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(71) Demandeurs/Applicants:
PIONEER HI-BRED INTERNATIONAL, INC., US;
E.I. DU PONT DE NEMOURS AND COMPANY, US

(72) Inventeurs/Inventors:
TAO, YONG, US;
CAHOON, REBECCA E., US;
OROZCO, EMIL M., JR., US;
BRUCE, WESLEY B., US;
WENG, ZUDE, US

(74) Agent: DIMOCK STRATTON CLARIZIO LLP

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(54) Title: AUXIN TRANSPORT PROTEINS

(57) **Abrégé/Abstract:**

This invention relates to an isolated nucleic acid fragment encoding an auxin transport protein. The invention also relates to the construction of a chimeric gene encoding all or a substantial portion of the auxin transport protein, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the auxin transport protein in a transformed host cell. The present invention also relates to methods using the auxin transport protein in modulating root development, and in discovering compounds with potential herbicidal activity.

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(71) Applicants (for all designated States except US): **E. I. DU PONT DE NEMOURS AND COMPANY** [US/US];
1007 Market Street, Wilmington, DE 19898 (US). **PIONEER HI-BRED INTERNATIONAL, INC.** [US/US];
7100 N.W. 62nd Avenue, Johnston, IA 50131 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **OROZCO, Emil, M., Jr.** [US/US]; 2 Dutton Farm Lane, West Grove, PA

19390 (US). **WENG, Zude** [CN/US]; Apartment 1B, 9122
Lincoln Drive, Des Plaines, IL 60016 (US). **BRUCE, Wesley, B.** [US/US]; 4625 96th Street, Des Moines, IA 50322
(US). **CAHOON, Rebecca, E.** [US/US]; 2331 West 18th
Street, Wilmington, DE 19806 (US). **TAO, Yong** [CN/US];
101-8 Thorn lane, Newark, DE 19711 (US).

(74) Agent: **GEIGER, Kathleen, W.**; E.I. du Pont de Nemours
and Company, Legal/Patent Records Center, 1007 Market
Street, Wilmington, DE 19898 (US).

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(54) Title: AUXIN TRANSPORT PROTEINS

SEQ ID NO:14
SEQ ID NO:30
SEQ ID NO:34
SEQ ID NO:38
SEQ ID NO:43
SEQ ID NO:44

*** * * * * ***** * * * * *
MITALDLYHVLTA VVPLYVAMT LAYGSVRWWRI FTPDQCSGINRFV ALFAVPLLSFHFI S
MITLTDFYHVM TAMPVLYVAMILAYGSVKWWKIFSPDQCSGINRFV ALFAVPLLSFHFI A
MITGKDIYDVFAAIVPLYVAMILAYGSVRWWKIFTPDQCSGINRFV AVFAVPLLSFHFI S
MITGKDIYDVLA AVVPLYVAMFMAYGSVRWWGIFTPDQCSGINRFV AVFAVPLLSFHFI S
MITGKDMYDVLA AVVPLYVAMILAYGSVRWWGIFTPDQCSGINRFV AVFAVPLLSFHFI S
MITAADFYHVM TAMPVLYVAMILAYGSVKWWKIFTPDQCSGINRFV ALFAVPLLSFHFI A
1 60

SEQ ID NO:14
SEQ ID NO:30
SEQ ID NO:34
SEQ ID NO:38
SEQ ID NO:43
SEQ ID NO:44

* * * * * * * * * * *
TNDPFAMNLRFLAADTLQKVA VLALLALASRGLSSPRALG-----LDWSITLFSLS
SNNPYEMNLRFLAADTLQKII ILVLLAVW----SNITKRG-----CLEWAITLFSLS
SNDPYAMNYHFIAADCLQKV VILGALFLWNT----FTKHG-----SLDWTITLFSLS
TNDPYAMDYRFLAADSLQKL VILAALAVWHNVLSRYRCRGTEAGEASSLDWTITLFSLA
SNDPYAMNYHFIAADSLQKV VILAALFLWQA----FSRRG-----SLEWMITLFSLS
ANNPYAMNLRFLAADSLQKVIVLSLLFLW----CKLSRNG-----SLDWTITLFSLS
61 120

SEQ ID NO:14
SEQ ID NO:30
SEQ ID NO:34
SEQ ID NO:38
SEQ ID NO:43
SEQ ID NO:44

***** * * * * * * * * * *
TLPNTLVMGIPLLRGMYGASSAGTLMVQVVVLQCI IWYTLMLFLFEYRAARALVDQFPD
TLPNTLVMGIPLLKGMYGDFS-GSLMVQIVVLQCI IWYTLMLFLFEYRGARMLISEQFP-
TLPNTLVMGIPLLKAMYGDFS-GSLMVQIVVLQSVI WYTLMLFMFEYRGAKLLITEQFP-
TLPNTLVMGIPLLRAMYGDFS-GSLMVQIVVLQSVI WYTLMLFLFEYRGAKALISEQFPF
TLPNTLVMGIPLLRAMYGDFS-GNLMVQIVVLQSI IWYTLMLFLFEYRGAKLLISEQFP-
TLPNTLVMGIPLLKGMYGDFS-GDLMVQIVVLQCI IWYILMLFLFEYRGAKLLISEQFP-
121 180

(57) Abstract: This invention relates to an isolated nucleic acid fragment encoding an auxin transport protein. The invention also relates to the construction of a chimeric gene encoding all or a substantial portion of the auxin transport protein, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the auxin transport protein in a transformed host cell. The present invention also relates to methods using the auxin transport protein in modulating root development, and in discovering compounds with potential herbicidal activity.

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TITLE

AUXIN TRANSPORT PROTEINS

This application claims the benefit of U.S. Provisional Application No. 60/133,040, filed May 7, 1999.

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FIELD OF THE INVENTION

This invention is in the field of plant molecular biology. More specifically, this invention pertains to nucleic acid fragments encoding auxin transport proteins in plants and seeds.

BACKGROUND OF THE INVENTION

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Auxins are a major class of plant hormones that influence diverse aspects of plant behavior and development including vascular tissue differentiation, apical development, tropic responses, and organ (e.g., flower, leaf) development. The term "auxin" refers to a diverse group of natural and synthetic chemical substances that are able to stimulate elongation growth in coleoptiles and many stems. Indole-3-acetic acid (IAA) is the principal auxin in higher plants, though other molecules such as 4-chloroindole-3-acetic acid and phenylacetic acid have been shown to have auxin activity. Synthetic auxins include 2,4,5-trichlorophenoxyacetic acid (2,4,5-T) and 2,4-dichlorophenoxyacetic acid (2,4-D); both are commonly used as herbicides.

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Distribution of auxins in concentration gradients within plant organs enables auxins to convey to cells their relative location, allowing the plants to respond accordingly to a given stimulus. A classic example that illustrates auxin action is the differential growth and curvature of etiolated coleoptiles exposed to light. It is believed that the phototropic stimulus results in a lateral redistribution of auxin in the coleoptile such that the shaded side has a higher auxin concentration than the illuminated side. With more auxin stimulating cell elongation on the shaded side, the end-result is the apparent bending of the coleoptile towards the light source.

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The foregoing description underscores the importance of polar transport in auxin function. Not surprisingly, a number of genetic and physiological studies have focused on the polar auxin transport system operating in plant cells. *Arabidopsis* mutants with impaired auxin transport capabilities exhibit varying phenotypes: *pin1* mutants develop naked, *pin*-like inflorescences with few normal flowers (Gälweiler, L. et al., (1998) *Science* 282:2226-2230), while defects in *pin2* (also called *eir1* and *agr1*) are restricted to the root, altering growth and gravitropic response (Luschnig, C. et al., (1998) *Genes Dev.* 12:2175-2187). Proteins encoded by *AUX1*, *PIN1* and *PIN2* genes which have been identified to be important for auxin transport and are putative membrane proteins that have significant homology with a number of bacterial membrane transporters (Luschnig, C. et al. *supra*; Gälweiler L. et al., (1998) *Science* 282:2226-2230; Bennett, M. J. et al., (1996)

Science 273:948-950; WO 99/63092-A1; U.S. Application No. 60/087,789; EP 0 814 161 A1), consistent with a role for these proteins in auxin transport.

Since auxin affects several aspects of plant development, and polar transport is a vital component of auxin function, it is envisioned that proteins involved in auxin polar transport may serve as potential targets for new herbicide discovery and design. Blocking of normal function of these auxin transport proteins can cause severe plant growth defects; this is supported by the phenotype of mutants where a particular auxin transport protein has been rendered nonfunctional, particularly the *Arabidopsis* pin1 mutants. In addition, since some of these auxin transport proteins have been shown to be root-specific and impact root development to a significant degree, manipulation of auxin transport proteins may be a powerful strategy for developing more robust root systems in plants, which in turn may enhance food production, especially in arid climates.

SUMMARY OF THE INVENTION

The present invention concerns an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a first nucleotide sequence encoding a polypeptide of at least 30 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:6; (b) a second nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:16, 28, 36, and 40; (c) a third nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:12; (d) a fourth nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 24; (e) a fifth nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 32; (f) a sixth nucleotide sequence encoding a polypeptide of at least 90 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:42; (g) a seventh nucleotide sequence encoding a polypeptide of at least 95 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:46; (h) an eighth nucleotide sequence encoding a polypeptide of at least 100 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:20; (i) a ninth nucleotide sequence encoding a polypeptide of at least 100 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2; (j) a tenth nucleotide sequence encoding a polypeptide of at least 150 amino acids having at least 95%

identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:4; (k) an eleventh nucleotide sequence encoding a polypeptide of at least 300 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:38; (l) a twelfth nucleotide sequence encoding a polypeptide
5 of at least 350 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:10; (m) a thirteenth nucleotide sequence encoding a polypeptide of at least 400 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22, 26 and 30; (n) a fourteenth nucleotide sequence
10 encoding a polypeptide of at least 500 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:34; (o) a fifteenth nucleotide sequence encoding a polypeptide of at least 200 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:14; (p) a sixteenth nucleotide sequence encoding a polypeptide
15 of at least 250 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:48; and (q) a seventeenth nucleotide sequence comprising the complement of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), (m), (n), (o), or (p).

In a second embodiment, it is preferred that the isolated polynucleotide of the claimed
20 invention comprises a first nucleotide sequence which comprises a nucleic acid sequence 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, 45, and 47 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46, and 48.

25 In a third embodiment, this invention concerns an isolated polynucleotide comprising a nucleotide sequence of at least one of 60 (preferably at least one of 40, most preferably at least one of 30) contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and the complement of such nucleotide sequences.

30 In a fourth embodiment, this invention relates to a chimeric gene comprising an isolated polynucleotide of the present invention operably linked to at least one suitable regulatory sequence.

In a fifth embodiment, the present invention concerns a host cell comprising a chimeric gene of the present invention or an isolated polynucleotide of the present invention. The
35 host cell may be eukaryotic, such as a yeast or a plant cell, or prokaryotic, such as a bacterial cell. The present invention also relates to a virus, preferably a baculovirus, comprising an isolated polynucleotide of the present invention or a chimeric gene of the present invention.

In a sixth embodiment, the invention also relates to a process for producing a host cell comprising a chimeric gene of the present invention or an isolated polynucleotide of the present invention, the process comprising either transforming or transfecting a compatible host cell with a chimeric gene or isolated polynucleotide of the present invention.

5 In a seventh embodiment, the invention concerns an auxin transport polypeptide selected from the group consisting of: (a) a polypeptide of at least 30 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:6; (b) a polypeptide of at least 50 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide
10 selected from the group consisting of SEQ ID NOs:16, 28, 36, and 40; (c) a polypeptide of at least 50 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:12; (d) a polypeptide of at least 50 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 24; (e) a
15 polypeptide of at least 50 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 32; (f) a polypeptide of at least 90 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:42; (g) a polypeptide of at least 95 amino acids having at least 95% identity based
20 on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:46; (h) a polypeptide of at least 100 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:20; (i) a polypeptide of at least 100 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2; (j) a polypeptide of at least 150 amino acids having at least 95% identity based on the Clustal
25 method of alignment when compared to a polypeptide of SEQ ID NO:4; (k) a polypeptide of at least 300 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:38; (l) a polypeptide of at least 350 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:10; (m) a polypeptide of at least 400 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22, 26 and 30; (n) a polypeptide of at least 500 amino acids having at least 80% identity based on the Clustal
30 method of alignment when compared to a polypeptide of SEQ ID NO:34; (o) a polypeptide of at least 200 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:14; and (p) a polypeptide of at least 250 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:48.

In an eighth embodiment, the invention relates to a method of selecting an isolated polynucleotide that affects the level of expression of an auxin transport polypeptide or enzyme activity in a host cell, preferably a plant cell, the method comprising the steps of: (a) constructing an isolated polynucleotide of the present invention or a chimeric gene of the present invention; (b) introducing the isolated polynucleotide or the chimeric gene into a host cell; (c) measuring the level of the auxin transport polypeptide or enzyme activity in the host cell containing the isolated polynucleotide; and (d) comparing the level of the auxin transport polypeptide or enzyme activity in the host cell containing the isolated polynucleotide with the level of the auxin transport polypeptide or enzyme activity in the host cell that does not contain the isolated polynucleotide.

In a ninth embodiment, the invention concerns a method of obtaining a nucleic acid fragment encoding a substantial portion of an auxin transport polypeptide, preferably a plant auxin transport polypeptide, comprising the steps of: synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 60 (preferably at least one of 40, most preferably at least one of 30) contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and the complement of such nucleotide sequences; and amplifying a nucleic acid fragment (preferably a cDNA inserted in a cloning vector) using the oligonucleotide primer. The amplified nucleic acid fragment preferably will encode a substantial portion of an auxin transport polypeptide amino acid sequence.

In a tenth embodiment, this invention relates to a method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding an auxin transport polypeptide comprising the steps of: probing a cDNA or genomic library with an isolated polynucleotide of the present invention; identifying a DNA clone that hybridizes with an isolated polynucleotide of the present invention; isolating the identified DNA clone; and sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

In an eleventh embodiment, this invention concerns a composition, such as a hybridization mixture, comprising an isolated polynucleotide or isolated polypeptide of the present invention.

In a twelfth embodiment, this invention concerns a method for positive selection of a transformed cell comprising: (a) transforming a host cell with the chimeric gene of the present invention or a construct of the present invention; and (b) growing the transformed host cell, preferably a plant cell, such as a monocot or a dicot, under conditions which allow expression of the auxin transport polypeptide polynucleotide in an amount sufficient to complement a null mutant to provide a positive selection means.

A further embodiment of the instant invention is a method for evaluating at least one compound for its ability to inhibit the activity of an auxin transport protein, the method comprising the steps of: (a) transforming a host cell with a chimeric gene comprising a

nucleic acid fragment encoding an auxin transport polypeptide, operably linked to at least one suitable regulatory sequence; (b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the encoded auxin transport protein in the transformed host cell;

5 (c) optionally purifying the auxin transport polypeptide expressed by the transformed host cell; (d) treating the auxin transport polypeptide with a compound to be tested; and (e) comparing the activity of the auxin transport polypeptide that has been treated with a test compound to the activity of an untreated auxin transport polypeptide, thereby selecting compounds with potential for inhibitory activity.

10 In a further embodiment, the instant invention concerns a method of modulating expression of an auxin transport protein in a plant, comprising the steps of: (a) transforming a plant cell with a nucleic acid fragment encoding the auxin transport protein operably linked in sense or antisense orientation to a promoter; and (b) growing the plant cell under plant growing conditions to produce a regenerated plant capable of expressing the nucleic acid for

15 a time sufficient to modulate expression of the nucleic acid fragment in the plant compared to a corresponding non-transformed plant, thereby resulting in at least one of the following: a more robust root system, an altered root angle, or redirected root growth.

BRIEF DESCRIPTION OF THE DRAWING AND SEQUENCE LISTINGS

20 The invention can be more fully understood from the following detailed description, the accompanying drawing and Sequence Listing which form a part of this application.

Figure 1 depicts the amino acid sequence alignment between the auxin transport protein encoded by the nucleotide sequences derived from the corn clone p0119.cmtn124r (SEQ ID NO:14), soybean clone sfl1.pk131.g9 (SEQ ID NO:30), soybean clone

25 src3c.pk026.o11 (SEQ ID NO:34), and wheat clone wdk1c.pk008.g12 (SEQ ID NO:38), the auxin transport protein EIR1 from *Arabidopsis thaliana* (NCBI GenBank Identifier (GI) No. 3377507; SEQ ID NO:43), and the auxin transport protein AtPIN1 from *Arabidopsis thaliana* (NCBI GenBank Identifier (GI) No. 4151319; SEQ ID NO:44). Amino acids which are conserved among all and at least two sequences with an amino acid at that position are

30 indicated with an asterisk (*). Dashes are used by the program to maximize alignment of the sequences.

Table 1 lists the polypeptides that are described herein, the designation of the cDNA clones that comprise the nucleic acid fragments encoding polypeptides representing all or a substantial portion of these polypeptides, and the corresponding identifier (SEQ ID NO:) as used in the attached Sequence Listing. Table 1 also identifies the cDNA clones as

35 individual ESTs ("EST"), sequences of the entire cDNA inserts comprising the indicated cDNA clones ("FIS"), contigs assembled from two or more ESTs ("Contig"), contigs assembled from an FIS and one or more ESTs ("Contig*"), or sequences encoding at a

minimum the mature protein derived from an EST, FIS, a contig, or an FIS and PCR ("CGS"). Nucleotide SEQ ID NOs:5, 7, 11, 17, 23, 27, 31, 35, and 41 correspond to nucleotide SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, and 17, respectively, presented in U.S. Provisional Application No. 60/133,040, filed May 7, 1999. Amino acid SEQ ID NOs:6, 8, 12, 18, 24, 28, 32, 36, and 42 correspond to amino acid SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, and 18, respectively, presented in U.S. Provisional Application No. 60/133,040, filed May 7, 1999. The sequence descriptions and Sequence Listing attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825.

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TABLE 1
Auxin Transport Proteins

Protein (Plant Source)	Clone Designation	Status	SEQ ID NO:	
			(Nucleotide)	(Amino Acid)
Auxin Transport Protein (Corn)	ceb1.pk0082.a5	EST	1	2
Auxin Transport Protein (Corn)	Contig of: cr1.pk0022.a4 cr1n.pk0033.e3 csi1n.pk0045.a5 csi1n.pk0050.d5 p0005.cbmej72r p0041.crtba02r	Contig	3	4
Auxin Transport Protein (Corn)	p0016.ctsag12r	EST	5	6
Auxin Transport Protein (Corn)	Contig of: p0097.cqrai63r p0094.csssh17r	Contig	7	8
Auxin Transport Protein (Corn)	p0094.csssh17r	FIS	9	10
Auxin Transport Protein (Corn)	p0119.cmtnl24r	EST	11	12
Auxin Transport Protein (Corn)	cil1c.pk001.b7	FIS	47	48
Auxin Transport Protein (Corn)	p0119.cmtnl24r	CGS	13	14
Auxin Transport Protein (Rice)	rr1.pk0019.c4	EST	15	16
Auxin Transport Protein (Rice)	rsl1n.pk003.n3	EST	17	18
Auxin Transport Protein (Rice)	rsl1n.pk003.n3	FIS	19	20
Auxin Transport Protein (Soybean)	scr1c.pk003.g7	FIS	21	22

Protein (Plant Source)	Clone Designation	Status	SEQ ID NO:	
			(Nucleotide)	(Amino Acid)
Auxin Transport Protein (Soybean)	sdp4c.pk003.h2	EST	23	24
Auxin Transport Protein (Soybean)	sdp4c.pk003.h2	FIS	25	26
Auxin Transport Protein (Soybean)	sfl1.pk131.g9	EST	27	28
Auxin Transport Protein (Soybean)	sfl1.pk131.g9(FIS)	CGS	29	30
Auxin Transport Protein (Soybean)	src3c.pk026.o11	EST	31	32
Auxin Transport Protein (Soybean)	src3c.pk026.o11(FIS)	CGS	33	34
Auxin Transport Protein (Wheat)	wdk1c.pk008.g12	EST	35	36
Auxin Transport Protein (Wheat)	wdk1c.pk008.g12(FIS)	CGS	37	38
Auxin Transport Protein (Wheat)	wdr1f.pk001.g9	EST	39	40
Auxin Transport Protein (Wheat)	wle1n.pk0109.h1	EST	41	42
Auxin Transport Protein (Wheat)	wle1n.pk0109.h1	FIS	45	46

5 The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in *Nucleic Acids Res.* 13:3021-3030 (1985) and in the *Biochemical J.* 219 (No. 2):345-373 (1984) which are herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

DETAILED DESCRIPTION OF THE INVENTION

10 In the context of this disclosure, a number of terms shall be utilized. The terms “polynucleotide”, “polynucleotide sequence”, “nucleic acid sequence”, and “nucleic acid fragment”/“isolated nucleic acid fragment” are used interchangeably herein. These terms encompass nucleotide sequences and the like. A polynucleotide may be a polymer of RNA or DNA that is single- or double-stranded, that optionally contains synthetic, non-natural or
15 altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA, synthetic DNA, or mixtures thereof. An isolated polynucleotide of the present invention may include at least one of 60 contiguous nucleotides, preferably at least one of 40 contiguous nucleotides, most preferably

one of at least 30 contiguous nucleotides derived from SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 47 or the complement of such sequences.

5 The term “isolated polynucleotide” refers to a polynucleotide that is substantially free from other nucleic acid sequences, such as and not limited to other chromosomal and extrachromosomal DNA and RNA. Isolated polynucleotides may be purified from a host cell in which they naturally occur. Conventional nucleic acid purification methods known to skilled artisans may be used to obtain isolated polynucleotides. The term also embraces recombinant polynucleotides and chemically synthesized polynucleotides.

10 The term “recombinant” means, for example, that a nucleic acid sequence is made by an artificial combination of two otherwise separated segments of sequence, e.g., by chemical synthesis or by the manipulation of isolated nucleic acids by genetic engineering techniques.

As used herein, “contig” refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of
15 sequence homology. For example, the nucleotide sequences of two or more nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acid fragments, the sequences (and thus their corresponding nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

20 As used herein, “substantially similar” refers to nucleic acid fragments wherein changes in one or more nucleotide bases results in substitution of one or more amino acids, but do not affect the functional properties of the polypeptide encoded by the nucleotide sequence. “Substantially similar” also refers to nucleic acid fragments wherein changes in one or more nucleotide bases does not affect the ability of the nucleic acid fragment to
25 mediate alteration of gene expression by gene silencing through for example antisense or co-suppression technology. “Substantially similar” also refers to modifications of the nucleic acid fragments of the instant invention such as deletion or insertion of one or more nucleotides that do not substantially affect the functional properties of the resulting transcript vis-à-vis the ability to mediate gene silencing or alteration of the functional
30 properties of the resulting protein molecule. It is therefore understood that the invention encompasses more than the specific exemplary nucleotide or amino acid sequences and includes functional equivalents thereof. The terms “substantially similar” and “corresponding substantially” are used interchangeably herein.

Substantially similar nucleic acid fragments may be selected by screening nucleic acid
35 fragments representing subfragments or modifications of the nucleic acid fragments of the instant invention, wherein one or more nucleotides are substituted, deleted and/or inserted, for their ability to affect the level of the polypeptide encoded by the unmodified nucleic acid fragment in a plant or plant cell. For example, a substantially similar nucleic acid fragment

representing at least one of 30 contiguous nucleotides derived from the instant nucleic acid fragment can be constructed and introduced into a plant or plant cell. The level of the polypeptide encoded by the unmodified nucleic acid fragment present in a plant or plant cell exposed to the substantially similar nucleic acid fragment can then be compared to the level of the polypeptide in a plant or plant cell that is not exposed to the substantially similar nucleic acid fragment.

For example, it is well known in the art that antisense suppression and co-suppression of gene expression may be accomplished using nucleic acid fragments representing less than the entire coding region of a gene, and by using nucleic acid fragments that do not share 100% sequence identity with the gene to be suppressed. Moreover, alterations in a nucleic acid fragment which result in the production of a chemically equivalent amino acid at a given site, but do not effect the functional properties of the encoded polypeptide, are well known in the art. Thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a functionally equivalent product. Nucleotide changes which result in alteration of the N-terminal and C-terminal portions of the polypeptide molecule would also not be expected to alter the activity of the polypeptide. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded products. Consequently, an isolated polynucleotide comprising a nucleotide sequence of at least one of 60 (preferably at least one of 40, most preferably at least one of 30) contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and the complement of such nucleotide sequences may be used in methods of selecting an isolated polynucleotide that affects the expression of an auxin transport polypeptide in a host cell. A method of selecting an isolated polynucleotide that affects the level of expression of a polypeptide in a virus or in a host cell (eukaryotic, such as plant or yeast, prokaryotic such as bacterial) may comprise the steps of: constructing an isolated polynucleotide of the present invention or a chimeric gene of the present invention; introducing the isolated polynucleotide or the chimeric gene into a host cell; measuring the level of a polypeptide or enzyme activity in the host cell containing the isolated polynucleotide; and comparing the level of a polypeptide or enzyme activity in the host cell containing the isolated polynucleotide with the level of a polypeptide or enzyme activity in a host cell that does not contain the isolated polynucleotide.

Moreover, substantially similar nucleic acid fragments may also be characterized by their ability to hybridize. Estimates of such homology are provided by either DNA-DNA or

DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (Hames and Higgins, Eds. (1985) *Nucleic Acid Hybridisation*, IRL Press, Oxford, U.K.). Stringency conditions can be adjusted to screen for moderately similar fragments, such as homologous sequences from distantly related organisms, to highly similar fragments, such as genes that duplicate functional enzymes from closely related organisms. Post-hybridization washes determine stringency conditions. One set of preferred conditions uses a series of washes starting with 6X SSC, 0.5% SDS at room temperature for 15 min, then repeated with 2X SSC, 0.5% SDS at 45°C for 30 min, and then repeated twice with 0.2X SSC, 0.5% SDS at 50°C for 30 min. A more preferred set of stringent conditions uses higher temperatures in which the washes are identical to those above except for the temperature of the final two 30 min washes in 0.2X SSC, 0.5% SDS was increased to 60°C. Another preferred set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65°C.

Substantially similar nucleic acid fragments of the instant invention may also be characterized by the percent identity of the amino acid sequences that they encode to the amino acid sequences disclosed herein, as determined by algorithms commonly employed by those skilled in this art. Suitable nucleic acid fragments (isolated polynucleotides of the present invention) encode polypeptides that are at least about 70% identical, preferably at least about 80% identical to the amino acid sequences reported herein. Preferred nucleic acid fragments encode amino acid sequences that are about 85% identical to the amino acid sequences reported herein. More preferred nucleic acid fragments encode amino acid sequences that are at least about 90% identical to the amino acid sequences reported herein. Most preferred are nucleic acid fragments that encode amino acid sequences that are at least about 95% identical to the amino acid sequences reported herein. Suitable nucleic acid fragments not only have the above identities but typically encode a polypeptide having at least 30 or 50 amino acids, preferably at least 90 or 100 amino acids, more preferably at least 150 amino acids, still more preferably at least 200 amino acids, and most preferably at least 250, 300, 350, 400 or 500 amino acids. Sequence alignments and percent identity calculations were performed using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-

based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively
5 identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or
10 more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a “substantial portion” of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that
15 comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

20 “Codon degeneracy” refers to divergence in the genetic code permitting variation of the nucleotide sequence without effecting the amino acid sequence of an encoded polypeptide. Accordingly, the instant invention relates to any nucleic acid fragment comprising a nucleotide sequence that encodes all or a substantial portion of the amino acid sequences set forth herein. The skilled artisan is well aware of the “codon-bias” exhibited
25 by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a nucleic acid fragment for improved expression in a host cell, it is desirable to design the nucleic acid fragment such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

“Synthetic nucleic acid fragments” can be assembled from oligonucleotide building
30 blocks that are chemically synthesized using procedures known to those skilled in the art. These building blocks are ligated and annealed to form larger nucleic acid fragments which may then be enzymatically assembled to construct the entire desired nucleic acid fragment. “Chemically synthesized”, as related to a nucleic acid fragment, means that the component nucleotides were assembled *in vitro*. Manual chemical synthesis of nucleic acid fragments
35 may be accomplished using well established procedures, or automated chemical synthesis can be performed using one of a number of commercially available machines. Accordingly, the nucleic acid fragments can be tailored for optimal gene expression based on optimization of the nucleotide sequence to reflect the codon bias of the host cell. The skilled artisan

appreciates the likelihood of successful gene expression if codon usage is biased towards those codons favored by the host. Determination of preferred codons can be based on a survey of genes derived from the host cell where sequence information is available.

“Gene” refers to a nucleic acid fragment that expresses a specific protein, including regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence. “Native gene” refers to a gene as found in nature with its own regulatory sequences. “Chimeric gene” refers any gene that is not a native gene, comprising regulatory and coding sequences that are not found together in nature. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that found in nature. “Endogenous gene” refers to a native gene in its natural location in the genome of an organism. A “foreign gene” refers to a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer. Foreign genes can comprise native genes inserted into a non-native organism, or chimeric genes. A “transgene” is a gene that has been introduced into the genome by a transformation procedure.

“Coding sequence” refers to a nucleotide sequence that codes for a specific amino acid sequence. “Regulatory sequences” refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences may include promoters, translation leader sequences, introns, and polyadenylation recognition sequences.

“Promoter” refers to a nucleotide sequence capable of controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an “enhancer” is a nucleotide sequence which can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue-specificity of a promoter. Promoters may be derived in their entirety from a native gene, or may be composed of different elements derived from different promoters found in nature, or may even comprise synthetic nucleotide segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. Promoters which cause a nucleic acid fragment to be expressed in most cell types at most times are commonly referred to as “constitutive promoters”. New promoters of various types useful in plant cells are constantly being discovered; numerous examples may be found in the compilation by Okamuro and Goldberg (1989) *Biochemistry of Plants* 15:1-82. It is further recognized that since in most cases the exact boundaries of regulatory sequences

have not been completely defined, nucleic acid fragments of different lengths may have identical promoter activity.

“Translation leader sequence” refers to a nucleotide sequence located between the promoter sequence of a gene and the coding sequence. The translation leader sequence is present in the fully processed mRNA upstream of the translation start sequence. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency. Examples of translation leader sequences have been described (Turner and Foster (1995) *Mol. Biotechnol.* 3:225-236).

“3' Non-coding sequences” refers to nucleotide sequences located downstream of a coding sequence and includes polyadenylation recognition sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al. (1989) *Plant Cell* 1:671-680.

“RNA transcript” refers to the product resulting from RNA polymerase-catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. “Messenger RNA (mRNA)” refers to the RNA that is without introns and that can be translated into polypeptides by the cell. “cDNA” refers to DNA that is complementary to and derived from an mRNA template. The cDNA can be single-stranded or converted to double stranded form using, for example, the Klenow fragment of DNA polymerase I. “Sense RNA” refers to an RNA transcript that includes the mRNA and can be translated into a polypeptide by the cell. “Antisense RNA” refers to an RNA transcript that is complementary to all or part of a target primary transcript or mRNA and that blocks the expression of a target gene (see U.S. Patent No. 5,107,065, incorporated herein by reference). The complementarity of an antisense RNA may be with any part of the specific nucleotide sequence, i.e., at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding sequence. “Functional RNA” refers to sense RNA, antisense RNA, ribozyme RNA, or other RNA that may not be translated but yet has an effect on cellular processes.

The term “operably linked” refers to the association of two or more nucleic acid fragments so that the function of one is affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of affecting the expression of that coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

The term “expression”, as used herein, refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from the nucleic acid fragment of the invention. “Expression” may also refer to translation of mRNA into a polypeptide. “Antisense inhibition” refers to the production of antisense RNA transcripts capable of suppressing the expression of the target protein. “Overexpression” refers to the production of a gene product in transgenic organisms that exceeds levels of production in normal or non-transformed organisms. “Co-suppression” refers to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar foreign or endogenous genes (U.S. Patent No. 5,231,020, incorporated herein by reference).

A “protein” or “polypeptide” is a chain of amino acids arranged in a specific order determined by the coding sequence in a polynucleotide encoding the polypeptide. In the context of this disclosure, a number of terms shall be utilized. The terms “protein” and “polypeptide” are used interchangeably herein. Each protein or polypeptide has a unique function.

“Altered levels” or “altered expression” refers to the production of gene product(s) in transgenic organisms in amounts or proportions that differ from that of normal or non-transformed organisms.

“Null mutant” refers to a host cell which either lacks the expression of a certain polypeptide or expresses a polypeptide which is inactive or does not have any detectable expected enzymatic function.

“Mature protein” refers to a post-translationally processed polypeptide; i.e., one from which any pre- or propeptides present in the primary translation product have been removed. “Precursor protein” refers to the primary product of translation of mRNA; i.e., with pre- and propeptides still present. Pre- and propeptides may be but are not limited to intracellular localization signals.

A “chloroplast transit peptide” is an amino acid sequence which is translated in conjunction with a protein and directs the protein to the chloroplast or other plastid types present in the cell in which the protein is made. “Chloroplast transit sequence” refers to a nucleotide sequence that encodes a chloroplast transit peptide. A “signal peptide” is an amino acid sequence which is translated in conjunction with a protein and directs the protein to the secretory system (Chrispeels (1991) *Ann. Rev. Plant Phys. Plant Mol. Biol.* 42:21-53). If the protein is to be directed to a vacuole, a vacuolar targeting signal (*supra*) can further be added, or if to the endoplasmic reticulum, an endoplasmic reticulum retention signal (*supra*) may be added. If the protein is to be directed to the nucleus, any signal peptide present should be removed and instead a nuclear localization signal included (Raikhel (1992) *Plant Phys.* 100:1627-1632).

“Transformation” refers to the transfer of a nucleic acid fragment into the genome of a host organism, resulting in genetically stable inheritance. Host organisms containing the

transformed nucleic acid fragments are referred to as “transgenic” organisms. Examples of methods of plant transformation include *Agrobacterium*-mediated transformation (De Blaere et al. (1987) *Meth. Enzymol.* 143:277) and particle-accelerated or “gene gun” transformation technology (Klein et al. (1987) *Nature (London)* 327:70-73; U.S. Patent No. 4,945,050, incorporated herein by reference). Thus, isolated polynucleotides of the present invention can be incorporated into recombinant constructs, typically DNA constructs, capable of introduction into and replication in a host cell. Such a construct can be a vector that includes a replication system and sequences that are capable of transcription and translation of a polypeptide-encoding sequence in a given host cell. A number of vectors suitable for stable transfection of plant cells or for the establishment of transgenic plants have been described in, e.g., Pouwels et al., *Cloning Vectors: A Laboratory Manual*, 1985, supp. 1987; Weissbach and Weissbach, *Methods for Plant Molecular Biology*, Academic Press, 1989; and Flevin et al., *Plant Molecular Biology Manual*, Kluwer Academic Publishers, 1990. Typically, plant expression vectors include, for example, one or more cloned plant genes under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant expression vectors also can contain a promoter regulatory region (e.g., a regulatory region controlling inducible or constitutive, environmentally- or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or a polyadenylation signal.

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook et al. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989 (hereinafter “Maniatis”).

“PCR” or “polymerase chain reaction” is a technique used for the amplification of specific DNA segments (U.S. Patent Nos. 4,683,195 and 4,800,159).

The present invention concerns an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a first nucleotide sequence encoding a polypeptide of at least 30 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:6; (b) a second nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:16, 28, 36, and 40; (c) a third nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:12; (d) a fourth nucleotide sequence encoding a polypeptide of at least 50 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 24; (e) a fifth nucleotide sequence encoding

a polypeptide of at least 50 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 32; (f) a sixth nucleotide sequence encoding a polypeptide of at least 90 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:42; (g) a seventh nucleotide sequence encoding a polypeptide of at least 95 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:46; (h) an eighth nucleotide sequence encoding a polypeptide of at least 100 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:20; (i) a ninth nucleotide sequence encoding a polypeptide of at least 100 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2; (j) a tenth nucleotide sequence encoding a polypeptide of at least 150 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:4; (k) an eleventh nucleotide sequence encoding a polypeptide of at least 300 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:38; (l) a twelfth nucleotide sequence encoding a polypeptide of at least 350 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:10; (m) a thirteenth nucleotide sequence encoding a polypeptide of at least 400 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22, 26 and 30; (n) a fourteenth nucleotide sequence encoding a polypeptide of at least 500 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:34; (o) a fifteenth nucleotide sequence encoding a polypeptide of at least 200 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:14; (p) a sixteenth nucleotide sequence encoding a polypeptide of at least 250 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:48; and (q) a seventeenth nucleotide sequence comprising the complement of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), (m), (n), (o) or (p).

Preferably, the first nucleotide sequence comprises a nucleic acid sequence 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, 45, and 47 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46, and 48.

Nucleic acid fragments encoding at least a substantial portion of several auxin transport proteins have been isolated and identified by comparison of random plant cDNA

sequences to public databases containing nucleotide and protein sequences using the BLAST algorithms well known to those skilled in the art. The nucleic acid fragments of the instant invention may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. Isolation of homologous genes using sequence-dependent
5 protocols is well known in the art. Examples of sequence-dependent protocols include, but are not limited to, methods of nucleic acid hybridization, and methods of DNA and RNA amplification as exemplified by various uses of nucleic acid amplification technologies (e.g., polymerase chain reaction, ligase chain reaction).

For example, genes encoding other auxin transport polypeptides, either as cDNAs or
10 genomic DNAs, could be isolated directly by using all or a substantial portion of the instant nucleic acid fragments as DNA hybridization probes to screen libraries from any desired plant employing methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the instant nucleic acid sequences can be designed and synthesized by methods known in the art (Maniatis). Moreover, the entire sequence(s) can
15 be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labeling, nick translation, end-labeling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers can be designed and used to amplify a part or all of the instant sequences. The resulting amplification products can be labeled directly during amplification reactions or labeled after amplification
20 reactions, and used as probes to isolate full length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, two short segments of the instant nucleic acid fragments may be used in polymerase chain reaction protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. The polymerase chain reaction may also be
25 performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the instant nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, the skilled artisan can follow
30 the RACE protocol (Frohman et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:8998-9002) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant sequences. Using commercially available 3' RACE or 5' RACE systems (BRL), specific 3' or 5' cDNA fragments can be isolated (Ohara et al. (1989) *Proc. Natl.*
35 *Acad. Sci. USA* 86:5673-5677; Loh et al. (1989) *Science* 243:217-220). Products generated by the 3' and 5' RACE procedures can be combined to generate full-length cDNAs (Frohman and Martin (1989) *Techniques* 1:165). Consequently, a polynucleotide comprising a nucleotide sequence of at least one of 60 (preferably one of at least 40, most preferably one

of at least 30) contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and the complement of such nucleotide sequences may be used in such methods to obtain a nucleic acid fragment encoding a substantial portion of an amino acid sequence of a polypeptide.

The present invention relates to a method of obtaining a nucleic acid fragment encoding a substantial portion of an auxin transport polypeptide, preferably a substantial portion of a plant auxin transport polypeptide, comprising the steps of: synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 60 (preferably at least one of 40, most preferably at least one of 30) contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and the complement of such nucleotide sequences; and amplifying a nucleic acid fragment (preferably a cDNA inserted in a cloning vector) using the oligonucleotide primer. The amplified nucleic acid fragment preferably will encode a substantial portion of an auxin transport polypeptide.

Availability of the instant nucleotide and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing substantial portions of the instant amino acid sequences may be synthesized. These peptides can be used to immunize animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. These antibodies can be then be used to screen cDNA expression libraries to isolate full-length cDNA clones of interest (Lerner (1984) *Adv. Immunol.* 36:1-34; Maniatis).

In another embodiment, this invention concerns viruses and host cells comprising either the chimeric genes of the invention as described herein or an isolated polynucleotide of the invention as described herein. Examples of host cells which can be used to practice the invention include, but are not limited to, yeast, bacteria, and plants.

As was noted above, the nucleic acid fragments of the instant invention may be used to create transgenic plants in which the disclosed polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of auxin efflux in those cells. In addition, since some of these auxin transport proteins may be root-specific and impact root development to a significant degree, these auxin transport proteins may lead to novel strategies for developing transgenic plants with more robust root systems, which may enhance food production, especially in arid climates. The nucleic acid fragments of the instant invention may also be used to regulate root angle, and thus modify plant susceptibility to root lodging, root angle being a determinant of lodging susceptibility. Modified root gravitropic responses (as mediated by manipulation of the nucleic acid fragments of the instant invention) would also be useful for redirecting root growth (by

inhibiting gravitropism in short durations) for soil remediation projects and alleviate soil erosion problems. Roots may also be made to grow deeper beyond the top layers of the soil, reducing root tip damage caused by insect feeding and possibly generating a root system that extends downward rather than laterally into neighboring root zones, thus minimizing competition for nutrients among different root systems, making planting at higher densities a possibility. The auxin transport proteins disclosed herein may also be engineered to transport other compounds into and/or out of the plant, for example, such as into storage compartments or into media for harvesting.

Overexpression of the proteins of the instant invention may be accomplished by first constructing a chimeric gene in which the coding region is operably linked to a promoter capable of directing expression of a gene in the desired tissues at the desired stage of development. The chimeric gene may comprise promoter sequences and translation leader sequences derived from the same genes. 3' Non-coding sequences encoding transcription termination signals may also be provided. The instant chimeric gene may also comprise one or more introns in order to facilitate gene expression.

Plasmid vectors comprising the instant isolated polynucleotide (or chimeric gene) may be constructed. The choice of plasmid vector is dependent upon the method that will be used to transform host plants. The skilled artisan is well aware of the genetic elements that must be present on the plasmid vector in order to successfully transform, select and propagate host cells containing the chimeric gene. The skilled artisan will also recognize that different independent transformation events will result in different levels and patterns of expression (Jones et al. (1985) *EMBO J.* 4:2411-2418; De Almeida et al. (1989) *Mol. Gen. Genetics* 218:78-86), and thus that multiple events must be screened in order to obtain lines displaying the desired expression level and pattern. Such screening may be accomplished by Southern analysis of DNA, Northern analysis of mRNA expression, Western analysis of protein expression, or phenotypic analysis.

For some applications it may be useful to direct the instant polypeptides to different cellular compartments, or to facilitate secretion from the cell. It is thus envisioned that the chimeric gene described above may be further supplemented by directing the coding sequence to encode the instant polypeptides with appropriate intracellular targeting sequences such as transit sequences (Keegstra (1989) *Cell* 56:247-253), signal sequences or sequences encoding endoplasmic reticulum localization (Chrispeels (1991) *Ann. Rev. Plant Phys. Plant Mol. Biol.* 42:21-53), or nuclear localization signals (Raikhel (1992) *Plant Phys.* 100:1627-1632) with or without removing targeting sequences that are already present. While the references cited give examples of each of these, the list is not exhaustive and more targeting signals of use may be discovered in the future.

It may also be desirable to reduce or eliminate expression of genes encoding the instant polypeptides in plants for some applications. In order to accomplish this, a chimeric

gene designed for co-suppression of the instant polypeptide can be constructed by linking a gene or gene fragment encoding that polypeptide to plant promoter sequences.

Alternatively, a chimeric gene designed to express antisense RNA for all or part of the instant nucleic acid fragment can be constructed by linking the gene or gene fragment in reverse orientation to plant promoter sequences. Either the co-suppression or antisense chimeric genes could be introduced into plants via transformation wherein expression of the corresponding endogenous genes are reduced or eliminated.

Molecular genetic solutions to the generation of plants with altered gene expression have a decided advantage over more traditional plant breeding approaches. Changes in plant phenotypes can be produced by specifically inhibiting expression of one or more genes by antisense inhibition or cosuppression (U.S. Patent Nos. 5,190,931, 5,107,065 and 5,283,323). An antisense or cosuppression construct would act as a dominant negative regulator of gene activity. While conventional mutations can yield negative regulation of gene activity these effects are most likely recessive. The dominant negative regulation available with a transgenic approach may be advantageous from a breeding perspective. In addition, the ability to restrict the expression of a specific phenotype to the reproductive tissues of the plant by the use of tissue specific promoters may confer agronomic advantages relative to conventional mutations which may have an effect in all tissues in which a mutant gene is ordinarily expressed.

The person skilled in the art will know that special considerations are associated with the use of antisense or cosuppression technologies in order to reduce expression of particular genes. For example, the proper level of expression of sense or antisense genes may require the use of different chimeric genes utilizing different regulatory elements known to the skilled artisan. Once transgenic plants are obtained by one of the methods described above, it will be necessary to screen individual transgenics for those that most effectively display the desired phenotype. Accordingly, the skilled artisan will develop methods for screening large numbers of transformants. The nature of these screens will generally be chosen on practical grounds. For example, one can screen by looking for changes in gene expression by using antibodies specific for the protein encoded by the gene being suppressed, or one could establish assays that specifically measure enzyme activity. A preferred method will be one which allows large numbers of samples to be processed rapidly, since it will be expected that a large number of transformants will be negative for the desired phenotype.

In another embodiment, the present invention concerns an auxin transport polypeptide selected from the group consisting of: (a) a polypeptide of at least 30 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:6; (b) a polypeptide of at least 50 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:16, 28, 36, and 40; (c) a polypeptide of at

least 50 amino acids having at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:12; (d) a polypeptide of at least 50 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 24; (e) a

5 polypeptide of at least 50 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 32; (f) a polypeptide of at least 90 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:42; (g) a polypeptide of at least 95 amino acids having at least 95% identity based on

10 the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:46; (h) a polypeptide of at least 100 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:20; (i) a polypeptide of at least 100 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2;

15 (j) a polypeptide of at least 150 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:4; (k) a polypeptide of at least 300 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:38; (l) a polypeptide of at least 350 amino acids having at least 95% identity based on the Clustal method of alignment when

20 compared to a polypeptide of SEQ ID NO:10; (m) a polypeptide of at least 400 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22, 26 and 30; (n) a polypeptide of at least 500 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:34; (o) a polypeptide

25 of at least 200 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:14; (p) a polypeptide of at least 250 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:48.

The instant polypeptides (or portions thereof) may be produced in heterologous host

30 cells, particularly in the cells of microbial hosts, and can be used to prepare antibodies to the proteins by methods well known to those skilled in the art. The antibodies are useful for detecting the polypeptides of the instant invention *in situ* in cells or *in vitro* in cell extracts. Preferred heterologous host cells for production of the instant polypeptides are microbial hosts. Microbial expression systems and expression vectors containing regulatory sequences

35 that direct high level expression of foreign proteins are well known to those skilled in the art. Any of these could be used to construct a chimeric gene for production of the instant polypeptides. This chimeric gene could then be introduced into appropriate microorganisms via transformation to provide high level expression of the encoded auxin transport protein.

An example of a vector for high level expression of the instant polypeptides in a bacterial host is provided (Example 6).

Additionally, the instant auxin transport proteins can be used as a target to facilitate design and/or identification of inhibitors of these proteins that may be useful as herbicides.

5 This is desirable because the auxin transport proteins described herein are essential components of the polar transport system involved in auxin redistribution and hence auxin function. Accordingly, inhibition of the activity of one or more of the enzymes described herein could lead to inhibition of plant growth. Thus, the instant auxin transport proteins could be appropriate for new herbicide discovery and design.

10 The present invention further provides a method for modulating (i.e., increasing or decreasing) the concentration or composition of the polypeptides of the present invention in a plant or part thereof. Modulation of the polypeptides can be effected by increasing or decreasing the concentration and/or the composition of the polypeptides in a plant. The method comprises transforming a plant cell with a construct comprising a nucleic acid
15 fragment of the present invention to obtain a transformed plant cell, growing the transformed plant cell under plant forming conditions, and expressing the nucleic acid fragment in the plant for a time sufficient to modulate concentration and/or composition of the polypeptides in the plant or plant part.

In some embodiments, the content and/or composition of polypeptides of the present
20 invention in a plant may be modulated by altering, *in vivo* or *in vitro*, the promoter of a non-isolated gene of the present invention to up- or down-regulate gene expression. In some embodiments, the coding regions of native genes of the present invention can be altered via substitution, addition, insertion, or deletion to decrease activity of the encoded enzyme. See, e.g., Kmiec, U.S. Patent No. 5,565,350; Zarling *et al.*, PCT/US93/03868.

25 In some embodiments, an isolated nucleic acid fragment (e.g., a vector) comprising a promoter sequence is transfected into a plant cell. Subsequently, a plant cell comprising the isolated nucleic acid is selected for by means known to those of skill in the art such as, but not limited to, Southern blot, DNA sequencing, or PCR analysis using primers specific to the promoter and to the nucleic acid and detecting amplicons produced therefrom. A plant or
30 plant part altered or modified by the foregoing embodiments is grown under plant forming conditions for a time sufficient to modulate the concentration and/or composition of polypeptides of the present invention in the plant. Plant forming conditions are well known in the art.

In general, concentration of the polypeptides is increased or decreased by at least 5%,
35 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% relative to a native control plant, plant part, or cell lacking the aforementioned transgene. Modulation in the present invention may occur during and/or subsequent to growth of the plant to the desired stage of development.

Modulating nucleic acid expression temporally and/or in particular tissues can be controlled by employing the appropriate promoter operably linked to a nucleic acid fragment of the present invention in, for example, sense or antisense orientation as discussed in greater detail above. Induction of expression of a nucleic acid fragment of the present invention can also be controlled by exogenous administration of an effective amount of inducing compound. Inducible promoters and inducing compounds that activate expression from these promoters are well known in the art.

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. Also useful are promoters which are chemically inducible.

Examples of promoters under developmental control include promoters that initiate transcription preferentially in certain tissues such as leaves, roots, fruit, seeds, or flowers. An exemplary promoter is the anther specific promoter 5126 (U.S. Patent Nos. 5,689,049 and 5,689,051). Examples of seed-preferred promoters include, but are not limited to, 27 kD gamma zein promoter and waxy promoter (Boronat et al. (1986) *Plant Sci.* 47:95-102; Reina et al. (1990) *Nucleic Acids Res.* 18(21):6426; Kloesgen et al. (1986) *Mol. Gen. Genet.* 203:237-244). Promoters that are expressed in the embryo, pericarp, and endosperm are disclosed in US applications Serial Nos. 60/097,233 filed August 20, 1998 and 60/098,230 filed August 28, 1998. The disclosures of each of these are incorporated herein by reference in their entirety.

Either heterologous or non-heterologous (i.e., endogenous) promoters can be employed to direct expression of the nucleic acids of the present invention. These promoters can also be used, for example, in chimeric genes to drive expression of antisense nucleic acids to reduce, increase, or alter concentration and/or composition of the proteins of the present invention in a desired tissue.

All or a substantial portion of the polynucleotides of the instant invention may also be used as probes for genetically and physically mapping the genes that they are a part of, and used as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. For example, the instant nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Maniatis) of restriction-digested plant genomic DNA may be probed with the nucleic acid fragments of the instant invention. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander et al. (1987) *Genomics* 1:174-181) in order to construct a genetic map. In addition, the nucleic acid fragments of the instant invention may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted

and used to calculate the position of the instant nucleic acid sequence in the genetic map previously obtained using this population (Botstein et al. (1980) *Am. J. Hum. Genet.* 32:314-331).

5 The production and use of plant gene-derived probes for use in genetic mapping is described in Bernatzky and Tanksley (1986) *Plant Mol. Biol. Reporter* 4:37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

10 Nucleic acid probes derived from the instant nucleic acid sequences may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel et al. In: *Nonmammalian Genomic Analysis: A Practical Guide*, Academic press 1996, pp. 319-346, and references cited therein).

15 In another embodiment, nucleic acid probes derived from the instant nucleic acid sequences may be used in direct fluorescence *in situ* hybridization (FISH) mapping (Trask (1991) *Trends Genet.* 7:149-154). Although current methods of FISH mapping favor use of large clones (several to several hundred KB; see Laan et al. (1995) *Genome Res.* 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

20 A variety of nucleic acid amplification-based methods of genetic and physical mapping may be carried out using the instant nucleic acid sequences. Examples include allele-specific amplification (Kazazian (1989) *J. Lab. Clin. Med.* 11:95-96), polymorphism of PCR-amplified fragments (CAPS; Sheffield et al. (1993) *Genomics* 16:325-332), allele-specific ligation (Landegren et al. (1988) *Science* 241:1077-1080), nucleotide extension reactions (Sokolov (1990) *Nucleic Acid Res.* 18:3671), Radiation Hybrid Mapping (Walter et al. (1997) *Nat. Genet.* 7:22-28) and Happy Mapping (Dear and Cook (1989) *Nucleic Acid Res.* 17:6795-6807). For these methods, the sequence of a nucleic acid fragment is used to design and produce primer pairs for use in the amplification reaction or in primer extension reactions. The design of such primers is well known to those skilled in the art. In methods employing PCR-based genetic mapping, it may be necessary to identify DNA sequence
25 differences between the parents of the mapping cross in the region corresponding to the instant nucleic acid sequence. This, however, is generally not necessary for mapping methods.

35 Loss of function mutant phenotypes may be identified for the instant cDNA clones either by targeted gene disruption protocols or by identifying specific mutants for these genes contained in a maize population carrying mutations in all possible genes (Ballinger and Benzer (1989) *Proc. Natl. Acad. Sci USA* 86:9402-9406; Koes et al. (1995) *Proc. Natl. Acad. Sci USA* 92:8149-8153; Bensen et al. (1995) *Plant Cell* 7:75-84). The latter approach may be accomplished in two ways. First, short segments of the instant nucleic acid

fragments may be used in polymerase chain reaction protocols in conjunction with a mutation tag sequence primer on DNAs prepared from a population of plants in which Mutator transposons or some other mutation-causing DNA element has been introduced (see Bensen, *supra*). The amplification of a specific DNA fragment with these primers indicates the insertion of the mutation tag element in or near the plant gene encoding the instant polypeptide. Alternatively, the instant nucleic acid fragment may be used as a hybridization probe against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer, such as that for a restriction enzyme site-anchored synthetic adaptor. With either method, a plant containing a mutation in the endogenous gene encoding the instant polypeptide can be identified and obtained. This mutant plant can then be used to determine or confirm the natural function of the instant polypeptides disclosed herein.

EXAMPLES

The present invention is further defined in the following Examples, in which parts and percentages are by weight and degrees are Celsius, unless otherwise stated. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Thus, various modifications of the invention in addition to those shown and described herein will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

The disclosure of each reference set forth herein is incorporated herein by reference in its entirety.

EXAMPLE 1

Composition of cDNA Libraries; Isolation and Sequencing of cDNA Clones

cDNA libraries representing mRNAs from various corn (*Zea mays*), rice (*Oryza sativa*), soybean (*Glycine max*), and wheat (*Triticum aestivum*) tissues were prepared. The characteristics of the libraries are described below. Corn developmental stages are explained in the publication "How a Corn Plant Develops" from the Iowa State University Coop. Ext. Service Special Report No. 48 reprinted June 1993.

TABLE 2
cDNA Libraries from Corn, Rice, Soybean, and Wheat

Library	Tissue	Clone
ceb1	Corn Embryo 10 to 11 Days After Pollination	ceb1.pk0082.a5
cil1c	Corn (EB90) Pooled Immature Leaf Tissue at V4, V6 and V8	cil1c.pk001.b7
cr1	Corn Root From 7 Day Old Seedlings	cr1.pk0022.a4
cr1n	Corn Root From 7 Day Old Seedlings*	cr1n.pk0033.e3
csi1n	Corn Silk*	csi1n.pk0045.a5 csi1n.pk0050.d5
p0005	Corn Immature Ear	p0005.cbmej72r
p0016	Corn Tassel Shoot, Pooled, 0.1-1.4 cm	p0016.ctsag12r
p0041	Corn Root Tip Smaller Than 5 mm in Length, Four Days After Imbibition	p0041.crtba02r
p0094	Corn Leaf Collars for the Ear Leaf (EL), screened 1 and the Next Leaf Above and Below the EL; Growth Conditions: Field; Control or Untreated Tissues	p0094.cssh17r
p0097	Corn V9 Whorl Section (7 cm) From Plant Infected Four Times With European Corn Borer	p0097.cqrai63r
p0119	Corn V12-Stage Ear Shoot With Husk, Night Harvested*	p0119.cmtnl24r
rr1	Rice Root of Two Week Old Developing Seedling	rr1.pk0019.c4
rsl1n	Rice 15-Day-Old Seedling*	rsl1n.pk003.n3
scr1c	Soybean Embryogenic Suspension Culture Subjected to 4 Vacuum Cycles and Collected 12 Hrs Later	scr1c.pk003.g7
sdp4c	Soybean Developing Pod (10-12 mm)	sdp4c.pk003.h2
sfl1	Soybean Immature Flower	sfl1.pk131.g9
src3c	Soybean 8 Day Old Root Infected With Cyst Nematode	src3c.pk026.o11
wdk1c	Wheat Developing Kernel, 3 Days After Anthesis	wdk1c.pk008.g12
wdr1f	Wheat Developing Root (Full Length)	wdr1f.pk001.g9
wle1n	Wheat Leaf From 7 Day Old Etiolated Seedling*	wle1n.pk0109.h1

*These libraries were normalized essentially as described in U.S. Patent No. 5,482,845, incorporated herein by reference.

5

cDNA libraries may be prepared by any one of many methods available. For example, the cDNAs may be introduced into plasmid vectors by first preparing the cDNA libraries in Uni-ZAP™ XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA). The Uni-ZAP™ XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut Bluescript II SK(+) vectors (Stratagene) using T4 DNA

10

ligase (New England Biolabs), followed by transfection into DH10B cells according to the manufacturer's protocol (GIBCO BRL Products). Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant pBluescript plasmids, or the insert cDNA sequences are amplified via

5 polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Amplified insert DNAs or plasmid DNAs are sequenced in dye-primer sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"; see Adams et al., (1991) *Science* 252:1651-1656). The resulting ESTs are analyzed using a Perkin Elmer Model 377 fluorescent sequencer.

10 EXAMPLE 2

Identification of cDNA Clones

cDNA clones encoding auxin transport protein were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/) searches for similarity to sequences contained in the

15 BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm

20 provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained

25 in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

EXAMPLE 3

Characterization of cDNA Clones Encoding Auxin Transport Protein

The BLASTX search using the EST sequences from clones p0016.ctsag12r, p0119.cmtnl24r and wle1n.pk0109.h1, and the contig assembled from EST sequences from clones p0097.cqrai63r and p0094.csssh17r revealed similarity of the proteins encoded by the cDNAs to the auxin transport protein encoded by REH1 (Rice EIR1 Homolog) from rice

35 (NCBI Gene Identifier No. 3377509). The BLAST results for each of these ESTs are shown in Table 3:

TABLE 3

BLAST Results for Clones Encoding Polypeptides Homologous to REH1 Protein

Clone	BLAST pLog Score 3377509
p0016.ctsag12r	10.5
Contig of: p0097.cqrai63r p0094.csssh17r	40.7
p0119.cmtnl24r	34.4
wle1n.pk0109.h1	52.0

The BLASTX search using the EST sequences from clones rsl1n.pk003.n3, src3c.pk026.o11 and wdk1c.pk008.g12 revealed similarity of the proteins encoded by the cDNAs to the auxin transport protein encoded by EIR1 from *Arabidopsis thaliana* (NCBI Gene Identifier No. 3377507). The BLAST results for each of these ESTs are shown in Table 4:

TABLE 4

BLAST Results for Clones Encoding Polypeptides Homologous to EIR1 Protein

Clone	BLAST pLog Score 3377507
rsl1n.pk003.n3	38.2
src3c.pk026.o11	39.2
wdk1c.pk008.g12	41.0

The BLASTX search using the EST sequences from clone sfl1.pk131.g9 revealed similarity of the protein encoded by the cDNA to the auxin transport protein encoded by PIN1 from *Arabidopsis thaliana* (NCBI Gene Identifier No. 4151319) with a pLog value of 30.2. The BLASTX search using the EST sequences from clone sdp4c.pk003.h2 revealed similarity of the protein encoded by the cDNA to a putative auxin transport protein encoded by a gene from *Arabidopsis thaliana* (NCBI Gene Identifier No. 3785972) with a pLog value of 37.7.

The sequence of a substantial portion of the cDNA insert from clone p0016.ctsag12r is shown in SEQ ID NO:5; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:6. The sequence of a contig assembled from a portion of the cDNA insert from clones p0097.cqrai63r and p0094.csssh17r is shown in SEQ ID NO:7; the deduced amino acid sequence of this contig is shown in SEQ ID NO:8. The sequence of a substantial portion of the cDNA insert from clone p0119.cmtnl24r is shown in SEQ ID NO:11; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:12. The sequence of a substantial portion of the cDNA insert from clone rsl1n.pk003.n3

is shown in SEQ ID NO:17; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:18. The sequence of a substantial portion of the cDNA insert from clone sdp4c.pk003.h2 is shown in SEQ ID NO:23; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:24. The sequence of a substantial portion of the cDNA insert from clone sfl1.pk131.g9 is shown in SEQ ID NO:27; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:28. The sequence of a substantial portion of the cDNA insert from clone src3c.pk026.o11 is shown in SEQ ID NO:31; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:32. The sequence of a substantial portion of the cDNA insert from clone wdk1c.pk008.g12 is shown in SEQ ID NO:35; the deduced amino acid sequence of this portion of the cDNA is shown in SEQ ID NO:36. The sequence of a substantial portion of the cDNA insert from wle1n.pk0109.h1 is shown in SEQ ID NO:41; the deduced amino acid sequence of this cDNA is shown in SEQ ID NO:42. BLAST scores and probabilities indicate that the instant nucleic acid fragments encode portions of auxin transport proteins.

The BLASTX search using the EST sequences from clones listed in Table 5 revealed similarity of the polypeptides encoded by the cDNAs to auxin transport proteins from rice (NCBI GenBank Identifier (GI) Nos. 3377509 and 7489524) and Arabidopsis (NCBI GenBank Identifier (GI) Nos. 5902405, 5817301, 4151319, 3377507, and 3785972). Shown in Table 5 are the BLAST results for individual ESTs ("EST"), the sequences of the entire cDNA inserts comprising the indicated cDNA clones ("FIS"), contigs assembled from two or more ESTs ("Contig"), contigs assembled from an FIS and one or more ESTs ("Contig*"), or sequences encoding the entire protein derived from an FIS, a contig, or an FIS and PCR ("CGS"):

TABLE 5

BLAST Results for Sequences Encoding Polypeptides Homologous to Auxin Transport Protein

Clone	Status	BLAST Results	
		NCBI GenBank Identifier (GI) No.	pLog Score
ceb1.pk0082.a5	EST	3377509	79.10
Contig of: cr1.pk0022.a4 cr1n.pk0033.e3 csi1n.pk0045.a5 csi1n.pk0050.d5 p0005.cbmej72r p0041.crtba02r	Contig	3377509	91.70
p0094.csssh17r	FIS	3377509	>254.00
p0119.cmtnl24r (FIS)	CGS	7489524	180.00
cil1.pk001.b7	FIS	7489524	135.00
rr1.pk0019.c4	EST	5902405	33.30

Clone	Status	BLAST Results	
		NCBI GenBank Identifier (GI) No.	pLog Score
rsl1n.pk003.n3	FIS	5817301	155.00
scr1c.pk003.g7	FIS	4151319	170.00
sdp4c.pk003.h2	FIS	5817301	>254.00
sfl1.pk131.g9(FIS)	CGS	4151319	>254.00
src3c.pk026.o11(FIS)	CGS	3377507	>254.00
wdk1c.pk008.g12(FIS)	CGS	3377507	>254.00
wdr1f.pk001.g9	EST	3785972	27.30
wle1n.pko109.hl	FIS	3377509	48.00

Figure 1 presents an alignment of the amino acid sequences set forth in SEQ ID NOs:14, 30, 34, and 38, the auxin transport protein EIR1 sequence from *Arabidopsis thaliana* (NCBI GenBank Identifier (GI) No. 3377507; SEQ ID NO:43), and the auxin transport protein AtPIN1 sequence from *Arabidopsis thaliana* (NCBI GenBank Identifier (GI) No. 4151319; SEQ ID NO:44). The data in Table 6 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:14, 30, 34, and 38, the auxin transport protein EIR1 sequence from *Arabidopsis thaliana* (NCBI GenBank Identifier (GI) No. 3377507; SEQ ID NO:43), and the auxin transport protein AtPIN1 from *Arabidopsis thaliana* (NCBI GenBank Identifier (GI) No. 4151319; SEQ ID NO:44).

TABLE 6

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Auxin Transport Protein

SEQ ID NO.	Percent Identity to	
	SEQ ID NO:43	SEQ ID NO:44
14	51.5	55.3
30	57.9	72.3
34	75.1	59.6
38	59.7	52.1

Sequence alignments and percent identity calculations were performed using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. Sequence alignments, BLAST scores and

probabilities indicate that the nucleic acid fragments comprising the instant cDNA clones encode all or a substantial portion of an auxin transport protein.

EXAMPLE 4

Expression of Chimeric Genes in Monocot Cells

5 A chimeric gene comprising a cDNA encoding the instant polypeptide in sense orientation with respect to the maize 27 kD zein promoter that is located 5' to the cDNA fragment, and the 10 kD zein 3' end that is located 3' to the cDNA fragment, can be constructed. The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites
10 (NcoI or SmaI) can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the digested vector pML103 as described below. Amplification is then performed in a standard PCR. The amplified DNA is then digested with restriction enzymes NcoI and SmaI and fractionated on an agarose gel. The appropriate band can be isolated from the gel and combined with a 4.9 kb NcoI-SmaI fragment of the
15 plasmid pML103. Plasmid pML103 has been deposited under the terms of the Budapest Treaty at ATCC (American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209), and bears accession number ATCC 97366. The DNA segment from pML103 contains a 1.05 kb Sall-NcoI promoter fragment of the maize 27 kD zein gene and a 0.96 kb SmaI-Sall fragment from the 3' end of the maize 10 kD zein gene in the vector
20 pGem9Zf(+) (Promega). Vector and insert DNA can be ligated at 15°C overnight, essentially as described (Maniatis). The ligated DNA may then be used to transform *E. coli* XL1-Blue (Epicurian Coli XL-1 Blue™; Stratagene). Bacterial transformants can be screened by restriction enzyme digestion of plasmid DNA and limited nucleotide sequence analysis using the dideoxy chain termination method (Sequenase™ DNA Sequencing Kit;
25 U.S. Biochemical). The resulting plasmid construct would comprise a chimeric gene encoding, in the 5' to 3' direction, the maize 27 kD zein promoter, a cDNA fragment encoding the instant polypeptide, and the 10 kD zein 3' region.

The chimeric gene described above can then be introduced into corn cells by the following procedure. Immature corn embryos can be dissected from developing caryopses
30 derived from crosses of the inbred corn lines H99 and LH132. The embryos are isolated 10 to 11 days after pollination when they are 1.0 to 1.5 mm long. The embryos are then placed with the axis-side facing down and in contact with agarose-solidified N6 medium (Chu et al. (1975) *Sci. Sin. Peking* 18:659-668). The embryos are kept in the dark at 27°C. Friable embryogenic callus consisting of undifferentiated masses of cells with somatic
35 proembryoids and embryoids borne on suspensor structures proliferates from the scutellum of these immature embryos. The embryogenic callus isolated from the primary explant can be cultured on N6 medium and sub-cultured on this medium every 2 to 3 weeks.

The plasmid, p35S/Ac (obtained from Dr. Peter Eckes, Hoechst Ag, Frankfurt, Germany) may be used in transformation experiments in order to provide for a selectable marker. This plasmid contains the *Pat* gene (see European Patent Publication 0 242 236) which encodes phosphinothricin acetyl transferase (PAT). The enzyme PAT confers
5 resistance to herbicidal glutamine synthetase inhibitors such as phosphinothricin. The *pat* gene in p35S/Ac is under the control of the 35S promoter from Cauliflower Mosaic Virus (Odell et al. (1985) *Nature* 313:810-812) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*.

The particle bombardment method (Klein et al. (1987) *Nature* 327:70-73) may be used
10 to transfer genes to the callus culture cells. According to this method, gold particles (1 μ m in diameter) are coated with DNA using the following technique. Ten μ g of plasmid DNAs are added to 50 μ L of a suspension of gold particles (60 mg per mL). Calcium chloride (50 μ L of a 2.5 M solution) and spermidine free base (20 μ L of a 1.0 M solution) are added to the particles. The suspension is vortexed during the addition of these solutions. After
15 10 minutes, the tubes are briefly centrifuged (5 sec at 15,000 rpm) and the supernatant removed. The particles are resuspended in 200 μ L of absolute ethanol, centrifuged again and the supernatant removed. The ethanol rinse is performed again and the particles resuspended in a final volume of 30 μ L of ethanol. An aliquot (5 μ L) of the DNA-coated gold particles can be placed in the center of a Kapton™ flying disc (Bio-Rad Labs). The
20 particles are then accelerated into the corn tissue with a Biolistic™ PDS-1000/He (Bio-Rad Instruments, Hercules CA), using a helium pressure of 1000 psi, a gap distance of 0.5 cm and a flying distance of 1.0 cm.

For bombardment, the embryogenic tissue is placed on filter paper over agarose-solidified N6 medium. The tissue is arranged as a thin lawn and covered a circular area of
25 about 5 cm in diameter. The petri dish containing the tissue can be placed in the chamber of the PDS-1000/He approximately 8 cm from the stopping screen. The air in the chamber is then evacuated to a vacuum of 28 inches of Hg. The macrocarrier is accelerated with a helium shock wave using a rupture membrane that bursts when the He pressure in the shock tube reaches 1000 psi.

30 Seven days after bombardment the tissue can be transferred to N6 medium that contains gluphosinate (2 mg per liter) and lacks casein or proline. The tissue continues to grow slowly on this medium. After an additional 2 weeks the tissue can be transferred to fresh N6 medium containing gluphosinate. After 6 weeks, areas of about 1 cm in diameter of actively growing callus can be identified on some of the plates containing the glufosinate-supplemented medium. These calli may continue to grow when sub-cultured on the
35 selective medium.

Plants can be regenerated from the transgenic callus by first transferring clusters of tissue to N6 medium supplemented with 0.2 mg per liter of 2,4-D. After two weeks the

tissue can be transferred to regeneration medium (Fromm et al. (1990) *Bio/Technology* 8:833-839).

EXAMPLE 5

Expression of Chimeric Genes in Dicot Cells

5 A seed-specific construct composed of the promoter and transcription terminator from the gene encoding the β subunit of the seed storage protein phaseolin from the bean *Phaseolus vulgaris* (Doyle et al. (1986) *J. Biol. Chem.* 261:9228-9238) can be used for expression of the instant polypeptides in transformed soybean. The phaseolin construct includes about 500 nucleotides upstream (5') from the translation initiation codon and about
10 1650 nucleotides downstream (3') from the translation stop codon of phaseolin. Between the 5' and 3' regions are the unique restriction endonuclease sites Nco I (which includes the ATG translation initiation codon), Sma I, Kpn I and Xba I. The entire construct is flanked by Hind III sites.

The cDNA fragment of this gene may be generated by polymerase chain reaction
15 (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the expression vector. Amplification is then performed as described above, and the isolated fragment is inserted into a pUC18 vector carrying the seed construct.

Soybean embryos may then be transformed with the expression vector comprising
20 sequences encoding the instant polypeptides. To induce somatic embryos, cotyledons, 3-5 mm in length dissected from surface sterilized, immature seeds of the soybean cultivar A2872, can be cultured in the light or dark at 26°C on an appropriate agar medium for 6-10 weeks. Somatic embryos which produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic
25 embryos which multiplied as early, globular staged embryos, the suspensions are maintained as described below.

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
30 35 mL of liquid medium.

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. Patent No. 4,945,050). A DuPont Biolistic™ PDS1000/HE instrument (helium retrofit) can be used for these transformations.

35 A selectable marker gene which can be used to facilitate soybean transformation is a chimeric gene 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 seed construct comprising the phaseolin 5' region, the fragment encoding the instant polypeptide and the phaseolin 3' region 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.

5 To 50 μ L of a 60 mg/mL 1 μ m gold particle suspension is added (in order): 5 μ L DNA (1 μ g/ μ L), 20 μ L spermidine (0.1 M), and 50 μ L 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 μ L 70% ethanol and resuspended in 40 μ L of anhydrous ethanol. The DNA/particle suspension can
10 be sonicated three times for one second each. Five μ L of the DNA-coated gold particles are then loaded on each macro carrier disk.

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty 60x15 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
15 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.

Five to seven days post bombardment, the liquid media may be exchanged with fresh
20 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
25 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 6

Expression of Chimeric Genes in Microbial Cells

30 The cDNAs encoding the instant polypeptides can be inserted into the T7 *E. coli* expression vector pBT430. This vector is a derivative of pET-3a (Rosenberg et al. (1987) *Gene* 56:125-135) which employs the bacteriophage T7 RNA polymerase/T7 promoter system. Plasmid pBT430 was constructed by first destroying the EcoR I and Hind III sites in pET-3a at their original positions. An oligonucleotide adaptor containing EcoR I and
35 Hind III sites was inserted at the BamH I site of pET-3a. This created pET-3aM with additional unique cloning sites for insertion of genes into the expression vector. Then, the Nde I site at the position of translation initiation was converted to an Nco I site using

oligonucleotide-directed mutagenesis. The DNA sequence of pET-3aM in this region, 5'-CATATGG, was converted to 5'-CCCATGG in pBT430.

Plasmid DNA containing a cDNA may be appropriately digested to release a nucleic acid fragment encoding the protein. This fragment may then be purified on a 1% NuSieve GTG™ low melting agarose gel (FMC). Buffer and agarose contain 10 µg/mL ethidium bromide for visualization of the DNA fragment. The fragment can then be purified from the agarose gel by digestion with GELase™ (Epicentre Technologies) according to the manufacturer's instructions, ethanol precipitated, dried and resuspended in 20 µL of water. Appropriate oligonucleotide adapters may be ligated to the fragment using T4 DNA ligase (New England Biolabs, Beverly, MA). The fragment containing the ligated adapters can be purified from the excess adapters using low melting agarose as described above. The vector pBT430 is digested, dephosphorylated with alkaline phosphatase (NEB) and deproteinized with phenol/chloroform as described above. The prepared vector pBT430 and fragment can then be ligated at 16°C for 15 hours followed by transformation into DH5 electrocompetent cells (GIBCO BRL). Transformants can be selected on agar plates containing LB media and 100 µg/mL ampicillin. Transformants containing the gene encoding the instant polypeptide are then screened for the correct orientation with respect to the T7 promoter by restriction enzyme analysis.

For high level expression, a plasmid clone with the cDNA insert in the correct orientation relative to the T7 promoter can be transformed into *E. coli* strain BL21(DE3) (Studier et al. (1986) *J. Mol. Biol.* 189:113-130). Cultures are grown in LB medium containing ampicillin (100 mg/L) at 25°C. At an optical density at 600 nm of approximately 1, IPTG (isopropylthio-β-galactoside, the inducer) can be added to a final concentration of 0.4 mM and incubation can be continued for 3 h at 25°. Cells are then harvested by centrifugation and re-suspended in 50 µL of 50 mM Tris-HCl at pH 8.0 containing 0.1 mM DTT and 0.2 mM phenyl methylsulfonyl fluoride. A small amount of 1 mm glass beads can be added and the mixture sonicated 3 times for about 5 seconds each time with a microprobe sonicator. The mixture is centrifuged and the protein concentration of the supernatant determined. One µg of protein from the soluble fraction of the culture can be separated by SDS-polyacrylamide gel electrophoresis. Gels can be observed for protein bands migrating at the expected molecular weight.

EXAMPLE 7

Evaluating Compounds for Their Ability to Inhibit the Activity of Auxin Transport Proteins

The polypeptides described herein may be produced using any number of methods known to those skilled in the art. Such methods include, but are not limited to, expression in bacteria as described in Example 6, or expression in eukaryotic cell culture, *in planta*, and using viral expression systems in suitably infected organisms or cell lines. The instant

polypeptides may be expressed either as mature forms of the proteins as observed *in vivo* or as fusion proteins by covalent attachment to a variety of enzymes, proteins or affinity tags. Common fusion protein partners include glutathione S-transferase ("GST"), thioredoxin ("Trx"), maltose binding protein, and C- and/or N-terminal hexahistidine polypeptide ("His)₆"). The fusion proteins may be engineered with a protease recognition site at the fusion point so that fusion partners can be separated by protease digestion to yield intact mature enzyme. Examples of such proteases include thrombin, enterokinase and factor Xa. However, any protease can be used which specifically cleaves the peptide connecting the fusion protein and the enzyme.

Purification of the instant polypeptides, if desired, may utilize any number of separation technologies familiar to those skilled in the art of protein purification. Examples of such methods include, but are not limited to, homogenization, filtration, centrifugation, heat denaturation, ammonium sulfate precipitation, desalting, pH precipitation, ion exchange chromatography, hydrophobic interaction chromatography and affinity chromatography, wherein the affinity ligand represents a substrate, substrate analog or inhibitor. When the instant polypeptides are expressed as fusion proteins, the purification protocol may include the use of an affinity resin which is specific for the fusion protein tag attached to the expressed enzyme or an affinity resin containing ligands which are specific for the enzyme. For example, the instant polypeptides may be expressed as a fusion protein coupled to the C-terminus of thioredoxin. In addition, a (His)₆ peptide may be engineered into the N-terminus of the fused thioredoxin moiety to afford additional opportunities for affinity purification. Other suitable affinity resins could be synthesized by linking the appropriate ligands to any suitable resin such as Sepharose-4B. In an alternate embodiment, a thioredoxin fusion protein may be eluted using dithiothreitol; however, elution may be accomplished using other reagents which interact to displace the thioredoxin from the resin. These reagents include β -mercaptoethanol or other reduced thiol. The eluted fusion protein may be subjected to further purification by traditional means as stated above, if desired. Proteolytic cleavage of the thioredoxin fusion protein and the enzyme may be accomplished after the fusion protein is purified or while the protein is still bound to the ThioBond™ affinity resin or other resin.

Crude, partially purified or purified enzyme, either alone or as a fusion protein, may be utilized in assays for the evaluation of compounds for their ability to inhibit enzymatic activation of the auxin transport proteins disclosed herein. Assays may be conducted under well known experimental conditions which permit optimal enzymatic activity. For example, assays for auxin transport proteins are presented by Chen, R. et al., (1998) *Proc. Natl. Acad. Sci. USA* 95:15112-15117.

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 50 55 60
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 65 70 75 80
 Met Val Leu Ala Met Leu Thr Ala Trp Ser His Leu Ser Arg Arg Gly
 85 90 95
 Ser Leu Glu Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asp Phe
 115 120 125

Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp
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 Tyr Thr Leu Met Leu Phe Met Phe Glu Tyr Arg Gly Ala Arg Met Leu
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 Ile Thr Glu Gln Phe Pro Asp Asn Ala Gly Ala Ile Ala Ser Ile Val
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 Val Asp Pro Asp Val Val Ser Leu Asp Gly Arg Arg Asp Ala Ile Glu
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 Thr Glu Ala Glu Val Lys Glu Asp Gly Arg Ile His Val Thr Val Arg
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 Arg Ser Asn Ala Ser Arg Ser Asp Ile Tyr Ser Arg Arg Ser Met Gly
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 Tyr Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe
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 Ala Ala Asp Ala Phe Gly Ile Arg Thr Gly Ala Thr Pro Arg Pro Ser
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 Ala Val Ala Ala Ala Pro Lys Gly Ala Arg Lys Ala Ala Thr Asn Gly
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Xaa Xaa Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45

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

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

Ala Val Leu Ala Leu Leu Ala Leu Xaa Ser Xaa Ala Ala Ser Ser Xaa
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Arg Xaa Arg Ser Gly Leu Asp Trp Ser Ile Lys Leu Xaa Xaa Leu Ser
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<212> DNA

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 <213> Zea mays

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 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
 50 55 60
 Phe Ala Met Asn Leu Arg Phe Leu Ala Ala Asp Thr Leu Gln Lys Val
 65 70 75 80
 Ala Val Leu Ala Leu Leu Ala Leu Ala Ser Arg Gly Leu Ser Ser Pro
 85 90 95
 Arg Ala Leu Gly Leu Asp Trp Ser Ile Thr Leu Phe Ser Leu Ser Thr
 100 105 110
 Leu Pro Asn Thr Leu Val Met Gly Ile Pro Leu Leu Arg Gly Met Tyr
 115 120 125
 Gly Ala Ser Ser Ala Gly Thr Leu Met Val Gln Val Val Val Leu Gln
 130 135 140
 Cys Ile Ile Trp Tyr Thr Leu Met Leu Phe Leu Phe Glu Tyr Arg Ala
 145 150 155 160

Ala	Arg	Ala	Leu	Val	Leu	Asp	Gln	Phe	Pro	Asp	Gly	Ala	Ala	Ala	Ser	165	170	175
Ile	Val	Ser	Phe	Arg	Val	Asp	Ser	Asp	Val	Val	Ser	Leu	Ala	Arg	Gly	180	185	190
Asp	Val	Glu	Leu	Glu	Ala	Glu	Pro	Asp	Gly	Val	Ala	Gly	Ala	Gly	Ala	195	200	205
Val	Ser	Ser	Arg	Gly	Gly	Asp	Ala	Gly	Arg	Val	Arg	Val	Thr	Val	Arg	210	215	220
Lys	Ser	Thr	Ser	Ser	Arg	Ser	Glu	Ala	Ala	Cys	Ser	His	Ser	His	Ser	225	230	235
Gln	Thr	Met	Gln	Pro	Arg	Val	Ser	Asn	Leu	Ser	Gly	Val	Glu	Ile	Tyr	245	250	255
Ser	Leu	Gln	Ser	Ser	Arg	Asn	Pro	Thr	Pro	Arg	Gly	Ser	Ser	Phe	Asn	260	265	270
His	Ala	Asp	Phe	Phe	Asn	Ile	Val	Gly	Ala	Ala	Ala	Lys	Gly	Gly	Gly	275	280	285
Gly	Ala	Ala	Gly	Asp	Glu	Glu	Lys	Gly	Ala	Cys	Gly	Gly	Gly	Gly	Gly	290	295	300
Gly	His	Ser	Pro	Gln	Pro	Gln	Ala	Val	Ala	Val	Pro	Ala	Lys	Arg	Lys	305	310	315
Asp	Leu	His	Met	Leu	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser	Glu	325	330	335
Arg	Ala	Ala	Val	His	Val	Phe	Gly	Ala	Gly	Gly	Ala	Asp	His	Ala	Asp	340	345	350
Val	Leu	Ala	Lys	Gly	Ala	Gln	Ala	Tyr	Asp	Glu	Tyr	Gly	Arg	Asp	Asp	355	360	365
Tyr	Ser	Ser	Arg	Thr	Lys	Asn	Gly	Ser	Gly	Gly	Ala	Asp	Lys	Gly	Gly	370	375	380
Pro	Thr	Leu	Ser	Lys	Leu	Gly	Ser	Asn	Ser	Thr	Ala	Gln	Leu	Tyr	Pro	385	390	395
Lys	Asp	Asp	Gly	Glu	Gly	Arg	Ala	Ala	Ala	Val	Ala	Met	Pro	Pro	Ala	405	410	415
Ser	Val	Met	Thr	Arg	Leu	Ile	Leu	Ile	Met	Val	Trp	Arg	Lys	Leu	Ile	420	425	430
Arg	Asn	Pro	Asn	Thr	Tyr	Ser	Ser	Leu	Ile	Gly	Val	Val	Trp	Ser	Leu	435	440	445
Val	Ser	Tyr	Arg	Trp	Gly	Ile	Glu	Met	Pro	Ala	Ile	Ile	Ala	Arg	Ser	450	455	460
Ile	Ser	Ile	Leu	Ser	Asp	Ala	Gly	Leu	Gly	Met	Ala	Met	Phe	Ser	Leu	465	470	475

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 35 40 45

Met Ser Met Phe Ser Met Gly Leu Phe Met Gly Gln Gln Glu Arg Val
 50 55 60

Ile Ala Cys Gly Ala Gly Leu Thr Ala Leu Gly Met Ala Leu Arg Phe
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Val Ala Gly Pro Leu Ala Thr Leu Val Gly Ala Ala Ala Leu Gly Leu
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Arg Gly Asp Val Leu His Leu Ala Ile Ile Gln Xaa Xaa Leu
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Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
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Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala
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 <212> DNA
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<211> 589

<212> PRT

<213> Oryza sativa

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35 40 45

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

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

Gly Ala Pro Arg Leu Asp Trp Ser Ile Thr Leu Phe Ser Leu Ser Thr
100 105 110

Leu Pro Asn Thr Leu Val Met Gly Ile Pro Leu Leu Ile Ala Met Tyr
115 120 125

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Arg	Met	Leu	Ile	Ala	Asp	Gln	Phe	Pro	Asp	Thr	Ala	Ala	Ser	Ile	Val
				165					170					175	
Ser	Leu	His	Val	Asp	Pro	Asp	Val	Val	Ser	Leu	Glu	Gly	Gly	His	Ala
			180					185					190		
Glu	Thr	Glu	Ala	Glu	Val	Ala	Ala	Asp	Gly	Arg	Leu	His	Val	Thr	Val
		195					200					205			
Arg	Arg	Ser	Ser	Val	Ser	Arg	Arg	Ser	Leu	Leu	Val	Thr	Pro	Arg	Pro
	210					215					220				
Ser	Asn	Leu	Thr	Gly	Ala	Glu	Ile	Tyr	Ser	Leu	Ser	Ser	Ser	Arg	Asn
225					230					235					240
Pro	Thr	Pro	Arg	Gly	Ser	Asn	Phe	Asn	His	Ala	Asp	Phe	Phe	Ala	Met
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Val	Gly	Gly	Gly	Pro	Pro	Pro	Pro	Thr	Pro	Ala	Ala	Val	Arg	Gly	Ser
			260					265					270		
Ser	Phe	Gly	Ala	Ser	Glu	Leu	Tyr	Ser	Leu	Gln	Ser	Ser	Arg	Gly	Pro
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His	Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser	Glu	Val	Ser
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Gly	Leu	Pro	Val	Phe	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Leu	Asp	Val
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Gly	Ala	Lys	Glu	Ile	His	Met	Val	Ile	Pro	Ala	Asp	Leu	Pro	Gln	Asn
		355					360					365			
Asn	Gly	Ser	Gly	Lys	Glu	His	Glu	Glu	Tyr	Gly	Ala	Val	Ala	Leu	Gly
	370					375					380				
Gly	Gly	Gly	Gly	Gly	Glu	Asn	Phe	Ser	Phe	Gly	Gly	Gly	Lys	Thr	Val
385					390					395					400
Asp	Gly	Ala	Glu	Ala	Val	Asp	Glu	Glu	Ala	Ala	Leu	Pro	Asp	Gly	Leu
				405					410					415	
Thr	Lys	Met	Gly	Ser	Ser	Ser	Thr	Ala	Glu	Leu	His	Pro	Lys	Val	Val
			420					425					430		
Asp	Val	Asp	Gly	Pro	Asn	Ala	Gly	Gly	Gly	Ala	Ala	Gly	Ala	Gly	Gln
		435					440					445			

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Tyr Gln Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met
 450 455 460
 Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Leu
 465 470 475 480
 Gly Leu Ala Trp Ser Leu Val Ala Phe Arg Leu Phe Met Ala Leu Gln
 485 490 495
 Pro Ser Ile Ile Ala Cys Gly Lys Ser Ala Ala Val Val Ser Met Ala
 500 505 510
 Val Arg Phe Leu Ala Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala
 515 520 525
 Ile Gly Leu Arg Gly Thr Leu Leu His Val Ala Ile Val Gln Ala Ala
 530 535 540
 Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val
 545 550 555 560
 His Pro Ala Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala
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 Leu Pro Ile Thr Leu Leu Tyr Tyr Ile Leu Leu Gly Leu
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<210> 21
 <211> 1618
 <212> DNA
 <213> Glycine max

<400> 21
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 aagaggacgg caagctccac gtcactgtca gaaaatccaa cgcttccaga tccgacatct 180
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 aatatgatca taaagaactc aagttaactg tatctccagg aaaagtggag ggtaatatta 720
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<210> 22
 <211> 443
 <212> PRT
 <213> Glycine max

<400> 22

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Thr	Asp	Ala	Gln	Ile	Lys	Glu	Asp	Gly	Lys	Leu	His	Val	Thr	Val	Arg
		35					40					45			
Lys	Ser	Asn	Ala	Ser	Arg	Ser	Asp	Ile	Phe	Ser	Arg	Arg	Ser	Gln	Gly
	50					55					60				
Phe	Ser	Ser	Thr	Thr	Pro	Arg	Pro	Ser	Asn	Leu	Thr	Asn	Ala	Glu	Ile
65					70					75					80
Tyr	Ser	Leu	Gln	Ser	Ser	Arg	Asn	Pro	Thr	Pro	Arg	Gly	Ser	Ser	Phe
				85					90					95	
Asn	His	Thr	Asp	Phe	Tyr	Ser	Met	Met	Ala	Ala	Gly	Arg	Asn	Ser	Asn
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Phe	Gly	Ala	Asn	Asp	Val	Tyr	Gly	Leu	Ser	Ala	Ser	Arg	Gly	Pro	Thr
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	210				215						220				
Lys	Leu	Thr	Val	Ser	Pro	Gly	Lys	Val	Glu	Gly	Asn	Ile	Asn	Arg	Asp
225					230					235					240
Thr	Gln	Glu	Glu	Tyr	Gln	Pro	Glu	Lys	Asp	Glu	Phe	Ser	Phe	Gly	Asn
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Arg	Gly	Ile	Glu	Asp	Glu	His	Glu	Gly	Glu	Lys	Val	Gly	Asn	Gly	Asn
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Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu
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Ile Gly Leu Thr Trp Ser Leu Ile Ser Phe Arg Trp Asn Val Lys Met
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Pro Ala Ile Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu
325 330 335

Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg
340 345 350

Ile Ile Ala Cys Gly Asn Ser Thr Ala Ala Phe Ser Met Ala Val Arg
355 360 365

Phe Leu Thr Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala Val Gly
370 375 380

Leu Lys Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro
385 390 395 400

Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro
405 410 415

Asp Ile Leu Ser Thr Gly Val Ile Phe Gly Met Leu Ile Ala Leu Pro
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Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu
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<210> 23
<211> 531
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (530)

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tcttctcacc ggaccagtgc tccggcataa accgcttcgt ggcgatcttc gccgtgccgc 420
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<210> 24
<211> 90
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (33)

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<220>

<221> UNSURE

<222> (78)

<400> 24

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Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Lys
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Xaa Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala
 35 40 45

Ile Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn
 50 55 60

Pro Tyr Ala Met Asn Phe Arg Phe Ile Arg Arg Arg Thr Xaa Thr Ser
 65 70 75 80

Lys Lys Ile Ile Met Leu Phe Ala Leu Ala
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<210> 25

<211> 2101

<212> DNA

<213> Glycine max

<400> 25

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<210> 26
 <211> 540
 <212> PRT
 <213> Glycine max

<400> 26
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 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro
 50 55 60
 Tyr Ala Met Asn Phe Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Ile
 65 70 75 80
 Ile Met Leu Phe Ala Leu Ala Ile Trp Thr Asn Leu Thr Lys Thr Gly
 85 90 95
 Ser Leu Glu Trp Met Ile Thr Ile Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Ile Ala Met Tyr Gly Asp Tyr
 115 120 125
 Ser Gly Ser Leu Met Val Gln Val Val Val Leu Gln Cys Ile Ile Trp
 130 135 140
 Tyr Thr Leu Leu Leu Phe Leu Phe Glu Tyr Arg Ala Ala Lys Ile Leu
 145 150 155 160
 Ile Met Glu Gln Phe Pro Glu Thr Ala Ala Ser Ile Val Ser Phe Lys
 165 170 175
 Val Asp Ser Asp Val Val Ser Leu Asp Gly Arg Asp Phe Leu Glu Thr
 180 185 190
 Asp Ala Glu Val Gly Asp Asp Gly Lys Leu His Val Thr Val Arg Lys
 195 200 205
 Ser Asn Ala Ser Arg Arg Ser Phe Met Met Thr Pro Arg Pro Ser Asn
 210 215 220
 Leu Thr Gly Ala Glu Ile Tyr Ser Leu Ser Ser Ser Arg Asn Pro Thr
 225 230 235 240
 Pro Arg Gly Ser Asn Phe Asn His Ala Asp Phe Phe Ser Met Met Gly
 245 250 255

Tyr Gln Pro Arg His Ser Asn Phe Thr Ala Asn Asp Leu Phe Ser Ser
 260 265 270
 Arg Gly Pro Thr Pro Arg Pro Ser Asn Phe Glu Glu Pro Ser Met Pro
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 Gln Ala Val Thr Val Ala Ser Pro Arg Phe Gly Phe Tyr Pro Ser Gln
 290 295 300
 Thr Val Pro Ala Ser Tyr Pro Pro Pro Asn Pro Asp Phe Ser Ser Ala
 305 310 315 320
 Thr Lys Asn Leu Lys Asn Gln Ser Gln Asn Gln Asn Pro Asn Gln Ser
 325 330 335
 Gln Ser Gln Asn Ser Gln Ala Pro Ala Lys Gly Ala His Asp Ala Lys
 340 345 350
 Glu Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Met Ser Glu
 355 360 365
 Asn Ala Gly Leu Asn Val Phe Ser Ser Thr Asp Leu Gly Thr Ser Glu
 370 375 380
 Gln Pro Asp Gln Gly Ala Lys Glu Ile Arg Met Leu Val Ala Asp Asn
 385 390 395 400
 Asn Ala His Leu Arg Asn Gly Glu Ala Asn Asn Lys Gly Gly Leu Glu
 405 410 415
 Ala Val Leu Gly Val Glu Asp Phe Lys Phe Leu Val Asn Gly Glu Glu
 420 425 430
 Gln Val Gly Glu Glu Lys Glu Gly Leu Asn Asn Gly Leu Asn Lys Leu
 435 440 445
 Gly Ser Ser Ser Thr Val Glu Leu Gln Pro Lys Ala Thr Val Ala Gly
 450 455 460
 Glu Ala Ser Ala Gly Lys His Met Pro Pro Ala Asn Val Met Thr Arg
 465 470 475 480
 Leu Ile Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr
 485 490 495
 Tyr Ser Ser Leu Ile Gly Val Val Trp Ser Leu Val Ala Phe Arg Trp
 500 505 510
 His Val His Met Pro Lys Ile Ile Glu Lys Ser Ile Ser Ile Leu Ser
 515 520 525
 Asp Ala Gly Leu Gly Met Ala Met Phe Ser Leu Gly
 530 535 540

<210> 27
 <211> 525
 <212> DNA
 <213> Glycine max

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<400> 27
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<210> 28
 <211> 64
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (38)

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 Ile Phe Ser Pro Asp Xaa Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ser Asn Asn Pro
 50 55 60

<210> 29
 <211> 2549
 <212> DNA
 <213> Glycine max

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<210> 30
 <211> 605
 <212> PRT
 <213> Glycine max

<400> 30

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Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Lys
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Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ser Asn Asn Pro
 50 55 60

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

Ile Ile Leu Val Leu Leu Ala Val Trp Ser Asn Ile Thr Lys Arg Gly
 85 90 95

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

Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asp Phe
 115 120 125

Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp
 130 135 140

Tyr Thr Leu Met Leu Phe Leu Phe Glu Phe Arg Gly Ala Arg Met Leu
 145 150 155 160

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Ile	Ser	Glu	Gln	Phe	Pro	Asp	Thr	Ala	Ala	Ser	Ile	Val	Ser	Ile	His			
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Val	Asp	Ser	Asp	Val	Met	Ser	Leu	Asp	Gly	Arg	Gln	Pro	Leu	Glu	Thr			
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Glu	Ala	Glu	Ile	Lys	Glu	Asp	Gly	Lys	Leu	His	Val	Thr	Val	Arg	Lys			
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Ser	Asn	Ala	Ser	Arg	Ser	Asp	Ile	Phe	Ser	Arg	Arg	Ser	Gln	Gly	Leu			
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Ser	Ser	Thr	Thr	Pro	Arg	Pro	Ser	Asn	Leu	Thr	Asn	Ala	Glu	Ile	Tyr			
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Ser	Leu	Gln	Ser	Ser	Arg	Asn	Pro	Thr	Pro	Arg	Gly	Ser	Ser	Phe	Asn			
				245					250					255				
His	Thr	Asp	Phe	Tyr	Ser	Met	Met	Ala	Ala	Gly	Gly	Arg	Asn	Ser	Asn			
			260					265					270					
Phe	Gly	Ala	Ser	Asp	Val	Tyr	Gly	Leu	Ser	Ala	Ser	Arg	Gly	Pro	Thr			
		275					280					285						
Pro	Arg	Pro	Ser	Asn	Tyr	Asp	Glu	Asp	Gly	Gly	Lys	Pro	Lys	Phe	His			
	290					295					300							
Tyr	His	Ala	Ala	Gly	Gly	Thr	Gly	His	Tyr	Pro	Ala	Pro	Asn	Pro	Gly			
305					310					315					320			
Met	Phe	Ser	Pro	Ser	Asn	Gly	Ser	Lys	Ser	Val	Ala	Ala	Asn	Ala	Asn			
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Ala	Lys	Arg	Pro	Asn	Gly	Gln	Ala	Gln	Leu	Lys	Pro	Glu	Asp	Gly	Asn			
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Arg	Asp	Leu	His	Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser			
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Asp	Val	Phe	Gly	Ala	His	Glu	Tyr	Gly	Gly	Gly	His	Asp	Gln	Lys	Glu			
	370					375					380							
Val	Lys	Leu	Asn	Val	Ser	Pro	Gly	Lys	Val	Glu	Asn	Asn	His	Arg	Asp			
385					390					395					400			
Thr	Gln	Glu	Asp	Tyr	Leu	Glu	Lys	Asp	Glu	Phe	Ser	Phe	Gly	Asn	Arg			
				405					410					415				
Glu	Met	Asp	Arg	Glu	Met	Asn	Gln	Leu	Glu	Gly	Glu	Lys	Val	Gly	Asp			
			420					425					430					
Gly	Lys	Pro	Lys	Thr	Met	Pro	Pro	Ala	Ser	Val	Met	Thr	Arg	Leu	Ile			
		435				440						445						
Leu	Ile	Met	Val	Trp	Arg	Lys	Leu	Ile	Arg	Asn	Pro	Asn	Thr	Tyr	Ser			
	450					455					460							
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PCT/US00/12061

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<222> (64)

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 20 25 30

Lys Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala
 35 40 45

Val Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Xaa
 50 55 60

Pro Tyr Ala Met Asn Tyr His Phe Ile Ala Ala Asp Cys Leu Gln Lys
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Val Val Ile Leu

<210> 33

<211> 2324

<212> DNA

<213> Glycine max

<400> 33

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gatatttatg atgttttcgc ggctattgtg cccctctacg ttgctatgat attagcatac 240
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gttgctgtgt tcgcagttcc acttctttct ttccacttca tctcctccaa tgacccttat 360
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 <211> 637
 <212> PRT
 <213> Glycine max

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 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Val
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Asp Pro
 50 55 60
 Tyr Ala Met Asn Tyr His Phe Ile Ala Ala Asp Cys Leu Gln Lys Val
 65 70 75 80
 Val Ile Leu Gly Ala Leu Phe Leu Trp Asn Thr Phe Thr Lys His Gly
 85 90 95
 Ser Leu Asp Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Lys Ala Met Tyr Gly Asp Phe
 115 120 125
 Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Ser Val Ile Trp
 130 135 140
 Tyr Thr Leu Met Leu Phe Met Phe Glu Tyr Arg Gly Ala Lys Leu Leu
 145 150 155 160
 Ile Thr Glu Gln Phe Pro Glu Thr Ala Gly Ser Ile Thr Ser Phe Arg
 165 170 175
 Val Asp Ser Asp Val Val Ser Leu Asn Gly Arg Glu Pro Leu Gln Thr
 180 185 190
 Asp Ala Glu Ile Gly Glu Asp Gly Lys Leu His Val Val Val Lys Arg
 195 200 205
 Ser Ala Ala Ser Ser Met Ile Ser Ser Phe Asn Lys Ser His Leu Thr
 210 215 220

Ser	Met	Thr	Pro	Arg	Ala	Ser	Asn	Leu	Thr	Gly	Val	Glu	Ile	Tyr	Ser	
225					230					235					240	
Val	Gln	Ser	Ser	Arg	Glu	Pro	Thr	Pro	Arg	Gly	Ser	Ser	Phe	Asn	Gln	
				245					250					255		
Thr	Asp	Phe	Tyr	Ala	Met	Phe	Ala	Ser	Lys	Ala	Pro	Ser	Pro	Lys	His	
			260					265					270			
Gly	Tyr	Thr	Asn	Ser	Phe	Gln	Ser	Asn	Asn	Gly	Gly	Ile	Gly	Asp	Val	
		275					280					285				
Tyr	Ser	Leu	Gln	Ser	Ser	Lys	Gly	Ala	Thr	Pro	Arg	Thr	Ser	Asn	Phe	
	290					295					300					
Glu	Glu	Glu	Met	Leu	Lys	Met	His	Lys	Lys	Arg	Gly	Gly	Arg	Ser	Met	
305					310					315					320	
Ser	Gly	Glu	Leu	Phe	Asn	Gly	Gly	Leu	Val	Ser	Ser	Asn	Tyr	Pro	Pro	
				325					330					335		
Pro	Asn	Pro	Met	Phe	Ser	Gly	Ser	Thr	Ser	Ala	Ala	Gly	Gly	Pro	Lys	
			340					345					350			
Lys	Lys	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Ala	Val	Ala	Pro	Asn	Lys	Glu	
		355					360					365				
Leu	His	Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser	Glu	Gly	
	370					375					380					
Asn	Leu	Arg	His	Ala	Val	Asn	Arg	Ala	Ala	Ser	Thr	Asp	Phe	Gly	Thr	
385					390					395					400	
Val	Asp	Pro	Ser	Lys	Ala	Val	Pro	His	Glu	Thr	Val	Ala	Ser	Lys	Ala	
				405					410					415		
Val	His	Glu	Leu	Ile	Glu	Asn	Met	Ser	Pro	Gly	Arg	Arg	Gly	Ser	Gly	
			420					425					430			
Glu	Arg	Glu	Pro	Glu	Met	Asp	Glu	Gly	Ala	Lys	Ile	Pro	Ala	Ser	Gly	
	435						440					445				
Ser	Pro	Tyr	Thr	Cys	Gln	Lys	Lys	Val	Asp	Met	Glu	Asp	Gly	Asn	Ala	
	450					455					460					
Asn	Lys	Asn	Gln	Gln	Met	Pro	Pro	Ala	Ser	Val	Met	Thr	Arg	Leu	Ile	
465					470					475					480	
Leu	Ile	Met	Val	Trp	Arg	Lys	Leu	Ile	Arg	Asn	Pro	Asn	Thr	Tyr	Ser	
				485					490					495		
Ser	Leu	Leu	Gly	Leu	Thr	Trp	Ser	Leu	Ile	Ser	Phe	Arg	Trp	His	Ile	
			500					505					510			
Glu	Met	Pro	Thr	Ile	Val	Lys	Gly	Ser	Ile	Ser	Ile	Leu	Ser	Asp	Ala	
		515					520					525				
Gly	Leu	Gly	Met	Ala	Met	Phe	Ser	Leu	Gly	Leu	Phe	Met	Ala	Leu	Gln	
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Pro Lys Ile Ile Ala Cys Gly Lys Ser Val Ala Ala Phe Ser Met Ala
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 Val Arg Phe Leu Thr Gly Pro Ala Val Ile Ala Ala Thr Ser Ile Gly
 565 570 575
 Ile Gly Leu Arg Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala
 580 585 590
 Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Leu
 595 600 605
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 Leu Pro Ile Thr Ile Leu Tyr Tyr Val Leu Leu Gly Val
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PCT/US00/12061

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<400> 35

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gncatgttca tggcgtacgg gtcggtgcgg tgggtggggca tcttcacgcc ggaccantgc 180
tcgggcatca aacgcttcgt ngccgtcttc gcggtggcgc tcctctcctt ccacttcac 240
tccaccaacg aaccctacgc catggactaa cgcttccttg gcgccgactc gctgcanaan 300
ntcgttatcc tcgccgncct cgccgtgtgg ganaangtgc tctcccncca acggtgcccn 360

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ggggganaga aggcggcgaa ggctcctcnc tgggctggga caacanactc ttctccttgg 420
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 <213> Triticum aestivum

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 20 25 30
 Ile Phe Thr Pro Asp Xaa Cys Ser Gly Ile Lys Arg Phe Val Ala Val
 35 40 45
 Phe Ala Val Ala Leu Leu Ser Phe His Phe Ile Ser Thr Asn Glu Pro
 50 55 60
 Tyr Ala Met Asp Xaa Arg Phe Leu Gly Ala Asp Ser Leu Xaa Xaa Xaa
 65 70 75 80
 Val Ile Leu Ala Xaa Leu Ala Val Trp
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<210> 37
 <211> 2293
 <212> DNA
 <213> Triticum aestivum

<400> 37

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<210> 38

<211> 632

<212> PRT

<213> *Triticum aestivum*

<400> 38

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          20             25             30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Val
          35             40             45

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

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Tyr Ala Met Asp Tyr Arg Phe Leu Ala Ala Asp Ser Leu Gln Lys Leu
 65 70 75 80
 Val Ile Leu Ala Ala Leu Ala Val Trp His Asn Val Leu Ser Arg Tyr
 85 90 95
 Arg Cys Arg Gly Gly Thr Glu Ala Gly Glu Ala Ser Ser Leu Asp Trp
 100 105 110
 Thr Ile Thr Leu Phe Ser Leu Ala Thr Leu Pro Asn Thr Leu Val Met
 115 120 125
 Gly Ile Pro Leu Leu Arg Ala Met Tyr Gly Asp Phe Ser Gly Ser Leu
 130 135 140
 Met Val Gln Ile Val Val Leu Gln Ser Val Ile Trp Tyr Thr Leu Met
 145 150 155 160
 Leu Phe Leu Phe Glu Tyr Arg Gly Ala Lys Ala Leu Ile Ser Glu Gln
 165 170 175
 Phe Pro Pro Asp Val Gly Ala Ser Ile Ala Ser Phe Arg Val Asp Ser
 180 185 190
 Asp Val Val Ser Leu Asn Gly Arg Glu Ala Leu His Ala Asp Ala Glu
 195 200 205
 Val Gly Arg Asp Gly Arg Val His Val Val Ile Arg Arg Ser Ala Ser
 210 215 220
 Gly Ser Thr Thr Gly Gly His Gly Ala Gly Arg Ser Gly Ile Tyr Arg
 225 230 235 240
 Gly Ala Ser Asn Ala Met Thr Pro Arg Ala Ser Asn Leu Thr Gly Val
 245 250 255
 Glu Ile Tyr Ser Leu Gln Thr Ser Arg Glu Pro Thr Pro Arg Gln Ser
 260 265 270
 Ser Phe Asn Gln Ser Asp Phe Tyr Ser Met Phe Asn Gly Ser Lys Leu
 275 280 285
 Ala Ser Pro Lys Gly Gln Pro Pro Val Ala Gly Gly Gly Gly Ala Arg
 290 295 300
 Gly Gln Gly Leu Asp Glu Gln Val Ala Asn Lys Phe Lys Gly Gly Glu
 305 310 315 320
 Ala Ala Ala Pro Tyr Pro Ala Pro Asn Pro Gly Met Met Met Pro Ala
 325 330 335
 Pro Arg Lys Lys Glu Leu Gly Gly Ser Asn Ser Asn Ser Asp Lys Glu
 340 345 350
 Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Ala
 355 360 365
 Asn Leu Arg Asn Ala Val Asn His Ala Ala Ser Thr Asp Phe Ala Ala
 370 375 380

Ala Pro Pro Ala Ala Ala Thr Pro Arg Asp Gly Ala Thr Pro Arg Gly
 385 390 395 400
 Val Ser Gly Ser Val Thr Pro Val Met Lys Lys Asp Ala Ser Ser Gly
 405 410 415
 Ala Val Glu Val Glu Ile Glu Asp Gly Met Met Lys Ser Pro Ala Thr
 420 425 430
 Gly Leu Gly Ala Lys Phe Pro Val Ser Gly Ser Pro Tyr Val Ala Pro
 435 440 445
 Arg Lys Lys Gly Ala Asp Val Pro Gly Leu Glu Glu Ala Ala His Pro
 450 455 460
 Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp
 465 470 475 480
 Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Ile Gly Leu
 485 490 495
 Val Trp Ser Leu Val Ser Phe Arg Trp Asn Ile Gln Met Pro Thr Ile
 500 505 510
 Ile Lys Gly Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala
 515 520 525
 Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Lys Ile Ile Ser
 530 535 540
 Cys Gly Lys Ser Val Ala Thr Phe Ala Met Ala Val Arg Phe Leu Thr
 545 550 555 560
 Gly Pro Ala Val Ile Ala Ala Thr Ser Ile Ala Val Gly Leu Arg Gly
 565 570 575
 Val Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile
 580 585 590
 Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Cys His Pro Gln Ile Leu
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tgggcgcgct gcgccaaggc caaggccggc gcctactcgt ggtcatcacg gggttctccc 360
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<212> PRT

<213> Triticum aestivum

<400> 40

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Phe Phe Thr Ala Glu Gln Cys Gly Ala Ile Asn Thr Leu Val Val Cys
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Phe Ser Met Pro Phe Phe Thr Phe Asp Phe Val Val Arg Ala Asp Pro
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Tyr Ala Met Asn Tyr Arg Val Ile Ala Ala Asp Ala Val Ala Lys Leu
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<212> DNA

<213> Triticum aestivum

<400> 41

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cgggcaagat gatcacgggc acggacttct accacgtgat gacggcggtg gtgccgctgt 180

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 tcatctccac caacaacccc tacaccatga acctgcgctt catcgccgcc gacacgctgc 360
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 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro
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 <212> PRT
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 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Asp Pro
 50 55 60
 Tyr Ala Met Asn Tyr His Phe Leu Ala Ala Asp Ser Leu Gln Lys Val
 65 70 75 80
 Val Ile Leu Ala Ala Leu Phe Leu Trp Gln Ala Phe Ser Arg Arg Gly
 85 90 95
 Ser Leu Glu Trp Met Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Arg Ala Met Tyr Gly Asp Phe
 115 120 125

Ser	Gly	Asn	Leu	Met	Val	Gln	Ile	Val	Val	Leu	Gln	Ser	Ile	Ile	Trp
	130					135					140				
Tyr	Thr	Leu	Met	Leu	Phe	Leu	Phe	Glu	Phe	Arg	Gly	Ala	Lys	Leu	Leu
145					150					155					160
Ile	Ser	Glu	Gln	Phe	Pro	Glu	Thr	Ala	Gly	Ser	Ile	Thr	Ser	Phe	Arg
				165					170					175	
Val	Asp	Ser	Asp	Val	Ile	Ser	Leu	Asn	Gly	Arg	Glu	Pro	Leu	Gln	Thr
			180					185					190		
Asp	Ala	Glu	Ile	Gly	Asp	Asp	Gly	Lys	Leu	His	Val	Val	Val	Arg	Arg
		195					200					205			
Ser	Ser	Ala	Ala	Ser	Ser	Met	Ile	Ser	Ser	Phe	Asn	Lys	Ser	His	Gly
		210				215					220				
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225					230					235					240
Gly	Val	Glu	Ile	Tyr	Ser	Val	Gln	Ser	Ser	Arg	Glu	Pro	Thr	Pro	Arg
				245					250					255	
Ala	Ser	Ser	Phe	Asn	Gln	Thr	Asp	Phe	Tyr	Ala	Met	Phe	Asn	Ala	Ser
			260					265					270		
Lys	Ala	Pro	Ser	Pro	Arg	His	Gly	Tyr	Thr	Asn	Ser	Tyr	Gly	Gly	Ala
		275					280					285			
Gly	Ala	Gly	Pro	Gly	Gly	Asp	Val	Tyr	Ser	Leu	Gln	Ser	Ser	Lys	Gly
	290					295					300				
Val	Thr	Pro	Arg	Thr	Ser	Asn	Phe	Asp	Glu	Glu	Val	Met	Lys	Thr	Ala
305					310					315					320
Lys	Lys	Ala	Gly	Arg	Gly	Gly	Arg	Ser	Met	Ser	Gly	Glu	Leu	Tyr	Asn
				325					330					335	
Asn	Asn	Ser	Val	Pro	Ser	Tyr	Pro	Pro	Pro	Asn	Pro	Met	Phe	Thr	Gly
			340					345					350		
Ser	Thr	Ser	Gly	Ala	Ser	Gly	Val	Lys	Lys	Lys	Glu	Ser	Gly	Gly	Gly
		355					360					365			
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	370					375					380				
Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser	Glu	Ala	Asn	Ala
385					390					395					400
Lys	Asn	Ala	Met	Thr	Arg	Gly	Ser	Ser	Thr	Asp	Val	Ser	Thr	Asp	Pro
				405					410					415	
Lys	Val	Ser	Ile	Pro	Pro	His	Asp	Asn	Leu	Ala	Thr	Lys	Ala	Met	Gln
			420					425					430		
Asn	Leu	Ile	Glu	Asn	Met	Ser	Pro	Gly	Arg	Lys	Gly	His	Val	Glu	Met
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Asp Gln Asp Gly Asn Asn Gly Gly Lys Ser Pro Tyr Met Gly Lys Lys
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 Gly Ser Asp Val Glu Asp Gly Gly Pro Gly Pro Arg Lys Gln Gln Met
 465 470 475 480
 Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp Arg
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 Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Phe Gly Leu Ala
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 Trp Ser Leu Val Ser Phe Lys Trp Asn Ile Lys Met Pro Thr Ile Met
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 Ser Gly Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala Met
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 Gly Lys Ser Val Ala Gly Phe Ala Met Ala Val Arg Phe Leu Thr Gly
 565 570 575
 Pro Ala Val Ile Ala Ala Thr Ser Ile Ala Ile Gly Ile Arg Gly Asp
 580 585 590
 Leu Leu His Ile Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile Val
 595 600 605
 Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro Asp Ile Leu Ser
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 <213> Arabidopsis thaliana

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 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ala Asn Asn Pro
 50 55 60
 Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala Asp Ser Leu Gln Lys Val
 65 70 75 80

Ile	Val	Leu	Ser	Leu	Leu	Phe	Leu	Trp	Cys	Lys	Leu	Ser	Arg	Asn	Gly	
				85					90					95		
Ser	Leu	Asp	Trp	Thr	Ile	Thr	Leu	Phe	Ser	Leu	Ser	Thr	Leu	Pro	Asn	
			100					105					110			
Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Lys	Gly	Met	Tyr	Gly	Asn	Phe	
		115					120					125				
Ser	Gly	Asp	Leu	Met	Val	Gln	Ile	Val	Val	Leu	Gln	Cys	Ile	Ile	Trp	
	130					135					140					
Tyr	Ile	Leu	Met	Leu	Phe	Leu	Phe	Glu	Tyr	Arg	Gly	Ala	Lys	Leu	Leu	
145					150					155					160	
Ile	Ser	Glu	Gln	Phe	Pro	Asp	Thr	Ala	Gly	Ser	Ile	Val	Ser	Ile	His	
				165					170					175		
Val	Asp	Ser	Asp	Ile	Met	Ser	Leu	Asp	Gly	Arg	Gln	Pro	Leu	Glu	Thr	
			180					185					190			
Glu	Ala	Glu	Ile	Lys	Glu	Asp	Gly	Lys	Leu	His	Val	Thr	Val	Arg	Arg	
		195					200					205				
Ser	Asn	Ala	Ser	Arg	Ser	Asp	Ile	Tyr	Ser	Arg	Arg	Ser	Gln	Gly	Leu	
	210					215					220					
Ser	Ala	Thr	Pro	Arg	Pro	Ser	Asn	Leu	Thr	Asn	Ala	Glu	Ile	Tyr	Ser	
225					230					235					240	
Leu	Gln	Ser	Ser	Arg	Asn	Pro	Thr	Pro	Arg	Gly	Ser	Ser	Phe	Asn	His	
				245					250					255		
Thr	Asp	Phe	Tyr	Ser	Met	Met	Ala	Ser	Gly	Gly	Gly	Arg	Asn	Ser	Asn	
			260					265					270			
Phe	Gly	Pro	Gly	Glu	Ala	Val	Phe	Gly	Ser	Lys	Gly	Pro	Thr	Pro	Arg	
		275					280					285				
Pro	Ser	Asn	Tyr	Glu	Glu	Asp	Gly	Gly	Pro	Ala	Lys	Pro	Thr	Ala	Ala	
	290					295					300					
Gly	Thr	Ala	Ala	Gly	Ala	Gly	Arg	Phe	His	Tyr	Gln	Ser	Gly	Gly	Ser	
305					310					315					320	
Gly	Gly	Gly	Gly	Gly	Ala	His	Tyr	Pro	Ala	Pro	Asn	Pro	Gly	Met	Phe	
				325					330					335		
Ser	Pro	Asn	Thr	Gly	Gly	Gly	Gly	Gly	Thr	Ala	Ala	Lys	Gly	Asn	Ala	
			340					345					350			
Pro	Val	Val	Gly	Gly	Lys	Arg	Gln	Asp	Gly	Asn	Gly	Arg	Asp	Leu	His	
		355					360					365				
Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser	Asp	Val	Phe	Gly	
	370					375					380					
Gly	Gly	Gly	Gly	Asn	His	His	Ala	Asp	Tyr	Ser	Thr	Ala	Thr	Asn	Asp	
385				390						395					400	

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 420 425 430
 Asp Ser Lys Val Leu Ala Thr Asp Gly Gly Asn Asn Ile Ser Asn Lys
 435 440 445
 Thr Thr Gln Ala Lys Val Met Pro Pro Thr Ser Val Met Thr Arg Leu
 450 455 460
 Ile Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Ser Tyr
 465 470 475 480
 Ser Ser Leu Phe Gly Ile Thr Trp Ser Leu Ile Ser Phe Lys Trp Asn
 485 490 495
 Ile Glu Met Pro Ala Leu Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp
 500 505 510
 Ala Gly Leu Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu
 515 520 525
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 530 535 540
 Ala Met Arg Phe Val Val Gly Pro Ala Val Met Leu Val Ala Ser Tyr
 545 550 555 560
 Ala Val Gly Leu Arg Gly Val Leu Leu His Val Ala Ile Ile Gln Ala
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 Ala Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn
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WO 00/68389

PCT/US00/12061

<212> PRT
 <213> Triticum aestivum

<400> 46

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 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro
 50 55 60

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

Met Met Leu Ala Met Leu Thr Ala Trp Ser His Leu Ser Arg Arg Gly
 85 90 95

<210> 47
 <211> 855
 <212> DNA
 <213> Zea mays

<400> 47

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 gccgagtaca acgac 855

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 <211> 285
 <212> PRT
 <213> Zea mays

<400> 48

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 1 5 10 15

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 20 25 30

Ser Thr Leu Pro Asn Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly
 35 40 45

Met	Tyr	Gly	Asp	Phe	Ser	Gly	Ser	Leu	Met	Val	Gln	Ile	Val	Val	Leu
	50					55					60				
Gln	Cys	Ile	Ile	Trp	Tyr	Thr	Leu	Met	Leu	Phe	Met	Phe	Glu	Tyr	Arg
65					70					75					80
Gly	Ala	Arg	Ile	Leu	Ile	Thr	Glu	Gln	Phe	Pro	Asp	Thr	Ala	Gly	Ala
				85					90					95	
Ile	Ala	Ser	Ile	Val	Val	Asp	Pro	Asp	Val	Val	Ser	Leu	Asp	Gly	Arg
			100					105					110		
Asn	Asp	Ala	Ile	Glu	Thr	Glu	Ala	Glu	Val	Lys	Glu	Asp	Gly	Lys	Ile
		115					120					125			
His	Val	Thr	Val	Arg	Arg	Ser	Asn	Ala	Ser	Arg	Ser	Asp	Ile	Tyr	Ser
	130					135					140				
Arg	Arg	Ser	Met	Gly	Phe	Ser	Ser	Thr	Thr	Pro	Arg	Pro	Ser	Asn	Leu
145					150					155					160
Thr	Asn	Ala	Glu	Ile	Tyr	Ser	Leu	Gln	Ser	Ser	Arg	Asn	Pro	Thr	Pro
				165					170					175	
Arg	Gly	Ser	Ser	Phe	Asn	His	Thr	Asp	Phe	Tyr	Ser	Met	Val	Gly	Arg
			180					185					190		
Ser	Ser	Asn	Phe	Ala	Ala	Gly	Asp	Ala	Phe	Gly	Leu	Arg	Thr	Gly	Ala
		195					200					205			
Thr	Pro	Arg	Pro	Ser	Asn	Tyr	Glu	Glu	Asp	Pro	Gln	Gly	Lys	Ala	Asn
	210					215					220				
Lys	Tyr	Gly	Gln	Tyr	Pro	Ala	Pro	Asn	Pro	Ala	Met	Ala	Ala	Gln	Pro
225					230					235					240
Ala	Lys	Gly	Leu	Lys	Lys	Ala	Ala	Asn	Gly	Gln	Ala	Lys	Gly	Glu	Asp
				245					250					255	
Gly	Lys	Asp	Leu	His	Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val
			260					265					270		
Ser	Asp	Val	Phe	Gly	Asn	Gly	Ala	Ala	Glu	Tyr	Asn	Asp			
		275					280					285			

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - 5 (a) a first nucleotide sequence encoding a polypeptide of at least 30 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:6;
 - (b) a second nucleotide sequence encoding a polypeptide of at least 50 amino
10 acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:16, 28, 36, and 40;
 - (c) a third nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:12;
 - 15 (d) a fourth nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 24;
 - (e) a fifth nucleotide sequence encoding a polypeptide of at least 50 amino
20 acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 32;
 - (f) a sixth nucleotide sequence encoding a polypeptide of at least 90 amino acids that has at least 95% identity based on the Clustal method of
25 alignment when compared to a polypeptide of SEQ ID NO:42;
 - (g) a seventh nucleotide sequence encoding a polypeptide of at least 95 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:46;
 - (h) an eighth nucleotide sequence encoding a polypeptide of at least 100 amino
30 acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:20;
 - (i) a ninth nucleotide sequence encoding a polypeptide of at least 100 amino acids that has at least 90% identity based on the Clustal method of
35 alignment when compared to a polypeptide of SEQ ID NO:2;
 - (j) a tenth nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:4;

- (k) an eleventh nucleotide sequence encoding a polypeptide of at least 300 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:38;
- (l) a twelfth nucleotide sequence encoding a polypeptide of at least 350 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:10;
- (m) a thirteenth nucleotide sequence encoding a polypeptide of at least 400 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22, 26 and 30;
- (n) a fourteenth nucleotide sequence encoding a polypeptide of at least 500 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:34;
- (o) a fifteenth nucleotide sequence encoding a polypeptide of at least 200 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:14;
- (p) a sixteenth nucleotide sequence encoding a polypeptide of at least 250 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:48; and
- (q) a seventeenth nucleotide sequence comprising a complement of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), (m), (n), (o) or (p).

2. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence comprises a nucleic acid sequence 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, 45, and 47 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46, and 48.

3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are DNA.

4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are RNA.

5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to at least one suitable regulatory sequence.

6. A host cell comprising the chimeric gene of Claim 5.

7. A host cell comprising the isolated polynucleotide of Claim 1.

8. The host cell of Claim 7 wherein the host cell is selected from the group consisting of yeast, bacteria, and plant.

9. A virus comprising the isolated polynucleotide of Claim 1.

10. A polypeptide selected from the group consisting of:

- 5 (a) a polypeptide of at least 30 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:6;
- (b) a polypeptide of at least 50 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:16, 28, 36, and 40;
- (c) a polypeptide of at least 50 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:12;
- 10 (d) a polypeptide of at least 50 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 24;
- (e) a polypeptide of at least 50 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 32;
- 15 (f) a polypeptide of at least 90 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:42;
- (g) a polypeptide of at least 95 amino acids having at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:46;
- 20 (h) a polypeptide of at least 100 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:20;
- 25 (i) a polypeptide of at least 100 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2;
- (j) a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:4;
- 30 (k) a polypeptide of at least 300 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:38;
- (l) a polypeptide of at least 350 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:10;
- 35

- (m) a polypeptide of at least 400 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:22, 26 and 30;
- 5 (n) a polypeptide of at least 500 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:34;
- (o) a polypeptide of at least 200 amino acids having at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:14; and
- 10 (p) a polypeptide of at least 250 amino acids having at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:48.

11. A method of selecting an isolated polynucleotide that affects the level of expression of a polypeptide in a plant cell, the method comprising the steps of:

- 15 (a) constructing the isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from the isolated polynucleotide of Claim 1;
- (b) introducing the isolated polynucleotide into the plant cell;
- (c) measuring the level of the polypeptide in the plant cell containing the
- 20 polynucleotide; and
- (d) comparing the level of the polypeptide in the plant cell containing the isolated polynucleotide with the level of the polypeptide in a plant cell that does not contain the isolated polynucleotide.

12. The method of Claim 11 wherein the isolated polynucleotide consists of the

25 nucleotide sequence 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, 45, and 47 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46, and 48.

13. A method of selecting an isolated polynucleotide that affects the level of

30 expression of a polypeptide in a plant cell, the method comprising the steps of:

- (a) constructing the isolated polynucleotide of Claim 1;
- (b) introducing the isolated polynucleotide into the plant cell;
- (c) measuring the level of the polypeptide in the plant cell containing the
- 35 polynucleotide; and
- (d) comparing the level of the polypeptide in the plant cell containing the isolated polynucleotide with the level of the polypeptide in a plant cell that does not contain the polynucleotide.

14. A method of obtaining a nucleic acid fragment encoding a polypeptide comprising the steps of:

- (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and a complement of such nucleotide sequences; and
- (b) amplifying the nucleic acid sequence using the oligonucleotide primer.

15. A method of obtaining a nucleic acid fragment encoding a polypeptide comprising the steps of:

- (a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence 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, 45, and 47 and a complement of such nucleotide sequences;
- (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;
- (c) isolating the identified DNA clone; and
- (d) sequencing a cDNA or genomic fragment that comprises the isolated DNA clone.

16. A method for evaluating at least one compound for its ability to inhibit the activity of a protein, the method comprising the steps of:

- (a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding the polypeptide, operably linked to at least one suitable regulatory sequence;
- (b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the auxin transport protein encoded by the operably linked nucleic acid fragment in the transformed host cell;
- (c) optionally purifying the auxin transport polypeptide expressed by the transformed host cell;
- (d) treating the auxin transport polypeptide with a compound to be tested; and
- (e) comparing the activity of the auxin transport polypeptide that has been treated with the test compound to the activity of an untreated auxin transport polypeptide,

thereby selecting compounds with potential for inhibitory activity.

17. A composition comprising the isolated polynucleotide of Claim 1.

18. A composition comprising the isolated polypeptide of Claim 10.

19. The isolated polynucleotide of Claim 1 comprising a nucleotide sequence having at least one of 30 contiguous nucleotides.
20. A method for positive selection of a transformed cell comprising:
- 5 (a) transforming a host cell with the chimeric gene of Claim 5; and
- (b) growing the transformed host cell under conditions which allow expression of a polynucleotide in an amount sufficient to complement a null mutant to provide a positive selection means.
21. The method of Claim 20 wherein the host cell is a plant.
22. The method of Claim 21 wherein the plant cell is a monocot.
- 10 23. The method of Claim 21 wherein the plant cell is a dicot.
24. A method of modulating expression of a polypeptide for modulating root development in a plant, comprising the steps of:
- (a) stably transforming a plant cell with an auxin transport protein polynucleotide operably linked to a promoter, wherein the polynucleotide is
- 15 in sense or antisense orientation; and
- (b) growing the plant cell under plant growing conditions to produce a regenerated plant capable of expressing the polynucleotide for a time sufficient to modulate root development in the plant.

[illegible]

FIGURE 1 CONTINUED

SEQ ID NO:14	** * **** * *	GAAASIVSFRVDSVSLARGDVELEAEPDGVAGAGAVSSRGGDAGRVRVTVRKSTSSRS	* *
SEQ ID NO:30		DTAASI VSIHVDSVMSLD-GRQPLETEAEI-----KEDGKLHVTVRKSNASRS	
SEQ ID NO:34		ETAGSITSFRVDSVSLN-GREPLQTD AEI-----GEDGKLHVVKRS-AASS	
SEQ ID NO:38		DVGASIASFRVDSVSLN-GREALHADA EV-----GRDGRVHVVI RRSASGST	
SEQ ID NO:43		ETAGSITSFRVDSVISLN-GREPLQTD AEI-----GDDGKLHV VRRSSAASS	
SEQ ID NO:44		DTAGSIVSIHVDSDIMSLD-GRQPLETEAEI-----KEDGKLHVTVRRSNASRS	

181 240

SEQ ID NO:14	** ** *	EAACSHSHSQ-----TMQPRVSNLSGVEIYSLQSSRNPTPRGSSFNHADFFNI VGAA-	*
SEQ ID NO:30		DI---FSRR---SQGLSSTTPRPSNLTNAEIYSLQSSRNPTPRGSSFNHTDFYSMMAAG-	
SEQ ID NO:34		MIS-SFNKSHLTSM-----TPRASNLTGVEIYSVQSSREPTPRGSSFNQTD FYAMF-ASK	
SEQ ID NO:38		TGGHGAGRSGIYRGASNAMTPRASNLTGVEIYSLQTSREPTPRQSSFNQSD FYSMFNGSK	
SEQ ID NO:43		MIS-SFNKSHGGGLNSSMITPRASNLTGVEIYSVQSSREPTPRASSFNQTD FYAMFNASK	
SEQ ID NO:44		DI---YSRR---SQGLSAT-PRPSNLTNAEIYSLQSSRNPTPRGSSFNHTDFYSMMAAG-	

241 300

SEQ ID NO:14	* * *	---AKGG-----GGAAGDE-----	*
SEQ ID NO:30		-----G-RNSNF-----GASD-VYGLSASRGPTPRPSNYDEDGK P--K-----	
SEQ ID NO:34		APSPKHGYTNSFQSNNGGIG-DVYSLQSSKGATPRTSNFEEEM LKMHKK--RGGRSMSGE	
SEQ ID NO:38		LASPKG-----QPPVAGGG-----ARGQLDEQVANK-----	
SEQ ID NO:43		APSPRHGYTNSYGGAGAGPGGDVYSLQSSKGVTPRTSNFDEE VMKTAKKAGRGRSMSGE	
SEQ ID NO:44		-----GGRNSNF-----GPGEAVFG---SKGPTPRPSNYEEDGGPA--KPTAAGTAAGAG	

301 360

FIGURE 1 CONTINUED

SEQ ID NO:14	* * *	* * *	*
SEQ ID NO:30	----	EKGACGGGGHSPQQA	-----VAVPAKRKDLHM
SEQ ID NO:34	----	FHYHA	----AGGTGHPAPNPGMFSPNSGSKSVAANANAKRPNQQAQLKPEDGNRDLHM
SEQ ID NO:38	----	LFN	----GGLVSSNYPPNP-MFSGSTSAAGPKKKDSSGG-----GAVAPNKELHM
SEQ ID NO:43	----	-FK	----GGEAAAPYPAPNP-GMM-----MPAPRKKELGGSNS-----DKELHM
SEQ ID NO:44	----	LYN	----NNSVPS-YPPNP-MFTGSTSGASGVKKKESGGGGVGVGGQNKEMNM
		REFHYQSGSGGGGAHYAPAPNPGMFSPNTGGGGTAAKGNAPVVGGK--RQDGNGRDLHM	
			361 420

SEQ ID NO:14	*****	*	*
SEQ ID NO:30	LVWSSASPVSE	-----RAAVHVEFGAGG	----DHADVLAQKAQAYDEY--GRDDY
SEQ ID NO:34	FVWSSASPVSDV	-----FGA	----HEYGG--HDQKEVKLNVS PGKVEN
SEQ ID NO:38	FVWSSASPVSEGNLRHAVNRAASTDFGTVDPSKAVPHETVASKAVHELIENTMS PGRRGS		
SEQ ID NO:43	FVWSSASPVSEANLRNAVNHAASTDFAAAPPAATPRDGATPRGVSGSVTPVMKKDASS		
SEQ ID NO:44	FVWSSASPVSEANAKNAMTRGSSTDVSTDPKVSIPPHDNLATKAMQNLIENMS PGKRGH		
	FVWSSASPVSDV	-----FEGGGGNHHADYSTATNDHQKDVKISVPQGSND	
			421 480

SEQ ID NO:14	SSRTKNGSGG	-ADKGGPTLS-KLGSNSTAQLYPKD	---DGEGRAAAVAMPPASVMTRLI
SEQ ID NO:30	NHRDT	--QEDYLEKDEFSGNR	---EMDREMNQLEGEKVGDGK---PKTMPPASVMTRLI
SEQ ID NO:34	GEREPEMDEG	-----AKIPASGSPYTCQKKVDMEDGNAN-KNQQMPASVMTRLI	
SEQ ID NO:38	GAVEVEIEDGMMKSPATGLGAKFPVSGSPYVAPRKKGADVPGLEEAHMPMPASVMTRLI		
SEQ ID NO:43	VEMDQDGNNG	-----GK-----SPYMGKGSVDVEDGGPGPRKQMPASVMTRLI	
SEQ ID NO:44	NQ	-----YVEREEFSFGNK	---DDDSKVLATDGGNNISNKTTOAKVMPPTSVMTRLI
			481 540

