu
420                 425                 430

Asn Lys Leu Gly Leu Leu Arg Ile Ser Ala Glu Asp Glu Met Ala Gly
435                 440                 445

Met Asp Gln Thr Arg His Gly Gly Phe Ala Tyr Ala Tyr His Asp Asp
450                 455                 460

Asp Ala Ser Gly Lys Pro Asp Arg Ser Phe Gly Gly Phe Met Leu Lys
465                 470                 475                 480

Ser Ala His Gly Thr Gln Val Ala Ala Glu Met Gly Gly His Val
485                 490                 495


<210> SEQ ID NO 35
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 35

atggcggcgg aggcggcgcc ggagtgggtg gagaaggggg acaacgcgtg gccgctagcg     60

gcggcgacgc tggtggggct gcagagcgtg ccgaggctgg tgatcctgta cggcgactgc    120

ggcgcggtcg gtccgaggac ggagaaggac agggaggcgt tcccgccgaa caacgtcctg    180

ctcacgctcg ccggagcggg gctgctgctg tggatggggt ggacggggtt caacggcggc    240

gcgccgtacg ccgccaacgt cgacgcgtcg gtcaccgtcg tgaacacgca cctctgcacg    300
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gcgacgagcc tcctggtgtg gctcctcctc gacagcttcg tcttcggccg cctctccgtc 360

atcagcgccg tgcagggcat gatcaccggc ctcgtctgcg tcaccccggc ggccaggctg 420

gtgctgcaca agcggagccg cctcctggcg cgcgtcgacg acacgctcgc cgtgctccac 480

acccacggcg tcgccggcag cctcagcggc gtcctgacgg ggctcctgct cctcgccgag 540

ccgcgcttcg ccaggctctt cttcggcgac gacccgcgct acgtcggcct cgcgtacgct 600

gtcagggacg gccgcgccgg ctcggggctc cggcaggtcg gcgtgcagct ggccgggatc 660

gcgttcgtgg tggcgctcaa cgtcgccgtg acgagcgccg tgtgcctggc cgtcagggtg 720

gccgtgccgc agctcgccgg cggcggcgac gccatacacg gcgaggacgc gtacgcggtg 780

tggggcgacg gcgagacgta cgagcagtac tccgtgcacg gcggcggcag caaccacggc 840

ggcttcccca tgacggccaa tcccgtggcg tccaaagccg acgagatgat atggatataa 900

<210> SEQ ID NO 36
<211> LENGTH: 299
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 36

Met Ala Ala Glu Ala Ala Pro Glu Trp Val Glu Lys Gly Asp Asn Ala
1 5 10 15

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

Leu Val Ile Leu Tyr Gly Asp Cys Gly Ala Val Gly Pro Arg Thr Glu
35 40 45

Lys Asp Arg Glu Ala Phe Pro Pro Asn Asn Val Leu Leu Thr Leu Ala
50 55 60

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

Ala Pro Tyr Ala Ala Asn Val Asp Ala Ser Val Thr Val Val Asn Thr
85 90 95

His Leu Cys Thr Ala Thr Ser Leu Leu Val Trp Leu Leu Leu Asp Ser
100 105 110

Phe Val Phe Gly Arg Leu Ser Val Ile Ser Ala Val Gln Gly Met Ile
115 120 125

Thr Gly Leu Val Cys Val Thr Pro Ala Ala Arg Leu Val Leu His Lys
130 135 140

Arg Ser Arg Leu Leu Ala Arg Val Asp Asp Thr Leu Ala Val Leu His
145 150 155 160

Thr His Gly Val Ala Gly Ser Leu Ser Gly Val Leu Thr Gly Leu Leu
165 170 175

Leu Leu Ala Glu Pro Arg Phe Ala Arg Leu Phe Phe Gly Asp Asp Pro
180 185 190

Arg Tyr Val Gly Leu Ala Tyr Ala Val Arg Asp Gly Arg Ala Gly Ser
195 200 205

Gly Leu Arg Gln Val Gly Val Gln Leu Ala Gly Ile Ala Phe Val Val
210 215 220

Ala Leu Asn Val Ala Val Thr Ser Ala Val Cys Leu Ala Val Arg Val
225 230 235 240

Ala Val Pro Gln Leu Ala Gly Gly Gly Asp Ala Ile His Gly Glu Asp
245 250 255

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Ala Tyr Ala Val Trp Gly Asp Gly Glu Thr Tyr Glu Gln Tyr Ser Val
260 265 270

His Gly Gly Gly Ser Asn His Gly Gly Phe Pro Met Thr Ala Asn Pro
275 280 285

Val Ala Ser Lys Ala Asp Glu Met Ile Trp Ile
290 295

<210> SEQ ID NO 37
<211> LENGTH: 2040
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 37

ggaggctttg gctaccctgc tcccctcgcc atttcattgg ccgtttcgtg gccatccatc 60

acgaactcga tcgattcccc tcttcgagcc cgtaccaatt attagctagt ttaactcgta 120

cgatgaatca cgccgaaaca caatataaat ggtggagtcg gctcgctgtc aaacgcgcgg 180

gagctcgcgc cacttgtaat ttttcgcgtc tcctctcgtc cggcacagca caggagcgcg 240

gacttgaaga cctcaagtag cgattcgtcc gtgcggcgcg gcgcaagaag ggaagggaag 300

gggactaggg gagggcgaga tggcggcggc gggggcgtac tcggcgagcc taccggcggt 360

gccggactgg ctgaacaagg gggacaacgc gtggcagctg acggcgtcga cgctggtggg 420

gatccagtcg atgcccgggc tggtggtgct gtacggcagc atcgtgaaga agaagtgggc 480

ggtgaactcg gcgttcatgg cgctctacgc ctacgcgtcg tcgctgctgg tgtgggtgct 540

ggtcggcttc cgcatggcgt tcggcgacca gctgctgccg ttctggggca aggccggcgt 600

ggcgctgacc cagagctacc tcgtcggccg cgccacgctg ccggccaccg cgcacggcgc 660

catcccgcgc accgagccct tctacccgga ggccacgctg gtgctcttcc agttcgagtt 720

cgccgccatc acgctcgtcc tcctcgccgg ctccgtcctc ggccgcatga acatcaaggc 780

ctggatggcc ttcaccccgc tctggctcct cctctcctac accgtcggcg ccttcagcct 840

ctggggcggc ggcttcctct accgctgggg cgtcatcgac tactccggcg gctacgtcat 900

ccacctctcc tccggcatcg ccggcttcac cgccgcctac tgggtggggc caaggctgaa 960

gagcgaccgt gagcggttct caccgaacaa catcctgctg atgatcgcgg gcggcgggct 1020

gctgtggatg gggtgggccg ggttcaacgg cggcgcgccg tacgccgcca acatcgcggc 1080

gtcggtcgcc gtgctcaaca ccaacgtctg cgccgccacc agcctcctca tgtggacctg 1140

cctcgacgtc atcttcttcc gcaagccgtc cgtcatcggc gccgtgcagg gcatgatgac 1200

cggcctcgtc tgcatcaccc ccggcgcagg gctggtgcag acctgggcgg ccgtggtaat 1260

gggcatcttc gccggcagcg tgccgtggtt caccatgatg atcctgcaca agaagtcagc 1320

gctgctgatg aaggtggacg acacgctcgc cgtgttccac acccacgccg tggcggggct 1380

cctcggcggc atcctcacgg gcctcctggc caccccggag ctcttctccc tcgagtccac 1440

ggtgccggga ctccgcggcg cgttctacgg cggcggtatc aagcagatcg gcaagcagct 1500

cggcggcgcc gcgttcgtga tcgcgtggaa cctcgtggtc accacggcca tcctcctcgg 1560

catcggcctg ttcatcccgc tgcggatgcc cgacgagcag ctcatgatcg gcgacgacgc 1620

ggcgcacggc gaggaggcct acgcgctgtg gggcgacggc gagaagttcg acgcgacgcg 1680

gcacgacctg tcgaggggcg gcggaggcgg cgacagggac ggccccgccg gcgagcgcct 1740

-continued

ctccgcccta ggcgccaggg gcgtcaccat ccagctctag gcgcgccacg ccacgccacg 1800

ccgcgccgcg ccgcggcctg gcctctaatt acacgcgcgt ttgtactgtt tttggacgtg 1860

ttattgttta ggagtagtga agtgaaccaa cgattgactg caaggtgaag ggtgagaacg 1920

cgagagacca gaccactata gtctatagta catatggatg ctgtaatgat gttgatccga 1980

gttcgttttt ccaacacgat aaaggccgac atgcctatta aatttaaaaa aaaaaaaaaa 2040

<210> SEQ ID NO 38
<211> LENGTH: 486
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 38

Met Ala Ala Ala Gly Ala Tyr Ser Ala Ser Leu Pro Ala Val Pro Asp
1 5 10 15

Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu Thr Ala Ser Thr Leu
20 25 30

Val Gly Ile Gln Ser Met Pro Gly Leu Val Val Leu Tyr Gly Ser Ile
35 40 45

Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala Leu Tyr Ala
50 55 60

Tyr Ala Ser Ser Leu Leu Val Trp Val Leu Val Gly Phe Arg Met Ala
65 70 75 80

Phe Gly Asp Gln Leu Leu Pro Phe Trp Gly Lys Ala Gly Val Ala Leu
85 90 95

Thr Gln Ser Tyr Leu Val Gly Arg Ala Thr Leu Pro Ala Thr Ala His
100 105 110

Gly Ala Ile Pro Arg Thr Glu Pro Phe Tyr Pro Glu Ala Thr Leu Val
115 120 125

Leu Phe Gln Phe Glu Phe Ala Ala Ile Thr Leu Val Leu Leu Ala Gly
130 135 140

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

Leu Trp Leu Leu Leu Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly
165 170 175

Gly Gly Phe Leu Tyr Arg Trp Gly Val Ile Asp Tyr Ser Gly Gly Tyr
180 185 190

Val Ile His Leu Ser Ser Gly Ile Ala Gly Phe Thr Ala Ala Tyr Trp
195 200 205

Val Gly Pro Arg Leu Lys Ser Asp Arg Glu Arg Phe Ser Pro Asn Asn
210 215 220

Ile Leu Leu Met Ile Ala Gly Gly Gly Leu Leu Trp Met Gly Trp Ala
225 230 235 240

Gly Phe Asn Gly Gly Ala Pro Tyr Ala Ala Asn Ile Ala Ala Ser Val
245 250 255

Ala Val Leu Asn Thr Asn Val Cys Ala Ala Thr Ser Leu Leu Met Trp
260 265 270

Thr Cys Leu Asp Val Ile Phe Phe Arg Lys Pro Ser Val Ile Gly Ala
275 280 285

Val Gln Gly Met Met Thr Gly Leu Val Cys Ile Thr Pro Gly Ala Gly
290 295 300

Leu Val Gln Thr Trp Ala Ala Val Val Met Gly Ile Phe Ala Gly Ser

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305 310 315 320

Val Pro Trp Phe Thr Met Met Ile Leu His Lys Lys Ser Ala Leu Leu
325 330 335

Met Lys Val Asp Asp Thr Leu Ala Val Phe His Thr His Ala Val Ala
340 345 350

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

Phe Ser Leu Glu Ser Thr Val Pro Gly Leu Arg Gly Ala Phe Tyr Gly
370 375 380

Gly Gly Ile Lys Gln Ile Gly Lys Gln Leu Gly Gly Ala Ala Phe Val
385 390 395 400

Ile Ala Trp Asn Leu Val Val Thr Thr Ala Ile Leu Leu Gly Ile Gly
405 410 415

Leu Phe Ile Pro Leu Arg Met Pro Asp Glu Gln Leu Met Ile Gly Asp
420 425 430

Asp Ala Ala His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu
435 440 445

Lys Phe Asp Ala Thr Arg His Asp Leu Ser Arg Gly Gly Gly Gly Gly
450 455 460

Asp Arg Asp Gly Pro Ala Gly Glu Arg Leu Ser Ala Leu Gly Ala Arg
465 470 475 480

Gly Val Thr Ile Gln Leu
485

<210> SEQ ID NO 39
<211> LENGTH: 1494
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 39

atggcgtcgc cgacccggcc ggggccgtac atgccgcgcc caccggcggt gccggagtgg 60

ctgaacaccg gggacaacgg gtggcagctc gcggcggcga cgttcgtcgg gctccagtcg 120

atgcctgggc tggtggtgct gtacggcagc atcgtgaaga agaagtgggc cgtcaactcg 180

gccttcatgg cgctgtacgc gtacgcgtcc acgctcatcg tgtgggtgct ggtcggcttc 240

cgcatggcgt tcggcgaccg gctgctcccg ttctgggggа aggccggcgc ggcgctgacg 300

gaggggttcc tcgtggcgcg cgcgtcggtc ccggccacgg cgcactacgg gaaggacggc 360

gccctggagt cgccgcgcac cgagccgttc tacccggagg cgtccatggt gctgttccag 420

ttcgagctcg ccgccatcac gctggtgctg ctcgccgggt cgctcctcgg gaggatgaac 480

atcaaggcgt ggatggcgtt cactccgctc tggctcctct tctcctacac cgtctgcgcc 540

ttcagcctct ggggcggcgg cttcctctac cagtggggcg tcatcgacta ctccggcgga 600

tacgtcatcc acctctcctc cggcatcgcc ggcttcaccg ccgcctactg ggtggggccg 660

aggctgaaga gcgacaggga gcggttctcg ccgaacaaca tcctcctcat gatcgccggc 720

ggcgggctgc tgtggctggg ctgggccggg ttcaacggcg gcgcgccgta cgccccaaac 780

atcaccgcgt ccatcgccgt gctcaacacc aacgtcagcg ccgcggcgag cctcctcacc 840

tggacctgcc tcgacgtcat cttcttcggc aagccctccg tcatcggcgc cgtgcagggc 900

atgatgaccg gtctcgtctg catcaccccc ggcgcaggtc tggtgcacac gtgggcggcc 960

atactgatgg gcatctgtgg cggcagcttg ccgtggttct ccatgatgat cctccacaag 1020

-continued

agatcggcgc tgctccagaa ggtggacgac accctcgccg tcttccacac ccacgccgtc 1080

gcgggcctcc tcggcggctt cctcacgggc ctgttcgcct tgccggacct caccgccgtc 1140

cacacccaca tccctggcgc gcgcggcgcg ttctacggcg gcggcatcgc ccaggtgggg 1200

aagcagatcg ccggcgcgct cttcgtcgtc gtgtggaacg tcgtggccac caccgtcatc 1260

ctgctcggcg tcggcctcgt cgtcccgctc cgcatgcccg acgagcagct caagatcggc 1320

gacgacgcgg cgcacgggga ggaggcctac gcgctatggg gagacggcga gaggttcgac 1380

gtgacgcgcc atgaggggggc gaggggcggc gcgtggggcg ccgcggtcgt ggacgaggcg 1440

atggatcacc ggctggccgg aatgggagcg agaggagtca cgattcagct gtag 1494

<210> SEQ ID NO 40
<211> LENGTH: 497
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 40

Met Ala Ser Pro Thr Arg Pro Gly Pro Tyr Met Pro Arg Pro Pro Ala
1 5 10 15

Val Pro Glu Trp Leu Asn Thr Gly Asp Asn Gly Trp Gln Leu Ala Ala
20 25 30

Ala Thr Phe Val Gly Leu Gln Ser Met Pro Gly Leu Val Val Leu Tyr
35 40 45

Gly Ser Ile Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala
50 55 60

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

Arg Met Ala Phe Gly Asp Arg Leu Leu Pro Phe Trp Gly Lys Ala Gly
85 90 95

Ala Ala Leu Thr Glu Gly Phe Leu Val Ala Arg Ala Ser Val Pro Ala
100 105 110

Thr Ala His Tyr Gly Lys Asp Gly Ala Leu Glu Ser Pro Arg Thr Glu
115 120 125

Pro Phe Tyr Pro Glu Ala Ser Met Val Leu Phe Gln Phe Glu Leu Ala
130 135 140

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

Ile Lys Ala Trp Met Ala Phe Thr Pro Leu Trp Leu Leu Phe Ser Tyr
165 170 175

Thr Val Cys Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu Tyr Gln Trp
180 185 190

Gly Val Ile Asp Tyr Ser Gly Gly Tyr Val Ile His Leu Ser Ser Gly
195 200 205

Ile Ala Gly Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg Leu Lys Ser
210 215 220

Asp Arg Glu Arg Phe Ser Pro Asn Asn Ile Leu Leu Met Ile Ala Gly
225 230 235 240

Gly Gly Leu Leu Trp Leu Gly Trp Ala Gly Phe Asn Gly Gly Ala Pro
245 250 255

Tyr Ala Pro Asn Ile Thr Ala Ser Ile Ala Val Leu Asn Thr Asn Val
260 265 270

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

Phe Gly Lys Pro Ser Val Ile Gly Ala Val Gln Gly Met Met Thr Gly
290                 295                 300

Leu Val Cys Ile Thr Pro Gly Ala Gly Leu Val His Thr Trp Ala Ala
305                 310                 315                 320

Ile Leu Met Gly Ile Cys Gly Gly Ser Leu Pro Trp Phe Ser Met Met
325                 330                 335

Ile Leu His Lys Arg Ser Ala Leu Leu Gln Lys Val Asp Asp Thr Leu
340                 345                 350

Ala Val Phe His Thr His Ala Val Ala Gly Leu Leu Gly Gly Phe Leu
355                 360                 365

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

Pro Gly Ala Arg Gly Ala Phe Tyr Gly Gly Gly Ile Ala Gln Val Gly
385                 390                 395                 400

Lys Gln Ile Ala Gly Ala Leu Phe Val Val Val Trp Asn Val Val Ala
405                 410                 415

Thr Thr Val Ile Leu Leu Gly Val Gly Leu Val Val Pro Leu Arg Met
420                 425                 430

Pro Asp Glu Gln Leu Lys Ile Gly Asp Asp Ala Ala His Gly Glu Glu
435                 440                 445

Ala Tyr Ala Leu Trp Gly Asp Gly Glu Arg Phe Asp Val Thr Arg His
450                 455                 460

Glu Gly Ala Arg Gly Gly Ala Trp Gly Ala Ala Val Val Asp Glu Ala
465                 470                 475                 480

Met Asp His Arg Leu Ala Gly Met Gly Ala Arg Gly Val Thr Ile Gln
485                 490                 495

Leu
```

<210> SEQ ID NO 41
<211> LENGTH: 1494
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 41

```
atggcgtcgc cgccgcagcc cgggccgtac atgccggacc tgccggcggt gccggcgtgg     60

ctgaacaagg gcgacaccgc gtggcagctg gtggcggcga cgttcgtcgg catccagtcg    120

atgcctgggc tggtggtgat ctacggcagc atcgtgaaga agaagtgggc cgtcaactcc    180

gccttcatgg cgctgtacgc ctacgcgtcc acgcttatcg tgtgggtgct cgtcggcttc    240

cgcatggcgt tcggcgaccg gctgctcccg ttctgggcca aggccgggcc ggcgctgacg    300

caggacttcc tggtgcaacg cgcggtgttc ccggcgacgg cgcactacgg cagcgacggc    360

acgctcgaga cgccgcgcac cgagccgttc tacgcggagg cggcgctggt gctgttcgag    420

ttcgagttcg cggccatcac gctggtgctg ctcgccgggt cgctcctggg gcggatgaac    480

atcaaggcgt ggatggcgtt caccccgctc tggctcctct tctcctacac cgtcggcgcg    540

ttcagcctct ggggcggcgg cttcctctac cagtggggcg tcatcgacta ctccggcgga    600

tacgtcatcc acctctcctc cggcgtcgcc ggcttcaccg ccgcctactg ggtgggcccg    660

aggctgaaga gcgacaggga gcggttctcg ccgaacaaca tcctgctcat gatcgccggc    720
```

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```
ggcgggctgc tgtggttggg ctgggccggg ttcaacggcg gcgcgccgta cgcccccaac    780

gtcaccgcca cggtcgccgt gctcaacacc aacgtcagcg ccgcgacgag cctcctcacc    840

tggacctgcc tcgacgtcat cttcttcggc aagccctccg tcatcggcgc cgtgcagggt    900

atgatgacgg ggctcgtctg catcacgccc ggcgccgggc tggtgcacac gtggtcagcg    960

atgctgatgg gcatgttcgc cggcagcgtc ccgtggttca cgatgatgat cctgcacaag   1020

aaatccacct tcctcatgaa ggtcgacgac accctcgccg tcttccacac ccacgccgtc   1080

gccggcatcc tgggcggcgt cctcacgggc ctcctcgcca cgccggagct ctgcgctctc   1140

gattgcccga tcccgaacat gcgcggcgtc ttctacggca gcggcatcgg ccagctcggg   1200

aagcagctcg gcggcgcgct gttcgtcacc gtctggaacc tcatcgtcac cagcgccatt   1260

ctcctctgca tcggcctctt catcccgctc cgcatgtccg acgaccagct catgatcggc   1320

gacgacgcgg cgcacgggga ggaggcctac gctctgtggg gggacggtga gaagttcgac   1380

gtgacgcggc cggagacgac gaggacggga ggtgcaggcg gcgcgggcag ggaggacacc   1440

atggagcaga ggctgaccaa catgggagcc aggggtgtca ccattcagtt gtag         1494
```

<210> SEQ ID NO 42
<211> LENGTH: 497
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 42

```
Met Ala Ser Pro Pro Gln Pro Gly Pro Tyr Met Pro Asp Leu Pro Ala
1               5                  10                  15

Val Pro Ala Trp Leu Asn Lys Gly Asp Thr Ala Trp Gln Leu Val Ala
20                  25                  30

Ala Thr Phe Val Gly Ile Gln Ser Met Pro Gly Leu Val Val Ile Tyr
35                  40                  45

Gly Ser Ile Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala
50                  55                  60

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

Arg Met Ala Phe Gly Asp Arg Leu Leu Pro Phe Trp Ala Lys Ala Gly
85                  90                  95

Pro Ala Leu Thr Gln Asp Phe Leu Val Gln Arg Ala Val Phe Pro Ala
100                 105                 110

Thr Ala His Tyr Gly Ser Asp Gly Thr Leu Glu Thr Pro Arg Thr Glu
115                 120                 125

Pro Phe Tyr Ala Glu Ala Ala Leu Val Leu Phe Glu Phe Glu Phe Ala
130                 135                 140

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

Ile Lys Ala Trp Met Ala Phe Thr Pro Leu Trp Leu Leu Phe Ser Tyr
165                 170                 175

Thr Val Gly Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu Tyr Gln Trp
180                 185                 190

Gly Val Ile Asp Tyr Ser Gly Gly Tyr Val Ile His Leu Ser Ser Gly
195                 200                 205

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

Gly Gly Leu Leu Trp Leu Gly Trp Ala Gly Phe Asn Gly Gly Ala Pro
245                 250                 255

Tyr Ala Pro Asn Val Thr Ala Thr Val Ala Val Leu Asn Thr Asn Val
260                 265                 270

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

Phe Gly Lys Pro Ser Val Ile Gly Ala Val Gln Gly Met Met Thr Gly
290                 295                 300

Leu Val Cys Ile Thr Pro Gly Ala Gly Leu Val His Thr Trp Ser Ala
305                 310                 315                 320

Met Leu Met Gly Met Phe Ala Gly Ser Val Pro Trp Phe Thr Met Met
325                 330                 335

Ile Leu His Lys Lys Ser Thr Phe Leu Met Lys Val Asp Asp Thr Leu
340                 345                 350

Ala Val Phe His Thr His Ala Val Ala Gly Ile Leu Gly Gly Val Leu
355                 360                 365

Thr Gly Leu Leu Ala Thr Pro Glu Leu Cys Ala Leu Asp Cys Pro Ile
370                 375                 380

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

Lys Gln Leu Gly Gly Ala Leu Phe Val Thr Val Trp Asn Leu Ile Val
405                 410                 415

Thr Ser Ala Ile Leu Leu Cys Ile Gly Leu Phe Ile Pro Leu Arg Met
420                 425                 430

Ser Asp Asp Gln Leu Met Ile Gly Asp Asp Ala Ala His Gly Glu Glu
435                 440                 445

Ala Tyr Ala Leu Trp Gly Asp Gly Glu Lys Phe Asp Val Thr Arg Pro
450                 455                 460

Glu Thr Thr Arg Thr Gly Gly Ala Gly Gly Ala Gly Arg Glu Asp Thr
465                 470                 475                 480

Met Glu Gln Arg Leu Thr Asn Met Gly Ala Arg Gly Val Thr Ile Gln
485                 490                 495

Leu
```

<210> SEQ ID NO 43
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 43

```
atgtcgtcgt cggcgacggt ggtgccgctg gcgtaccagg ggaacacgtc ggcgtcggtg     60

gcggactggc tgaacaaggg cgacaacgcg tggcagctgg tggcggcgac ggtggtgggg    120

ctgcagagcg tgccgggctt ggtggtgctg tacggcggcg tggtgaagaa gaagtgggcg    180

gtgaactcgg cgttcatggc gctctacgcc ttcgccgccg tgtggatctg ctgggtcacc    240

tgggcgtaca acatgtcgtt cggggagaag ctcctcccga tctgggggaa ggcgcggccg    300

gcgctggacc agggcctcct cgtcggccgc gccgcgctgc cggcgacggt ccactaccgc    360

gccgacggca gcgtggagac ggcggcggtg gagccgctgt acccgatggc gacggtggtg    420

tacttccagt gcgtgttcgc cgccatcacc ctcatcctcg tcgccggctc cctcctcggc    480
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cgcatgagct tcctcgcctg gatgatcttc gtcccgctct ggctcacctt ctcctacacc    540

gtcggcgcct tctccctctg gggcggcggc ttcctcttcc actggggcgt catcgactac    600

tgcggcggct acgtcatcca cgtctccgcc ggcatcgccg gcttcaccgc cgcctactgg    660

gtggggccaa gggcacagaa ggacagggag aggttcccgc cgaacaacat actgttcacg    720

ctgacggggg cagggttact atggatgggg tgggcagggt tcaacggcgg tggtccgtac    780

gccgccaact ccgtcgcctc catggccgtc ctcaacacca acatctgcac cgccatgagc    840

ctcatcgtct ggacatgcct cgacgtcatc ttcttcaaga agccctccgt cgtcggcgcc    900

gtccagggca tgatcaccgg cctcgtctgc atcacccccg ctgcaggggt ggtgcagggg    960

tgggcggcgc tggtgatggg ggtgctcgcc ggcagcatcc cgtggtacac catgatgatc   1020

ctccacaagc gctccaagat cctgcagcgc gtcgacgaca ccctcggcgt cttccacacc   1080

cacggcgtcg ccggcctcct cggcggcctc ctcaccggcc tcttcgccga gcccaccctc   1140

tgcaacctct tcctccccgt cgccgactcc cggggcgcct tctacggcgg cgccggcggc   1200

gcccagttcg gcaagcagat cgccggtggc ctcttcgtcg tcgcctggaa cgtcgccgtc   1260

acctccctca tctgcctcgc catcaacctc ctcgtcccgc tccgcatgcc cgacgacaag   1320

ctcgaggtcg gcgacgacgc cgtccacggc gaggaggcct acgcgctctg gggcgacggc   1380

gagatgtacg acgtcaccaa gcacggctcc gacgccgccg ttgcgcccgt cgtcgtatga   1440
```

<210> SEQ ID NO 44
<211> LENGTH: 479
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 44

```
Met Ser Ser Ser Ala Thr Val Val Pro Leu Ala Tyr Gln Gly Asn Thr
1               5                  10                  15

Ser Ala Ser Val Ala Asp Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln
20                  25                  30

Leu Val Ala Ala Thr Val Val Gly Leu Gln Ser Val Pro Gly Leu Val
35                  40                  45

Val Leu Tyr Gly Gly Val Val Lys Lys Lys Trp Ala Val Asn Ser Ala
50                  55                  60

Phe Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Thr
65                  70                  75                  80

Trp Ala Tyr Asn Met Ser Phe Gly Glu Lys Leu Leu Pro Ile Trp Gly
85                  90                  95

Lys Ala Arg Pro Ala Leu Asp Gln Gly Leu Leu Val Gly Arg Ala Ala
100                 105                 110

Leu Pro Ala Thr Val His Tyr Arg Ala Asp Gly Ser Val Glu Thr Ala
115                 120                 125

Ala Val Glu Pro Leu Tyr Pro Met Ala Thr Val Val Tyr Phe Gln Cys
130                 135                 140

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

Arg Met Ser Phe Leu Ala Trp Met Ile Phe Val Pro Leu Trp Leu Thr
165                 170                 175

Phe Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu
180                 185                 190
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```
Phe His Trp Gly Val Ile Asp Tyr Cys Gly Gly Tyr Val Ile His Val
195                 200                 205

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

Ala Gln Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Phe Thr
225                 230                 235                 240

Leu Thr Gly Ala Gly Leu Leu Trp Met Gly Trp Ala Gly Phe Asn Gly
245                 250                 255

Gly Gly Pro Tyr Ala Ala Asn Ser Val Ala Ser Met Ala Val Leu Asn
260                 265                 270

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

Val Ile Phe Phe Lys Lys Pro Ser Val Val Gly Ala Val Gln Gly Met
290                 295                 300

Ile Thr Gly Leu Val Cys Ile Thr Pro Ala Ala Gly Val Val Gln Gly
305                 310                 315                 320

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

Thr Met Met Ile Leu His Lys Arg Ser Lys Ile Leu Gln Arg Val Asp
340                 345                 350

Asp Thr Leu Gly Val Phe His Thr His Gly Val Ala Gly Leu Leu Gly
355                 360                 365

Gly Leu Leu Thr Gly Leu Phe Ala Glu Pro Thr Leu Cys Asn Leu Phe
370                 375                 380

Leu Pro Val Ala Asp Ser Arg Gly Ala Phe Tyr Gly Gly Ala Gly Gly
385                 390                 395                 400

Ala Gln Phe Gly Lys Gln Ile Ala Gly Gly Leu Phe Val Val Ala Trp
405                 410                 415

Asn Val Ala Val Thr Ser Leu Ile Cys Leu Ala Ile Asn Leu Leu Val
420                 425                 430

Pro Leu Arg Met Pro Asp Asp Lys Leu Glu Val Gly Asp Asp Ala Val
435                 440                 445

His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu Met Tyr Asp
450                 455                 460

Val Thr Lys His Gly Ser Asp Ala Ala Val Ala Pro Val Val Val
465                 470                 475


<210> SEQ ID NO 45
<211> LENGTH: 1497
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 45

atgtcggggg acgcgttcaa catgtcggtg gcgtaccagc cgtcggggat ggcggtgccg     60

gagtggctga acaagggcga caacgcgtgg cagatgatct cggcgacgct ggtggggatg    120

cagagcgtgc cggggctggt gatcctgtac ggcagcatcg tgaagaagaa gtgggcggtg    180

aactcggcgt tcatggcgct ctacgccttc gccgccgtgt ggctgtgctg ggtcacctgg    240

ggctacaaca tgtcgttcgg ccacaagctc ctcccgttct ggggcaaggc gcggccggcg    300

ctgggccaga gcttcctcct cgcccaggcc gtgctcccgc agacgacgca gttctacaag    360

ggcggcggcg gcgccgacgc cgtggtggag acgccatggg tgaacccgct ctacccgatg    420
```

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gccaccatgg tgtacttcca gtgcgtgttc gccgccatca cgctcatcct cctcgccggc 480

tcgctgctgg ggcggatgaa catcaaggcg tggatgctgt tcgtcccgct ctggctcacc 540

ttctcctaca ccgtcggcgc cttctcgctg tggggcggcg gcttcctctt ccactggggg 600

gtcatggact actccggcgg ctacgtcatc cacctctcgt cgggtgtcgc cggcttcacc 660

gcggcgtact gggtggggcc caggtcgacc aaggacaggg agaggttccc gccaaacaac 720

gtgctgctca tgctcaccgg cgccggcata ctgtggatgg ggtgggcggg gttcaacggc 780

ggcgacccgt actccgccaa catcgactcc tcgctcgccg tgctcaacac caacatctgc 840

gccgccacca gcctcctcgt ctggacttgc ctcgacgtca tcttcttcaa gaagccgtcc 900

gtcatcggcg ccgtccaggg catgatcacc ggcctcgtct gcatcactcc cggcgcaggc 960

ctggtgcagg gttgggcggc gatcgtgatg ggcatcctct ccggcagcat cccgtggttc 1020

acgatgatgg tggtgcacaa gcggtcgcgc ctcctgcagc aggtggacga caccctgggc 1080

gtcttccaca cccacgccgt cgccggattc ctcggcggcg ccaccacggg cctcttcgcc 1140

gagcccgtcc tctgctccct cttcctcccc gtcaccaact cccgcggcgc cttctacccc 1200

ggccgcggcg gcggcctcca gttcgtccgc caggtggccg gcgccctctt catcatctgc 1260

tggaacgtgg tggtcaccag cctcgtctgc ctcgccgtcc gcgccgtggt tcccctccgg 1320

atgcccgagg aggagctcgc catcggcgac gacgccgtgc acggggagga ggcgtacgcg 1380

ctgtggggcg acggcgagaa gtacgactcc accaagcacg gatggtactc cgacaacaac 1440

gacacgcacc acaacaacaa caaggccgcg cccagcggcg tcacgcagaa cgtctga 1497

<210> SEQ ID NO 46
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 46

Met Ser Gly Asp Ala Phe Asn Met Ser Val Ala Tyr Gln Pro Ser Gly
1 5 10 15

Met Ala Val Pro Glu Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Met
20 25 30

Ile Ser Ala Thr Leu Val Gly Met Gln Ser Val Pro Gly Leu Val Ile
35 40 45

Leu Tyr Gly Ser Ile Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe
50 55 60

Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Leu Cys Trp Val Thr Trp
65 70 75 80

Gly Tyr Asn Met Ser Phe Gly His Lys Leu Leu Pro Phe Trp Gly Lys
85 90 95

Ala Arg Pro Ala Leu Gly Gln Ser Phe Leu Leu Ala Gln Ala Val Leu
100 105 110

Pro Gln Thr Thr Gln Phe Tyr Lys Gly Gly Gly Gly Ala Asp Ala Val
115 120 125

Val Glu Thr Pro Trp Val Asn Pro Leu Tyr Pro Met Ala Thr Met Val
130 135 140

Tyr Phe Gln Cys Val Phe Ala Ala Ile Thr Leu Ile Leu Leu Ala Gly
145 150 155 160

Ser Leu Leu Gly Arg Met Asn Ile Lys Ala Trp Met Leu Phe Val Pro

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165                 170                 175

Leu Trp Leu Thr Phe Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly
180                 185                 190

Gly Gly Phe Leu Phe His Trp Gly Val Met Asp Tyr Ser Gly Gly Tyr
195                 200                 205

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

Val Gly Pro Arg Ser Thr Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn
225                 230                 235                 240

Val Leu Leu Met Leu Thr Gly Ala Gly Ile Leu Trp Met Gly Trp Ala
245                 250                 255

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

Ala Val Leu Asn Thr Asn Ile Cys Ala Ala Thr Ser Leu Leu Val Trp
275                 280                 285

Thr Cys Leu Asp Val Ile Phe Phe Lys Lys Pro Ser Val Ile Gly Ala
290                 295                 300

Val Gln Gly Met Ile Thr Gly Leu Val Cys Ile Thr Pro Gly Ala Gly
305                 310                 315                 320

Leu Val Gln Gly Trp Ala Ala Ile Val Met Gly Ile Leu Ser Gly Ser
325                 330                 335

Ile Pro Trp Phe Thr Met Met Val Val His Lys Arg Ser Arg Leu Leu
340                 345                 350

Gln Gln Val Asp Asp Thr Leu Gly Val Phe His Thr His Ala Val Ala
355                 360                 365

Gly Phe Leu Gly Gly Ala Thr Thr Gly Leu Phe Ala Glu Pro Val Leu
370                 375                 380

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

Gly Arg Gly Gly Gly Leu Gln Phe Val Arg Gln Val Ala Gly Ala Leu
405                 410                 415

Phe Ile Ile Cys Trp Asn Val Val Val Thr Ser Leu Val Cys Leu Ala
420                 425                 430

Val Arg Ala Val Val Pro Leu Arg Met Pro Glu Glu Glu Leu Ala Ile
435                 440                 445

Gly Asp Asp Ala Val His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp
450                 455                 460

Gly Glu Lys Tyr Asp Ser Thr Lys His Gly Trp Tyr Ser Asp Asn Asn
465                 470                 475                 480

Asp Thr His His Asn Asn Asn Lys Ala Ala Pro Ser Gly Val Thr Gln
485                 490                 495

Asn Val


<210> SEQ ID NO 47
<211> LENGTH: 1497
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 47

atggcgacgt gcgcggcgga cctggcgccg ctgctggggc cggtggcggc gaacgcgacg     60

gactacctgt gcaaccggtt cgccgacacg acgtcggcgg tggacgcgac gtacctgctc    120
```

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ttctcggcgt acctcgtgtt cgccatgcag ctcgggttcg cgatgctctg cgccgggtcg    180

gtgcgggcca agaacacgat gaacatcatg ctcaccaacg tgctcgacgc cgcggccggg    240

gcgctcttct actacctctt cggcttcgcc ttcgccttcg gcacgccgtc caacggcttc    300

atcgggaagc agttcttcgg cctcaagcac atgccgcaga ccgggttcga ctacgacttc    360

ttcctcttcc agtgggcctt cgccatcgcc gccgccggga tcacgtcggg ctccatcgcc    420

gagaggacgc agttcgtcgc ctacctcatc tactccgcct tcctcaccgg gttcgtctac    480

ccggtggtgt cccactggat ctggtccgcc gatgggtggg cctctgcctc ccgcacgtcc    540

ggacctctgc tgttcggctc cggtgtcatc gacttcgccg gctccggcgt cgtccacatg    600

gtcggcggtg tcgccgggct ctggggcgcg ctcatcgagg gcccccgcat cgggaggttc    660

gaccacgccg gccgatcggt ggcgctcaag ggccacagcg cgtcgctcgt cgtgcttggc    720

accttcctgc tgtggttcgg ctggtacgga ttcaaccccg ggtcgttcac caccatcctc    780

aagacgtacg gcccggccgg cggcatcaac gggcagtggt ccggagtcgg ccgcaccgcc    840

gtgacgacga ccctggccgg cagcgtggcg gcgctcacca cgctgttcgg gaagcggctc    900

cagacggggc actggaacgt ggtcgacgtc tgcaacggcc tcctcggcgg gttcgccgcc    960

atcaccgccg ggtgcagcgt cgtcgacccg tgggccgcga tcatctgcgg gttcgtctcg   1020

gcgtgggtgc tcatcggcct caacgcgctc gccgcgcgcc tcaagttcga cgacccgctc   1080

gaggccgccc agctccacgg cgggtgcggc gcgtggggga tcctcttcac cgcgctcttc   1140

gcgaggcaga agtacgtcga ggagatctac ggcgccggcc ggccgtacgg cctgttcatg   1200

ggcggcggcg gcaagctgct cgccgcgcac gtcatccaga tcctggtcat cttcgggtgg   1260

gtcagctgca ccatgggacc tctcttctac gggctcaaga agctcggcct gctccgcatc   1320

tccgccgagg acgagacgtc cggcatggac ctgacacggc acggcgggtt cgcgtacgtc   1380

taccacgacg aggacgagca cgacaagtct ggggttggtg ggttcatgct ccggtccgcg   1440

cagacccgcg tcgagccggc ggcggcggct gcctccaaca gcaacaacca agtgtaa      1497
```

<210> SEQ ID NO 48
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 48

```
Met Ala Thr Cys Ala Ala Asp Leu Ala Pro Leu Leu Gly Pro Val Ala
1               5                  10                  15

Ala Asn Ala Thr Asp Tyr Leu Cys Asn Arg Phe Ala Asp Thr Thr Ser
20                  25                  30

Ala Val Asp Ala Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
35                  40                  45

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
50                  55                  60

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

Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Thr Pro
85                  90                  95

Ser Asn Gly Phe Ile Gly Lys Gln Phe Phe Gly Leu Lys His Met Pro
100                 105                 110

Gln Thr Gly Phe Asp Tyr Asp Phe Phe Leu Phe Gln Trp Ala Phe Ala
```

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```
115                 120                 125

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln
130                 135                 140

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

Pro Val Val Ser His Trp Ile Trp Ser Ala Asp Gly Trp Ala Ser Ala
165                 170                 175

Ser Arg Thr Ser Gly Pro Leu Leu Phe Gly Ser Gly Val Ile Asp Phe
180                 185                 190

Ala Gly Ser Gly Val Val His Met Val Gly Gly Val Ala Gly Leu Trp
195                 200                 205

Gly Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly
210                 215                 220

Arg Ser Val Ala Leu Lys Gly His Ser Ala Ser Leu Val Val Leu Gly
225                 230                 235                 240

Thr Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe
245                 250                 255

Thr Thr Ile Leu Lys Thr Tyr Gly Pro Ala Gly Gly Ile Asn Gly Gln
260                 265                 270

Trp Ser Gly Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser
275                 280                 285

Val Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His
290                 295                 300

Trp Asn Val Val Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala
305                 310                 315                 320

Ile Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ala Ile Ile Cys
325                 330                 335

Gly Phe Val Ser Ala Trp Val Leu Ile Gly Leu Asn Ala Leu Ala Ala
340                 345                 350

Arg Leu Lys Phe Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly
355                 360                 365

Cys Gly Ala Trp Gly Ile Leu Phe Thr Ala Leu Phe Ala Arg Gln Lys
370                 375                 380

Tyr Val Glu Glu Ile Tyr Gly Ala Gly Arg Pro Tyr Gly Leu Phe Met
385                 390                 395                 400

Gly Gly Gly Gly Lys Leu Leu Ala Ala His Val Ile Gln Ile Leu Val
405                 410                 415

Ile Phe Gly Trp Val Ser Cys Thr Met Gly Pro Leu Phe Tyr Gly Leu
420                 425                 430

Lys Lys Leu Gly Leu Leu Arg Ile Ser Ala Glu Asp Glu Thr Ser Gly
435                 440                 445

Met Asp Leu Thr Arg His Gly Gly Phe Ala Tyr Val Tyr His Asp Glu
450                 455                 460

Asp Glu His Asp Lys Ser Gly Val Gly Gly Phe Met Leu Arg Ser Ala
465                 470                 475                 480

Gln Thr Arg Val Glu Pro Ala Ala Ala Ala Ala Ser Asn Ser Asn Asn
485                 490                 495

Gln Val


<210> SEQ ID NO 49
<211> LENGTH: 438
```

-continued

<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 49

atggcgtggg tgagcttcac catggcgctg ctgttcctgg tgctcaacaa gctgggcttg 60

ctgcgcatct cggccgagga caagatggcc ggcatggacc agacgcgcca cggcgggtta 120

ccacgacgac gacgcgagcg gcaagccaga ccttggcatt ggcgggttca tgctcaagtc 180

ggtgcacggc acgcaggttc gtcggtgtcg acggaggcga cgactgcggg gatggtggcc 240

gcgagggccg tgcaggagtt gtggaacggt tcggacaccg agcagaagag gacataccca 300

ccggttctgc tcgccggaga gggaggggac aacgactgcg gtgtccatca ctggctgcgc 360

ttgccactac catcgctggt ctcgtggaag agaggagagg ggagaaagag gaagaagaag 420

gaaagaaggg caatttga 438

<210> SEQ ID NO 50
<211> LENGTH: 145
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 50

Met Ala Trp Val Ser Phe Thr Met Ala Leu Leu Phe Leu Val Leu Asn
1 5 10 15

Lys Leu Gly Leu Leu Arg Ile Ser Ala Glu Asp Lys Met Ala Gly Met
20 25 30

Asp Gln Thr Arg His Gly Gly Leu Pro Arg Arg Arg Arg Glu Arg Gln
35 40 45

Ala Arg Pro Trp His Trp Arg Val His Ala Gln Val Gly Ala Arg His
50 55 60

Ala Gly Ser Ser Val Ser Thr Glu Ala Thr Thr Ala Gly Met Val Ala
65 70 75 80

Ala Arg Ala Val Gln Glu Leu Trp Asn Gly Ser Asp Thr Glu Gln Lys
85 90 95

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

Cys Gly Val His His Trp Leu Arg Leu Pro Leu Pro Ser Leu Val Ser
115 120 125

Trp Lys Arg Gly Glu Gly Arg Lys Arg Lys Lys Lys Glu Arg Arg Ala
130 135 140

Ile
145

<210> SEQ ID NO 51
<211> LENGTH: 1497
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 51

atggcgacgt gcttggacag cctcgggccg ctgctcggcg gcgcggcgaa ctccaccgac 60

gcggccaact acatctgcaa caggttcacg gacacctcct ccgcggtgga cgcgacgtac 120

ctgctcttct cggcctacct cgtgttcgcc atgcagctcg ggttcgccat gctctgcgcg 180

ggctccgtcc gcgccaagaa ctccatgaac atcatgctca ccaacgtgct cgacgccgcc 240

gccggcgcgc tcttctacta cctcttcggc ttcgccttcg cgttcgggac gccgtccaag 300

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ggcttcatcg ggaagcagtt cttcgggctg aagcacatgc cgcagacagg gtacgactac    360

gacttcttcc tcttccagtg ggccttcgcc atcgccgccg ccggcatcac gtccggttcc    420

atcgccgagc ggacgcgctt cagcgcgtat ctcatctact ccgccttcct caccgggttc    480

gtgtacccgg tggtgtcgca ctggttctgg tccaccgacg ggtgggcttc ggccggccgg    540

ttgacgggtc cgttgctgtt caagtcgggc gtcatcgact tcgccggctc cggcgtcgtc    600

catctggtcg gtggcattgc tggcctgtgg ggtgccttca tcgagggccc tcgcatcggg    660

cggttcgacg ccgccggccg cacggtggcg atgaaagggc acagcgcctc actggtcgtg    720

ctcggcacct tcctgctgtg gttcgggtgg ttcggcttca acccggggtc cttcaccacc    780

atctccaaga tctacggcga gtcgggcacg atcgacgggc agtggtcggc ggtgggccgc    840

accgccgtga cgacgtcgct ggcggggagc gtcgccgcgc tgacgacgct ctacggcaag    900

agatggctga cggggcactg gaacgtgacc gacgtctgca acggtctcct cggcggcttc    960

gccgcgatca ccgcgggctg ctccgtggtc gacccgtggg cgtcggtgat ctgcgggttc   1020

gtgtcggcgt gggtcctcat cggctgcaac aagctgtcgc tgattctcaa gttcgacgac   1080

ccgctggagg cgacgcagct gcacgccggg tgcggcgcgt gggggatcat cttcaccgcg   1140

ctgttcgcgc gcagggagta cgtcgagctg atctacgggg tgccggggag gccgtacggg   1200

ctgttcatgg gcggcggcgg gaggcttctc gcggcgcaca tcgtgcagat cctggtgatc   1260

gtcgggtggg tcagcgccac catggggacg ctcttctacg tgctgcacag gttcgggctg   1320

ctccgcgtct cgcccgcgac agagatggaa ggcatggacc cgacgtgcca cggcgggttc   1380

gggtacgtgg acgaggacga aggcgagcgc cgcgtcaggg ccaagtcggc ggcggagacg   1440

gctcgcgtgg agcccagaaa gtcgccggag caagccgcgg cgggccagtt tgtgtag      1497
```

<210> SEQ ID NO 52
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 52

```
Met Ala Thr Cys Leu Asp Ser Leu Gly Pro Leu Leu Gly Gly Ala Ala
1               5                  10                  15

Asn Ser Thr Asp Ala Ala Asn Tyr Ile Cys Asn Arg Phe Thr Asp Thr
20                  25                  30

Ser Ser Ala Val Asp Ala Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val
35                  40                  45

Phe Ala Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg
50                  55                  60

Ala Lys Asn Ser Met Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala
65                  70                  75                  80

Ala Gly Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly
85                  90                  95

Thr Pro Ser Lys Gly Phe Ile Gly Lys Gln Phe Phe Gly Leu Lys His
100                 105                 110

Met Pro Gln Thr Gly Tyr Asp Tyr Asp Phe Phe Leu Phe Gln Trp Ala
115                 120                 125

Phe Ala Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg
130                 135                 140
```

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```
Thr Arg Phe Ser Ala Tyr Leu Ile Tyr Ser Ala Phe Leu Thr Gly Phe
145                 150                 155                 160

Val Tyr Pro Val Val Ser His Trp Phe Trp Ser Thr Asp Gly Trp Ala
165                 170                 175

Ser Ala Gly Arg Leu Thr Gly Pro Leu Leu Phe Lys Ser Gly Val Ile
180                 185                 190

Asp Phe Ala Gly Ser Gly Val Val His Leu Val Gly Gly Ile Ala Gly
195                 200                 205

Leu Trp Gly Ala Phe Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp Ala
210                 215                 220

Ala Gly Arg Thr Val Ala Met Lys Gly His Ser Ala Ser Leu Val Val
225                 230                 235                 240

Leu Gly Thr Phe Leu Leu Trp Phe Gly Trp Phe Gly Phe Asn Pro Gly
245                 250                 255

Ser Phe Thr Thr Ile Ser Lys Ile Tyr Gly Glu Ser Gly Thr Ile Asp
260                 265                 270

Gly Gln Trp Ser Ala Val Gly Arg Thr Ala Val Thr Thr Ser Leu Ala
275                 280                 285

Gly Ser Val Ala Ala Leu Thr Thr Leu Tyr Gly Lys Arg Trp Leu Thr
290                 295                 300

Gly His Trp Asn Val Thr Asp Val Cys Asn Gly Leu Leu Gly Gly Phe
305                 310                 315                 320

Ala Ala Ile Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ser Val
325                 330                 335

Ile Cys Gly Phe Val Ser Ala Trp Val Leu Ile Gly Cys Asn Lys Leu
340                 345                 350

Ser Leu Ile Leu Lys Phe Asp Asp Pro Leu Glu Ala Thr Gln Leu His
355                 360                 365

Ala Gly Cys Gly Ala Trp Gly Ile Ile Phe Thr Ala Leu Phe Ala Arg
370                 375                 380

Arg Glu Tyr Val Glu Leu Ile Tyr Gly Val Pro Gly Arg Pro Tyr Gly
385                 390                 395                 400

Leu Phe Met Gly Gly Gly Gly Arg Leu Leu Ala Ala His Ile Val Gln
405                 410                 415

Ile Leu Val Ile Val Gly Trp Val Ser Ala Thr Met Gly Thr Leu Phe
420                 425                 430

Tyr Val Leu His Arg Phe Gly Leu Leu Arg Val Ser Pro Ala Thr Glu
435                 440                 445

Met Glu Gly Met Asp Pro Thr Cys His Gly Gly Phe Gly Tyr Val Asp
450                 455                 460

Glu Asp Glu Gly Glu Arg Arg Val Arg Ala Lys Ser Ala Ala Glu Thr
465                 470                 475                 480

Ala Arg Val Glu Pro Arg Lys Ser Pro Glu Gln Ala Ala Ala Gly Gln
485                 490                 495

Phe Val


<210> SEQ ID NO 53
<211> LENGTH: 1853
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 53
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acagcccaca cttccattgc tcctcccctc tcctctacag tctgtgttga gcgcgcgtcg 60

aggcggcgag gatggcaacg tgcgcggata ccctcggccc gctgctgggc acggcggcgg 120

cgaacgcgac ggactacctg tgcaaccagt tcgcggacac gacgtcggcc gtggactcga 180

cgtacctgct cttctcggcg tacctcgtgt tcgccatgca gctcggcttc gccatgctct 240

gcgccgggtc cgtccgcgcc aagaacacca tgaacatcat gcttaccaac gtgctcgacg 300

ccgccgccgg cgcgctcttc tactacctct tcggcttcgc cttcgccttc ggggcgccgt 360

ccaacggctt catcgggaag cacttcttcg gcctcaagca ggtcccacag gtcggcttcg 420

actacagctt cttcctcttc cagtgggcct tcgccatcgc cgccgcgggc atcacgtccg 480

gctccatcgc cgagcggacc cagttcgtgg cgtacctcat ctactccgcc ttcctcaccg 540

gcttcgtcta cccggtggtg tcccactgga tctggtccgc cgacgggtgg gcctcggctt 600

cccggacgtc ggggtcgctg ctcttcgggt ccggcgtcat cgacttcgcc gggtcagggg 660

ttgtccacat ggtgggcggc gtggccggac tctggggcgc cctcatcgag ggcccccgca 720

ttgggcggtt cgaccacgcc ggccgctcgg tggcgctgcg cggccacagc gcgtcgctcg 780

tcgtgctcgg cagcttcctt ctgtggttcg ggtggtacgg gtttaacccc ggctcgttcc 840

tcaccatcct caaatcctac ggcccgcccg gtagcatcca cgggcagtgg tcggcggtgg 900

gacgcaccgc cgtgaccacc accctcgccg gcagcacggc ggcgctcacg acgctcttcg 960

ggaagaggct ccagacgggg cactggaacg tgatcgacgt ctgcaacggc ctcctcggcg 1020

gcttcgcggc gatcaccgcc ggttgctccg tcgtcgaccc gtgggccgcg atcatctgcg 1080

ggttcgtctc ggcgtgggtg ctcatcggcc tcaacgcgct ggcggcgagg ctcaagttcg 1140

acgacccgct cgaggcggcg cagctgcacg gcgggtgcgg cgcgtggggg gtcatcttca 1200

cggcgctgtt cgcgcgcaag gagtacgtgg accagatctt cggccagccc gggcgcccgt 1260

acgggctgtt catgggcggc ggcggccggc tgctcggggc gcacatagtg gtcatcctgg 1320

tcatcgcggc gtgggtgagc ttcaccatgg cgccgctgtt cctggtgctc aacaagctgg 1380

gcttgctgcg catctcggcc gaggacgaga tggccggcat ggaccagacg cgccacggcg 1440

ggttcgcgta cgcgtaccac gacgacgacg cgagcggcaa gccggaccgc agcgtcggcg 1500

ggttcatgct caagtcggcg cacggcacgc aggtcgccgc cgagatggga ggccatgtct 1560

agtggaaccg gaggagctga gctagtagta catacatgca gcatcatcga tcgaacgaaa 1620

tgcatataag cgtttttcaa ggttgatctg atgctgcagg tttcgtgatt gtataatagg 1680

aagaaaaaga tagtagtatt ttttatctga gatcatctgt ttggaacagg ggatttgact 1740

aagatttgat ataaatttac acaaaatctt agcaaaaatc cctttatctc aactctcaag 1800

tagagctttg ctttgtacaa caaagtatca tgtgtgatat aattgtcagg tgg 1853

<210> SEQ ID NO 54
<211> LENGTH: 496
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 54

Met Ala Thr Cys Ala Asp Thr Leu Gly Pro Leu Leu Gly Thr Ala Ala
1 5 10 15

Ala Asn Ala Thr Asp Tyr Leu Cys Asn Gln Phe Ala Asp Thr Thr Ser
20 25 30

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Ala Val Asp Ser Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ala
35                  40                  45

Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys
50                  55                  60

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

Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ala Pro
85                  90                  95

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

Gln Val Gly Phe Asp Tyr Ser Phe Phe Leu Phe Gln Trp Ala Phe Ala
115                 120                 125

Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln
130                 135                 140

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

Pro Val Val Ser His Trp Ile Trp Ser Ala Asp Gly Trp Ala Ser Ala
165                 170                 175

Ser Arg Thr Ser Gly Ser Leu Leu Phe Gly Ser Gly Val Ile Asp Phe
180                 185                 190

Ala Gly Ser Gly Val Val His Met Val Gly Gly Val Ala Gly Leu Trp
195                 200                 205

Gly Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly
210                 215                 220

Arg Ser Val Ala Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly
225                 230                 235                 240

Ser Phe Leu Leu Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe
245                 250                 255

Leu Thr Ile Leu Lys Ser Tyr Gly Pro Pro Gly Ser Ile His Gly Gln
260                 265                 270

Trp Ser Ala Val Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser
275                 280                 285

Thr Ala Ala Leu Thr Thr Leu Phe Gly Lys Arg Leu Gln Thr Gly His
290                 295                 300

Trp Asn Val Ile Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala
305                 310                 315                 320

Ile Thr Ala Gly Cys Ser Val Val Asp Pro Trp Ala Ala Ile Ile Cys
325                 330                 335

Gly Phe Val Ser Ala Trp Val Leu Ile Gly Leu Asn Ala Leu Ala Ala
340                 345                 350

Arg Leu Lys Phe Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly
355                 360                 365

Cys Gly Ala Trp Gly Val Ile Phe Thr Ala Leu Phe Ala Arg Lys Glu
370                 375                 380

Tyr Val Asp Gln Ile Phe Gly Gln Pro Gly Arg Pro Tyr Gly Leu Phe
385                 390                 395                 400

Met Gly Gly Gly Gly Arg Leu Leu Gly Ala His Ile Val Val Ile Leu
405                 410                 415

Val Ile Ala Ala Trp Val Ser Phe Thr Met Ala Pro Leu Phe Leu Val
420                 425                 430

Leu Asn Lys Leu Gly Leu Leu Arg Ile Ser Ala Glu Asp Glu Met Ala
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435 440 445

Gly Met Asp Gln Thr Arg His Gly Gly Phe Ala Tyr Ala Tyr His Asp
450 455 460

Asp Asp Ala Ser Gly Lys Pro Asp Arg Ser Val Gly Gly Phe Met Leu
465 470 475 480

Lys Ser Ala His Gly Thr Gln Val Ala Ala Glu Met Gly Gly His Val
485 490 495

<210> SEQ ID NO 55
<211> LENGTH: 1870
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 55

cactagtact ccctccgtcc caatataagt gcatttagga caggatgtga tatatcctag 60

gactacaaat ctggacagtt gtctgttcat attcgtagtc ctaggatatg tcacatacta 120

tactaggtgt atttatattg ggacggaggg agcagtactt aaagtatatt tgcaactttt 180

tactgaactt ggtgtgctgt gtcaggcgac tactccagag gattgattac ttcatgcctt 240

gacaatgatg tgaagtagca tgaccttgcg attcatatgg tcggggatcg aggcatatat 300

acacccaacc cagttcattg agtgatcagt agagagattc ttcccctctt ctcctgccag 360

ctcttccagg ttctgagttc tgaccatggc ggctggagcg attccaatgg cgtaccagac 420

cactccgtca tcgccagact ggctgaacaa gggcgacaac gcatggcaga tgacatcggc 480

gaccctcgtc ggcctgcaga gcatgccagg gctggtgatc ctgtacggca gcattgtcaa 540

gaagaagtgg gctatcaact cggcgttcat ggcgctgtat gccttcgctg ctgtctggat 600

ctgctgggtt gtctgggcat acaacatgtc gttcggcgac cgcctcctgc cattctgggg 660

taaggcacgg ccagcgctcg ggcagagctt cctcgtggcg cagtctgagc tcactgctac 720

cgctattcgc taccacaatg ggtcagctga ggcgcccatg ctcaagccgt tgtacccagt 780

cgccaccatg gtgtacttcc agtgcatgtt tgcgagcatc accatcatca tcctcgcagg 840

ctcactgctt gggcgcatga acatcaaggc gtggatggcc tttgtgccgc tctggatcac 900

cttctcttac acggtctgcg ccttctcgct ctggggtggc ggtttcctct tccagtgggg 960

tgtcatagac tactctggtg gctatgtcat ccatctctct tctggcatcg caggcctcac 1020

tgctgcctac tgggttggac caaggtcagc atcagatagg gagagattcc cgcccaacaa 1080

catactgctg gtgctagcag gggcggggct gctgtggctt gggtggacag gtttcaatgg 1140

aggagaccca tattcagcca atattgattc atccatggca gtgctcaaca cacatatctg 1200

cgcatccacc agcctactcg tgtggacaat cctggatgtc ttcttcttcg ggaagccatc 1260

ggtaattggc gcggtgcagg gcatgatcac tggcctggta tgcatcaccc ctggtgcagg 1320

cctggtgcaa ggttgggcag ctattgtgat gggaattctc tctggtagca ttccatggta 1380

caccatgatg gtgctgcaca agaaatggtc attcatgcag aggattgatg acacgcttgg 1440

tgtcttccac acccatgcgg tggctgggtt ccttggtggc gccaccactg gactcttcgc 1500

cgagcccatc ctatgcagtc tcttcctatc tatcccagat tctaaaggtg cattctacgg 1560

tggccccggt ggatcacagt tcgggaagca gattgctggc gcactatttg tcactgcctg 1620

gaatattgtt atcacctcca tcatctgtgt catcatcagc ctaatcctgc ccctccgtat 1680

agctgatcaa gaactgctta ttggagatga tgctgtacac ggtgaggagg catatgctat 1740

-continued

ctgggcagag ggagagctca atgacatgac ccaccacaat gagagcacac atagtggtgt 1800

ctctgtagga gtgacacaga atgtttgaac agtacccact ttattgagga aaaagaaata 1860

taattgtctt 1870

<210> SEQ ID NO 56
<211> LENGTH: 480
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 56

Met Ala Ala Gly Ala Ile Pro Met Ala Tyr Gln Thr Thr Pro Ser Ser
1 5 10 15

Pro Asp Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Met Thr Ser Ala
20 25 30

Thr Leu Val Gly Leu Gln Ser Met Pro Gly Leu Val Ile Leu Tyr Gly
35 40 45

Ser Ile Val Lys Lys Lys Trp Ala Ile Asn Ser Ala Phe Met Ala Leu
50 55 60

Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Val Trp Ala Tyr Asn
65 70 75 80

Met Ser Phe Gly Asp Arg Leu Leu Pro Phe Trp Gly Lys Ala Arg Pro
85 90 95

Ala Leu Gly Gln Ser Phe Leu Val Ala Gln Ser Glu Leu Thr Ala Thr
100 105 110

Ala Ile Arg Tyr His Asn Gly Ser Ala Glu Ala Pro Met Leu Lys Pro
115 120 125

Leu Tyr Pro Val Ala Thr Met Val Tyr Phe Gln Cys Met Phe Ala Ser
130 135 140

Ile Thr Ile Ile Ile Leu Ala Gly Ser Leu Leu Gly Arg Met Asn Ile
145 150 155 160

Lys Ala Trp Met Ala Phe Val Pro Leu Trp Ile Thr Phe Ser Tyr Thr
165 170 175

Val Cys Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu Phe Gln Trp Gly
180 185 190

Val Ile Asp Tyr Ser Gly Gly Tyr Val Ile His Leu Ser Ser Gly Ile
195 200 205

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

Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Leu Val Leu Ala Gly Ala
225 230 235 240

Gly Leu Leu Trp Leu Gly Trp Thr Gly Phe Asn Gly Gly Asp Pro Tyr
245 250 255

Ser Ala Asn Ile Asp Ser Ser Met Ala Val Leu Asn Thr His Ile Cys
260 265 270

Ala Ser Thr Ser Leu Leu Val Trp Thr Ile Leu Asp Val Phe Phe Phe
275 280 285

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

Val Cys Ile Thr Pro Gly Ala Gly Leu Val Gln Gly Trp Ala Ala Ile
305 310 315 320

Val Met Gly Ile Leu Ser Gly Ser Ile Pro Trp Tyr Thr Met Met Val

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325 330 335

Leu His Lys Lys Trp Ser Phe Met Gln Arg Ile Asp Asp Thr Leu Gly
340 345 350

Val Phe His Thr His Ala Val Ala Gly Phe Leu Gly Gly Ala Thr Thr
355 360 365

Gly Leu Phe Ala Glu Pro Ile Leu Cys Ser Leu Phe Leu Ser Ile Pro
370 375 380

Asp Ser Lys Gly Ala Phe Tyr Gly Gly Pro Gly Gly Ser Gln Phe Gly
385 390 395 400

Lys Gln Ile Ala Gly Ala Leu Phe Val Thr Ala Trp Asn Ile Val Ile
405 410 415

Thr Ser Ile Ile Cys Val Ile Ile Ser Leu Ile Leu Pro Leu Arg Ile
420 425 430

Ala Asp Gln Glu Leu Leu Ile Gly Asp Asp Ala Val His Gly Glu Glu
435 440 445

Ala Tyr Ala Ile Trp Ala Glu Gly Glu Leu Asn Asp Met Thr His His
450 455 460

Asn Glu Ser Thr His Ser Gly Val Ser Val Gly Val Thr Gln Asn Val
465 470 475 480

<210> SEQ ID NO 57
<211> LENGTH: 981
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 57

atggcgtcgg cggcggtgcc ggagtggctg aacaagggcg acaatgcctg gcagatgctc 60

tccgccacgc tcgtcgccct tcagggcttc ccgggcctcg ccctcttcta cgtcggtgcc 120

gtcccccgca agtgggcgct cacctccgca ttcatggcgc tctacgccat ggccgccacc 180

atgccgtgct gggcgctctg ggcgcacaac atggccttcg gccgccgcct cctccccttc 240

gtcggccgcc ccgccccggc gctcgcccag gactacatgc tcagccaggc gctgctcccc 300

tccaccctcc acctccgctc caacggcgag gttgagacgg ccgcggtggc gccgctgtac 360

ccgtcggcga gcatggtgtt cttccagtgg gccttcgccg gcgtcaccgt ggggctggtc 420

gccggcgccg tgctcgggcg catgagcgtc aaggcgtgga tggcgttcgt gccgctgtgg 480

acgacgctgt cctacacggt gggagcgtac agcatctggg gcggaggctt cctcttccac 540

tggggcgtca tggactactc cggcggctac gtcgtgctcc tcgccgccgg cgtctccggc 600

tacacggccg cgtactgggt gggacccagg aggaaggagg aggacgagga ggaaatggca 660

acggcgagtg gtggcaacct ggtggtgatg gtggccggcg cgggcatcct gtggatgggg 720

tggaccggct tcaacggcgg cgaccccttc tccgccaaca ccgactcgtc ggtggcggtg 780

ctcaacacgc acatctgcgc caccaccagc atcgtcgctt gggtttgctg cgacgtcgcc 840

gtccgcggga ggccgtcggt ggtgggcgcg gtgcagggca tgatcaccgg cctggtgtgc 900

atcactccaa ggtcaaacat caagtacagc tttcttctag tagtaatttc tgatgagatg 960

cctgttcctg atctgagcta g 981

<210> SEQ ID NO 58
<211> LENGTH: 326
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

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<400> SEQUENCE: 58

Met Ala Ser Ala Ala Val Pro Glu Trp Leu Asn Lys Gly Asp Asn Ala
1 5 10 15

Trp Gln Met Leu Ser Ala Thr Leu Val Ala Leu Gln Gly Phe Pro Gly
20 25 30

Leu Ala Leu Phe Tyr Val Gly Ala Val Pro Arg Lys Trp Ala Leu Thr
35 40 45

Ser Ala Phe Met Ala Leu Tyr Ala Met Ala Ala Thr Met Pro Cys Trp
50 55 60

Ala Leu Trp Ala His Asn Met Ala Phe Gly Arg Arg Leu Leu Pro Phe
65 70 75 80

Val Gly Arg Pro Ala Pro Ala Leu Ala Gln Asp Tyr Met Leu Ser Gln
85 90 95

Ala Leu Leu Pro Ser Thr Leu His Leu Arg Ser Asn Gly Glu Val Glu
100 105 110

Thr Ala Ala Val Ala Pro Leu Tyr Pro Ser Ala Ser Met Val Phe Phe
115 120 125

Gln Trp Ala Phe Ala Gly Val Thr Val Gly Leu Val Ala Gly Ala Val
130 135 140

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

Thr Thr Leu Ser Tyr Thr Val Gly Ala Tyr Ser Ile Trp Gly Gly Gly
165 170 175

Phe Leu Phe His Trp Gly Val Met Asp Tyr Ser Gly Gly Tyr Val Val
180 185 190

Leu Leu Ala Ala Gly Val Ser Gly Tyr Thr Ala Ala Tyr Trp Val Gly
195 200 205

Pro Arg Arg Lys Glu Glu Asp Glu Glu Glu Met Ala Thr Ala Ser Gly
210 215 220

Gly Asn Leu Val Val Met Val Ala Gly Ala Gly Ile Leu Trp Met Gly
225 230 235 240

Trp Thr Gly Phe Asn Gly Gly Asp Pro Phe Ser Ala Asn Thr Asp Ser
245 250 255

Ser Val Ala Val Leu Asn Thr His Ile Cys Ala Thr Thr Ser Ile Val
260 265 270

Ala Trp Val Cys Cys Asp Val Ala Val Arg Gly Arg Pro Ser Val Val
275 280 285

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

Ser Asn Ile Lys Tyr Ser Phe Leu Leu Val Val Ile Ser Asp Glu Met
305 310 315 320

Pro Val Pro Asp Leu Ser
325

<210> SEQ ID NO 59
<211> LENGTH: 1377
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 59

atggcgtcgg tggcggtgcc ggagtggctg aacaagggcg acaacgcctg gcagatgctc 60

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tccgccacgc tcgtcgccct gcagggcttc cccggtctcg ccctcttcta cgccggcgcc 120

gtcacccgca agtgcgcgct cacctccgca ttcatggcgc tctacgccat ggccgccacc 180

atgccgtgct gggcgctctg ggcgcacaac atggccttcg gccaccgcct cctgcccttc 240

gtcggccgcc ccgccccggc gctcgcccag cactacatgc tcacccaggc gctgctcccc 300

ttcaccctcc acctccactc caacggcgag gtggagacgg ccgcggtggc gccgctgtac 360

ccgtcggcga gcatggtgtt cttccagtgg gcctccgccg gcgtcaccgt ggggctggtc 420

gccggcgccg tgctcgggcg catgagcgtc aaggcgtgga tggcgttcgt gccgctgtgg 480

acgacgctgt cctatacggt gggagcgtac agcatttggg gcgggggctt cctcttccac 540

tggggcgtca tggactactc cggcggctac gtcgttcacc tcgccgccgg cgtctccggc 600

tacacggccg cgtactgggt gggaccaagg aggaaggagg aggaggaaat gacaatggcg 660

ggtggtggca acctggtggc gatggtggcc ggcgcgggca tcctgtggat ggggtggacc 720

ggcttcaacg gcggcgaccc cttctccgcc aacaccgact cgtcggtggc ggtgctcaac 780

acgcacatct gcaccaccac cagcatcctc gcttgggttt gctgcgacat cgccgtccgc 840

gggaggccgt cggtggtggg cgcggtgcag ggcatgatca ccggcctggt gtgcataact 900

ccggcggcag ggctggtgca ggggtgggca gctctgctaa tgggcgtcgc gtcggggaca 960

ctgccatgct acaccatgaa cgccgccatg tcgttcaagg tagacgacac gctgggcatc 1020

ctgcacaccc acgcggtgtc cggtgttctg ggcggcgtcc tcaccggcgt tttcgcgcac 1080

cctactctct gtgacatgtt ccttccggtg accggctcaa ggggcctcgt ctacggcgtc 1140

cgcgccggcg gggtgcaggt gttgaagcag gtcgccgccg cattgttcgt tgccgcatgg 1200

aacgtggccg ccacgtccat catcttggtc gtcgtcaggg cgttcgtgcc gctgaggatg 1260

acggaagatg agctgctcgc cggagacatt gccgtacatg gggaacaagc ttattatttt 1320

tcgagtggca ccaattgtag tttaagccat gagaccattg aggtcggaaa ttcataa 1377

<210> SEQ ID NO 60
<211> LENGTH: 458
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 60

Met Ala Ser Val Ala Val Pro Glu Trp Leu Asn Lys Gly Asp Asn Ala
1 5 10 15

Trp Gln Met Leu Ser Ala Thr Leu Val Ala Leu Gln Gly Phe Pro Gly
20 25 30

Leu Ala Leu Phe Tyr Ala Gly Ala Val Thr Arg Lys Cys Ala Leu Thr
35 40 45

Ser Ala Phe Met Ala Leu Tyr Ala Met Ala Ala Thr Met Pro Cys Trp
50 55 60

Ala Leu Trp Ala His Asn Met Ala Phe Gly His Arg Leu Leu Pro Phe
65 70 75 80

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

Ala Leu Leu Pro Phe Thr Leu His Leu His Ser Asn Gly Glu Val Glu
100 105 110

Thr Ala Ala Val Ala Pro Leu Tyr Pro Ser Ala Ser Met Val Phe Phe
115 120 125

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Gln Trp Ala Ser Ala Gly Val Thr Val Gly Leu Val Ala Gly Ala Val
130                 135                 140

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

Thr Thr Leu Ser Tyr Thr Val Gly Ala Tyr Ser Ile Trp Gly Gly Gly
165                 170                 175

Phe Leu Phe His Trp Gly Val Met Asp Tyr Ser Gly Gly Tyr Val Val
180                 185                 190

His Leu Ala Ala Gly Val Ser Gly Tyr Thr Ala Ala Tyr Trp Val Gly
195                 200                 205

Pro Arg Arg Lys Glu Glu Glu Glu Met Thr Met Ala Gly Gly Gly Asn
210                 215                 220

Leu Val Ala Met Val Ala Gly Ala Gly Ile Leu Trp Met Gly Trp Thr
225                 230                 235                 240

Gly Phe Asn Gly Gly Asp Pro Phe Ser Ala Asn Thr Asp Ser Ser Val
245                 250                 255

Ala Val Leu Asn Thr His Ile Cys Thr Thr Thr Ser Ile Leu Ala Trp
260                 265                 270

Val Cys Cys Asp Ile Ala Val Arg Gly Arg Pro Ser Val Val Gly Ala
275                 280                 285

Val Gln Gly Met Ile Thr Gly Leu Val Cys Ile Thr Pro Ala Ala Gly
290                 295                 300

Leu Val Gln Gly Trp Ala Ala Leu Leu Met Gly Val Ala Ser Gly Thr
305                 310                 315                 320

Leu Pro Cys Tyr Thr Met Asn Ala Ala Met Ser Phe Lys Val Asp Asp
325                 330                 335

Thr Leu Gly Ile Leu His Thr His Ala Val Ser Gly Val Leu Gly Gly
340                 345                 350

Val Leu Thr Gly Val Phe Ala His Pro Thr Leu Cys Asp Met Phe Leu
355                 360                 365

Pro Val Thr Gly Ser Arg Gly Leu Val Tyr Gly Val Arg Ala Gly Gly
370                 375                 380

Val Gln Val Leu Lys Gln Val Ala Ala Ala Leu Phe Val Ala Ala Trp
385                 390                 395                 400

Asn Val Ala Ala Thr Ser Ile Ile Leu Val Val Val Arg Ala Phe Val
405                 410                 415

Pro Leu Arg Met Thr Glu Asp Glu Leu Leu Ala Gly Asp Ile Ala Val
420                 425                 430

His Gly Glu Gln Ala Tyr Tyr Phe Ser Ser Gly Thr Asn Cys Ser Leu
435                 440                 445

Ser His Glu Thr Ile Glu Val Gly Asn Ser
450                 455


<210> SEQ ID NO 61
<211> LENGTH: 1750
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 61

atttcatata tgtatatata gcatcagaga gagaacaatt ctttgaaggg tgaaaaacct     60

tgatcaagaa ttgaagcatt aatcttcaac catggccaca cccttggcct accaagagca    120

ccttccggcg gcacccggtt ggctgaacaa aggtgacaac gcatggcagt taacagcagc    180
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caccctcgtt ggtcttcaaa gcatgccggg tctcgtgatc ctctacgcaa gcatagtgaa 240

gaagaaatgg gcagtgaatt cagctttcat ggctctctat gcctttgcag cagttctaat 300

atgttgggtg cttgtgtgtt accgcatggc ctttggagaa gaacttttac ccttctgggg 360

taagggtgct ccagcactag gccagaagtt cctcacaaaa cgagccgtag tcaatgaaac 420

catccaccac tttgataatg gcactgttga atcacctcct gaggaaccct tttaccctat 480

ggcctcgctt gtgtatttcc aattcacttt tgctgctatt actcttattt tgttggctgg 540

ctctgtcctt ggccgaatga acatcaaggc ttggatggct tttgtgcctc tttggttgat 600

cttttcctac acagtcgggg cttttagtct ttggggtggt ggctttctct accaatgggg 660

cgttattgat tattctggcg gctatgtcat acacctttct tctggaatcg ctggcttcac 720

tgctgcttac tgggttggac caaggttgaa gagtgatagg gagaggttcc caccaaacaa 780

tgtgcttctc atgcttgctg gtgctgggtt gttgtggatg ggttggtcag ggttcaacgg 840

tggagcacca tatgctgcaa acattgcatc ttcaattgcg gtgttgaaca caaacatttg 900

tgcagccact agcttccttg tgtggacaac tttggatgtc attttttttg ggaaaccttc 960

ggtgattgga gctgtgcagg gcatgatgac tggacttgta tgcatcaccc caggggcagg 1020

gcttgtgcat tcatgggctg ttatagtgat gggaatatta tttgggagca ttccatgggt 1080

gactatgatg attttgcata aaaagtcaac tttgctacag aaggtagatg acacccttgg 1140

tgtgtttcac acacatgctg tggctggcct tttgggtggt ctcctcacag gtctattagc 1200

agaaccagcc ctttgtagac ttctattgcc agtaacaaat tcaaggggtg cattctatgg 1260

tggaggtggt ggtgtgcagt tcttcaagca attggtggcg gccatgtttg ttattggatg 1320

gaacttggtg tccaccacca ttattctcct tgtcataaaa ttgttcatac ccttgaggat 1380

gccggacgag cagctggaaa tcggtgacga cgccgtccac ggtgaggaag cttatgccct 1440

ttggggtgat ggagaaaaat atgacccaac taggcatggt tccttgcaaa gtggcaacac 1500

tactgtctca ccttatgtta atggtgcaag aggggtgact ataaacttat gagtcaagaa 1560

attaggctgt gccttgctca cacatgcatg tgtataaatt tatatgatta acaaatgtga 1620

tgaatccgtg agtggtataa gtagatattt gattttgtca tgaaagaaaa tttccaaatt 1680

ttgagatgtg atgttcctct ggtcatcttg cattcgaaga ctctggtcat atatttctgg 1740

cacagaatgt 1750

<210> SEQ ID NO 62
<211> LENGTH: 486
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 62

Met Ala Thr Pro Leu Ala Tyr Gln Glu His Leu Pro Ala Ala Pro Gly
1 5 10 15

Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu Thr Ala Ala Thr Leu
20 25 30

Val Gly Leu Gln Ser Met Pro Gly Leu Val Ile Leu Tyr Ala Ser Ile
35 40 45

Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala Leu Tyr Ala
50 55 60

Phe Ala Ala Val Leu Ile Cys Trp Val Leu Val Cys Tyr Arg Met Ala

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65                  70                  75                  80

Phe Gly Glu Glu Leu Leu Pro Phe Trp Gly Lys Gly Ala Pro Ala Leu
85                  90                  95

Gly Gln Lys Phe Leu Thr Lys Arg Ala Val Val Asn Glu Thr Ile His
100                 105                 110

His Phe Asp Asn Gly Thr Val Glu Ser Pro Pro Glu Glu Pro Phe Tyr
115                 120                 125

Pro Met Ala Ser Leu Val Tyr Phe Gln Phe Thr Phe Ala Ala Ile Thr
130                 135                 140

Leu Ile Leu Leu Ala Gly Ser Val Leu Gly Arg Met Asn Ile Lys Ala
145                 150                 155                 160

Trp Met Ala Phe Val Pro Leu Trp Leu Ile Phe Ser Tyr Thr Val Gly
165                 170                 175

Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu Tyr Gln Trp Gly Val Ile
180                 185                 190

Asp Tyr Ser Gly Gly Tyr Val Ile His Leu Ser Ser Gly Ile Ala Gly
195                 200                 205

Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg Leu Lys Ser Asp Arg Glu
210                 215                 220

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

Leu Trp Met Gly Trp Ser Gly Phe Asn Gly Gly Ala Pro Tyr Ala Ala
245                 250                 255

Asn Ile Ala Ser Ser Ile Ala Val Leu Asn Thr Asn Ile Cys Ala Ala
260                 265                 270

Thr Ser Phe Leu Val Trp Thr Thr Leu Asp Val Ile Phe Phe Gly Lys
275                 280                 285

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

Ile Thr Pro Gly Ala Gly Leu Val His Ser Trp Ala Val Ile Val Met
305                 310                 315                 320

Gly Ile Leu Phe Gly Ser Ile Pro Trp Val Thr Met Met Ile Leu His
325                 330                 335

Lys Lys Ser Thr Leu Leu Gln Lys Val Asp Asp Thr Leu Gly Val Phe
340                 345                 350

His Thr His Ala Val Ala Gly Leu Leu Gly Gly Leu Leu Thr Gly Leu
355                 360                 365

Leu Ala Glu Pro Ala Leu Cys Arg Leu Leu Leu Pro Val Thr Asn Ser
370                 375                 380

Arg Gly Ala Phe Tyr Gly Gly Gly Gly Gly Val Gln Phe Phe Lys Gln
385                 390                 395                 400

Leu Val Ala Ala Met Phe Val Ile Gly Trp Asn Leu Val Ser Thr Thr
405                 410                 415

Ile Ile Leu Leu Val Ile Lys Leu Phe Ile Pro Leu Arg Met Pro Asp
420                 425                 430

Glu Gln Leu Glu Ile Gly Asp Asp Ala Val His Gly Glu Glu Ala Tyr
435                 440                 445

Ala Leu Trp Gly Asp Gly Glu Lys Tyr Asp Pro Thr Arg His Gly Ser
450                 455                 460

Leu Gln Ser Gly Asn Thr Thr Val Ser Pro Tyr Val Asn Gly Ala Arg
465                 470                 475                 480
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Gly Val Thr Ile Asn Leu
485

<210> SEQ ID NO 63
<211> LENGTH: 2191
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 63

cgtaatacac taaccaaccc accatgtcgc tgcctgcttg tcccgccgaa caactggccc 60

aacttctcgg cccaaacacc acagacgcct ccgccgccgc ctcccttatc tgcggccatt 120

tcgccgccgt ggacagcaag ttcgtcgaca cggccttcgc cgtcgacaac acctacctcc 180

tcttttccgc ctacctcgtt ttttctatgc agctcggctt cgccatgctc tgcgccggct 240

ccgtccgcgc caagaacacc atgaacatca tgctcaccaa cgtcctggac gctgccgccg 300

gcggcctctt ctactacctc ttcggcttcg ccttcgcttt cggctccccc tccaacggct 360

tcatcggtaa acatttcttc ggcctcaagg acatcccttc atcctcctac gactacagct 420

acttcctcta ccaatgggcc ttcgccatcg ccgccgccgg catcaccagc ggaagcatcg 480

ccgaacgcac acagttcgtg gcctatctca tctactcctc cttcctcacc ggcttcgtct 540

atccggtggt ctcccactgg ttctggtccc cagacggctg ggcctctgcc tttaagatca 600

ccgaccggct attttccacc ggcgtaatag acttcgccgg ttccggcgta gtccacatgg 660

tcggcggaat agccggccta tggggagcgc tgatcgaagg cccaagaatg ggacgtttcg 720

atcatgcagg acgagctgtg gccttgcgag gccacagcgc gtccttagta gtcctgggaa 780

ccttcttgct ttggttcggt tggtacggat ttaaccccgg ttcatttaac aaaatcctac 840

ttacttacgg taactcagga aattactacg gtcaatggag cgcggttggc agaaccgcgg 900

tcaccactac cctagcgggg tcaacagctg ccttgaccac gctattcggt aaacgggtga 960

tatccggtca ctggaacgtg accgatgtct gcaacgggct gttaggcggt ttcgcggcga 1020

taacagccgg ttgctccgtg gttgagccat gggcagccat cgtatgcggt tttgttgctt 1080

ctatagtatt aatagcttgc aacaaattag cagagaaggt taagttcgac gatcctctgg 1140

aggcggcgca gttgcacggt gggtgtggca cgtggggggt gatattcacg gcgttgttcg 1200

caaaaaagga gtatgtgaag gaggtttacg ggttggggag ggcgcacggg ttgctcatgg 1260

ggggtggtgg gaagttgctg gcggcgcacg tgattcagat tctggtgatt gctgggtggg 1320

ttagtgcgac catgggaccc ttgttttggg ggttgaataa actgaagctg ttgaggattt 1380

cttcagagga tgagcttgcg gggatggaca tgactcgcca tggaggcttt gcttatgctt 1440

atgaggatga tgagacgcac aagcatggga tgcagttgag gagggttggg cccaacgcgt 1500

cttccacacc caccactgat gaatgatctt tttttcccat atgcatgtct cattagtcaa 1560

acattaaatt tggatacata ttccttgtaa ggattcaaac cttggttact tgttacttct 1620

gttagatcca actccggttg atactcatga ctttttactt ctttttttt tatttgtctt 1680

gggtcttctt ttttcgtaga ttttttcttt tatgatgatg ggcaattagg gattttgatt 1740

tgtaattgtc attggtcgtg cattggtgga tgctggaagt taaagattct ggtggaagat 1800

gcgtacgttt ctgtgggggg tggttgttga ctaaggcatg ttggtcctgg aaatgacaga 1860

tggctgtgga aaatggaaat ttgtgggatt tatttttgta gttttcacca aaaaagaagg 1920

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aagaagattg gtatatagta gaaatactac tgtttggccg tgaggcatat agtttttttt 1980

tcttttcctt aatttgagac ttttatgtta aacttttttca ttatgtctaa tgtaaatata 2040

tggaagtagt ttttatattt tactgcctga atgtttgttt tttgtgttat atgtttttgt 2100

ttatatggaa ttgaaatcga ttgtaatatg ttacgtggaa gtaatgtaag ttaaaagatg 2160

atgtaggtag tgttatttag tgttttttttt t 2191

<210> SEQ ID NO 64
<211> LENGTH: 500
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 64

Met Ser Leu Pro Ala Cys Pro Ala Glu Gln Leu Ala Gln Leu Leu Gly
1 5 10 15

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

Phe Ala Ala Val Asp Ser Lys Phe Val Asp Thr Ala Phe Ala Val Asp
35 40 45

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

Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys Asn Thr Met
65 70 75 80

Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Ala Gly Gly Leu Phe
85 90 95

Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ser Pro Ser Asn Gly
100 105 110

Phe Ile Gly Lys His Phe Phe Gly Leu Lys Asp Ile Pro Ser Ser Ser
115 120 125

Tyr Asp Tyr Ser Tyr Phe Leu Tyr Gln Trp Ala Phe Ala Ile Ala Ala
130 135 140

Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe Val Ala
145 150 155 160

Tyr Leu Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Val Val
165 170 175

Ser His Trp Phe Trp Ser Pro Asp Gly Trp Ala Ser Ala Phe Lys Ile
180 185 190

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

Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile
210 215 220

Glu Gly Pro Arg Met Gly Arg Phe Asp His Ala Gly Arg Ala Val Ala
225 230 235 240

Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu
245 250 255

Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Asn Lys Ile Leu
260 265 270

Leu Thr Tyr Gly Asn Ser Gly Asn Tyr Tyr Gly Gln Trp Ser Ala Val
275 280 285

Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser Thr Ala Ala Leu
290 295 300

Thr Thr Leu Phe Gly Lys Arg Val Ile Ser Gly His Trp Asn Val Thr

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305 310 315 320

Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ala Gly
325 330 335

Cys Ser Val Val Glu Pro Trp Ala Ala Ile Val Cys Gly Phe Val Ala
340 345 350

Ser Ile Val Leu Ile Ala Cys Asn Lys Leu Ala Glu Lys Val Lys Phe
355 360 365

Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Thr Trp
370 375 380

Gly Val Ile Phe Thr Ala Leu Phe Ala Lys Lys Glu Tyr Val Lys Glu
385 390 395 400

Val Tyr Gly Leu Gly Arg Ala His Gly Leu Leu Met Gly Gly Gly Gly
405 410 415

Lys Leu Leu Ala Ala His Val Ile Gln Ile Leu Val Ile Ala Gly Trp
420 425 430

Val Ser Ala Thr Met Gly Pro Leu Phe Trp Gly Leu Asn Lys Leu Lys
435 440 445

Leu Leu Arg Ile Ser Ser Glu Asp Glu Leu Ala Gly Met Asp Met Thr
450 455 460

Arg His Gly Gly Phe Ala Tyr Ala Tyr Glu Asp Asp Glu Thr His Lys
465 470 475 480

His Gly Met Gln Leu Arg Arg Val Gly Pro Asn Ala Ser Ser Thr Pro
485 490 495

Thr Thr Asp Glu
500

<210> SEQ ID NO 65
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 65

gcttctccca cctcaaacgc cgtcgtttcg accaccttct tcggtcgcgg cacaaccaat 60

aaccatgtcg ctgccagatt gtcccgccgt ccaacttgcc caactcctgg gcccaaatac 120

cacaaacgct gccgccgccg cctccttcat ctgcgaccgg ttcaccgccg tggacaacaa 180

gttcgtcgac acggccttcg cggtcgacaa cacttacctc ctcttctccg cctacctcgt 240

cttctcgatg cagctcggct tcgccatgct ctgcgccggc tccgtccgcg ccaagaacac 300

catgaacatc atgctcacca acgtcctcga cgccgccgcc ggcggcctct tctactacct 360

cttcggcttc gccttcgcct tcggctcccc ctccaacggc ttcattggca aacacttctt 420

cggcctcaag gaactccccc cccaaagctt cgactacagc aactttctct atcaatgggc 480

cttcgccatc gccgccgccg gcatcaccag cggctccatc gccgaacgca cacagttcgt 540

ggcctatctc atctactcct ccttcctcac cggcttcgtc taccccgtcg tctcccactg 600

gttctggtcc gcagacggct gggcttctgc catttccccc ggagaccggc tattttccac 660

cggcgtgata gacttcgccg gctccggcgt agtccacatg gttggtggag tagccggctt 720

ctggggcgca ctgatagaag gcccgagaat cggacgcttc gaccacgcgg gacgcgccgt 780

tgccctcaga ggccacagcg 800

<210> SEQ ID NO 66

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<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 66

Met Ser Leu Pro Asp Cys Pro Ala Val Gln Leu Ala Gln Leu Leu Gly
1 5 10 15

Pro Asn Thr Thr Asn Ala Ala Ala Ala Ala Ser Phe Ile Cys Asp Arg
20 25 30

Phe Thr Ala Val Asp Asn Lys Phe Val Asp Thr Ala Phe Ala Val Asp
35 40 45

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

Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys Asn Thr Met
65 70 75 80

Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Ala Gly Gly Leu Phe
85 90 95

Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ser Pro Ser Asn Gly
100 105 110

Phe Ile Gly Lys His Phe Phe Gly Leu Lys Glu Leu Pro Ser Gln Ser
115 120 125

Phe Asp Tyr Ser Asn Phe Leu Tyr Gln Trp Ala Phe Ala Ile Ala Ala
130 135 140

Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe Val Ala
145 150 155 160

Tyr Leu Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Val Val
165 170 175

Ser His Trp Phe Trp Ser Ala Asp Gly Trp Ala Ser Ala Ile Ser Pro
180 185 190

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

Val Val His Met Val Gly Gly Val Ala Gly Phe Trp Gly Ala Leu Ile
210 215 220

Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala Gly Arg Ala Val Ala
225 230 235 240

Leu Arg Gly His Ser
245

<210> SEQ ID NO 67
<211> LENGTH: 644
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 67

cggtgcttaa caccaacatt tgcgccgcca ccagcctcct cgtatggacg tggttggacg 60

ttatttttctt caagaaaccc tcagttattg gagccgttca gggcatgata actggccttg 120

tttgcatcac tcccggagct ggtctggttc aaggatgggc tgccatagtg atgggacttc 180

tttcaggcag tgtcccatgg ttcagcatga tggtattagg gaaaaagctg aaattgtttc 240

aaatggttga tgacaccctt gctgtgttcc acactcatgc tgtggctggc cttcttggag 300

gcatactcac tggcctattt gccgaacctc gtctgtgtgc actctttcta cctgtcacca 360

actccaaaag aggagtctat ggaggccctg gtggagtcca aatccttaaa caaatcgtgg 420

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gagctttgtt catcattggg tggaaccttg tggtcacttc aattatttgt gtggttatta 480

gtttcatagt tccacttaga atgacagagg aagagcttct cattggagat gatgcggttc 540

atggggaaga ggcttatgct ctgtggggtg atggagagaa acttagcatc tacaaagatg 600

ataccactca ccatggagtt gtgtctagtg gtgccactca agtg 644

<210> SEQ ID NO 68
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 68

Val Leu Asn Thr Asn Ile Cys Ala Ala Thr Ser Leu Leu Val Trp Thr
1 5 10 15

Trp Leu Asp Val Ile Phe Phe Lys Lys Pro Ser Val Ile Gly Ala Val
20 25 30

Gln Gly Met Ile Thr Gly Leu Val Cys Ile Thr Pro Gly Ala Gly Leu
35 40 45

Val Gln Gly Trp Ala Ala Ile Val Met Gly Leu Leu Ser Gly Ser Val
50 55 60

Pro Trp Phe Ser Met Met Val Leu Gly Lys Lys Leu Lys Leu Phe Gln
65 70 75 80

Met Val Asp Asp Thr Leu Ala Val Phe His Thr His Ala Val Ala Gly
85 90 95

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

Ala Leu Phe Leu Pro Val Thr Asn Ser Lys Arg Gly Val Tyr Gly Gly
115 120 125

Pro Gly Gly Val Gln Ile Leu Lys Gln Ile Val Gly Ala Leu Phe Ile
130 135 140

Ile Gly Trp Asn Leu Val Val Thr Ser Ile Ile Cys Val Val Ile Ser
145 150 155 160

Phe Ile Val Pro Leu Arg Met Thr Glu Glu Glu Leu Leu Ile Gly Asp
165 170 175

Asp Ala Val His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu
180 185 190

Lys Leu Ser Ile Tyr Lys Asp Asp Thr Thr His His
195 200

<210> SEQ ID NO 69
<211> LENGTH: 749
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 69

gccacaaaca attcatcagc tcatacacgt aatttctttt cctcttttcc tcttatccaa 60

ttctaatcac gatcagacat taaatgtaaa cacttctcta tcaaaaattt gaacttagtt 120

cgcctcacac ttttgttttg tcaccttgtg agagactaat tccctctaat aaacgcaacg 180

ttgttcatca gtggcacata catatacagc atcacaattc tttgaagggt gaaaaagctt 240

gatcaagaat tgaagcatat tgatcttcag ccatggctac acccttggcc taccaagagc 300

accttccggc ggcacccgaa tggctgaaca aaggtgacaa cgcatggcag ctaacagcag 360

ccaccctcgt cggtcttcaa agcatgccgg gtctcgtgat cctctacgcc agcatagtga 420

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agaaaaaatg ggcagtgaac tcagctttca tggctctcta cgcctttgcg gcggttctaa 480

tatgttgggt gcttgtgtgt taccgcatgg cctttggaga aaaactttta cccttctggg 540

ggaagggtgc tcccagactt aggccagaat tcgtcacaaa acgagccgga gtcaatgaaa 600

cgctgcacca ctttgatagt ggcactgtag aatcccctcg cgaagagcca ctttacccta 660

atggcgtact tgtgtatgtc cgattgactt ttgctgctat gtaccatata gtgatggctg 720

gctctgtgct gccacgaaga acatcgaag 749

<210> SEQ ID NO 70
<211> LENGTH: 159
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 70

Met Ala Thr Pro Leu Ala Tyr Gln Glu His Leu Pro Ala Ala Pro Glu
1 5 10 15

Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu Thr Ala Ala Thr Leu
20 25 30

Val Gly Leu Gln Ser Met Pro Gly Leu Val Ile Leu Tyr Ala Ser Ile
35 40 45

Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala Leu Tyr Ala
50 55 60

Phe Ala Ala Val Leu Ile Cys Trp Val Leu Val Cys Tyr Arg Met Ala
65 70 75 80

Phe Gly Glu Lys Leu Leu Pro Phe Trp Gly Lys Gly Ala Pro Arg Leu
85 90 95

Arg Pro Glu Phe Val Thr Lys Arg Ala Gly Val Asn Glu Thr Leu His
100 105 110

His Phe Asp Ser Gly Thr Val Glu Ser Pro Arg Glu Glu Pro Leu Tyr
115 120 125

Pro Asn Gly Val Leu Val Tyr Val Arg Leu Thr Phe Ala Ala Met Tyr
130 135 140

His Ile Val Met Ala Gly Ser Val Leu Pro Arg Arg Thr Ser Lys
145 150 155

<210> SEQ ID NO 71
<211> LENGTH: 1871
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 71

ctctaacagc caaagcatgg cttctctctc ttgctccgcc aacgaccttg ccccactctt 60

caacgacacc gccgccgcca actacctctg cgcccaattc gattccattt ctagaaagct 120

cgccgaaaca acctacgccg tcgacaacac ctaccttctg ttttcagcgt atcttgtctt 180

cgccatgcag ctcggcttcg ccatgctctg cgccggctcc gtcagagcca aaaacaccat 240

gaacatcatg ctcaccaacg tcctcgacgc cgccgccggc ggtctctcct actacctatt 300

cggctttgca ttcgccttcg gcggcccctc caacggcttc atcggccgcc acttcttcgg 360

cctacgagat tacccaatgg gctcctctcc ctccggcgac tacagcttct tcctctacca 420

gtgggccttc gccatcgccg ccgcaggaat caccagcggc tccatcgccg agagaacaca 480

gttcgtggct taccttatct actcttcttt cttaaccggt ttcgtttacc ccatcgtttc 540

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gcattggttc tggtcctcag acggttgggc cagcgcgact cgtagccacg gaaatgtttt 600

attcgggtct ggagtcatcg acttcgcggg ctcaggcgtt gttcacatgg ttggcgggat 660

agcgggcctg tgggggggctt taattgaagg cccgagaatc ggccggttcg accgttcggg 720

ccggtcggtt gctttacgtg gccacagcgc gtctttagtt gtgcttggta cgtttttgtt 780

atggttcggc tggtacggct tcaaccctgg ttcgtttgtg acaatagaca aggggtatga 840

aagtggaggg tattatggtc aatggagcgc tatagggagg acagctgtca cgacgacatt 900

ggctgggagc actgcggctc tgacgacgtt gttcagcaag cggttattgg ttggccactg 960

gaacgtgatt gacgtgtgta acggcctgct tggcgggttc gctgccatta catcgggctg 1020

tgccgttgtg gaaccgtggg ccgcgattgt gtgtgggttt gtggcggcgt gggttttgat 1080

tgggcttaat aagcttgccg cgaaggtaga gtacgatgat ccgttggagg cggcgcagct 1140

tcacggcggg tgcggcgcgt ggggtgtttt cttcacggga ttgtttgcga agaaagtgta 1200

cgtggaggag atttacggtg ttggaaggcc gttcggggct ttgatgggtg gcggagggag 1260

gctgctggcg gcgcaggtga ttcagatatt ggtggtgtgc gggtgggtta cggcgaccat 1320

ggcgccgttg ttctatgggc ttcataagat gaaactgttg agaatttcga gggatgatga 1380

gactgcgggg atggatttga cgaggcatgg tgggtttgct tatgcatacc atgatgatga 1440

agatggttca agcaggggag tagggttcat gctgcgtaga attgagcctg ctgctagtac 1500

cactccctct ccccccgctg caccacaagt ttaatcaaaa tgtggtttat gattttcaag 1560

cgtttttag tttcgtacct gcacatagct atgggcaaag ctagccttgt caaaaccata 1620

tacaagcaag acacgaggga tgcatatatg aagtataaaa attaatgcgt gggggtcaac 1680

atttaggaaa tgtcttctag agttactgta cattttaaaa tgtttgttgg cttggtttat 1740

tattttcatc tttgaattcc aagactagtt tggtcgactg ttgtcacgtt agtttgtatc 1800

ctgctgcaga ataacttgct tgtaattgta tactgattag ttggtatata gtgatatatt 1860

atatatacta a 1871

<210> SEQ ID NO 72
<211> LENGTH: 505
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 72

Met Ala Ser Leu Ser Cys Ser Ala Asn Asp Leu Ala Pro Leu Phe Asn
1 5 10 15

Asp Thr Ala Ala Ala Asn Tyr Leu Cys Ala Gln Phe Asp Ser Ile Ser
20 25 30

Arg Lys Leu Ala Glu Thr Thr Tyr Ala Val Asp Asn Thr Tyr Leu Leu
35 40 45

Phe Ser Ala Tyr Leu Val Phe Ala Met Gln Leu Gly Phe Ala Met Leu
50 55 60

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

Asn Val Leu Asp Ala Ala Ala Gly Gly Leu Ser Tyr Tyr Leu Phe Gly
85 90 95

Phe Ala Phe Ala Phe Gly Gly Pro Ser Asn Gly Phe Ile Gly Arg His
100 105 110

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Phe Phe Gly Leu Arg Asp Tyr Pro Met Gly Ser Ser Pro Ser Gly Asp
115                 120                 125

Tyr Ser Phe Phe Leu Tyr Gln Trp Ala Phe Ala Ile Ala Ala Ala Gly
130                 135                 140

Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe Val Ala Tyr Leu
145                 150                 155                 160

Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Ile Val Ser His
165                 170                 175

Trp Phe Trp Ser Ser Asp Gly Trp Ala Ser Ala Thr Arg Ser His Gly
180                 185                 190

Asn Val Leu Phe Gly Ser Gly Val Ile Asp Phe Ala Gly Ser Gly Val
195                 200                 205

Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile Glu
210                 215                 220

Gly Pro Arg Ile Gly Arg Phe Asp Arg Ser Gly Arg Ser Val Ala Leu
225                 230                 235                 240

Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu Trp
245                 250                 255

Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Val Thr Ile Asp Lys
260                 265                 270

Gly Tyr Glu Ser Gly Gly Tyr Tyr Gly Gln Trp Ser Ala Ile Gly Arg
275                 280                 285

Thr Ala Val Thr Thr Thr Leu Ala Gly Ser Thr Ala Ala Leu Thr Thr
290                 295                 300

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

Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ser Gly Cys Ala
325                 330                 335

Val Val Glu Pro Trp Ala Ala Ile Val Cys Gly Phe Val Ala Ala Trp
340                 345                 350

Val Leu Ile Gly Leu Asn Lys Leu Ala Ala Lys Val Glu Tyr Asp Asp
355                 360                 365

Pro Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Ala Trp Gly Val
370                 375                 380

Phe Phe Thr Gly Leu Phe Ala Lys Lys Val Tyr Val Glu Glu Ile Tyr
385                 390                 395                 400

Gly Val Gly Arg Pro Phe Gly Ala Leu Met Gly Gly Gly Gly Arg Leu
405                 410                 415

Leu Ala Ala Gln Val Ile Gln Ile Leu Val Val Cys Gly Trp Val Thr
420                 425                 430

Ala Thr Met Ala Pro Leu Phe Tyr Gly Leu His Lys Met Lys Leu Leu
435                 440                 445

Arg Ile Ser Arg Asp Asp Glu Thr Ala Gly Met Asp Leu Thr Arg His
450                 455                 460

Gly Gly Phe Ala Tyr Ala Tyr His Asp Asp Glu Asp Gly Ser Ser Arg
465                 470                 475                 480

Gly Val Gly Phe Met Leu Arg Arg Ile Glu Pro Ala Ala Ser Thr Thr
485                 490                 495

Pro Ser Pro Pro Ala Ala Pro Gln Val
500                 505
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<210> SEQ ID NO 73
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 73

tttcacacac atgctgtggc tggccttttg ggtggtctcc tcacaggtct attagcagaa 60

ccagcccttt gtagactact attgccagtt accaactcaa ggggtgcatt ctatggtggt 120

ggtggtggta tgcagttctt caagcaattg gtggcggcca tgtttgtcat tggatggaac 180

ttggtgtcca ccaccatcat tctccttgtc ataaaattgt tcataccctt gaggatgccg 240

gatgagcagc tggaaatcgg cgacgacgcc gtccacggcg aggaagctta tgccctctgg 300

ggtgatggag aaaaatatga cccaactagg catggttcct tgcaaagtgg caacactttt 360

gtgtcacctt atgttaatgg tgcaagaggg gtgaccataa acttatgagt caagaaattc 420

ggctgtgctt tgctcacaca tatgtataaa gttatgtgat gaatccgtga gtggtgtaag 480

tagaaatttg attttgtcat gaaagaaaat tcaagttttg agatctgatg ttcctctggc 540

catccagcat tcgaagacct gatcatatat ttctggcaca gattgtgttg acatgtttat 600

aaaatttaga tttgtcaatt tttgaaggag cttgtgatta gttttctttt ccacttatat 660

gttttaatta ctagaagaat atcaaatttt ctttttacga aatgcttagt acataattgt 720

taaaaaaaat catcatgtaa tgggtacgaa atatttatca attctatgaa tgagtatttt 780

tttcttagat aacttcagtg accactttta gaaaatttat cctatgtata aattttaaaa 840

gaatggtttt aactccaaaa ttttcaccta gtccttgtca aacaaatttt attttggctc 900

acttaaaggt aaaattattt agttatgcat ttcagaatga agtttggttc gaaatatttt 960

gacagtgtgt caaatataaa ttcttcaaaa gaaaaagcca agactacttt acaacaaaat 1020

agataagttt ctcataaact gagcacaagt ttt 1053

<210> SEQ ID NO 74
<211> LENGTH: 135
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 74

Phe His Thr His Ala Val Ala Gly Leu Leu Gly Gly Leu Leu Thr Gly
1 5 10 15

Leu Leu Ala Glu Pro Ala Leu Cys Arg Leu Leu Leu Pro Val Thr Asn
20 25 30

Ser Arg Gly Ala Phe Tyr Gly Gly Gly Gly Gly Met Gln Phe Phe Lys
35 40 45

Gln Leu Val Ala Ala Met Phe Val Ile Gly Trp Asn Leu Val Ser Thr
50 55 60

Thr Ile Ile Leu Leu Val Ile Lys Leu Phe Ile Pro Leu Arg Met Pro
65 70 75 80

Asp Glu Gln Leu Glu Ile Gly Asp Asp Ala Val His Gly Glu Glu Ala
85 90 95

Tyr Ala Leu Trp Gly Asp Gly Glu Lys Tyr Asp Pro Thr Arg His Gly
100 105 110

Ser Leu Gln Ser Gly Asn Thr Phe Val Ser Pro Tyr Val Asn Gly Ala
115 120 125

Arg Gly Val Thr Ile Asn Leu

-continued

130 135

<210> SEQ ID NO 75
<211> LENGTH: 799
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 75

gtgtgtggtt ttgtcgcttc agtgtttctg atagcgtgca acaaattagc agagaaggtt 60

aagttcgatg atcctttgga agcggcgcag ttacacggtg ggtgtggcgc gtgggggggtg 120

atattcacgg cgctgttcgc gaaaaaggag tatgtgagcc aggtttatgg ggaggggagg 180

gcgcacgggt tgttcatgag gggtggaggg aagttgctgg cggcgcacgt gattcagatt 240

ttggttattg ttgggtgggt gagtgcgacc atgggaccct tgttttgggg gttgaataaa 300

ttgaaattgt tgaggatttc ttccgaggat gagcttgcgg ggatggatct tacccgtcat 360

ggaggatttg cttatgctta tgaggatgat gagtcgcaca agcatgggat tcagctgagg 420

aaggttgggc ccaacgcgtc gtccacaccc accactgatg aatgattacg atcacgatta 480

attcggcccc gacagtatta tcttcaattg aaattacgtg tgacttagaa gaagaaaaaa 540

agatgatgat gattttgttt gtaatttatt ttatttgttt tgggtttttt ttttaatttt 600

gtagattttt ctttttatga tgggtaagta gggattttaa tttgtaattg ttattggccg 660

tatattggta gatgctggaa attgaagatt ctgctggaag atgcgaacgt ttctgaaaat 720

gatagatggc tgtggaaaat gaaaatattt tatttgtggg atttaatttt cgtagttttc 780

gccaaaaaag aaggaagag 799

<210> SEQ ID NO 76
<211> LENGTH: 154
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 76

Val Cys Gly Phe Val Ala Ser Val Phe Leu Ile Ala Cys Asn Lys Leu
1 5 10 15

Ala Glu Lys Val Lys Phe Asp Asp Pro Leu Glu Ala Ala Gln Leu His
20 25 30

Gly Gly Cys Gly Ala Trp Gly Val Ile Phe Thr Ala Leu Phe Ala Lys
35 40 45

Lys Glu Tyr Val Ser Gln Val Tyr Gly Glu Gly Arg Ala His Gly Leu
50 55 60

Phe Met Arg Gly Gly Gly Lys Leu Leu Ala Ala His Val Ile Gln Ile
65 70 75 80

Leu Val Ile Val Gly Trp Val Ser Ala Thr Met Gly Pro Leu Phe Trp
85 90 95

Gly Leu Asn Lys Leu Lys Leu Leu Arg Ile Ser Ser Glu Asp Glu Leu
100 105 110

Ala Gly Met Asp Leu Thr Arg His Gly Gly Phe Ala Tyr Ala Tyr Glu
115 120 125

Asp Asp Glu Ser His Lys His Gly Ile Gln Leu Arg Lys Val Gly Pro
130 135 140

Asn Ala Ser Ser Thr Pro Thr Thr Asp Glu
145 150

-continued

<210> SEQ ID NO 77
<211> LENGTH: 90
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 77

tttctctacc aatgggggt tattgactat tctggcggct atgtcatcca cctttcttct 60

ggaatcgctg gtttaactgc tgcttactgg 90

<210> SEQ ID NO 78
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 78

Phe Leu Tyr Gln Trp Gly Val Ile Asp Tyr Ser Gly Gly Tyr Val Ile
1 5 10 15

His Leu Ser Ser Gly Ile Ala Gly Leu Thr Ala Ala Tyr Trp
20 25 30

<210> SEQ ID NO 79
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 79

caaattcgct ttacatacag tatggtaatt gtccaaattt ttacgaccga tttgtcaggt 60

acatcattta atgcatggca acatacatga taagatgaat caataaatac attccagctt 120

ccacgtacgt acgtctgcca acatagccgg cctcataatg tctcatccaa gtaaataaaa 180

cgacaaaatg attgattgta taaacctgct gcaaataact cagtatcata aagccttggc 240

cttgaacacc ctcactcgag ttttcagcca attaaccaaa tcacactgaa acactgaagt 300

actagttatt caactactag taataagcat aattaaatat agaggagccg aagacgaagc 360

aagcccagaa aggttgaaca aaggagacaa cgcatggcag ttaatggcag ccacagtggt 420

gggtatggtg attctctatg gaagcctaga gtgaaaaag 459

<210> SEQ ID NO 80
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 80

Pro Glu Arg Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu Met Ala Ala
1 5 10 15

Thr Val Val Gly Met Val Ile Leu Tyr Gly Ser Leu
20 25

<210> SEQ ID NO 81
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 81

acttgtgcta cccatggcca ctcccacagc ataccaagaa cacctccctg catcccccca 60

ctggctaaac aaaggggaca acgcatggca gctgacagca gccactctcg taggtctcca 120

-continued

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aagcatgccg ggtctggtga tcctctacgc cagcatggtg aagaagaaat gggccgtgaa    180

ctctgcattc atggccctct acgcctttgc agcagtccta atatgctggg tgctcgtttg    240

tcaccgaatg gccttcggtg acaaactcct tcccttctgg gggaagggcg ccccagcact    300

aggccagaag tttttaacac accgcgccaa agtccccgaa agcacgcact attataacaa    360

tggtacggtc gaaagcgcga cttcggaacc gttgtttgcc acggcttctc ttgtgtattt    420

tcaattcacg tttgcggcta tcacgcttat c                                   451
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<210> SEQ ID NO 82
<211> LENGTH: 146
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 82

Met Ala Thr Pro Thr Ala Tyr Gln Glu His Leu Pro Ala Ser Pro His
1               5                  10                  15

Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln Leu Thr Ala Ala Thr Leu
20                  25                  30

Val Gly Leu Gln Ser Met Pro Gly Leu Val Ile Leu Tyr Ala Ser Met
35                  40                  45

Val Lys Lys Lys Trp Ala Val Asn Ser Ala Phe Met Ala Leu Tyr Ala
50                  55                  60

Phe Ala Ala Val Leu Ile Cys Trp Val Leu Val Cys His Arg Met Ala
65                  70                  75                  80

Phe Gly Asp Lys Leu Leu Pro Phe Trp Gly Lys Gly Ala Pro Ala Leu
85                  90                  95

Gly Gln Lys Phe Leu Thr His Arg Ala Lys Val Pro Glu Ser Thr His
100                 105                 110

Tyr Tyr Asn Asn Gly Thr Val Glu Ser Ala Thr Ser Glu Pro Leu Phe
115                 120                 125

Ala Thr Ala Ser Leu Val Tyr Phe Gln Phe Thr Phe Ala Ala Ile Thr
130                 135                 140

Leu Ile
145
```

What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:

a. a polynucleotide having at least 70% sequence identity, as determined by the GAP algorithm under default parameters, to the full length sequence of a polynucleotide selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81; wherein the polynucleotide encodes a polypeptide that functions as a modifier of AMT;

b. a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80 or 82;

c. a polynucleotide selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81; and

d. A polynucleotide which is complementary to the polynucleotide of (a), (b) or (c).

2. A recombinant expression cassette, comprising the polynucleotide of claim **1**, wherein the polynucleotide is operably linked, in sense or anti-sense orientation, to a promoter.

3. A host cell comprising the expression cassette of claim **2**.

4. A transgenic plant comprising the recombinant expression cassette of claim **2**.

5. The transgenic plant of claim **4**, wherein said plant is a monocot.

6. The transgenic plant of claim **4**, wherein said plant is a dicot.

7. The transgenic plant of claim **4**, wherein said plant is selected from the group consisting of: maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, peanut, switchgrass, myscanthus, triticale and cocoa.

8. A transgenic seed from the transgenic plant of claim **4**.

9. A method of modulating the AMT in plants, comprising:
a. introducing into a plant cell a recombinant expression cassette comprising the polynucleotide of claim **1** operably linked to a promoter; and
b. culturing the plant under plant cell growing conditions; wherein the
AMT in said plant cell is modulated.

10. The method of claim **9**, wherein the plant cell is from a plant selected from the group consisting of: maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, peanut, switchgrass, myscanthus, triticale and cocoa.

11. A method of modulating the AMT in a plant, comprising:
a. introducing into a plant cell a recombinant expression cassette comprising the polynucleotide of claim **1** operably linked to a promoter;
b. culturing the plant cell under plant cell growing conditions; and
c. regenerating a plant form said plant cell; wherein the AMT in said plant is modulated.

12. The method of claim **11**, wherein the plant is selected from the group consisting of: maize, soybean, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, peanut, switchgrass, myscanthus, triticale and cocoa.

13. A method of decreasing the AMT transporter polypeptide activity in a plant cell, comprising:
a. providing a nucleotide sequence comprising at least 15 consecutive nucleotides of the complement of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81;
b. providing a plant cell comprising an mRNA having the sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79 or 81; and
c. introducing the nucleotide sequence of step (a) into the plant cell, wherein the nucleotide sequence inhibits expression of the mRNA in the plant cell.

14. The method of claim **13**, wherein said plant cell is from a monocot.

15. The method of claim **14**, wherein said monocot is maize, wheat, rice, barley, sorghum, switchgrass, myscanthus, triticale or rye.

16. The method of claim **13**, wherein said plant cell is from a dicot.

17. The transgenic plant of claim **4**, wherein the AMT transporter activity in said plant is decreased.

18. The transgenic plant of claim **17**, wherein the plant has enhanced root growth.

19. The transgenic plant of claim **17**, wherein the plant has increased seed size.

20. The transgenic plant of claim **17**, wherein the plant has increased seed weight.

21. The transgenic plant of claim **17**, wherein the plant has seed with increased embryo size.

22. The transgenic plant of claim **17**, wherein the plant has increased leaf size.

23. The transgenic plant of claim **17**, wherein the plant has increased seedling vigor.

24. The transgenic plant of claim **17**, wherein the plant has enhanced silk emergence.

25. The transgenic plant of claim **17**, wherein the plant has increased ear size.

26. The transgenic plant of claim **4**, wherein the AMT transporter activity in said plant is increased.

* * * * *