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(57) **Abrégé/Abstract:**

The preparation and use of nucleic acid fragments useful in altering the oil phenotype in plants are disclosed. Recombinant DNA construct incorporating such nucleic acid fragments and suitable regulatory sequences can be used to create transgenic plants having altered lipid profiles. Methods for altering the oil phenotype in plants using such nucleic acid fragments also are disclosed.



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(54) Title: ALTERATION OF OIL TRAITS IN PLANTS

(57) Abstract: The preparation and use of nucleic acid fragments useful in altering the oil phenotype in plants are disclosed. Recombinant DNA construct incorporating such nucleic acid fragments and suitable regulatory sequences can be used to create transgenic plants having altered lipid profiles. Methods for altering the oil phenotype in plants using such nucleic acid fragments also are disclosed.



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TITLE

ALTERATION OF OIL TRAITS IN PLANTS

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FIELD OF THE INVENTION

The present invention is in the field of plant breeding and genetics and, in particular, relates to the alteration of oil phenotype in plants through the controlled expression of selective genes.

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BACKGROUND OF THE INVENTION

Plant lipids have a variety of industrial and nutritional uses and are central to plant membrane function and climatic adaptation. These lipids represent a vast array of chemical structures, and these structures determine the physiological and industrial properties of the lipid. Many of these structures result either directly or indirectly from metabolic processes that alter the degree of unsaturation of the lipid. Different metabolic regimes in different plants produce these altered lipids, and either domestication of exotic plant species or modification of agronomically adapted species is usually required to produce economically large amounts of the desired lipid.

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There are serious limitations to using mutagenesis to alter fatty acid composition. Screens will rarely uncover mutations that a) result in a dominant ("gain-of-function") phenotype, b) are in genes that are essential for plant growth, and c) are in an enzyme that is not rate-limiting and that is encoded by more than one gene. In cases where desired phenotypes are available in mutant corn lines, their introgression into elite lines by traditional breeding techniques is slow and expensive, since the desired oil compositions are likely the result of several recessive genes.

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Recent molecular and cellular biology techniques offer the potential for overcoming some of the limitations of the mutagenesis approach, including the need for extensive breeding. Some of the particularly useful technologies are seed-specific expression of foreign genes in transgenic plants [see Goldberg et al (1989) *Cell* 56:149-160], and the use of antisense RNA to inhibit plant target genes in a dominant and tissue-specific manner [see van der Krol et al (1988) *Gene* 72:45-50]. Other advances include the transfer of foreign genes into elite commercial varieties of commercial oilcrops, such as soybean [Chee et al (1989) *Plant Physiol.* 91:1212-1218; Christou et al (1989) *Proc. Natl. Acad. Sci. U.S.A.* 86:7500-7504; Hinchey et al (1988) *Bio/Technology* 6:915-922; EPO publication 0 301 749 A2], rapeseed [De Block et al (1989) *Plant Physiol.* 91:694-701], and sunflower [Everett

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et al(1987) *Bio/Technology* 5:1201-1204], and the use of genes as restriction fragment length polymorphism (RFLP) markers in a breeding program, which makes introgression of recessive traits into elite lines rapid and less expensive [Tanksley et al (1989) *Bio/Technology* 7:257-264]. However, application of each of these technologies requires identification and isolation of commercially-important genes.

The regulation of transcription of most eukaryotic genes is coordinated through sequence-specific binding of proteins to the promoter region located upstream of the gene. Many of these protein-binding sequences have been conserved during evolution and are found in a wide variety of organisms. One such feature is the "CCAAT" sequence element. (Edwards et al, 1998, *Plant Physiol.* 117:1015-1022). CCAAT boxes are a feature of gene promoters in many eukaryotes including several plant gene promoters.

Heme-Activated Protein (HAP) proteins constitute a large family of transcription factors first identified in yeast. They combine to form a heteromeric protein complex that activates transcription by binding to CCAAT boxes in eukaryotic promoters. The orthologous Hap proteins display a high degree of evolutionary conservation in their functional domains in all species studied to date (Li et al, 1991).

WO 00/28058 published on May 18, 2000 describes Hap3-type CCAAT-box binding transcriptional activator polynucleotides and polypeptides, especially, the Leafy Cotyledon 1 (LEC1) transcriptional activator polynucleotides and polypeptides.

WO 99/67405 describes leafy cotyledon1 genes and their uses.

The human, murine and plant homologues of CCAAT-binding proteins have been isolated and characterized based on their sequence similarity with their yeast counterparts (Li et al, 1991). This high degree of sequence homology translates remarkably into functional interchangeability among orthologue proteins of different species (Sinha et al, 1995). Unlike yeast, multiple forms of each HAP homolog have been identified in plants (Edwards et al, 1998).

Molecular and genetic analysis revealed HAP members to be involved in the control of diverse and critical biological processes ranging from development and cell cycle regulation to metabolic control and homeostasis (Lotan et al, 1998; Lopez et al, 1996). In yeast, HAPs are involved in the transcriptional control of metabolic relevant processes such as the regulation of catabolic derepression of *cyc1* and other genes involved in respiration (Becker et al., 1991).

In mammalian systems, several reports describe HAPs as direct or indirect regulators of several important genes involved in lipid biosynthesis such as fatty acid synthase (Roder et al, 1997), farnesyl diphosphate (FPP) synthase (Jackson et al, 1995; Ericsson et al, 1996), glycerol-3-phosphate acyltransferase (GPA, Jackson et al, 1997), acetyl-CoA carboxylase (ACC, Lopez et al, 1996) and 3-

hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) synthase (Jackson et al, 1995), among others.

In addition, other CCAAT-binding transcription factors have also been reported to be involved in different aspects of the control of lipid biosynthesis and adipocyte growth and differentiation in mammalian systems (see McKnight et al, 1989).

It appears that the currently available evidence to date points to a family of proteins of the CCAAT-binding transcription factors as important modulators of metabolism and lipid biosynthesis in mammalian systems. Such a determination has not been made for plant systems.

SUMMARY OF THE INVENTION

This invention concerns an isolated nucleotide fragment comprising a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence encoding a fifth polypeptide having Hap2-like transcription factor activity, the fifth polypeptide having at least 70% identity based on the Clustal method of alignment when compared to a sixth polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 5, 6, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, or 208, 210, 212, 214, or 216;

(b) a nucleic acid sequence encoding a seventh polypeptide having Hap5-like transcription factor activity, the seventh polypeptide having at least 80% identity based on the Clustal method of alignment when compared to an eighth polypeptide selected from the group consisting of SEQ ID NOs:84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, or 221;

(c) a nucleic acid sequence encoding a seventeenth polypeptide having Hap3/Lec1-like activity, the seventeenth polypeptide having at least 70% identity based on the Clustal method of alignment when compared to a eighteenth polypeptide selected from the group consisting of SEQ ID NOs:130, 132, 134, or 136.

Also of interest are the complements of such nucleotide fragment as well as the use of such fragments or a part thereof in antisense inhibition or co-suppression in a transformed plant.

In a second embodiment, this invention concerns recombinant DNA constructs comprising such fragments, plants comprising such recombinant DNA constructs in their genome, seeds obtained from such plants and oil obtained from these seeds.

In a third embodiment, this invention concerns a method for altering oil phenotype in a plant which comprises: (a) transforming a plant with a recombinant DNA construct the invention, (b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and (c) selecting those

transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

In a fourth embodiment, this invention concerns a method for altering oil phenotype in a plant which comprises:

5 (a) transforming a plant with a recombinant DNA construct comprising isolated nucleotide fragment comprising a nucleic acid sequence selected from the group consisting of:

(i) a nucleic acid sequence encoding a plant Hap3/Lec1 transcription factor having at least 60% identity based on the Clustal method of alignment when
10 compared to a second polypeptide selected from the group consisting of even SEQ ID NOs: from 130 to 148, and SEQ ID NOs:195 and 196;

(ii) the complement of the nucleic acid sequence of (i);

(iii) the sequence of (i) or (ii) or a part thereof which is useful in antisense inhibition or co-suppression in a transformed plant;

15 (iv) a nucleic acid sequence encoding a plant Lec1-related CCAAT binding transcription factor having at least 60% identity based on the Clustal method of alignment when compared to a second polypeptide selected from the group consisting of even SEQ ID NOs: from 150 to 178, and SEQ ID NOs:197 to 202;

(v) the complement of the nucleic acid sequence of (iv);

20 (vi) the sequence of (iv) or (v) or a part thereof which is useful in antisense inhibition or co-suppression in a transformed plant;

wherein said nucleic acid sequence is operably linked to at least one regulatory sequence;

(b) growing the transformed plant under conditions suitable for expression of
25 the recombinant DNA construct; and

(c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

In a fifth embodiment, this invention concerns a method for altering oil phenotype in a plant which comprises:

30 (a) transforming a plant with a recombinant DNA construct comprising an isolated nucleic acid fragment operably linked to at least one regulatory sequence wherein said fragment has a nucleic acid sequence encoding a polypeptide having a sequence identity of at least 60% based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of even SEQ ID NOs:
35 from 2 to 178, and 206 to 214, and SEQ ID NOs:179 to 202, 216 to 219, 221, and 222;

(b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and

(c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

In a sixth embodiment, this invention concerns method of mapping genetic variations related to altered oil phenotypes in a plant comprising:

- 5 (a) crossing two plant varieties; and
- (b) evaluating genetic variations with respect to nucleic acid sequences set forth in any one of the odd SEQ ID NOs: from 1 to 177, or 207 to 215, or SEQ ID NO:220 in progeny plants resulting from the cross of step (a) wherein the evaluation is made using a method selected from the group consisting of: RFLP analysis, SNP
- 10 analysis, and PCR-based analysis.

In a seventh embodiment, this invention concerns a method of molecular breeding to obtain altered oil phenotypes in a plant comprising:

- (a) crossing two plant varieties; and
- (b) evaluating genetic variations with respect to nucleic acid sequences set
- 15 forth in any one of the odd SEQ ID NOs: from 1 to 177, or 207 to 215, or SEQ ID NO:220 in progeny plants resulting from the cross of step (a) wherein the evaluation is made using a method selected from the group consisting of: RFLP analysis, SNP analysis, and PCR-based analysis.

In an eighth embodiment, this invention concerns a method for altering oil

20 phenotype in a plant which comprises:

- (a) transforming a plant with a recombinant DNA construct comprising isolated nucleotide fragment comprising a nucleic acid sequence selected from the group consisting of:

(i) a nucleic acid sequence encoding a plant Hap3/Lec1 transcription

25 factor having at least 70% identity based on the Clustal method of alignment when compared to a second polypeptide selected from the group consisting of SEQ ID NOs:130 to 148, and SEQ ID NOs:195, 196, and 206;

(ii) the complement of the nucleic acid sequence of (iv);

(iii) the sequence of (iv) or (v) or a part thereof which is useful in

30 antisense inhibition or co-suppression in a transformed plant;

(b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and

(c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

35 In a ninth embodiment, this invention concerns a method to isolate nucleic acid fragments associated with altering oil phenotype in a plant which comprises:

(a) comparing even SEQ ID NOs: from 2 to 178, and 206 to 214, and SEQ ID NOs: 179 to 202, 216 to 219, 221, and 222 with other polypeptide sequences for the purpose of identifying polypeptides associated with altering oil phenotype in a plant;

(b) identifying the conserved sequence(s) or 4 or more amino acids obtained in step (a);

(c) making region-specific nucleotide probe(s) or oligomer(s) based on the conserved sequences identified in step (b); and

(d) using the nucleotide probe(s) or oligomer(s) of step (c) to isolate sequences associated with altering oil phenotype by sequence dependent protocols.

BRIEF DESCRIPTION OF THE FIGURES AND SEQUENCE LISTINGS

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

Figure 1 shows the fatty acid composition of maize somatic embryos over-expressing Hap3/Lec1 (solid bars, "Hap3/Lec1") compared to control embryos (striped bars, "con"). A ubiquitin promoter was used to drive Hap3/Lec1 expression in maize embryogenic callus. More than ten different events were analyzed by GC for fatty acid content/composition and compared to controls transformed with the selectable marker (BAR gene) plasmid alone. The somatic embryos over-expressing Lec1 contain elevated fatty acid contents averaging 119 % over control oil levels.

Figure 2 shows the fatty acid composition of maize embryos transformed with additional copies of Hap3/Lec1 (solid bars, "+ transgene") compared to control embryos (cross-hatched bars, "- transgene"). An oleosin promoter was used to direct the expression of a transgenic copy of Hap3/Lec 1. More than twenty events producing segregating T1 seed were analyzed by NMR for embryo oil content. Six to twelve embryos were analyzed for each of five different events. Some embryos within each event contained elevated oil content. The same embryos from these five events were analyzed by PCR to determine the presence or absence of the Lec1 construct. Embryos with high oil were always found to contain the Lec1 construct (darkly shaded bars), whereas embryos with normal levels of oil were typically found not to contain the Lec1 construct (cross-hatched bars). These data demonstrate the presence of the Lec1 gene does lead to increased oil in the embryo. It is believed that embryos containing sharply higher levels of oil were homozygous for the Lec1 construct, as these events were segregating 1:2:1. The oil concentration in the embryos containing the Lec1 construct greatly surpassed any increase previously achieved through enzymatic modification of the fatty acid

biosynthetic pathway, with some embryos containing an average increase of 56% in embryo oil content.

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 (for the corresponding SEQ ID NO: identifier as used in the attached Sequence Listing see Table 3). 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.

TABLE 1

Genes Involved in Alteration of Oil Traits in Plants

Gene Name	Clone	Plant
Hap2a transcription factor	ncs.pk0013.c4	Catalpa [Catalpa speciosa]
Hap2c-like transcription factor	etr1c.pk006.f9	cattail [Typha latifolia]
Hap2a transcription factor	vmb1na.pk015.d18:fis	grape [Vitis sp.]
Hap2a transcription factor	vpl1c.pk008.o5:fis	grape [Vitis sp.]
Hap2c-like transcription factor	vdb1c.pk001.m5:fis	grape [Vitis sp.]
Hap2 transcription factor	cho1c.pk004.b19:fis	maize [Zea mays]
Hap2 transcription factor	p0015.cdpgu90r:fis	maize [Zea mays]
Hap2a transcription factor	cta1n.pk0070.f3:fis	maize [Zea mays]
Hap2a-like transcription factor	cco1n.pk0014.d4:fis	maize [Zea mays]
Hap2a-like transcription factor	cco1n.pk086.d20:fis	maize [Zea mays]
Hap2b transcription factor	p0126.cnlau71r:fis	maize [Zea mays]
Hap2b-like transcription factor	p0104.cabav52r	maize [Zea mays]
Hap2c transcription factor	cho1c.pk007.l21:fis	maize [Zea mays]
Hap2c-like transcription factor	contig of:	maize [Zea mays]
	cca.pk0026.d6	
	cen3n.pk0061.e10:fis	
	cen3n.pk0135.c2	
	cho1c.pk001.n24	
	p0092.chwae40r	
Hap2c-like transcription factor	cpf1c.pk006.e3:fis	maize [Zea mays]
Hap2c-like transcription factor	contig of:	maize [Zea mays]
	cr1n.pk0080.g6	
	p0003.cgpg51r	

TABLE 1 (Continued)

Gene Name	Clone	Plant
Hap2c-like transcription factor	p0015.cpdfm55r:fis	maize [Zea mays]
Hap2c-like transcription factor	p0083.cldct11r:fis	maize [Zea mays]
Hap2c-like transcription factor	p0083.cldeu68r:fis	maize [Zea mays]
Hap2a transcription factor	pps1c.pk001.h3:fis	prickly poppy [Argemone mexicana]
Hap2c-like transcription factor	pps1c.pk007.j21:fis	prickly poppy [Argemone mexicana]
Hap2 transcription factor	rr1.pk0030.f7:fis	rice [Oryza sativa]
Hap2a transcription factor	rls72.pk0023.c8:fis	rice [Oryza sativa]
Hap2a-like transcription factor	rca1n.pk002.c15	rice [Oryza sativa]
Hap2a-like transcription factor	rds3c.pk001.g9	rice [Oryza sativa]
Hap2b transcription factor	rca1n.pk002.j3:fis	rice [Oryza sativa]
Hap2c-like transcription factor	rca1n.pk029.n22:fis	rice [Oryza sativa]
Hap2c-like transcription factor	rl0n.pk131.j17	rice [Oryza sativa]
Hap2a transcription factor	sdp3c.pk018.b9:fis	soybean [Glycine max]
Hap2a transcription factor	sfl1.pk0102.h8	soybean [Glycine max]
Hap2a transcription factor	srr3c.pk001.l10:fis	soybean [Glycine max]
Hap2a-like transcription factor	sdp2c.pk003.o5:fis	soybean [Glycine max]
Hap2b transcription factor	sif1c.pk001.m16:fis	soybean [Glycine max]
Hap2c-like transcription factor	src1c.pk003.o16:fis	soybean [Glycine max]
Hap2c-like transcription factor	src3c.pk012.m6:fis	soybean [Glycine max]
Hap2c-like transcription factor	hss1c.pk011.h10:fis	sunflower [Helianthus sp.]
Hap2 transcription factor	wr1.pk0094.f2:fis	wheat-common [Triticum aestivum]
Hap2a-like transcription factor	wre1n.pk0143.h2:fis	wheat-common [Triticum aestivum]
Hap2b transcription factor	wds1f.pk002.p21:fis	wheat-common [Triticum aestivum]

TABLE 1 (Continued)

Gene Name	Clone	Plant
Hap2c transcription factor	contig of: wdi1c.pk002.b10 wr1.pk0153.c7:fis	wheat-common [Triticum aestivum]
Hap2c-like transcription factor	wre1n.pk0066.e4:fis	wheat-common [Triticum aestivum]
Hap2c-like transcription factor	ncs.pk0013.c4:fis	catalpa [Catalpa speciosa]
Hap2c-like transcription factor	p0117.chcln94r:fis	maize [Zea mays]
Hap2c-like transcription factor	rdi2c.pk011.f19:fis	rice [Oryza sativa]
Hap2c-like transcription factor	sfl1.pk0101.g7:fis	soybean [Glycine max]
Hap2c-like transcription factor	wdi1c.pk002.b10:fis	wheat-common [Triticum aestivum]
Hap5c-like transcription factor	ect1c.pk001.k17:fis	Canna [Canna edulis]
Hap5a-like transcription factor	vrr1c.pk004.o20:fis	grape [Vitis sp.]
Hap5a-like transcription factor	clm1f.pk001.k17:fis	maize [Zea mays]
Hap5b-like transcription factor	cde1n.pk003.a5:fis	maize [Zea mays]
Hap5b-like transcription factor	cen3n.pk0164.a10:fis	maize [Zea mays]
Hap5b-like transcription factor	p0118.chsbc77r	maize [Zea mays]
Hap5c-like transcription factor	cco1n.pk055.o18:fis	maize [Zea mays]
Hap5c-like transcription factor	cho1c.pk001.l23:fis	maize [Zea mays]
Hap5c-like transcription factor	cse1c.pk001.h6:fis	maize [Zea mays]
Hap5a-like transcription factor	rlm3n.pk005.d20:fis	rice [Oryza sativa]
Hap5b-like transcription factor	rr1.pk0003.a3:fis	rice [Oryza sativa]
Hap5b-like transcription factor	rr1.pk0039.d4:fis	rice [Oryza sativa]
Hap5c-like transcription factor	rca1n.pk021.b20:fis	rice [Oryza sativa]
Hap5a-like transcription factor	sdp2c.pk029.k17:fis	soybean [Glycine max]
Hap5a-like transcription factor	sdp2c.pk044.e5:fis	soybean [Glycine max]
Hap5b-like transcription factor	sgs4c.pk004.j2	soybean [Glycine max]

TABLE 1 (Continued)

Gene Name	Clone	Plant
Hap5b-like transcription factor	src3c.pk002.h4:fis	soybean [Glycine max]
Hap5b-like transcription factor	src3c.pk009.b15:fis	soybean [Glycine max]
Hap5b-like transcription factor	src3c.pk019.d4:fis	soybean [Glycine max]
Hap5c-like transcription factor	sls1c.pk032.j4:fis	soybean [Glycine max]
Hap5 transcription factor	wdk2c.pk009.e4:fis	wheat-common [Triticum aestivum]
Hap5a-like transcription factor	contig of: wlm96.pk036.j11 wlm96.pk060.d5:fis	wheat-common [Triticum aestivum]
Hap5c-like transcription factor	wle1n.pk0076.h7:fis	wheat-common [Triticum aestivum]
Hap5c-like transcription factor	sgs4c.pk004.j2:fis	soybean [Glycine max]
Lec1-embryonic type	eas1c.pk003.e16	amaranth [Amaranthus retroflexus]
Lec1-embryonic type	fds1n.pk008.m14	balsam pear [Momordica charantia]
Lec1-embryonic type	p0015.cdp75rb:fis	maize [Zea mays]
Lec1-embryonic type	p0083.clder12r:fis	maize [Zea mays]
Lec1-embryonic type	pps1c.pk002.l19	prickly poppy [Argemone mexicana]
Lec1-embryonic type	Contig of: scb1c.pk004.j10 se1.pk0042.d8:fis	soybean [Glycine max]
Lec1-embryonic type	se2.11d12:fis	soybean [Glycine max]
Lec1-embryonic type	ses2w.pk0015.a4:fis	soybean [Glycine max]
Lec1-embryonic type	vs1n.pk013.m13:fis	vernonia [Vernonia mespilifolia]
Lec1-embryonic type	wdk3c.pk023.h15:fis	wheat-common [Triticum aestivum]
Lec1-related CCAAT binding protein	ect1c.pk007.p18:fis	Canna [Canna edulis]
Lec1-related CCAAT binding protein	fds.pk0003.h5:fis	balsam pear [Momordica charantia]
Lec1-related CCAAT binding protein	eef1c.pk004.c8:fis	eucalyptus [Eucalyptus grandis]
Lec1-related CCAAT binding protein	cbn10.pk0005.e6:fis	maize [Zea mays]
Lec1-related CCAAT binding protein	p0006.cbysa51r:fis	maize [Zea mays]

TABLE 1 (Continued)

Gene Name	Clone	Plant
Lec1-related CCAAT binding protein	rl0n.pk0061.c8:fis	rice [Oryza sativa]
Lec1-related CCAAT binding protein	rsl1n.pk002.g10:fis	rice [Oryza sativa]
Lec1-related CCAAT binding protein	ses4d.pk0037.e3:fis	soybean [Glycine max]
Lec1-related CCAAT binding protein	src2c.pk003.i13:fis	soybean [Glycine max]
Lec1-related CCAAT binding protein	src2c.pk011.m12:fis	soybean [Glycine max]
Lec1-related CCAAT binding protein	src2c.pk025.b3:fis	soybean [Glycine max]
Lec1-related CCAAT binding protein	src3c.pk028.j21:fis	soybean [Glycine max]
Lec1-related CCAAT binding protein	wkm1c.pk0002.d7:fis	wheat-common [Triticum aestivum]
Lec1-related CCAAT binding protein	wlk8.pk0001.e10:fis	wheat-common [Triticum aestivum]
Lec1-related CCAAT binding protein	wlm96.pk037.k9:fis	wheat-common [Triticum aestivum]

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 may be referred to herein. 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

As used herein, an "isolated nucleic acid fragment" is a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. An isolated nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA. Nucleotides (usually found in their 5'-monophosphate form) are referred to by their single letter designation as follows: "A" for adenylate or deoxyadenylate (for RNA or DNA, respectively), "C" for cytidylate or deoxycytidylate, "G" for guanylate or deoxyguanylate, "U" for uridylate, "T" for deoxythymidylate, "R" for purines (A or G), "Y" for pyrimidines (C or T), "K" for g or T, "H" for A or C or T, "I" for inosine, and "N" for any nucleotide.

The terms “subfragment that is functionally equivalent” and “functionally equivalent subfragment” are used interchangeably herein. These terms refer to a portion or subsequence of an isolated nucleic acid fragment in which the ability to alter gene expression or produce a certain phenotype is retained whether or not the fragment or subfragment encodes an active enzyme. For example, the fragment or subfragment can be used in the design of recombinant DNA constructs to produce the desired phenotype in a transformed plant. Recombinant DNA constructs can be designed for use in co-suppression or antisense by linking a nucleic acid fragment or subfragment thereof, whether or not it encodes an active enzyme, in the appropriate orientation relative to a plant promoter sequence.

The terms “homology”, “homologous”, “substantially similar” and “corresponding substantially” are used interchangeably herein. They refer to nucleic acid fragments wherein changes in one or more nucleotide bases does not affect the ability of the nucleic acid fragment to mediate gene expression or produce a certain phenotype. These terms also refer 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 alter the functional properties of the resulting nucleic acid fragment relative to the initial, unmodified fragment. It is therefore understood, as those skilled in the art will appreciate, that the invention encompasses more than the specific exemplary sequences.

Moreover, the skilled artisan recognizes that substantially similar nucleic acid sequences encompassed by this invention are also defined by their ability to hybridize, under moderately stringent conditions (for example, 0.5 X SSC, 0.1% SDS, 60°C) with the sequences exemplified herein, or to any portion of the nucleotide sequences reported herein and which are functionally equivalent to the promoter of the invention. 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 involves 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 involves the use of 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 involves the use of two final washes in 0.1X SSC, 0.1% SDS at 65°C.

With respect to the degree of substantial similarity between the target (endogenous) mRNA and the RNA region in the construct having homology to the target mRNA, such sequences should be at least 25 nucleotides in length, preferably at least 50 nucleotides in length, more preferably at least 100 nucleotides in length, again more preferably at least 200 nucleotides in length, and most preferably at least 300 nucleotides in length; and should be at least 80% identical, preferably at least 85% identical, more preferably at least 90% identical, and most preferably at least 95% identical.

Sequence alignments and percent similarity calculations may be determined using a variety of comparison methods designed to detect homologous sequences including, but not limited to, the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences are 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 and calculation of percent identity of protein sequences using the Clustal method are KTUPLE=1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. For nucleic acids these parameters are KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

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).

In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively 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 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 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.

“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 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 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 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. The term “recombinant DNA construct” and “recombinant DNA construct” are used interchangeably herein. A recombinant DNA construct comprises an artificial combination of nucleic acid

fragments, e.g., regulatory and coding sequences that are not found together in nature. For example, a recombinant DNA construct 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
5 arranged in a manner different than that found in nature. 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 recombinant DNA constructs. A “transgene” is a gene
that has been introduced into the genome by a transformation procedure.

10 “Coding sequence” refers to a DNA 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.

15 Regulatory sequences may include, but are not limited to, promoters, translation leader sequences, introns, and polyadenylation recognition sequences.

“Promoter” refers to a DNA sequence capable of controlling the expression of a coding sequence or functional RNA. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as
20 enhancers. Accordingly, an “enhancer” is a DNA 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 be composed of different elements derived from different promoters found in nature, or even comprise
25 synthetic DNA 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 gene to be expressed in most cell types at most times are commonly referred to as “constitutive promoters”. New promoters of
30 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, DNA fragments of some variation may have identical promoter activity.

35 An “intron” is an intervening sequence in a gene that does not encode a portion of the protein sequence. Thus, such sequences are transcribed into RNA but are then excised and are not translated. The term is also used for the excised RNA sequences. An “exon” is a portion of the sequence of a gene that is

transcribed and is found in the mature messenger RNA derived from the gene, but is not necessarily a part of the sequence that encodes the final gene product.

The "translation leader sequence" refers to a DNA 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, R. and Foster, G. D. (1995) *Molecular Biotechnology* 3:225).

The "3' non-coding sequences" refer to DNA sequences located downstream of a coding sequence and include 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 post-transcriptional 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 protein by the cell. "cDNA" refers to a DNA that is complementary to and synthesized from a mRNA template using the enzyme reverse transcriptase. The cDNA can be single-stranded or converted into the double-stranded form using the Klenow fragment of DNA polymerase I. "Sense" RNA refers to RNA transcript that includes the mRNA and can be translated into protein within a cell or *in vitro*. "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 (U.S. Patent No. 5,107,065). The complementarity of an antisense RNA may be with any part of the specific gene transcript, i.e., at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding sequence. "Functional RNA" refers to antisense RNA, ribozyme RNA, or other RNA that may not be translated but yet has an effect on cellular processes. The terms "complement" and "reverse complement" are used interchangeably herein with respect to mRNA transcripts, and are meant to define the antisense RNA of the message.

The term "endogenous RNA" refers to any RNA which is encoded by any nucleic acid sequence present in the genome of the host prior to transformation with

the recombinant construct of the present invention, whether naturally-occurring or non-naturally occurring, i.e., introduced by recombinant means, mutagenesis, etc.

The term “non-naturally occurring” means artificial, not consistent with what is normally found in nature.

5 The term “operably linked” refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is regulated by the other. For example, a promoter is operably linked with a coding sequence when it is capable of regulating the expression of that coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences
10 can be operably linked to regulatory sequences in a sense or antisense orientation. In another example, the complementary RNA regions of the invention can be operably linked, either directly or indirectly, 5' to the target mRNA, or 3' to the target mRNA, or within the target mRNA, or a first complementary region is 5' and its complement is 3' to the target mRNA.

15 The term “expression”, as used herein, refers to the production of a functional end-product. Expression of a gene involves transcription of the gene and translation of the mRNA into a precursor or mature protein. “Antisense inhibition” refers to the production of antisense RNA transcripts capable of suppressing the expression of the target protein. “Co-suppression” refers to the production of sense
20 RNA transcripts capable of suppressing the expression of identical or substantially similar foreign or endogenous genes (U.S. Patent No. 5,231,020).

 “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
25 of mRNA; i.e., with pre- and propeptides still present. Pre- and propeptides may be but are not limited to intracellular localization signals.

 “Stable transformation” refers to the transfer of a nucleic acid fragment into a genome of a host organism, including both nuclear and organellar genomes, resulting in genetically stable inheritance. In contrast, “transient transformation”
30 refers to the transfer of a nucleic acid fragment into the nucleus, or DNA-containing organelle, of a host organism resulting in gene expression without integration or stable inheritance. Host organisms containing the transformed nucleic acid fragments are referred to as “transgenic” organisms. The preferred method of cell transformation of rice, corn and other monocots is the use of particle-accelerated or
35 “gene gun” transformation technology (Klein et al, (1987) *Nature (London)* 327:70-73; U.S. Patent No. 4,945,050), or an *Agrobacterium*-mediated method using an appropriate Ti plasmid containing the transgene (Ishida Y. et al, 1996,

Nature Biotech. 14:745-750). The term “transformation” as used herein refers to both stable transformation and transient transformation.

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

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
10 acids by genetic engineering techniques. A “recombinant DNA construct” comprises an isolated polynucleotide operably linked to at least one regulatory sequence. The term also embraces an isolated polynucleotide comprising a region encoding all or part of a functional RNA and at least one of the naturally occurring regulatory sequences directing expression in the source (e.g., organism) from which the
15 polynucleotide was isolated, such as, but not limited to, an isolated polynucleotide comprising a nucleotide sequence encoding a herbicide resistant target gene and the corresponding promoter and 3' end sequences directing expression in the source from which sequences were isolated.

A “transgene” is a recombinant DNA construct that has been introduced into
20 the genome by a transformation procedure.

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 sequence homology. For example, the nucleotide sequences of two or more nucleic acid fragments can be compared and aligned in
25 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.

“PCR” or “Polymerase Chain Reaction” is a technique for the synthesis of
30 large quantities of specific DNA segments, consists of a series of repetitive cycles (Perkin Elmer Cetus Instruments, Norwalk, CT). Typically, the double stranded DNA is heat denatured, the two primers complementary to the 3' boundaries of the target segment are annealed at low temperature and then extended at an intermediate temperature. One set of these three consecutive steps is referred to
35 as a cycle.

The terms “recombinant construct”, “expression construct”, “recombinant expression construct”, “recombinant DNA construct” and “recombinant DNA construct” are used interchangeably herein. Such construct may be itself or may be

used in conjunction with a vector. If a vector is used then the choice of vector is dependent upon the method that will be used to transform host plants as is well known to those skilled in the art. For example, a plasmid vector can be used. The skilled artisan is well aware of the genetic elements that must be present on the vector in order to successfully transform, select and propagate host cells comprising any of the isolated nucleic acid fragments of the invention. 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.

Co-suppression constructs in plants previously have been designed by focusing on overexpression of a nucleic acid sequence having homology to an endogenous mRNA, in the sense orientation, which results in the reduction of all RNA having homology to the overexpressed sequence (see Vaucheret et al (1998) *Plant J* 16:651-659; and Gura (2000) *Nature* 404:804-808). The overall efficiency of this phenomenon is low, and the extent of the RNA reduction is widely variable. Recent work has described the use of "hairpin" structures that incorporate all, or part, of an mRNA encoding sequence in a complementary orientation that results in a potential "stem-loop" structure for the expressed RNA (PCT Publication WO 99/53050 published on October 21, 1999). This increases the frequency of co-suppression in the recovered transgenic plants. Another variation describes the use of plant viral sequences to direct the suppression, or "silencing", of proximal mRNA encoding sequences (PCT Publication WO 98/36083 published on August 20, 1998). Both of these co-suppressing phenomena have not been elucidated mechanistically, although recent genetic evidence has begun to unravel this complex situation (Elmayan et al (1998) *Plant Cell* 10:1747-1757).

Alternatively, a recombinant DNA construct 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 recombinant DNA constructs 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 recombinant DNA constructs 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.

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 polypeptides. 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 polypeptides 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.

The terms Hap3, Lec1, and Hap3/Lec1 are used interchangeably herein and refer to a class of transcription factors. The Hap3/Lec1 class is part of a broader family that includes other transcription factors such as Hap5, Hap2, and Lec1-CCAAT. The terms Hap3-like, Lec1-like, Hap3/Lec1-like, Hap5-like, Hap2-like, Lec1-CCAAT-like, etc. refer to any transcription factors that share sequence identity as disclosed herein and/or functionality with the nucleotide sequences and the corresponding amino acid sequences encoded by such nucleotide sequences disclosed in the present invention.

Surprisingly and unexpectedly, it has been found that there are a variety of regulatory/structural nucleic acid fragments, which heretofore have not been associated with altering oil phenotype in plants, that appear to be useful in altering oil phenotype in plants. In addition to the CCAAT-binding transcription factors, other proteins which heretofore have not been associated with altering oil phenotype in plants, have been identified. The nucleic acids identified encode a diverse class of regulatory and structural polypeptides whose expression correlates with altered oil phenotypes in plants. Altering the expression of these polypeptides would be expected to have an effect in altering oil accumulation in plants.

Other protein classes identified herein include:

a Hap2 transcription factor;

a Hap5 transcription factor;

a Hap3/Lec1 or Lec1-CCAAT binding transcription factor.

They can be characterized as an isolated nucleotide fragment comprising a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence encoding a fifth polypeptide having Hap2-like transcription factor activity, the fifth polypeptide having at least 70% identity based on the Clustal method of alignment when compared to a sixth polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 5, 6, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, or 208, 210, 212, 214, or 216; or

(b) a nucleic acid sequence encoding a seventh polypeptide having Hap5-like transcription factor activity, the seventh polypeptide having at least 80% identity

based on the Clustal method of alignment when compared to an eighth polypeptide selected from the group consisting of SEQ ID NOs:84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, or 221; or

- 5 (c) a nucleic acid sequence encoding a seventeenth polypeptide having Hap3/Lec1-like activity, the seventeenth polypeptide having at least 70% identity based on the Clustal method of alignment when compared to a eighteenth polypeptide selected from the group consisting of SEQ ID NOs:130, 132, 134, or 136.

10 It is understood by one skilled in the art that other percent identity ranges may be useful in the above mentioned characterization. Useful percent identities would include, but not be limited to, 45%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and all integer percentages from 45 to 100%.

The complement of the nucleotide fragments of this inventions are
15 encompassed within the scope of this invention.

Those skilled in the art with also appreciate that the nucleotide fragment of this invention and/or the complement thereof can be used in whole or in part in antisense inhibition or co-suppression of a transformed plant.

In a more preferred embodiment, the first polypeptide mentioned above is as
20 follows with respect to each part, the first polypeptide in

part (a) is a Hap2 transcription factor;

part (b) is a Hap5 transcription factor;

part (c) is a Hap3/Lec1 or Lec1-CCAAT binding transcription factor

Lec1 homologs may be further identified by using conserved sequence motifs.

25 The following amino acid sequence (given in single letter code, with "x" representing any amino acid). Under lined amino acids are those that are conserved in Lec1 but not found in Lec1-related proteins.

REQDxxMPxANVxRIMRxxLPxxAKISDDAKExIQECVSExISFxxEANxRCxxxx
RKTxxxE

30 In a further embodiment, this invention encompasses recombinant DNA construct comprising any of the isolated nucleic acid fragments of the invention or complement thereof operably linked to at least one regulatory sequence. It is also understood that recombinant DNA constructs comprising such fragments or complements thereof or parts of either can be used in antisense inhibition or
35 suppression of a transformed plant.

Also within the scope of this invention is a plant comprising in its genome a recombinant DNA construct as described herein. Recombinant DNA constructs designed for plant expression such as those described herein can be introduced into

a plant cell in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of plant (i.e, monocot or dicot) and/or organelle (i.e., nucleus, chloroplast, mitochondria) targeted for transformation. Suitable methods for transforming plant cells include

5 microinjection, electroporation, Agrobacterium mediated transformation, direct gene transfer and particle-accelerated or "gene gun" transformation technology as is discussed above.

Examples of plants which can be transformed include, but are not limited to, corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower, and coconut.

10 The regeneration, development and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, In, Methods for Plant Molecular Biology, (Eds.), Academic Press, Inc., San Diego, CA (1988)). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those

15 individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous

20 gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the

25 present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated. Methods for transforming dicots,

30 primarily by use of *Agrobacterium tumefaciens*, and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863, U.S. Patent No. 5,159,135, U.S. Patent No. 5,518, 908); soybean (U.S. Patent No. 5,569,834, U.S. Patent No. 5,416,011, McCabe et. al., *BioTechnology* 6:923 (1988), Christou et al., *Plant Physiol.* 87:671-674 (1988)); *Brassica* (U.S. Patent No. 5,463,174); peanut

35 (Cheng et al., *Plant Cell Rep.* 15:653-657 (1996), McKently et al., *Plant Cell Rep.* 14:699-703 (1995)); papaya; and pea (Grant et al., *Plant Cell Rep.* 15:254-258, (1995)).

Transformation of monocotyledons using electroporation, particle bombardment, and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier et al., *Proc. Natl. Acad. Sci. (USA)* 84:5354, (1987)); barley (Wan and Lemaux, *Plant Physiol* 104:37 (1994)); *Zea mays* (Rhodes et al., *Science* 240:204 (1988), Gordon-Kamm et al., *Plant Cell* 2:603-618 (1990), Fromm et al., *BioTechnology* 8:833 (1990), Koziel et al., *BioTechnology* 11: 194, (1993), Armstrong et al., *Crop Science* 35:550-557 (1995)); oat (Somers et al., *BioTechnology* 10: 15 89 (1992)); orchard grass (Horn et al., *Plant Cell Rep.* 7:469 (1988)); rice (Toriyama et al., *TheorAppl. Genet.* 205:34, (1986); Part et al., *Plant Mol. Biol.* 32:1135-1148, (1996); Abedinia et al., *Aust. J. Plant Physiol.* 24:133-141 (1997); Zhang and Wu, *Theor. Appl. Genet.* 76:835 (1988); Zhang et al. *Plant Cell Rep.* 7:379, (1988); Battraw and Hall, *Plant Sci.* 86:191-202 (1992); Christou et al., *Bio/Technology* 9:957 (1991)); rye (De la Pena et al., *Nature* 325:274 (1987)); sugarcane (Bower and Birch, *Plant J.* 2:409 (1992)); tall fescue (Wang et al., *BioTechnology* 10:691 (1992)), and wheat (Vasil et al., *Bio/Technology* 10:667 (1992); U.S. Patent No. 5,631,152).

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte et al., *Nature* 335:454-457 (1988); Marcotte et al., *Plant Cell* 1:523-532 (1989); McCarty et al., *Cell* 66:895-905 (1991); Hattori et al., *Genes Dev.* 6:609-618 (1992); Goff et al., *EMBO J.* 9:2517-2522 (1990)).

Transient expression systems may be used to functionally dissect gene constructs (see generally, Maliga et al., *Methods in Plant Molecular Biology*, Cold Spring Harbor Press (1995)). It is understood that any of the nucleic acid molecules of the present invention can be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters, enhancers etc.

In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (e.g., DNA molecules, plasmids, etc.), generation of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989); Maliga et al., *Methods in Plant Molecular Biology*, Cold Spring Harbor Press (1995); Birren et al., *Genome Analysis: Detecting Genes*, 1, Cold Spring Harbor, New York (1998); Birren et al., *Genome Analysis: Analyzing DNA*, 2, Cold Spring Harbor, New York (1998); *Plant Molecular Biology: A Laboratory Manual*, eds. Clark, Springer, New York (1997)).

Seeds obtained from such plants and oil obtained from these seeds constitute another aspect of the present invention.

In an even further aspect, the invention concerns a method for altering oil phenotype in a plant which comprises:

- 5 (a) transforming a plant with a recombinant DNA construct of the invention;
- (b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and
- (c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

10 In a more specific embodiment, the invention concerns a method for altering oil phenotype in a plant which comprises:

(a) transforming a plant with a recombinant DNA construct comprising isolated nucleotide fragment comprising a nucleic acid sequence selected from the group consisting of:

- 15 (i) a nucleic acid sequence encoding a plant Hap3/Lec1 transcription factor having at least 60% identity based on the Clustal method of alignment when compared to a second polypeptide selected from the group consisting of even SEQ ID NOs: from 130 to 148, and SEQ ID NOs:195 and 196;
- (ii) the complement of the nucleic acid sequence of (i);
- 20 (iii) the sequence of (i) or (ii) or a part thereof which is useful in antisense inhibition or co-suppression in a transformed plant;
- (iv) a nucleic acid sequence encoding a plant Lec1-related CCAAT binding transcription factor having at least 60% identity based on the Clustal method of alignment when compared to a second polypeptide selected from the group
- 25 consisting of even SEQ ID NOs: from 150 to 178, and SEQ ID NOs:197 to 202;
- (v) the complement of the nucleic acid sequence of (vii);
- (vi) the sequence of (iv) or (v) or a part thereof which is useful in antisense inhibition or co-suppression in a transformed plant;
- wherein said nucleic acid sequence is operably linked to at least one
- 30 regulatory sequence;
- (b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and
- (c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

35 It is understood by one skilled in the art that other percent identity ranges may be useful in the above mentioned method. Useful percent identities would include, but not be limited to, 45%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and all integer percentages from 45 to 100%.

In an even further aspect, this invention concerns a method to isolate nucleic acid fragments associated with altering oil phenotype in a plant which comprises:

(a) comparing even SEQ ID NOs: from 2 to 178, and 206 to 214, and SEQ ID NOs: 179 to 202, 216 to 219, 221, and 222 with other polypeptide sequences for the purpose of identifying polypeptides associated with altering oil phenotype in a plant;

(b) identifying the conserved sequences(s) or 4 or more amino acids obtained in step (a);

(c) making region-specific nucleotide probe(s) or oligomer(s) based on the conserved sequences identified in step (b); and

(d) using the nucleotide probe(s) or oligomer(s) of step (c) to isolate sequences associated with altering oil phenotype by sequence dependent protocols.

In a most preferred aspect, this invention concerns a method for altering oil phenotype in a plant which comprises:

(a) transforming a plant with a recombinant DNA construct comprising an isolated nucleic acid fragment operably linked to at least one regulatory sequence wherein said fragment has a nucleic acid sequence encoding a polypeptide having a sequence identity of at least 60% based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of even ;

(b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and

(c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

It is understood by one skilled in the art that other percent identity ranges may be useful in the above mentioned method. Useful percent identities would include, but not be limited to, 45%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and all integer percentages from 45 to 100%.

In another aspect, this invention also concerns a method of mapping genetic variations related to altered oil phenotypes in a plant comprising:

(a) crossing two plant varieties; and

(b) evaluating genetic variations with respect to nucleic acid sequences set forth in any one of the odd SEQ ID NOs: from 1 to 177, or 207 to 215, or SEQ ID NO: 220 in progeny plants resulting from the cross of step (a) wherein the evaluation is made using a method selected from the group consisting of: RFLP analysis, SNP analysis, and PCR-based analysis.

In another embodiment, this invention concerns a method of molecular breeding to obtain altered oil phenotypes in a plant comprising:

(a) crossing two plant varieties; and

(b) evaluating genetic variations with respect to nucleic acid sequences set forth in any one of the odd SEQ ID NOs: from 1 to 177, or 207 to 215, or SEQ ID NO:220 in progeny plants resulting from the cross of step (a) wherein the evaluation is made using a method selected from the group consisting of: RFLP analysis, SNP analysis, and PCR-based analysis.

The genetic variability at a particular locus (gene) due to even minor base changes can alter the pattern of restriction enzyme digestion fragments that can be generated. Pathogenic alterations to the genotype can be due to deletions or insertions within the gene being analyzed or even single nucleotide substitutions that can create or delete a restriction enzyme recognition site. RFLP analysis takes advantage of this and utilizes Southern blotting with a probe corresponding to the gene of interest.

Thus, if a polymorphism (i.e., a commonly occurring variation in a gene or segment of DNA; also, the existence of several forms of a gene (alleles) in the same species) creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (e.g., a variable nucleotide tandem repeat (VNTR) polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms: ("RFLPs"). RFLPs have been widely used in human and plant genetic analyses (Glassberg, UK Patent Application 2135774; Skolnick et al, *Cytogen. Cell Genet.* 32:58-67 (1982); Botstein et al, *Ann. J. Hum. Genet.* 32:314-331 (1980); Fischer et al (PCT Application WO 90/13668; Uhlen, PCT Application WO 90/11369).

A central attribute of "single nucleotide polymorphisms" or "SNPs" is that the site of the polymorphism is at a single nucleotide. SNPs have certain reported advantages over RFLPs or VNTRs. First, SNPs are more stable than other classes of polymorphisms. Their spontaneous mutation rate is approximately 10^{-9} (Kornberg, *DNA Replication*, W.H. Freeman & Co., San Francisco, 1980), approximately, 1,000 times less frequent than VNTRs (U.S. Patent 5,679,524). Second, SNPs occur at greater frequency, and with greater uniformity than RFLPs and VNTRs. As SNPs result from sequence variation, new polymorphisms can be identified by sequencing random genomic or cDNA molecules. SNPs can also result from deletions, point mutations and insertions. Any single base alteration, whatever the cause, can be a SNP. The greater frequency of SNPs means that they can be more readily identified than the other classes of polymorphisms.

SNPs can be characterized using any of a variety of methods. Such methods include the direct or indirect sequencing of the site, the use of restriction enzymes where the respective alleles of the site create or destroy a restriction site, the use of allele-specific hybridization probes, the use of antibodies that are specific for the proteins encoded by the different alleles of the polymorphism or by other biochemical interpretation. SNPs can be sequenced by a number of methods. Two basic methods may be used for DNA sequencing, the chain termination method of Sanger et al, *Proc. Natl. Acad. Sci. (U.S.A.)* 74:5463-5467 (1977), and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci. (U.S.A.)* 74: 560—564 (1977).

Polymerase chain reaction ("PCR") is a powerful technique used to amplify DNA millions of fold, by repeated replication of a template, in a short period of time. (Mullis et al, *Cold Spring Harbor Symp. Quant. Biol.* 51:263-273 (1986); Erlich et al, European Patent Application 50,424; European Patent Application 84,796; European Patent Application 258,017, European Patent Application 237,362; Mullis, European Patent Application 201,184, Mullis et al U.S. Patent No. 4,683,202; Erlich, U.S. Patent No. 4,582,788; and Saiki et al, U.S. Patent No. 4,683,194). The process utilizes sets of specific in vitro synthesized oligonucleotides to prime DNA synthesis. The design of the primers is dependent upon the sequences of DNA that are desired to be analyzed. The technique is carried out through many cycles (usually 20-50) of melting the template at high temperature, allowing the primers to anneal to complementary sequences within the template and then replicating the template with DNA polymerase.

The products of PCR reactions are analyzed by separation in agarose gels followed by ethidium bromide staining and visualization with UV transillumination. Alternatively, radioactive dNTPs can be added to the PCR in order to incorporate label into the products. In this case the products of PCR are visualized by exposure of the gel to x-ray film. The added advantage of radiolabeling PCR products is that the levels of individual amplification products can be quantitated.

Furthermore, single point mutations can be detected by modified PCR techniques such as the ligase chain reaction ("LCR") and PCR-single strand conformational polymorphisms ("PCR-SSCP") analysis. The PCR technique can also be used to identify the level of expression of genes in extremely small samples of material, e.g., tissues or cells from a body. The technique is termed reverse transcription-PCR ("RT-PCR").

In another embodiment, this invention concerns a method for altering oil phenotype in a plant which comprises:

(a) transforming a plant with a recombinant DNA construct comprising isolated nucleotide fragment comprising a nucleic acid sequence selected from the group consisting of:

(i) a nucleic acid sequence encoding a plant Hap3/Lec1 transcription factor having at least 70% identity based on the Clustal method of alignment when compared to a second polypeptide selected from the group consisting of SEQ ID NOs:130 to 148, and SEQ ID NOs:195 and 196;

(ii) the complement of the nucleic acid sequence of (iv);

(iii) the sequence of (iv) or (v) or a part thereof which is useful in antisense inhibition or co-suppression in a transformed plant;

(b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and

(c) selecting those transformed plants whose oil phenotype has been altered compared to the oil phenotype of an untransformed plant.

It is understood by one skilled in the art that other percent identity ranges may be useful in the above mentioned method. Useful percent identities would include, but not be limited to, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95% and all integer percentages from 45 to 100%.

In another aspect this invention concerns a method to isolate nucleic acid fragments associated with altering oil phenotype in a plant which comprises:

(a) comparing SEQ ID NOs:130 to 148, and SEQ ID NOs:195, 196, and 206 with other polypeptide sequences for the purpose of identifying polypeptides associated with altering oil phenotype in a plant;

(b) identifying the conserved sequences(s) or 4 or more amino acids obtained in step (a);

(c) making region-specific nucleotide probe(s) or oligomer(s) based on the conserved sequences identified in step (b); and

(d) using the nucleotide probe(s) or oligomer(s) of step (c) to isolate sequences associated with altering oil phenotype by sequence dependent protocols.

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. The disclosure of each reference set forth herein may be referred to herein.

EXAMPLE 1

Composition of cDNA Libraries; Isolation and Sequencing of cDNA Clones

cDNA libraries representing mRNAs from various plant tissues were prepared. The characteristics of the libraries are described below.

TABLE 2
cDNA Libraries from Various Plants

Library	Tissue	Clone
cbn10	Corn Developing Kernel (Embryo and Endosperm); 10 Days After Pollination	cbn10.pk0005.e6:fis cbn10.pk0064.e6
cc71se-a	Corn Callus Type II Tissue, Somatic Embryo Formed	cc71se-a.pk0002.e11:fis
cc71se-b	Corn Callus Type II Tissue, Somatic Embryo Formed	cc71se-b.pk0018.e4:fis
cca	Corn Callus Type II Tissue, Undifferentiated, Highly Transformable	cca.pk0026.d6
ccase-b	Corn Callus Type II Tissue, Somatic Embryo Formed, Highly Transformable	ccase-b.pk0003.b9:fis
cco1n	Corn Cob of 67 Day Old Plants Grown in Green House*	cco1n.pk062.j7 cco1n.pk086.d20:fis cco1n.pk0014.d4:fis cco1n.pk055.o18 cco1n.pk089.g17 cco1n.pk068.f18:fis
cde1c	Corn (Zea Mays, B73) developing embryo 20 DAP	cde1c.pk003.o22:fis
cde1n	Corn (Zea mays, B73) developing embryo 20 DAP normalized	cde1n.pk003.a5 cde1n.pk001.n24:fis
cdo1c	Corn (Zea mays L.) ovary, 5 days after silking (includes pedicel and glumes)	cdo1c.pk001.c1:fis
ceb3	Corn Embryo 20 Days After Pollination	ceb3.pk0012.a7
ceb5	Corn Embryo 30 Days After Pollination	ceb5.pk0081.b4
cen3n	Corn Endosperm 20 Days After Pollination*	cen3n.pk0164.a10 cen3n.pk0044.b8:fis cen3n.pk0112.e10:fis cho1c.pk003.p17:fis cho1c.pk003.n23
cho1c	Corn (Zea mays L., Alexho Synthetic High Oil) embryo 20 DAP	cho1c.pk004.b19:fis cho1c.pk007.l21:fis cho1c.pk001.l23:fis cho1c.pk009.g10
clm1f	Corn (Zea mays, B73) leaf at V6-VT (full length)	clm1f.pk001.k17 clm1f.pk002.o13:fis
cpd1c	Corn (Zea mays L.) pooled BMS treated with chemicals related to protein kinases	cpd1c.pk011.i5:fis cpd1c.pk008.e21
cpf1c	Corn (Zea mays L.) pooled BMS treated with chemicals related to protein synthesis	cpf1c.pk006.e3:fis
cpj1c	Corn (Zea mays L.) pooled BMS treated with chemicals related to membrane ionic force	cpj1c.pk005.m20:fis
cr1n	Corn Root From 7 Day Old Seedlings*	cr1n.pk0080.g6
cse1c	Corn (Zea mays L.) seedling at V2 stage treated with Ethylene collected at 6 hr, 23 hr, 72 hr	cse1c.pk001.h6

TABLE 2 (Continued)

Library	Tissue	Clone
cta1n	Corn Tassel*	cta1n.pk0070.f3:fis cta1n.pk0074.h11
ctn1c	Corn (<i>Zea mays</i> L., B73) night harvested tassel (v12 stage).	ctn1c.pk002.o4
ect1c	<i>Canna edulis</i> Tubers	ect1c.pk001.k17:fis ect1c.pk007.p18:fis
eef1c	<i>Eucalyptus tereticornis</i> flower buds from adult tree	eef1c.pk004.c8:fis
etr1c	Cattail (<i>Typha latifolia</i>) root	etr1c.pk006.f9
fds	<i>Momordica charantia</i> Developing Seed	fds.pk0003.h5:fis
hss1c	<i>Sclerotinia</i> infected sunflower plants	hss1c.pk011.h10:fis
ncs	<i>Catalpa speciosa</i> Developing Seed	ncs.pk0013.c4
p0006	Young shoot	p0006.cbysa51r:fis
p0015	13 DAP embryo	p0015.cdpгу90r:fis p0015.cdpmf55r:fis
p0016	Tassel shoTassel shoots, pooled, 0.1-1.4 cm	p0016.ctsbf56rb
p0026	Regenerating callus 5 days after auxin removal Hi-II callus 223a, 1129e GS3 shoot cultures that were transformed with PHP5869 and were maintained on 273T shoot multiplication medium since 3/17/94 (sample received on 5/29/96 for RNA prep). The original transformation was done on 11/6/93	p0026.ccrab39r
p0027	CM45 shoot culture. It was initiated on 2/28/96 from seed derived meristems. The culture was maintained on 273N medium.	p0027.cgsag51r
p0031	Regenerating callus, 10 and 14 days after auxin removal. Hi-II callus 223a, 1129e 10 days. Hi-II callus 223a, 1129e 14 days	p0031.ccmau15r:fis p0031.ccmbc81r
p0032	corn Root Worm infested V5 roots	p0032.crcav77r:fis
p0037		p0037.crwbs90r:fis
p0083	7 DAP whole kernels	p0083.cldct11r:fis p0083.cldeu68r:fis p0083.clder12r
p0086	P0067 screened 1; 11 DAP pericarp	p0086.cbsaa24r
p0118	Night harvested, pooled stem tissue from the 4-5 internodes subtending the tassel; V8-V12 stages, Screened 1	p0118.chsbc77r p0118.chsbh89r
p0125	Anther: Prophase I sceened 1	p0125.czaab60rb:fis
p0126	Night harvested leaf tissue; V8-V10	p0126.cnlau71r:fis
p0134	Hi-II callus 223a, 1129e, 10days hi-II callus 233a, 1129e, 14days	p0134.carah47r
pps1c	Prickly poppy developing seeds	pps1c.pk001.h3:fis pps1c.pk007.j21:fis
rbm5c	Rice (<i>Oryza sativa</i> , Cypress) bran 10 days after milling	rbm5c.pk001.a19
rca1c	Rice Nipponbare Callus.	rca1c.pk007.b22:fis

TABLE 2 (Continued)

Library	Tissue	Clone
rca1n	Rice (<i>Oryza sativa</i> L., Nipponbare) callus normalized.	rca1n.pk029.n22 rca1n.pk002.j3 rca1n.pk021.b20:fis rca1n.pk004.j14:fis rca1n.pk026.m9 rca1n.pk008.o5:fis r10n.pk096.h23
rl0n	Rice 15 Day Old Leaf*	rl0n.pk0061.c8:fis rl0n.pk131.j17 r10n.pk0015.a4:fis
rlm3n	Rice (<i>Oryza Sativa</i> , YM) leaf mixture (rsr9) normalized at 45 C for 24 hrs using 20 fold excess of driver	rlm3n.pk005.d20:fis
rlr2	Rice (<i>Oryza sativa</i> L.) leaf (15 DAG) 2 hrs after infection of strain 4360-R-62 (AVR2-YAMO); Resistant	rlr2.pk0012.d2
rlr24	Rice Leaf 15 Days After Germination, 24 Hours After Infection of Strain <i>Magnaporthe grisea</i> 4360-R-62 (AVR2-YAMO); Resistant	rlr24.pk0032.e10
rls6	Rice Leaf 15 Days After Germination, 6 Hours After Infection of Strain <i>Magnaporthe grisea</i> 4360-R-67 (AVR2-YAMO); Susceptible	rls6.pk0033.a9:fis
rls72	Rice Leaf 15 Days After Germination, 72 Hours After Infection of Strain <i>Magnaporthe grisea</i> 4360-R-67 (AVR2-YAMO); Susceptible	rls72.pk0023.c8:fis
rr1	Rice Root of Two Week Old Developing Seedling	rr1.pk0039.d4:fis rr1.pk0003.a3:fis rr1.pk097.f22:fis rr1.pk0047.g12:fis rsl1n.pk002.g10:fis
rsl1n	Rice (<i>Oryza sativa</i> , YM) 15 day old seedling normalized	rsl1n.pk002.j2:fis rsl1n.pk006.n24:fis rsl1n.pk013.g2
scb1c	Soybean (<i>Glycine max</i> L., 2872) Embryogenic suspension culture subjected to 4 bombardments and collected 12 hrs later.	scb1c.pk004.n19:fis
sde4c	Soybean Developing Embryo (9-11 mm)	sde4c.pk0001.a2:fis
sdp2c	Soybean (<i>Glycine max</i> L.) developing pods 6-7 mm	sdp2c.pk003.o5:fis sdp2c.pk023.n6:fis sdp2c.pk029.k17:fis sdp2c.pk044.e5:fis
sdp3c	Soybean Developing Pods (8-9 mm)	sdp3c.pk018.b9:fis sdp3c.pk019.n1:fis
sdp4c	Soybean (<i>Glycine max</i> L.) developing pods 10-12 mm	sdp4c.pk009.e3 s dp4c.pk016.e10
sdr1f	Soybean (<i>Glycine max</i> , Wye) 10 day old root	sdr1f.pk001.p7

TABLE 2 (Continued)

Library	Tissue	Clone
sds1f	Soybean (Glycine max, Wye) 11 day old seedling full length library using trehalose	sds1f.pk001.f7:fis
se1	Soybean Embryo, 6 to 10 Days After Flowering	se1.pk0042.d8:fis
se2	Soybean Embryo, 13 Days After Flowering	se2.11d12:fis
ses2w	Soybean Embryogenic Suspension 2 Weeks After Subculture	ses2w.pk0015.a4:fis ses2w.pk0035.a9:fis ses2w.pk0012.d10:fis ses4d.pk0037.e3:fis
ses4d	Soybean Embryogenic Suspension 4 Days After Subculture	ses4d.pk0044.c12 ses4d.pk0006.a12 ses4d.pk0006.a12:fis ses4d.pk0043.d10:fis sfl1.pk0102.h8
sfl1	Soybean Immature Flower	sfl1.pk131.j19 sfl1.pk135.g3 sfl1.pk0029.h10:fis
sgc5c	Soybean (Glycine max L., Wye) germanating cotyledon (3/4 yellow; 15-24 DAG)	sgc5c.pk001.h16
sgs1c	Soybean Seeds 4 Hours After Germination	sgs1c.pk004.f19:fis
sgs4c	Soybean (Glycine max L.) seeds 2 days after germination.	sgs4c.pk004.j2 sgs4c.pk006.g6 sgs4c.pk006.n21
sic1c	Soybean (Glycine max) pooled tissue of root, stem, and leaf with iron chlorosis conditions	sic1c.pk003.o13:fis sic1c.pk003.o18:fis
sif1c	Soybean (Glycine max) pooled tissue of basal stem and root infected with fusarium	sif1c.pk001.m16:fis
sls1c	Soybean (Glycine max L., S1990) infected with Sclerotinia sclerotiorum mycelium.	sls1c.pk010.l1:fis sls1c.pk032.j4
sls1c	Soybean (Glycine max L., S1990) infected with Sclerotinia sclerotiorum mycelium.	sls1c.pk010.l1:fis sls1c.pk020.h24
sls2c	Soybean (Glycine max L., Manta) infected with Sclerotinia sclerotiorum mycelium.	sls2c.pk007.c23:fis
sr1	Soybean Root	sr1.pk0041.a11:fis sr1.pk0049.c2
srb	Scarlett runner bean (R.Goldberg)	srb.08g04
src1c	Soybean 8 Day Old Root Infected With Cyst Nematode	src1c.pk003.o16:fis
src2c	Soybean (Glycine max L., 437654) 8 day old root inoculated with eggs of cyst Nematode (Race 1) for 4 days.	src2c.pk025.b3:fis src2c.pk011.m12:fis src2c.pk009.g9:fis src2c.pk003.i13:fis src3c.pk018.d10:fis sr3c.pk011.g22
src3c	Soybean 8 Day Old Root Infected With Cyst Nematode	src3c.pk012.m6:fis src3c.pk019.d4:fis src3c.pk009.b15 src3c.pk028.j21:fis

TABLE 2 (Continued)

Library	Tissue	Clone
srr1c	Soybean 8-Day-Old Root	srr1c.pk001.i24:fis
srr3c	Soybean 8-Day-Old Root	srr3c.pk001.l10:fis
tlw1c	Tobacco (<i>Nicotiana benthamiana</i>) Leaves Wounded by Abrasion and Harvested After 1.5 Hour.	tlw1c.pk006.o16
vdb1c	Grape (<i>Vitis</i> sp.) developing bud	vdb1c.pk001.m5:fis
vmb1na	Grape (<i>Vitis</i> sp.) midstage berries normalized	vmb1na.pk015.d18:fis
vpl1c	Grape (<i>Vitis</i> sp.) In vitro plantlets	vpl1c.pk008.o5:fis
vrr1c	Grape (<i>Vitis</i> sp.) resistant roots	vrr1c.pk004.o20:fis
vs1n	<i>Vernonia</i> Seed*	vs1n.pk013.m13:fis
wde1f	Wheat (<i>Triticum aestivum</i> , Hi Line) developing endosperm 2-7 DPA	wde1f.pk003.h2:fis
wdk2c	Wheat Developing Kernel, 7 Days After Anthesis.	wdk2c.pk009.e4
wdk2c	Wheat Developing Kernel, 7 Days After Anthesis.	wdk2c.pk018.c16:fis
wdk3c	Wheat Developing Kernel, 14 Days After Anthesis.	wdk3c.pk023.h15:fis
wdk5c	Wheat Developing Kernel, 30 Days After Anthesis	wdk5c.pk006.m13
wdk9n	Wheat (<i>Triticum aestivu</i> , Spring Wheat) kernels 3, 7, 14 and 21 days after anthesis	wdk9n.pk001.k5
wdr1f	Wheat (<i>Triticum aestivum</i>) developing root (full length)	wdr1f.pk003.b21:fis
wds1f	Wheat developing seedling full length	wds1f.pk002.p21:fis
wia1c	Wheat (<i>Triticum aestivum</i> , Hi Line) immature anthers	wia1c.pk001.d20:fis
wkm1c	Wheat Kernel malted 55 Hours at 22 Degrees Celsius	wkm1c.pk0002.d7:fis
wl1n	Wheat Leaf From 7 Day Old Seedling*	wl1n.pk0114.f9
wle1n	Wheat Leaf From 7 Day Old Etiolated Seedling*	wle1n.pk0076.h7:fis
wlk8	Wheat Seedlings 8 Hours After Treatment With Fungicide**	wlk8.pk0001.e10:fis
wlm96	Wheat Seedlings 96 Hours After Inoculation With <i>Erysiphe graminis f. sp tritici</i>	wlm96.pk060.d5 wlm96.pk037.k9:fis wlm96.pk035.j11:fis wlm96.pk0007.e4:fis
wr1	Wheat Root From 7 Day Old Seedling	wr1.pk0094.f2:fis wr1.pk0153.c7:fis wr1.pk148.f7:fis
wre1n	Wheat Root From 7 Day Old Etiolated Seedling*	wre1n.pk0066.e4:fis wre1n.pk0143.h2:fis

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

** Application of 6-iodo-3-propyl-2-propyloxy-4(3H)-quinazolinone; synthesis and methods of using this compound are described in U.S. Pat No. 5,747,497.

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
5 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 ligase (New England Biolabs), followed by transfection into DH10B cells according to the manufacturer's protocol (GIBCO BRL
10 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 polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Amplified insert DNAs or plasmid DNAs are sequenced in dye-
15 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.

Full-insert sequence (FIS) data is generated utilizing a modified transposition
20 protocol. Clones identified for FIS are recovered from archived glycerol stocks as single colonies, and plasmid DNAs are isolated via alkaline lysis. Isolated DNA templates are reacted with vector primed M13 forward and reverse oligonucleotides in a PCR-based sequencing reaction and loaded onto automated sequencers. Confirmation of clone identification is performed by sequence alignment to the
25 original EST sequence from which the FIS request is made.

Confirmed templates are transposed via the Primer Island transposition kit (PE Applied Biosystems, Foster City, CA) which is based upon the *Saccharomyces cerevisiae* Ty1 transposable element (Devine and Boeke (1994) *Nucleic Acids Res.* 22:3765-3772). The *in vitro* transposition system places unique binding sites
30 randomly throughout a population of large DNA molecules. The transposed DNA is then used to transform DH10B electro-competent cells (Gibco BRL/Life Technologies, Rockville, MD) via electroporation. The transposable element contains an additional selectable marker (named DHFR; Fling and Richards (1983) *Nucleic Acids Res.* 11:5147-5158), allowing for dual selection on agar plates of only
35 those subclones containing the integrated transposon. Multiple subclones are randomly selected from each transposition reaction, plasmid DNAs are prepared via alkaline lysis, and templates are sequenced (ABI Prism dye-terminator

ReadyReaction mix) outward from the transposition event site, utilizing unique primers specific to the binding sites within the transposon.

Sequence data is collected (ABI Prism Collections) and assembled using Phred/Phrap (P. Green, University of Washington, Seattle). Phrep/Phrap is a public domain software program which re-reads the ABI sequence data, re-calls the bases, assigns quality values, and writes the base calls and quality values into editable output files. The Phrap sequence assembly program uses these quality values to increase the accuracy of the assembled sequence contigs. Assemblies are viewed by the Consed sequence editor (D. Gordon, University of Washington, Seattle).

10 In some of the clones the cDNA fragment corresponds to a portion of the 3'-terminus of the gene and does not cover the entire open reading frame. In order to obtain the upstream information one of two different protocols are used. The first of these methods results in the production of a fragment of DNA containing a portion of the desired gene sequence while the second method results in the production of
15 a fragment containing the entire open reading frame. Both of these methods use two rounds of PCR amplification to obtain fragments from one or more libraries. The libraries some times are chosen based on previous knowledge that the specific gene should be found in a certain tissue and some times are randomly-chosen. Reactions to obtain the same gene may be performed on several libraries in parallel
20 or on a pool of libraries. Library pools are normally prepared using from 3 to 5 different libraries and normalized to a uniform dilution. In the first round of amplification both methods use a vector-specific (forward) primer corresponding to a portion of the vector located at the 5'-terminus of the clone coupled with a gene-specific (reverse) primer. The first method uses a sequence that is
25 complementary to a portion of the already known gene sequence while the second method uses a gene-specific primer complementary to a portion of the 3'-untranslated region (also referred to as UTR). In the second round of amplification a nested set of primers is used for both methods. The resulting DNA fragment is ligated into a pBluescript vector using a commercial kit and following the
30 manufacturer's protocol. This kit is selected from many available from several vendors including Invitrogen (Carlsbad, CA), Promega Biotech (Madison, WI), and Gibco-BRL (Gaithersburg, MD). The plasmid DNA is isolated by alkaline lysis method and submitted for sequencing and assembly using Phred/Phrap, as above.

EXAMPLE 2

Identification of cDNA Clones

35 cDNA clones encoding proteins involved in altering plant oil traits were identified by gene profiling (see Example 7) and by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al (1993) *J. Mol. Biol.* 215:403-410.

searches for similarity to sequences contained in the 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 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 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.

ESTs submitted for analysis are compared to the genbank database as described above. ESTs that contain sequences more 5- or 3-prime can be found by using the BLASTn algorithm (Altschul et al (1997) *Nucleic Acids Res.* 25:3389-3402.) against the DuPont proprietary database comparing nucleotide sequences that share common or overlapping regions of sequence homology. Where common or overlapping sequences exist between two or more nucleic acid fragments, the sequences can be assembled into a single contiguous nucleotide sequence, thus extending the original fragment in either the 5 or 3 prime direction. Once the most 5-prime EST is identified, its complete sequence can be determined by Full Insert Sequencing as described in Example 1. Homologous genes belonging to different species can be found by comparing the amino acid sequence of a known gene (from either a proprietary source or a public database) against an EST database using the tBLASTn algorithm. The tBLASTn algorithm searches an amino acid query against a nucleotide database that is translated in all 6 reading frames. This search allows for differences in nucleotide codon usage between different species, and for codon degeneracy.

EXAMPLE 3

Characterization of cDNA Clones Encoding Proteins Involved in Altering Oil Phenotypes

The BLASTX search using the EST sequences from clones listed in Table 3 revealed similarity of the polypeptides encoded by the cDNAs to Hap2 homologs,

Hap5 homologs, and Lec1 transcription factors from various species including *Arabidopsis thaliana*, rice (*Oryza sativa*), corn (*Zea mays*), soybean (*Glycine max*), cucumber (*Cucumis sativus*), *Sordaria* (*Sordaria macrospora*), sesame (*Sesamum indicum*), grape (*Vitis* sp.), Brassica (*Brassica napus*), and tobacco (*Nicotiana tabacum*). Shown in Table 3 are the BLAST results for individual ESTs ("EST"), the sequences of the entire cDNA inserts comprising the indicated cDNA clones ("FIS"), the sequences of contigs assembled from two or more ESTs ("Contig"), sequences of contigs assembled from an FIS and one or more ESTs ("Contig*"), or sequences encoding an entire protein derived from an FIS, a contig, or an FIS and PCR ("CGS"):

TABLE 3
BLAST Results for Sequences Encoding Polypeptides Homologous
to Proteins Involved in Altering Oil Phenotypes

SEQ ID NO.	Gene Name	Clone	Homolog	Genbank #	pLOG
2	Hap2a	ncs.pk0013.c4	No hits		-
4	Hap2c	etr1c.pk006.f9	No hits		-
6	Hap2a	vmb1na.pk015.d18	Arabidopsis	11282597	8.1
8	Hap2a	vpl1c.pk008.o5: fis	Grape	7141243	91.2
10	Hap2c	vdb1c.pk001.m5: fis	Rice	7489565	38.0
12	Hap2c	cho1c.pk004.b19: fis	Rice	7489565	94.3
14	Hap2c	p0015.cdpгу90r: fis	Rice	7489565	96.2
16	Hap2a	cta1n.pk0070.f3: fis	Rice	7489565	38.1
18	Hap2a	cco1n.pk0014.d4: fis	Arabidopsis	6634774	37.2
20	Hap2a	cco1n.pk086.d20: fis	Arabidopsis	6634774	36.3
22	Hap2b	p0126.cnlau71r: fis	Rice	7489565	23.7
24	Hap2b	p0104.cabav52r	Rice	7489565	16.7
26	Hap2b	cho1c.pk007.l21: fis	Rice	7489565	35.0
		contig of:			
		cca.pk0026.d6			
28	Hap2c	cen3n.pk0061.e10: fis	Rice	7489565	43.5
		cen3n.pk0135.c2			
		cho1c.pk001.n24			
		p0092.chwae40r			
30	Hap2c	cpf1c.pk006.e3: fis	Rice	7489565	44.0
		contig of:	Rice	7489565	
32	Hap2c	cr1n.pk0080.g6			35.0
		p0003.cgpgе51r			
34	Hap2c	p0015.cdpfm55r: fis	Arabidopsis	4587559	26.4
36	Hap2	p0083.cldct11r: fis	Rice	7489565	91.4
38	Hap2	p0083.cldeu68r: fis	Rice	7489565	14.2
40	Hap2a	pps1c.pk001.h3: fis	Arabidopsis	9293997	45.5
42	Hap2c	pps1c.pk007.j21: fis	Arabidopsis	5903072	53.7
44	Hap2	rr1.pk0030.f7: fis	Rice	7489565	identical

TABLE 3 (Continued)

46	Hap2a	rls72.pk0023.c8:fis	Arabidopsis	9293997	36.5
48	Hap2a	rca1n.pk002.c15	Grape	7141243	7.7
50	Hap2a	rds3c.pk001.g9	Rice	7489565	18.2
52	Hap2b	rca1n.pk002.j3:fis	Rice	7489565	26.0
54	Hap2c	rca1n.pk029.n22:fis	Arabidopsis	8778470	29.2
56	Hap2b	r10n.pk131.j17	Rice	7489565	10.5
58	Hap2a	sdp3c.pk018.b9:fis	Arabidopsis	2398521	74.5
60	Hap2a	sfl1.pk0102.h8	Grape	7141243	36.7
62	Hap2a	srr3c.pk001.l10:fis	Brassica	1586551	48.7
64	Hap2a	sdp2c.pk003.o5:fis	Arabidopsis	6634774	53.0
66	Hap2b	sif1c.pk001.m16:fis	Arabidopsis	6714441	180.0
68	Hap2c	src1c.pk003.o16:fis	Rice	7489565	33.5
70	Hap2c	src3c.pk012.m6:fis	Rice	7489565	31.5
72	Hap2a	hss1c.pk011.h10:fis	Arabidopsis	9293997	48.7
74	Hap2c	wr1.pk0094.f2:fis	Rice	7489565	92.7
76	Hap2a	wre1n.pk0143.h2:fis	Arabidopsis	6634774	35.0
78	Hap2b	wds1f.pk002.p21:fis	Arabidopsis	6714441	26.5
		contig of:	Rice	7489565	
80	Hap2b	wdi1c.pk002.b10			38.5
		wr1.pk0153.c7:fis			
82	Hap2c	wre1n.pk0066.e4:fis	Rice	7489565	42.7
84	Hap5c	ect1c.pk001.k17:fis	Rice	5257260	57.0
86	Hap5a	vrr1c.pk004.o20:fis	Arabidopsis	6523090	93.0
88	Hap5a	clm1f.pk001.k17:fis	Arabidopsis	6523090	66.7
90	Hap5b	cde1n.pk003.a5:fis	Arabidopsis	3776575	57.0
92	Hap5b	cen3n.pk0164.a10:fis	Arabidopsis	3776575	57.0
94	Hap5b	p0118.chsbc77r	Arabidopsis	3776575	58.5
96	Hap5c	cco1n.pk055.o18	Rice	5257260	41.0
98	Hap5c	cho1c.pk001.l23:fis	Rice	5257260	82.0
100	Hap5c	cse1c.pk001.h6:fis	Rice	5257260	86.4
102	Hap5a	rlm3n.pk005.d20:fis	Arabidopsis	6523090	66.7
104	Hap5b	rr1.pk0003.a3:fis	Arabidopsis	6289057	58.5
106	Hap5b	rr1.pk0039.d4:fis	Arabidopsis	3776575	57.2
108	Hap5c	rca1n.pk021.b20:fis	Rice	5257260	74.0
110	Hap5a	sdp2c.pk029.k17:fis	Arabidopsis	6523090	90.5
112	Hap5a	sdp2c.pk044.e5:fis	Arabidopsis	6523090	92.4
114	Hap5b	sgs4c.pk004.j2	Arabidopsis	3776575	18.5
116	Hap5b	src3c.pk002.h4:fis	Arabidopsis	6289057	61.1
118	Hap5b	src3c.pk009.b15:fis	Arabidopsis	6289057	61.5
120	Hap5b	src3c.pk019.d4:fis	Arabidopsis	6056368	51.5
122	Hap5c	sls1c.pk032.j4:fis	Arabidopsis	6289057	74.5
124	Hap5	wdk2c.pk009.e4:fis	Rice	5257260	20.0

TABLE 3 (Continued)

SEQ ID NO.	Gene Name	Clone	Homolog	Genbank #	pLOG
126	Hap5a	Contig of: wlm96.pk036.j11	Arabidopsis	9758288	19.7
128	Hap5c	wlm96.pk060.d5: fis wle1n.pk0076.h7: fis	Rice	5257260	82.0
130	Lec1	eas1c.pk003.e16	Arabidopsis	9758795	49.2
132	Lec1	fds1n.pk008.m14	Arabidopsis	9758795	46.1
134	Lec1	p0015.cdpg75rb: fis	Arabidopsis	9758795	45.4
136	Lec1	p0083.clder12r: fis	Arabidopsis	6552738	35.2
138	Lec1	pps1c.pk002.l19	Arabidopsis	9758795	45.2
140	Lec1	Contig of: scb1c.pk004.j10	Arabidopsis	9758795	47.4
142	Lec1	se1.pk0042.d8: fis se2.11d12: fis	Arabidopsis	9758795	52.2
144	Lec1	ses2w.pk0015.a4: fis	Arabidopsis	9758795	43.7
146	Lec1	vs1n.pk013.m13: fis	Arabidopsis	9758795	53.1
148	Lec1	wdk3c.pk023.h15: fis	Arabidopsis	9758795	36.7
150	Lec1-CCAAT	ect1c.pk007.p18: fis	Zea mays	22380	44.7
152	Lec1-CCAAT	fds.pk0003.h5: fis	Arabidopsis	6729485	57.7
154	Lec1-CCAAT	eef1c.pk004.c8: fis	Zea mays	22380	61.7
156	Lec1-CCAAT	cbn10.pk0005.e6: fis	Zea mays	22380	72.2
158	Lec1-CCAAT	p0006.cbysa51r: fis	Arabidopsis	2244810	55.5
160	Lec1-CCAAT	rl0n.pk0061.c8: fis	Zea mays	22380	46.5
162	Lec1-CCAAT	rsl1n.pk002.g10: fis	Zea mays	22380	68.7
164	Lec1-CCAAT	ses4d.pk0037.e3: fis	Arabidopsis	2398529	49.0
166	Lec1-CCAAT	src2c.pk003.i13: fis	Arabidopsis	3738293	41.1
168	Lec1-CCAAT	src2c.pk011.m12: fis	Arabidopsis	6729485	62.0
170	Lec1-CCAAT	src2c.pk025.b3: fis	Zea mays	22380	45.5
172	Lec1-CCAAT	src3c.pk028.j21: fis	Zea mays	22380	54.3
174	Lec1-CCAAT	wkm1c.pk0002.d7: fis	Zea mays	22380	79.5
176	Lec1-CCAAT	wlk8.pk0001.e10: fis	Arabidopsis	2398529	52.7
178	Lec1-CCAAT	wlm96.pk037.k9: fis	Zea mays	22380	73.5
206	Lec1	rice genome seq	Oryza sativa	7378310	180
208	Hap2	ncs.pk0013.c4: fis	Arabidopsis	9293997	46.7
210	Hap2	p0117.chcln94r: fis	Oryza sativa	1489565	26.0
212	Hap2	rdi2c.pk011.f19: fis	Oryza sativa	1489565	45.0
214	Hap2	sfl1.pk0101.g7: fis	Vitis sp.	7141243	38.4
216	Hap2	wdi1c.pk002.b10: fis	Oryza sativa	1489565	40.3
221	Hap5	sgs4c.pk004.j2: fis	Arabidopsis	15223482	69.0

The sequence of the entire cDNA insert in the clones listed in Table 3 was determined. Further sequencing and searching of the DuPont proprietary database allowed the identification of other corn, rice, soybean and/or wheat clones encoding polypeptides involved in altering oil phenotypes. The BLASTX search using the

sequences from clones listed in Table 4 revealed similarity of the polypeptides encoded by the various cDNAs from plant and fungal species (noted by their NCBI General Identifier No. in Tables 3 and 4). Shown in Table 4 are the BLAST results for individual ESTs ("EST"), the sequences of the entire cDNA inserts comprising the indicated cDNA clones ("FIS"), sequences of contigs assembled from two or more ESTs ("Contig"), sequences of 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 4

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to Polypeptides Involved in Altering Plant Oil Phenotypes

SEQ ID NO.	Accession No. (SEQ ID NO)	Percent Identity
2	1586551 (187)	23.4%
4	7489565 (181)	27.4%
6	11282597 (179)	22.1%
10	7489565 (181)	36.1%
12	7489565 (181)	67.2%
14	7489565 (181)	70.6%
16	7489565 (181)	33.2%
18	6634774 (182)	40.1%
20	6634774 (182)	39.1%
22	7489565 (181)	28.2%
24	7489565 (181)	53.2%
26	7489565 (181)	34.0%
28	7489565 (181)	39.5%
30	7489565 (181)	39.5%
32	7489565 (181)	35.5%
34	4587559 (202)	54.1%
36	7489565 (181)	67.2%
38	7489565 (181)	29.0%
40	9293997 (217)	31.5%
42	5903072 (184)	35.3%
46	5903072 (184)	33.7%
48	7141243 (180)	34.5%
50	7489565 (181)	35.7%
52	7489565 (181)	27.2%
54	8778470 (185)	40.5%
56	7489565 (181)	22.1%
58	2398521 (186)	49.1%
60	7141243 (180)	40.9%
62	1586551 (187)	37.8%

TABLE 4 (Continued)

SEQ ID NO.	Accession No. (SEQ ID NO)	Percent Identity
64	6634774 (182)	49.2%
66	6714441 (188)	32.5%
68	7489565 (181)	32.4%
70	7489565 (181)	31.1%
72	9293997 (217)	40.6%
74	7489565 (181)	68.5%
76	6634774 (182)	36.5%
78	6714441 (188)	23.7%
80	7489565 (181)	34.5%
82	7489565 (181)	37.4%
84	5257260 (189)	62.9%
86	6523090 (190)	77.7%
88	6523090 (190)	53.8%
90	3776575 (191)	50.7%
92	3776575 (191)	51.6%
94	3776575 (191)	60.0%
96	5257260 (189)	62.7%
98	5257260 (189)	75.0%
100	5257260 (189)	77.5%
102	6523090 (190)	53.8%
104	6289057 (192)	50.6%
106	3776575 (191)	52.1%
108	5257260 (189)	77.9%
110	6523090 (190)	70.3%
112	6523090 (190)	70.7%
114	3776575 (191)	35.7%
116	6289057 (192)	53.2%
118	6289057 (192)	52.8%
120	6056368 (193)	73.0%
122	6289057 (192)	57.1%
124	5257260 (189)	27.3%
126	9758288 (194)	46.3%
128	5257260 (189)	74.9%
130	9758795 (196)	49.0%
132	9758795 (196)	49.7%
134	9758795 (196)	49.8%
136	6552738 (195)	38.9%
208	9293997 (217)	34.9%
210	7489565 (218)	28.6%
212	7489565 (218)	35.7%
214	7141243 (219)	42.3%
216	7489565 (218)	34.9%
221	15223482 (222)	64.8%

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 and BLAST scores and probabilities indicate that the nucleic acid fragments comprising the instant cDNA clones encode a substantial portion of cDNAs to receptor protein kinases, MEK3 homologs, Hap2 homologs, LIP 15 homologs, calcium EF-hand proteins, ATP citrate lyase, glucose metabolism proteins such as SNF1 homologs, Lec1 transcription factors, and seed developmentally regulated transcription factors such as CKC (Aintegumenta-like) homologs.

EXAMPLE 4

Expression of Recombinant DNA constructs in Monocot Cells

A recombinant DNA construct comprising a cDNA encoding the instant polypeptides 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 (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 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 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; U.S. Biochemical). The resulting plasmid construct would comprise a recombinant DNA construct encoding, in the 5' to 3' direction, the maize 27 kD zein promoter, a cDNA fragment encoding the instant polypeptides, and the 10 kD zein 3' region.

5 The recombinant DNA construct described above can then be introduced into corn cells by the following procedure. Immature corn embryos can be dissected from developing caryopses 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
10 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 proembryoids and embryoids borne on suspensor structures proliferates from the scutellum of these immature embryos. The embryogenic callus isolated from the primary explant can
15 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).
20 The enzyme PAT confers 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*.

25 The particle bombardment method (Klein et al (1987) *Nature* 327:70-73) may be used to transfer genes to the callus culture cells. According to this method, gold particles (1 µm in diameter) are coated with DNA using the following technique. Ten µg of plasmid DNAs are added to 50 µL of a suspension of gold particles (60 mg per ml). Calcium chloride (50 µL of a 2.5 M solution) and spermidine free
30 base (20 µL of a 1.0 M solution) are added to the particles. The suspension is vortexed during the addition of these solutions. After 10 minutes, the tubes are briefly centrifuged (5 sec at 15,000 rpm) and the supernatant removed. The particles are resuspended in 200 µL of absolute ethanol, centrifuged again and the supernatant removed. The ethanol rinse is performed again and the particles
35 resuspended in a final volume of 30 µL of ethanol. An aliquot (5 µL) of the DNA-coated gold particles can be placed in the center of a Kapton™ flying disc (Bio-Rad Labs). The 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 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.

Seven days after bombardment the tissue can be transferred to N6 medium that contains bialophos (5 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 bialophos. After 6 weeks, areas of about 1 cm in diameter of actively growing callus can be identified on some of the plates containing the bialophos-supplemented medium. These calli may continue to grow when sub-cultured on the 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 Recombinant DNA constructs in Dicot Cells

A seed-specific expression cassette 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 cassette includes about 500 nucleotides upstream (5') from the translation initiation codon and about 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 cassette is flanked by Hind III sites.

The cDNA fragment of this gene may be generated by polymerase chain reaction (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 expression cassette.

Soybean embryos may then be transformed with the expression vector comprising 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 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 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.

A selectable marker gene which can be used to facilitate soybean transformation is a recombinant DNA construct 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 expression cassette comprising the phaseolin 5' region, the fragment encoding the instant polypeptides 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.

To 50 µL of a 60 mg/mL 1 µm gold particle suspension is added (in order): 5 µL DNA (1 µg/µL), 20 µL spermidine (0.1 M), and 50 µL CaCl₂ (2.5 M). The particle preparation is then agitated for three minutes, spun in a microfuge for 10 seconds and the supernatant removed. The DNA-coated particles are then washed once in 400 µL 70% ethanol and resuspended in 40 µL of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five µL 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 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.

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

EXAMPLE 6

Expression Vector for Plant Transformation by Particle Gun Bombardment.

A seed specific gene expression cassette was used for making recombinant DNA constructs for expression of candidate genes in corn. The expression cassette
20 is composed of the 0.9kb oleosin promoter, the intron 1 of the maize shrunken 1 gene and adjacent exon (Vasil et al, 1989, *Plant Physiol* 91: 1575-1579; Mascarenhas et al, 1990, *Plant Mol Biol* 15:913-920) and 3' transcription termination region from the nopaline synthase (Nos) gene. In between the exon adjacent to the shrunken 1 gene and the nopaline synthase (Nos) gene are unique restriction
25 endonuclease sites MfeI and XmaI. This vector has been designated pBN256.

pMUT256 refers to a pBN256 plasmid in which a EcoRI site has been removed by site directed mutagenesis. A modified version of pMUT256, designated pMUT256e was modified by addition of a synthetic multiple cloning site. The synthetic polylinker was generated by annealing of oligos (5'-
30 acagtacagtacagtacagtacagt-3') and (5'-actgtactgtactgtacgtgactgt-3') [SEQ ID NOs:430 and 431, respectively] and subsequent subcloning into the pMut256 open with MfeI and XmaI. Additional expression cassettes/vectors will be described in reference to specific examples where they have been used (see below).

EXAMPLE 7Isolation and Cloning of Candidate Genes into Embryo-specific Plant Expression Vectors.HAP3/LEC1 (Heme-Activated Protein 3/ Leafy Cotyledon 1):

5 A full length clone (p0015.cdpgp75rb, SEQ ID NOs:134) for the corn homolog of the HAP3/Lec1 gene was obtained from Dupont/Pioneer EST Database. The ORF of maize HAP3/Lec1 (a 1 kb Sall/HpaI fragment, PCT Application No. WO 00/28058, published on May 18, 2000) was moved into an expression cassette containing a maize oleosin promoter (a 0.9 kb BamHI/XhoI fragment, PCT

10 Application No. WO 99/64579, published on December 16, 1999) and a polyadenylation sequence from the *Agrobacterium* nopaline synthase gene. This expression cassette was then subcloned adjacent to a 35S::Bar expression cassette (Sidorenko et al (2000) *Plant J* 22:471-482). The resulting expression cassettes flanked by T-DNA border sequences were then mobilized into the *Agrobacterium*

15 "super-binary" vector (Komari, 1990) using electroporation. Additional constructs were made to confer expression patterns different from those obtained with the oleosin promoter. A ubiquitin promoter (UBI, Christensen et al (1992) *Plant Mol Biol* 18:675-680), a lipid transfer protein (LTP) promoter (U.S. Patent No. 5,525,716), and a gamma zein promoter (GZP) (Boronat et al (1986) *Plant Science* 47: 95-102)

20 were each fused to Lec1 as described above for the oleosin promoter. The two transcription units, LTP-Lec1 and GZP-Lec1, were combined into one expression construct next to the 35S:Bar expression construct and flanked by T-DNA border sequences (as described above).

HAP2 (Heme-Activated Protein 2):

25 A full length clone (cho1c.pk006.b14, a 30 nucleotide shorter cDNA than cho1c.pk004.b19: fis, shown in SEQ ID NO:27) for the corn homolog of the HAP2 gene was obtained from Dupont/Pioneer EST Database. The Apol/ApaI 1.1 kb fragment of cho1c.pk006.b14 was isolated and subcloned into pMUT256e opened by digestion with EcoRI/ApaI. One clone was selected for corn transformation by

30 restriction digestion analysis for correct insert size. Subcloning artifacts were excluded by 5' and 3' sequence of the vector-insert boundaries.

HAP5 (Heme-Activated Protein 5):

A full length clone (cho1c.pk001.l23, shown in SEQ ID NO:113) for the corn homolog of HAP5 gene was obtained from Dupont/Pioneer EST Database. The

35 EcoRI/ApaI 1.1 kb fragment of cho1c.pk001.l23 was isolated and subcloned into pMUT256e opened by digestion with EcoRI/ApaI. One clone was selected for corn transformation after restriction digestion analysis for correct insert size. Subcloning artifacts were excluded by 5' and 3' sequence of the vector-insert boundaries.

EXAMPLE 8

Transformation of Immature Embryos By Particle Bombardment and Regeneration of Corn Plants

Immature maize embryos from greenhouse donor plants are bombarded with a
5 plasmid containing the gene of the invention operably linked to a weak promoter,
such as the nos promoter, or an inducible promoter, such as In2, plus a plasmid
containing the selectable marker gene PAT (Wohlleben et al (1988) *Gene* 70:25-37)
that confers resistance to the herbicide Bialaphos. Transformation is performed as
follows. The ears are surface sterilized in 30% Chloral bleach plus 0.5% Micro
10 detergent for 20 minutes, and rinsed two times with sterile water. The immature
embryos are excised and placed embryo axis side down (scutellum side up), 25
embryos per plate. These are cultured on 560 L medium 4 days prior to
bombardment in the dark. Medium 560 L is an N6-based medium containing
Eriksson's vitamins, thiamine, sucrose, 2,4-D, and silver nitrate. The day of
15 bombardment, the embryos are transferred to 560 Y medium for 4 hours and are
arranged within the 2.5-cm target zone. Medium 560Y is a high osmoticum medium
(560 L with high sucrose concentration). A plasmid vector comprising the gene of
the invention operably linked to the selected promoter is constructed. This plasmid
DNA plus plasmid DNA containing a PAT selectable marker is precipitated onto
20 1.1 μm (average diameter) tungsten pellets using a CaCl_2 precipitation procedure
as follows: 100 μl prepared tungsten particles in water, 10 μl (1 μg) DNA in
TrisEDTA buffer (1 μg total), 100 μl 2.5 M CaCl_2 , 10 μl 0.1 M spermidine. Each
reagent is added sequentially to the tungsten particle suspension, while maintained
on the multitube vortexer. The final mixture is sonicated briefly and allowed to
25 incubate under constant vortexing for 10 minutes. After the precipitation period, the
tubes are centrifuged briefly, liquid removed, washed with 500 ml 100% ethanol,
and centrifuged for 30 seconds. Again the liquid is removed, and 105 μl 100%
ethanol is added to the final tungsten particle pellet. For particle gun bombardment,
the tungsten/DNA particles are briefly sonicated and 10 μl spotted onto the center of
30 each macrocarrier and allowed to dry about 2 minutes before bombardment. The
sample plates are bombarded at level #4 in particle gun #HE34-1 or #HE34-2. All
samples receive a single shot at 650 PSI, with a total of ten aliquots taken from
each tube of prepared particles/DNA. Following bombardment, the embryos are
kept on 560Y medium, an N6 based medium, for 2 days, then transferred to 560R
35 selection medium, an N6 based medium containing 3 mg/liter Bialaphos, and
subcultured every 2 weeks. After approximately 10 weeks of selection, selection-
resistant callus clones are sampled for PCR and activity of the gene of interest.
Positive lines are transferred to 288J medium, an N6 based medium with lower

sucrose and hormone levels, to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to medium for germination and transferred to the lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to classic 600 pots (1.6 gallon) and grown to maturity. Plants are monitored for expression of the gene of interest.

EXAMPLE 9

Transformation of callus and Regeneration of Corn Plants – Particle Gun.

Type II Callus Isolation and Maintenance.

After 10-21 days, type II callus is initiated from the scutellum and appears as a friable, embryogenic outgrowth of rapidly dividing cells. Callus is subcultured every 5-10 days and maintained on N6 medium supplemented with 1 mg/L 2,4-D (CM). These cultures are used in transformation experiments from 5 to 12 weeks after initiation.

Preparation of Callus for Transformation.

Proembryogenic type II callus is transferred to #4 Whatman filter paper on CM media. The CM plates with callus is wrapped with parafilm and incubated in the dark Conviron growth chamber (45% humidity, 27 -28°C) for two days before bombardment. Prior to bombardment, the osmotic plates are left partially ajar for thirty minutes in the laminar flow hood to allow moisture on the tissue to dissipate.

Gold Particle Preparation

Sixty mg of 0.6 micron gold is weighed out in a siliconized eppendorf tube (Axgen Microtubes - 1.7 ml clear tube). The tube is left stationary for 15 minutes and spun down. The pellet is rinsed with sterile water three more times. Subsequently, one ml of sterile water is added to the gold pellet and vortexed for 10 minutes. The gold particles are divided into 50 ul aliquots.

DNA/Gold Preparation

Fifty µL of 0.6 micron gold in sterile dd H₂O. A 2:1 molar ratio of trait gene:bar gene (usually ~5-10 ug in total DNA) is added and vortexed.. Subsequently, fifty µL of 2.5 M CaCl₂ is added quickly into the suspension and vortexed followed by the addition of 20 µL of 0.1 M spermidine and vortexed and spun down. The pellet is rinsed 3x in 100% ethanol. The pellet is gently resuspended by tapping the side of the eppendorf tube several times. The DNA prep is stored in the 20°C freezer.

Loading of the Macrocarrier

The DNA/gold prep is thawed and sonicated (2 strokes) in the Branson 200 Ultrasonic cleaner prior to the addition to macrocarriers. The suspension is mixed well by pipetting in and out. Immediately, 6 μ l of DNA/gold suspension is dispensed quickly to the center of each macrocarrier. Once the DNA prep is dried onto the macrocarrier, the PDS-100/He Gun is used to bombard the maize callus cells with the DNA-coated gold particles.

Particle Gun Parameters.

Plates containing callus are the bombarded with the PDS-1000/He Gun using the following parameters: 1) DNA precipitated onto 0.6 μ M Gold particles; 2) 8 cm distance from stopping screen; 3) 27-29 inches Hg vacuum; 4) 1050-1100 PSI He pressure.

Selection of Transgenic Callus Lines.

After 3-4 days of incubation in the dark chamber the callus is transferred (3-4 mm clumps) onto media containing 3-5 ppm bialaphos (SM3 or SM5). The SM plates are incubated in the dark at 27°C for ~7-14 days. Thereafter, all callus is transferred onto SM (5 ppm bialaphos) keeping track of unique lines as above. Each clump may be split into several pieces at this transfer.

Regeneration of Transgenic Maize Plants.

Callus events are isolated onto fresh SM medium, sampled for PCR (polymerase chain reaction) and placed on first-stage regeneration media (RM31). After 10-14 days, the proembryogenic callus are transferred onto fresh RM3 plates and placed in the light chamber at 26°C. Plantlets approximately 2-3 cm are removed and transfer to RM4 media tubs. After 1-2 weeks plants from RM4 are potted to a maximum of two plantlets per pot. The pots are then placed in the Conviron growth chamber (photolight = 20 hours, humidity = 65%, temperature = 24°C) and watered with Roots2 solution. Plants (~20 cm tall) are tested for expression of the *bar* gene by performing a 2% basta swipe test.

EXAMPLE 10

Analysis of fatty acid content and composition by gas chromatography (GC)

Fatty acid (FA) determination was done from a total of 300-400 mg of tissue lyophilized for 24 hours. The tissue was then ground using a FastPrep mill (Bio101) at 4.5 speed and 20 seconds in the presence of 0.5 ml of 2.5% Sulfuric Acid + 97.5% Methanol and Heptadecanoic acid (17:0, stock 10 mg/ml in Tuloene) as an external standard. Thereafter, another 0.5 ml 2.5% Sulfuric Acid + 97.5% Methanol was used to wash each tube and incubate in 95°C for 1 hour for transesterification. The tubes were removed from the water bath and allowed to cool down to RT. FAs

were extracted in one volume of heptane:H₂O (1:1) and cleared by centrifugation. The supernatant (50 ul) containing the fatty acid methyl esters were loaded into a Hewlett Packard 6890 gas chromatograph fitted with a 30 m x 0.32 mm Omegawax column and the separated peaks were analyzed and characterized.

5

EXAMPLE 11

Lec 1 Over-expression Leads to Altered Fatty Acid Accumulation in Maize Somatic Embryos

The ubiquitin promoter (Christensen et al (1992) *Plant Mol Biol* 18:675-89) was used to drive Hap3/Lec1 expression (outlined in Example 7) in maize embryogenic callus to test what phenotype would arise from over-expression of Lec1 in somatic embryos. Transformation of the construct into maize embryogenic callus and generation of somatic embryos is outlined in Example 9.

More than ten different events were analysed by GC for fatty acid content/composition and compared to controls transformed with the selectable marker (BAR gene) plasmid alone. A pool of three embryos each from XX different events showed that the somatic embryos overexpressing Lec1 contain elevated fatty acid content (average 119% increase over control) with no significant alteration in fatty acid composition when compared to the control somatic embryos (Figure 1).

EXAMPLE 12

20

Nuclear Magnetic Resonance (NMR) ANALYSIS

Seed are imbibed in distilled water for 12-24 hours at 4°C. The embryo is dissected away and stored in a 48 well plate. The samples are lyophilized overnight in a Virtis 24x48 lyophilizer. The NMR (Process Control Technologies – PCT (Ft. Collins, CO) is set up as per the manufacturer's instructions. The NMR is calibrated using a series of 5 mm NMR tubes containing precisely measured amounts of corn oil (Mazola). The calibration standards are 3, 6, 9, 12, 15, 18, 21, 27, 33, and 40 mg of oil.

EXAMPLE 13

Lec 1 Over-expression Leads to Altered Oil Accumulation in Maize Kernels

30

The Hap3/Lec1 expression construct with the oleosin promoter (outlined in Example 7) was introduced into maize to test what phenotype would arise from seed specific over-expression. Transformation of the construct into maize was accomplished using *Agrobacterium tumefaciens* as follows.

Freshly isolated immature embryos of maize, about 10 days after pollination (DAP), are incubated with the *Agrobacterium*. The preferred genotype for transformation is the highly transformable genotype Hi-II (Armstrong, C. L., 1991, Development and Availability of Germplasm with High Type II Culture Formation Response, *Maize Genetics Cooperation Newsletter*, 65:92-93). An F₁ hybrid

created by crossing with an Hi-II with an elite inbred may also be used. After *Agrobacterium* treatment of immature embryos, the embryos are cultured on medium containing toxic levels of herbicide. Only those cells which receive the herbicide-resistance gene, and the linked gene(s), grow on selective medium.

- 5 Transgenic events so selected are propagated and regenerated to whole plants, produce seed, and transmit transgenes to progeny.

The engineered *Agrobacterium tumefaciens* LBA4404 is constructed as per U.S. Patent No. 5,591,616 to contain the linked gene(s) and the selectable marker gene. Typically either BAR (D'Halluin et al (1992) *Methods Enzymol.* 216:415-426) or PAT (Wohlleben et al (1988) *Gene* 70:25-37) may be used.

To use the engineered vector in plant transformation, a master plate of single bacterial colonies is first prepared by inoculating the bacteria on minimal AB medium and then incubating the bacteria plate inverted at 28°C in darkness for about 3 days. A working plate is then prepared by selecting a single colony from the plate of minimal A medium and streaking it across a plate of YP medium. The YP-medium bacterial plate is then incubated inverted at 28°C in darkness for 1-2 days.

Agrobacterium for plant transfection and co-cultivation is prepared 1 day prior to transformation. Into 30 ml of minimal A medium in a flask is placed 50 µg/ml spectinomycin (or appropriate bacterial antibiotic depending on marker in co-integrate), 100 µM acetosyringone, and about a 1/8 loopful of *Agrobacterium* from a 1 to 2-day-old working plate. The *Agrobacterium* is then grown at 28°C at 200 rpm in darkness overnight (about 14 hours). In mid-log phase, the *Agrobacterium* is harvested and resuspended at 3 to 5 X 10⁸ CFU/ml in 561Q medium + 100 µM acetosyringone using standard microbial techniques and standard curves.

25 Immature Embryo Preparation

Nine to ten days after controlled pollination of a corn plant, developing immature embryos are opaque and 1-1.5 mm long and are the appropriate size for *Agro*-infection. The husked ears are sterilized in 50% commercial bleach and 1 drop Tween for 30 minutes, and then rinsed twice with sterile water. The immature embryos are aseptically removed from the caryopsis and placed into 2 ml of sterile holding solution comprising of 561Q + 100 µM acetosyringone.

Agrobacterium Infection and Co-cultivation of Embryos

Holding solution is decanted from excised immature embryos and replaced with prepared *Agrobacterium*. Following gentle mixing and incubation for about 5 minutes, the *Agrobacterium* is decanted from the immature embryos. Immature embryos are then moved to a plate of 562P medium, scutellum surface upwards, and incubated at 20°C for 3 days in darkness followed by incubation at 28°C for 3

days in darkness on medium 562P + 100 mg/ml carbenecillin (see U.S. Patent 5,981,840).

Selection of Transgenic Events

Following incubation, the immature embryos are transferred to 563O medium for selection of events. The transforming DNA possesses a herbicide-resistance gene, in this example the PAT gene, which confers resistance to bialaphos. At 10- to 14-day intervals, embryos are transferred to 563O medium. Actively growing putative transgenic embryogenic tissue is visible in 6-8 weeks.

Regeneration of T₀ Plants

Transgenic embryogenic tissue is transferred to 288W medium and incubated at 28°C in darkness until somatic embryos matured, or about 10 to 18 days. Individual matured somatic embryos with well-defined scutellum and coleoptile are transferred to 272 embryo germination medium and incubated at 28°C in the light. After shoots and roots emerge, individual plants are potted in soil and hardened-off using typical horticultural methods.

Confirmation of Transformation

Putative transgenic events are subjected to analysis to confirm their transgenic nature. Events are tested for the presence of Lec1 by PCR amplification. Additionally, T₀ plants are painted with bialaphos herbicide. The subsequent lack of a herbicide-injury lesion indicates the presence and action of the herbicide resistance gene. The plants are monitored and scored for altered Lec1 expression and/or phenotype such as increased organic sulfur compounds.

Media Recipes

Medium 561 Q contains the following ingredients: 950.000 ml of D-I Water, Filtered; 4.000 g of Chu (N6) Basal Salts (Sigma C-1416); 1.000 ml of Eriksson's Vitamin Mix (1000x Sigma-1511); 1.250 ml of Thiamine.HCL.4 mg/ml; 3.000 ml of 2, 4-D 0.5 mg/ml (No. 2A); 0.690 g of L-proline; 68.500 g of Sucrose; and 36.000 g of Glucose. Directions are: dissolve ingredients in polished deionized water in sequence; adjust pH to 5.2 w/KOH; Q.S. to volume with polished deionized water after adjusting pH; and filter sterilize (do not autoclave).

Medium 562 P contains the following ingredients: 950.000 ml of D-I Water, Filtered; 4.000 g of Chu (N6) Basal Salts (Sigma C-1416); 1.000 ml of Eriksson's Vitamin Mix (1000x Sigma-1511); 1.250 ml of Thiamine.HCL.4 mg/ml; 4.000 ml of 2, 4-D 0.5 mg/ml; 0.690 g of L-proline; 30.000 g of Sucrose; 3.000 g of Gelrite, which is added after Q.S. to volume; 0.425 ml of Silver Nitrate 2 mg/ml #; and 1.000 ml of Aceto Syringone 100 mM #. Directions are: dissolve ingredients in polished deionized water in sequence; adjust pH to 5.8 w/KOH; Q.S. to volume with polished

deionized water after adjusting pH; and sterilize and cool to 60°C. Ingredients designated with a # are added after sterilizing and cooling to temperature.

Medium 563 O contains the following ingredients: 950.000 ml of D-I Water, Filtered; 4.000 g of Chu (N6) Basal Salts (Sigma C-1416); 1.000 ml of Eriksson's Vitamin Mix (1000x Sigma-1511); 1.250 ml of Thiamine.HCL.4 mg/ml; 30.000 g of Sucrose; 3.000 ml of 2, 4-D 0.5 mg/ml (No. 2A); 0.690 g of L-proline; 0.500 g of Mes Buffer; 8.000 g of Agar (Sigma A-7049, Purified), which is added after Q.S. to volume; 0.425 ml of Silver Nitrate 2 mg/ml #; 3.000 ml of Bialaphos 1 mg/ml #; and 2.000 ml of Agribio Carbenicillin 50 mg/ml #. Directions are: dissolve ingredients in polished deionized water in sequence; adjust to pH 5.8 w/koh; Q.S. to volume with polished deionized water after adjusting pH; sterilize and cool to 60°C. Ingredients designated with a # are added after sterilizing and cooling to temperature.

Medium 288 W contains the following ingredients: 950.000 ml of D-I H₂O; 4.300 g of MS Salts; 0.100 g of Myo-Inositol; 5.000 ml of MS Vitamins Stock Solution (No. 36J); 1.000 ml of Zeatin.5 mg/ml; 60.000 g of Sucrose; 8.000 g of Agar (Sigma A-7049, Purified), which is added after Q.S. to volume; 2.000 ml of IAA 0.5 mg/ml #; 1.000 ml of .1 Mm ABA #; 3.000 ml of Bialaphos 1 mg/ml #; and 2.000 ml of Agribio Carbenicillin 50 mg/ml #. Directions are: dissolve ingredients in polished deionized water in sequence; adjust to pH 5.6; Q.S. to volume with polished deionized water after adjusting pH; sterilize and cool to 60°C. Add 3.5 g/L of Gelrite for cell biology. Ingredients designated with a # are added after sterilizing and cooling to temperature.

Medium 272 contains the following ingredients: 950.000 ml of deionized water; 4.300 g of MS Salts; 0.100 g of Myo-Inositol; 5.000 of MS Vitamins Stock Solution; 40.000 g of Sucrose; and 1.500 g of Gelrite, which is added after Q.S. to volume. Directions are: dissolve ingredients in polished deionized water in sequence; adjust to pH 5.6; Q.S. to volume with polished deionized water after adjusting pH; and sterilize and cool to 60°C.

Medium minimal A contains the following ingredients: 950.000 ml of deionized water; 10.500 g of potassium phosphate dibasic K₂HPO₄; 4.500 g of potassium phosphate monobasic KH₂PO₄; 1.000 g of ammonium sulfate; 0.500 g of sodium citrate dihydrate; 10.000 ml of sucrose 20% solution #; and 1.000 ml of 1M magnesium sulfate #. Directions are: dissolve ingredients in polished deionized water in sequence; Q.S. to volume with deionized water; sterilize and cool to 60°C. Ingredients designated with a # are added after sterilizing and cooling to temperature.

Medium minimal AB contains the following ingredients: 850.000 ml of deionized water; 50.000 ml of stock solution 800A; 9 g of Phytagar which is added after Q.S. to volume; 50.000 ml of stock solution 800B #; 5.000 g of glucose #; and 2.000 ml of spectinomycin 50/mg/ml stock #. Directions are: dissolve ingredients in polished deionized water in sequence; Q.S. to volume with polished deionized water less 100 ml per liter; sterilize and cool to 60°C. Ingredients designated with a # are added after sterilizing and cooling to temperature. Stock solution 800A contains the following ingredients: 950.000 ml of deionized water; 60.000 g of potassium phosphate dibasic K₂HPO₄; and 20.000 g of sodium phos. monobasic, hydrous. Directions are: dissolve ingredients in polished deionized water in sequence; adjust pH to 7.0 with potassium hydroxide; Q.S. to volume with polished deionized water after adjusting pH; and sterilize and cool to 60°C. Stock solution 800B contains the following ingredients: 950.000 ml of deionized water; 20.000 g of ammonium chloride; 6.000 g of magnesium sulfate 7-H₂O, MgSO₄, 7 H₂O; 3.000 g of potassium chloride; 0.200 g of calcium chloride (anhydrate); and 0.050 g of ferrous sulfate 7-hydrate. Directions are: dissolve ingredients in polished deionized water in sequence; Q.S. to volume with polished deionized water; and sterilize and cool to 60°C.

Medium minimal YP contains the following ingredients: 950.000 ml of deionized water; 5.000 g of yeast extract (Difco); 10.000 g of peptone (Difco); 5.000 g of sodium chloride; 15.000 g of bacto-agar, which is added after Q.S. to volume; and 1.000 ml of spectinomycin 50 mg/ml stock #. Directions are: dissolve ingredients in polished deionized water in sequence; adjust pH to 6.8 with potassium hydroxide; Q.S. to volume with polished deionized water after adjusting pH; sterilize and cool to 60°C. Ingredients designated with a # are added after sterilizing and cooling to temperature.

More than twenty events producing segregating T1 seed were analyzed by NMR for embryo oil content (see Example 12). Six to twelve embryos analyzed for each of five different events showed that some embryos within each event contained elevated oil content. These results are shown in Figure 2. The same embryos from these five events were analyzed by PCR to determine the presence or absence of the Lec1 construct. Embryos with high oil are always found to contain the Lec1 construct (darkly shaded bars), whereas embryos with normal levels of oil were typically found not to contain the Lec1 construct (cross-hatched bars). These data demonstrate the presence of the Lec1 gene does lead to increased oil in the embryo. It is believed that embryos containing sharply higher levels of oil were homozygous for the Lec1 construct, as these events were segregating 1:2:1. For these events, the oil concentration in the embryos containing the Lec1 construct

greatly surpassed any increase previously achieved through enzymatic modification of the fatty acid biosynthetic pathway, with some embryos containing an average increase of 56% in embryo oil content (Figure 2, Event 277267). Plants derived from seed that contained high oil exhibit some phenotypic changes in growth and
5 development. There is an accumulation of additional leaves during early growth and development phase, and strong leaf curling throughout plant growth and development.

EXAMPLE 14

Additional Promoters Coupled to Lec1 Also Result in Altered Maize Kernel Oil Accumulation

10

Other types of seed-specific promoters, the lipid transfer protein promoter and the gamma zein promoter, were also tested for their ability to alter oil accumulation in maize kernels when expressing Lec1. Transformation and analysis of these constructs was essentially the same as protocols outlined in Example 13. More
15 than twenty events producing segregating T1 seed are analyzed by NMR for embryo oil content (see Example 12). Six to twelve embryos were analyzed for each event. Events containing embryos with high oil content were analyzed further. The same embryos from these events are analyzed by PCR to determine the presence or absence of the Lec1 construct. As with the oleosin promoter containing
20 construct, all embryos with high oil contents are found to contain the Lec1 construct, whereas embryos with lower or normal oil contents are typically found not to contain the Lec1 construct. Like the events containing Lec1 and the oleosin promoter, the oil concentration in the embryo for these events also greatly surpass any increase previously achieved through enzymatic modification, with some embryos containing
25 an average increase of more than 50% in embryo oil content.

Surprisingly, plants derived from seed containing high oil using this construct do not show the abnormal phenotype found for plants expressing Lec1 under the control of the oleosin promoter. It is believed that these data demonstrate that high oil can be achieved in the embryo without negative agronomic effects when the
30 appropriate expression is employed.

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 aag 1203

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 <212> PRT
 <213> Zea mays

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Ala Glu Glu Arg Ser Lys Gln Gly Gly Lys Glu Ala Ala Ala Arg Ala
 20 25 30

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Ala Gly Cys Arg Lys Gly Asn Met Leu Pro Pro His Leu Thr Glu Asn
35 40 45

Gly Ala Val Met Ile Gln Phe Gly His Gln Met Pro Asp Tyr Asp Ser
50 55 60

Pro Ala Thr Gln Ser Thr Ser Glu Thr Ser His Gln Glu Ala Ser Gly
65 70 75 80

Met Ser Glu Gly Ser Leu Asn Glu His Asn Asn Asp His Ser Gly Asn
85 90 95

Leu Asp Gly Tyr Ser Lys Ser Asp Glu Asn Lys Met Met Ser Ala Leu
100 105 110

Ser Leu Gly Asn Pro Glu Thr Ala Tyr Ala His Asn Pro Lys Pro Asp
115 120 125

Arg Thr Gln Ser Phe Ala Ile Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr
130 135 140

Gly Gly Ala Val Ala Ala Ala Tyr Gly Pro His Ala Ile Met His Pro
145 150 155 160

Gln Leu Val Gly Met Val Pro Ser Ser Arg Val Pro Leu Pro Ile Glu
165 170 175

Pro Ala Ala Glu Glu Pro Ile Tyr Val Asn Ala Lys Gln Tyr His Ala
180 185 190

Ile Leu Arg Arg Arg Gln Leu Arg Ala Lys Leu Glu Ala Glu Asn Lys
195 200 205

Leu Val Lys Ser Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His
210 215 220

Ala Met Lys Arg Ala Arg Gly Thr Gly Gly Arg Phe Leu Asn Thr Lys
225 230 235 240

Gln Gln Pro Glu Ser Pro Gly Ser Gly Gly Ser Ser Asp Ala Gln Arg
245 250 255

Val Pro Ala Thr Ala Ser Gly Gly Leu Phe Thr Lys His Glu His Ser
260 265 270

Leu Pro Pro Gly Gly Arg His His Tyr His Ala Arg Gly Gly Gly Glu
275 280 285

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<211> 1301

<212> DNA

<213> Zea mays

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1301

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<210> 16

<211> 264

<212> PRT

<213> Zea mays

<400> 16

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Met Ser Ser Met Glu Ser Arg Pro Gly Arg Thr Asn Leu Val Glu Pro
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Ile Gly His Gly Ala Ala Leu Pro Ser Gly Gly Gln Ala Val Gln Pro
          20              25              30

Trp Trp Thr Ser Ser Gly Ala Val Leu Gly Ala Val Ser Pro Ala Val
      35              40              45

Val Ala Val Ala Pro Gly Ser Gly Thr Gly Ile Ser Leu Ser Ser Ser
 50              55              60

Pro Ala Gly Gly Ser Gly Gly Gly Gly Ala Ala Lys Gly Ala Ala Ser
 65              70              75              80

Asp Glu Ser Ser Glu Asp Ser Arg Arg Ser Gly Glu Pro Lys Asp Gly
          85              90              95

Ser Ala Ser Gln Glu Lys Asn His Ala Thr Ser Gln Ile Pro Ala Leu
      100              105              110

Ala Pro Glu Tyr Leu Ala Pro Tyr Ser Gln Leu Glu Leu Asn Gln Ser
      115              120              125

Ile Ala Ser Ala Ala Tyr Gln Tyr Pro Asp Pro Tyr Tyr Ala Gly Met
      130              135              140

Val Ala Pro Tyr Gly Ser His Ala Val Ala His Phe Gln Leu Pro Gly
      145              150              155              160

Leu Thr Gln Ser Arg Met Pro Leu Pro Leu Glu Val Ser Glu Glu Pro
          165              170              175

Val Tyr Val Asn Ala Lys Gln Tyr His Gly Ile Leu Arg Arg Arg Gln
      180              185              190

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Ser Arg Ala Lys Ala Glu Leu Glu Lys Lys Val Val Lys Ala Arg Lys
 195 200 205

Pro Tyr Leu His Glu Ser Arg His Gln His Ala Met Arg Arg Ala Arg
 210 215 220

Gly Asn Gly Gly Arg Phe Leu Asn Thr Lys Lys Ser Asp Ser Gly Ala
 225 230 235 240

Pro Asn Gly Gly Glu Asn Ala Glu His Leu His Val Pro Pro Asp Leu
 245 250 255

Leu Gln Leu Arg Gln Asn Glu Ala
 260

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 <211> 1258
 <212> DNA
 <213> Zea mays

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 gaacctgggg accagcaaga agccccagtt actagttcag atagccaacc aacagtaggc 360
 acaccatcaa cagattatgt ggcaccctat gccctcatg acatgagcca tgcaatgggt 420
 caatacgctt atccaaatat tgaccatac tatggaagcc tttatgcagc agcttacggt 480
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 cagaacggag ttgcgccccca caggagcggc caaccgtcaa cccctccgtc tcccaacggt 840
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 gaagagattt cagccccctga gctagatatg gcagcagttt tgtacagaaa acgctagcaa 960
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<210> 18
 <211> 214
 <212> PRT
 <213> Zea mays

<400> 18
 Met Thr Ser Val Val His Ser Val Ser Gly Asp His Arg Ala Glu Asp
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 Gln Asn Gln Gln Lys Lys Gln Ala Glu Pro Gly Asp Gln Gln Glu Ala
 20 25 30
 Pro Val Thr Ser Ser Asp Ser Gln Pro Thr Val Gly Thr Pro Ser Thr
 35 40 45

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

<210> 19
 <211> 1170
 <212> DNA
 <213> Zea mays

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 gaagagccag tgtatgtaaa tgcaaagcaa tacaatgcca tattaagacg gcgtcaatct 660
 cgggctaaag ctgaatcaga acggaagctt gtcaagggcc gcaagcccta tctccatgag 720
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<210> 20
 <211> 215
 <212> PRT
 <213> Zea mays

<400> 20
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 Gln Ser His Gln Lys Lys Gln Thr Glu Pro Gly Asp Gln Gln Glu Ala
 20 25 30
 Pro Val Thr Ser Ser Asp Ser Gln Pro Thr Val Gly Thr Pro Ser Thr
 35 40 45
 Asp Tyr Val Ala Pro Tyr Ala Pro His Asp Met Ser His Ala Met Gly
 50 55 60
 Gln Tyr Ala Tyr Pro Asn Ile Asp Pro Tyr Tyr Gly Ser Leu Tyr Ala
 65 70 75 80
 Ala Ala Tyr Gly Gly His Pro Leu Met His Pro Thr Leu Val Gly Met
 85 90 95
 His Pro Ala Gly Leu Pro Leu Pro Thr Asp Ala Ile Glu Glu Pro Val
 100 105 110
 Tyr Val Asn Ala Lys Gln Tyr Asn Ala Ile Leu Arg Arg Arg Gln Ser
 115 120 125
 Arg Ala Lys Ala Glu Ser Glu Arg Lys Leu Val Lys Gly Arg Lys Pro
 130 135 140
 Tyr Leu His Glu Ser Arg His Gln His Ala Leu Lys Arg Ala Arg Gly
 145 150 155 160
 Ala Gly Gly Arg Phe Leu Asn Ser Lys Ser Asp Asp Lys Glu Glu Asn
 165 170 175
 Ser Asp Ser Ser Gln Lys Glu Ile Gln Asn Gly Val Ala Pro Gln Lys
 180 185 190
 Gly Gly Gln Pro Ser Thr Pro Pro Ser Pro Asn Gly Ala Ser Ser Ala
 195 200 205
 Tyr Gln Ala Pro Ser Arg Glu
 210 215

<210> 21
 <211> 1892
 <212> DNA
 <213> Zea mays

<400> 21
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tctgtgctct ggtgccgagg tgttcgttct gaatatattga ttcaattcaa aatcttcagc 1860
taagttacta ctgggacaaa aaaaaaaaaa aa 1892

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<210> 22

<211> 341

<212> PRT

<213> Zea mays

<400> 22

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```

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Gly Met Ser Gln Ala Ser His Gly Ala Ala Pro Ala Gly Ala Pro Leu
                20                      25                      30

```

```

Pro Trp Trp Ala Gly Ala Gln Leu Leu Ser Gly Glu Pro Ala Pro Leu
                35                      40                      45

```

```

Ser Pro Glu Glu Ala Pro Arg Asp Thr Gln Phe Gln Val Val Pro Gly
                50                      55                      60

```

```

Ala Ser Gln Gly Thr Pro Asp Pro Ala Pro Pro Lys Gly Gly Thr Pro
        65                      70                      75                      80

```

```

Lys Val Leu Lys Phe Ser Val Phe Gln Gly Asn Leu Glu Ser Gly Gly
                85                      90                      95

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Lys Gly Glu Lys Thr Pro Lys Asn Ser Thr Ala Val Val Leu Gln Ser
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<223> n = A, C, G, or T
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 <222> (276)
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<220>
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<220>
 <221> unsure
 <222> (296)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (320)
 <223> n = A, C, G, or T

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 gctctggcgg acgcttcctg aacacaaaga aagaatccag cgggaaggat gctgggtggtg 180
 gcagcaaggc aatgtttcaa ncaaccccct catgcgccag gtggcggttct cccaagctcc 240
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 tccaaagttt tttcaacctn ttt 323

<210> 24
 <211> 77
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (67)
 <223> Xaa = any amino acid

<400> 24
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 20 25 30
 His Ala Leu Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr
 35 40 45
 Lys Lys Glu Ser Ser Gly Lys Asp Ala Gly Gly Gly Ser Lys Ala Met
 50 55 60
 Phe Gln Xaa Thr Pro Ser Cys Ala Arg Trp Arg Ser Pro
 65 70 75

<210> 25
 <211> 1195

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<212> DNA

<213> Zea mays

<400> 25

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ccgcttccgc ttccgcttcc aaaggtaact cctttgggaa aaccgttaac gatcatctga 180
ggtcaacttt gagttttgat aacaagcaac ctccatttgc aagtcaaaac tttgactacg 240
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<210> 26

<211> 273

<212> PRT

<213> Zea mays

<400> 26

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Met Leu Leu Pro Ser Ser Ser Ser Ser Ser Ala Ser Ala Ser Ala Ser
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Lys Gly Asn Ser Phe Gly Lys Thr Val Asn Asp His Leu Arg Ser Thr
      20              25              30

Leu Ser Phe Asp Asn Lys Gln Pro Pro Phe Ala Ser Gln Asn Phe Asp
      35              40              45

Tyr Gly Gln Thr Ile Ala Cys Ile Ser Tyr Pro Tyr Asn His Ser Gly
      50              55              60

Ser Gly Asp Val Trp Ala Ala Tyr Glu Ser Arg Thr Ser Ala Ala Thr
      65              70              75              80

Val Phe Arg Ser Gln Ile Ala Gly Gly Gly Thr Ser Thr Arg Ile Pro
      85              90              95

Leu Pro Leu Glu Leu Ala Glu Asn Glu Pro Ile Tyr Val Asn Pro Lys
      100             105             110

Gln Tyr His Gly Ile Leu Arg Arg Arg Gln Leu Arg Ala Lys Leu Glu
      115             120             125

Ala Gln Asn Lys Leu Val Arg Ala Arg Lys Pro Tyr Leu His Glu Ser
      130             135             140

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Arg His Leu His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly Arg Phe
 145 150 155 160
 Leu Asn Thr Lys Gln Leu Gln Gln Ser His Thr Ala Leu Thr Arg Ser
 165 170 175
 Thr Thr Thr Ser Gly Thr Ser Ser Ser Gly Ser Thr His Leu Arg Leu
 180 185 190
 Gly Gly Gly Ala Ala Ala Ala Gly Asp Arg Ser Val Leu Ala Pro Lys
 195 200 205
 Thr Met Ala Ser Gln Asp Ser Ser Lys Lys Ala Val Ser Ser Ala Leu
 210 215 220
 Ala Phe Thr Ala Thr Pro Met Leu Arg Arg Asp Asp Gly Phe Leu Gln
 225 230 235 240
 His Pro Ser His Leu Phe Ser Phe Ser Gly His Phe Gly Gln Ala Ser
 245 250 255
 Ala Gln Ala Gly Val His Asn Gly Ser Gln His Arg Val Pro Val Met
 260 265 270

Arg

<210> 27
 <211> 1376
 <212> DNA
 <213> Zea mays

<400> 27
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 aagcaaaatg ttgtttggag ctcaagtaca ccatcttgta atgcctgtga ttttacggga 180
 aatggaggat cattctgtcc atcccatgtc taagtctaac catggctcct tgtcaggaaa 240
 tggttatgag atgaaacatt caggccataa agtttgcatg agggattcat catcggagtc 300
 tgatcgggtct caccaagaag catcagcagc aagtgaagc agtccaaatg aacacacatc 360
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 ccttaggagg aggcaaacac gtgctaaatt ggaggccag aacaagatgg tgaaaaatcg 720
 gaagccatat cttcatgagt cccgacatcg tcatgccatg aaacgggctc gtggatcagg 780
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<210> 28
 <211> 300
 <212> PRT
 <213> Zea mays

<400> 28

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Ser	Lys	Ser	Asn	His	Gly	Ser	Leu	Ser	Gly	Asn	Gly	Tyr	Glu	Met	Lys
			20					25					30		
His	Ser	Gly	His	Lys	Val	Cys	Asp	Arg	Asp	Ser	Ser	Ser	Glu	Ser	Asp
		35					40					45			
Arg	Ser	His	Gln	Glu	Ala	Ser	Ala	Ala	Ser	Glu	Ser	Ser	Pro	Asn	Glu
	50					55						60			
His	Thr	Ser	Thr	Gln	Ser	Asp	Asn	Asp	Glu	Asp	His	Gly	Lys	Asp	Asn
65					70					75					80
Gln	Asp	Thr	Met	Lys	Pro	Val	Leu	Ser	Leu	Gly	Lys	Glu	Gly	Ser	Ala
				85					90					95	
Phe	Leu	Ala	Pro	Lys	Leu	His	Tyr	Ser	Pro	Ser	Phe	Ala	Cys	Ile	Pro
			100					105					110		
Tyr	Thr	Ala	Asp	Ala	Tyr	Tyr	Ser	Ala	Val	Gly	Val	Leu	Thr	Gly	Tyr
		115					120					125			
Pro	Pro	His	Ala	Ile	Val	His	Pro	Gln	Gln	Asn	Asp	Thr	Thr	Asn	Thr
	130					135					140				
Pro	Gly	Met	Leu	Pro	Val	Glu	Pro	Ala	Glu	Glu	Pro	Ile	Tyr	Val	Asn
145					150					155					160
Ala	Lys	Gln	Tyr	His	Ala	Ile	Leu	Arg	Arg	Arg	Gln	Thr	Arg	Ala	Lys
				165					170					175	
Leu	Glu	Ala	Gln	Asn	Lys	Met	Val	Lys	Asn	Arg	Lys	Pro	Tyr	Leu	His
			180					185					190		
Glu	Ser	Arg	His	Arg	His	Ala	Met	Lys	Arg	Ala	Arg	Gly	Ser	Gly	Gly
		195					200					205			
Arg	Phe	Leu	Asn	Thr	Lys	Gln	Leu	Gln	Glu	Gln	Asn	Gln	Gln	Tyr	Gln
	210					215						220			
Ala	Ser	Ser	Gly	Ser	Leu	Cys	Ser	Lys	Ile	Ile	Ala	Asn	Ser	Ile	Ile
225					230					235					240
Ser	Gln	Ser	Gly	Pro	Thr	Cys	Thr	Pro	Ser	Ser	Gly	Thr	Ala	Gly	Ala
				245					250					255	
Ser	Thr	Ala	Gly	Gln	Asp	Arg	Ser	Cys	Leu	Pro	Ser	Val	Gly	Phe	Arg
			260					265					270		
Pro	Thr	Thr	Asn	Phe	Ser	Asp	Gln	Gly	Arg	Gly	Gly	Leu	Lys	Leu	Ala
		275					280					285			

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Val Ile Gly Met Gln Gln Arg Val Ser Thr Ile Arg
 290 295 300

<210> 29
 <211> 1492
 <212> DNA
 <213> Zea mays

<400> 29
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 gtgtcagttc atctgatttc tcagaagcaa aatgttggtt ggagctcagt gacaccatct 180
 tgtaatgcat gtgcctttta cgggaaatgg aggatcattc tgtccatcca aagtctaagt 240
 ctaaccatgg ttccttgtca ggaaatggtt atgagatgaa aaatccaggc catgaagttt 300
 gtgataggga ttcatcatca gagtctgata gatctcacc cagaagcatca gcagtgagtg 360
 aaagcagtct agatgaacac acatcaactc aatcagacaa tgatgaagat catgggaagg 420
 ataatcagga cacattgaag ccagtattgt ccttggggaa ggaagggtct gccttttttg 480
 ccccaaaaat agattacaac ccgtcttttc cttatatctc ttatactgct gacgcttact 540
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 atgatacaac aaatagtccg gttatgttgc ctgcggaacc tgcagaagaa gaaccaatat 660
 atgtcaatgc aaaacaatac catgcaatcc ttaggaggag gcagacacgt gctaaactgg 720
 aggcgcagaa caagatggtg aaaggctcga agccatacct tcatgagtct cgacaccgtc 780
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 tgagtttctg aggtgaagcc atcgaaacat gaccgtgtgg ttcagtaaaa aaaaaaaaaa 1380
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<210> 30
 <211> 301
 <212> PRT
 <213> Zea mays

<400> 30
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 Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
 20 25 30
 Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
 35 40 45
 Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His
 50 55 60
 Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
 65 70 75 80
 Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
 85 90 95

Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Pro Tyr Ile Pro Tyr
 100 105 110
 Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
 115 120 125
 Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
 130 135 140
 Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
 145 150 155 160
 Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
 165 170 175
 Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu His
 180 185 190
 Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
 195 200 205
 Arg Phe Leu Asn Thr Lys Gln Gln Leu Gln Glu Gln Asn Gln Arg Tyr
 210 215 220
 Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asn Ser Val
 225 230 235 240
 Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly
 245 250 255
 Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
 260 265 270
 Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
 275 280 285
 Val Met Asn Gly Met Gln Gln Arg Val Ser Thr Ile Arg
 290 295 300

<210> 31
 <211> 725
 <212> DNA
 <213> Zea mays

<220>
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 <222> (546)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (554)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (636)
 <223> n = A, C, G, or T

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<220>

<221> unsure

<222> (671)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (697)

<223> n = A, C, G, or T

<400> 31

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agtgcttcaa actggagtgg cagcctagct catcaagagc acgttagctt cgcactctgt 420
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gctggnacca tcantgggcg cgctccgtgt gcccggtggca attcatcttg gcttatgatg 600
tatcttatag ttaatttgct ttcactttca tatggnactt gtctcagatt aaactcgtga 660
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aaaaa                                           725

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<210> 32

<211> 169

<212> PRT

<213> Zea mays

<400> 32

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

Gln Lys Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Val Lys Gly Arg
                35                      40                      45

Lys Pro Tyr Leu His Glu Ser Arg His Arg His Ala Met Lys Arg Val
                50                      55                      60

Arg Gly Pro Gly Arg Phe Leu Asn Lys Lys Glu Leu Gln Glu Gln Gln
        65                      70                      75                      80

Leu Lys Ala Leu Pro Ser Leu Gln Thr Pro Thr Gly Gly Val Ser Lys
                85                      90                      95

Met Ala Phe Gly Arg Asn Leu Cys Pro Glu Ser Ser Thr Ser His Ser
                100                      105                      110

Pro Ser Thr Ser Ser Thr Ile Ser Ser Ala Ser Asn Trp Ser Gly Thr
                115                      120                      125

Leu Ala His Gln Glu His Val Ser Phe Ala Ser Ala Asn Lys Phe Leu
        130                      135                      140

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Pro Ser Met Asn Phe His Ala Glu Asn Gly Val Lys Arg Trp Pro Ser
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Met Ala Ser Ala Thr Thr Pro Leu Ser
 165

<210> 33
 <211> 831
 <212> DNA
 <213> Zea mays

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 gagtctaggc atcttcatgc aatgaagagg gcacgagggt ccggtggacg attcctcaac 180
 actaagcagc tccagcagtc tcacacagcc ctcaccagggt ccaccaccac aagtggcaca 240
 agctcctcag gctcaactca tctgcggctt ggtggtggcg cagccgcagc tggagatcga 300
 tctgtgctgg cacccaaaac aatggcctca caagacagta gcaagaaggc cgtttcttca 360
 gccctcgcct tcaactgcgac tccaatgctg cgcagagatg acggcttctt gcagcaccca 420
 agccatcttt tcagtttttc tgggtcathtt gggcaggcaa gcgcgcaagc tggcgtccat 480
 aatggaagtc agcatagggt tccagttatg agatgaccgg tttgcgaacc atagctgggtg 540
 atccaggcgt ctaggggtcaa cttcgctgtg gtgtcttagt ctctcaggca attcatcctt 600
 ggcttaattt ctggcttttt attagaaggt accaaaatgt gttccatacc gttgtggcca 660
 cagagcccat aaaccagggg gtttgatggt tggcactcct acccaaacta ttgttgagcgt 720
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<210> 34
 <211> 98
 <212> PRT
 <213> Zea mays

<400> 34
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 Leu Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Val Arg Ala Arg Lys
 20 25 30
 Ser Tyr Leu His Glu Ser Arg His Leu His Ala Met Lys Arg Ala Arg
 35 40 45
 Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Gln Leu Gln Gln Ser His
 50 55 60
 Thr Ala Leu Thr Arg Ser Thr Thr Thr Ser Gly Thr Ser Ser Ser Gly
 65 70 75 80
 Ser Thr His Leu Arg Leu Gly Gly Gly Ala Ala Ala Ala Gly Asp Arg
 85 90 95
 Ser Val

<210> 35
 <211> 1307

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<212> DNA

<213> Zea mays

<400> 35

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gcgggctgcc ggaaggggaa catgctccct cctcatctca cagtacgaac tgaaaaacaa 180
gagtaaagaa tttccgtgag atgagacaga atggcgcggt gatgattcag tttggccatc 240
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cgtctggaat gagcgaaggg agcctcaacg agcataataa tgaccattca ggcaaccttg 360
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<210> 36

<211> 244

<212> PRT

<213> Zea mays

<400> 36

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

Glu Ala Ser Gly Met Ser Glu Gly Ser Leu Asn Glu His Asn Asn Asp
          35             40             45

His Ser Gly Asn Leu Asp Gly Tyr Ser Lys Ser Asp Glu Asn Lys Met
          50             55             60

Met Ser Ala Leu Ser Leu Gly Asn Pro Glu Thr Ala Tyr Ala His Asn
          65             70             75             80

Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile Ser Tyr Pro Tyr Ala
          85             90             95

Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Ala Tyr Gly Pro His Ala
          100            105            110

Ile Met His Pro Gln Leu Val Gly Met Val Pro Ser Ser Arg Val Pro
          115            120            125

Leu Pro Ile Glu Pro Ala Ala Glu Glu Pro Ile Tyr Val Asn Ala Lys
          130            135            140

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Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Leu Arg Ala Lys Leu Glu
 145 150 155 160

Ala Glu Asn Lys Leu Val Lys Ser Arg Lys Pro Tyr Leu His Glu Ser
 165 170 175

Arg His Leu His Ala Met Lys Arg Ala Arg Gly Thr Gly Gly Arg Phe
 180 185 190

Leu Asn Thr Lys Gln Gln Pro Glu Ser Pro Gly Ser Gly Gly Ser Ser
 195 200 205

Asp Ala Gln Arg Val Pro Ala Thr Ala Ser Gly Gly Leu Phe Thr Lys
 210 215 220

His Glu His Ser Leu Pro Pro Gly Gly Arg His His Tyr His Ala Arg
 225 230 235 240

Gly Gly Gly Glu

<210> 37
 <211> 816
 <212> DNA
 <213> Zea mays

<400> 37
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 gcagccccag gagcagaacc agcagtacca ggcgtcgagt ggttcaatgt gctcaaagac 180
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 gcgtgtttcc accataaggt gaagagaagt gggcacgaca ccattcccag gcgcgcactg 420
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<210> 38
 <211> 78
 <212> PRT
 <213> Zea mays

<400> 38
 His Ala Ser Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu
 1 5 10 15

His Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly
 20 25 30

Gly Arg Phe Leu Asn Thr Lys Gln Gln Pro Gln Glu Gln Asn Gln Gln
 35 40 45

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Tyr Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asn Ser
 50 55 60

Val Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp
 65 70 75

<210> 39

<211> 1630

<212> DNA

<213> Argemone mexicana

<400> 39

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aaaaaaaaaa 1630

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<210> 40

<211> 333

<212> PRT

<213> Argemone mexicana

<400> 40

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

Val Tyr Asn Thr Gly Ser Ser Ala Glu Leu Gly Glu Ser Thr Ile Lys
 35 40 45

Ser Ser Ser Met Glu Gln Pro Asp Gly Gly Met Gly Ile Asp Thr Arg
 50 55 60

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

<210> 41

<211> 1565

<212> DNA

<213> Argemone mexicana

<400> 41

caagaaagaa aagagagaag aaagaaaatt ttttgaaggt gggtttgaac agaggagaca 60

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tgaccagatc tatcccaaca tctcttctcc ttattttctct cactttacca aatcccaaag 120
taaattcact ccagaagcgc gtaatatagg ttttcaaaaa cagttctgag gatttttagat 180
tgttttcatc ttggtttgga atttacatag tgaagttaag tgaacaagaa tgcaagacaa 240
gtcaattttca catagtgttg ttagttgtcc aatttggtgg acttctactg gatcccaagt 300
tccacagagt tgtttatcaa agagtttaag cgtaaccttc gactcttctc gtcaagattg 360
cggtagtttg aagcagctag gttttcaact tcaagatcag gattcatcct cgactcaatc 420
aactggtcag tcgcatcatg aagtgggaaa tatgtctgga agcaacccta ctgggcaatg 480
catttcagct cagtgcgaaa aagttactta cgggaaacaa ggagatgttc aaacgaaatc 540
aattctatca cttggagctc cagaagttgt tctccctcaa caagttgatt ataaccacca 600
ctcagtggct cgtataccct atcattacgt tgatccgtat tacgggtggca taatggcgctc 660
ttatggacca caggctatta ttcaccaca aatgatgggt ataacacctg cagcagttccc 720
attgcctctt gatccttgag aaaatgagcc catgtatgtt aatgcaaaac agtaccgagc 780
aattcttaga cggaggcagt cccgtgctaa gcttgaggct caaaataaac ttatcaaaga 840
tcgcaagcct tatctacatg aatctcggca tcttcatgca ttgaagaggg ctaggggatc 900
tggtggacgt tttctcaaca cgaagcagct gcaagagttg aaacaaaaca actctaattg 960
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1560
aaaaaa 1565

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<210> 42

<211> 326

<212> PRT

<213> Argemone mexicana

<400> 42

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Met Gln Asp Lys Ser Ile Ser His Ser Val Val Ser Cys Pro Ile Trp
  1                      5                      10                      15

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```

Trp Thr Ser Thr Gly Ser Gln Val Pro Gln Ser Cys Leu Ser Lys Ser
          20                      25                      30

```

```

Leu Ser Val Thr Phe Asp Ser Ser Arg Gln Asp Cys Gly Ser Leu Lys
          35                      40                      45

```

```

Gln Leu Gly Phe Gln Leu Gln Asp Gln Asp Ser Ser Ser Thr Gln Ser
          50                      55                      60

```

```

Thr Gly Gln Ser His His Glu Val Gly Asn Met Ser Gly Ser Asn Pro
          65                      70                      75                      80

```

```

Thr Gly Gln Cys Ile Ser Ala Gln Cys Glu Lys Val Thr Tyr Gly Lys
          85                      90                      95

```

```

Gln Gly Asp Val Gln Thr Lys Ser Ile Leu Ser Leu Gly Ala Pro Glu
          100                      105                      110

```

```

Val Val Leu Pro Gln Gln Val Asp Tyr Asn His His Ser Val Ala Arg
          115                      120                      125

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```

Ile Pro Tyr His Tyr Val Asp Pro Tyr Tyr Gly Gly Ile Met Ala Ser
          130                      135                      140

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Tyr Gly Pro Gln Ala Ile Ile His Pro Gln Met Met Gly Ile Thr Pro
 145 150 155 160
 Ala Arg Val Pro Leu Pro Leu Asp Leu Ala Glu Asn Glu Pro Met Tyr
 165 170 175
 Val Asn Ala Lys Gln Tyr Arg Ala Ile Leu Arg Arg Arg Gln Ser Arg
 180 185 190
 Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys Asp Arg Lys Pro Tyr
 195 200 205
 Leu His Glu Ser Arg His Leu His Ala Leu Lys Arg Ala Arg Gly Ser
 210 215 220
 Gly Gly Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Leu Lys Gln Asn
 225 230 235 240
 Asn Ser Asn Gly Gln Asn Thr Ser Glu Ser Ala Tyr Leu Gln Leu Gly
 245 250 255
 Gly Asn Leu Ser Glu Ser Glu Phe Gly Asn Gly Gly Gly Ala Ser Thr
 260 265 270
 Thr Ser Cys Ser Asp Ile Thr Thr Ala Ser Asn Ser Asp His Ile Phe
 275 280 285
 Arg Gln Gln Asn Leu Arg Phe Ala Gly Tyr Thr His Met Gly Gly Thr
 290 295 300
 Met Gln Asp Gly Gly Gly Gly Gly Ile Met Ser Asn Gly Ser His His
 305 310 315 320
 Arg Val Pro Val Thr Gln
 325

<210> 43

<211> 1187

<212> DNA

<213> Oryza sativa

<400> 43

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 tggtcataaa atgcctgact acgagtcac agctacccaa tcaactagtg gatctcctcg 180
 tgaagtgtct ggaatgagcg aaggaagcct caatgagcag aatgatcaat ctggtaatat 240
 tgatggttac acgaagagtg atgaaggtaa gatgatgtca gctttatctc tgggcaaate 300
 agaaactgtg tatgcacatt cggaacctga ccgtagccaa ccctttggca tatcatatcc 360
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 tccccagatt gtgggcgtga tgtcatcctc ccgagtcccc ctaccaatag aaccagccac 480
 cgaagagcct atttatgtaa atgcaaagca ataccatgag attctccgaa ggagacagct 540
 ccgtgcaaag ttagaggctg aaaacaagct ggtgaaaaac cgcaagccgt acctccatga 600
 atcccggcat caacacgcga tgaagagagc tcgggggaaca ggggggagat tcctcaacac 660
 aaagcagcag cctgaagctt cagatgggtg caccccaagg ctctgtctctg caaacggcgt 720
 tgtgtttctca aagcacgagc acagcttgct gtccagtgat ctccatcatc gtcgtgtgaa 780
 agagggcgct tgagatcctc gccgtttctg tcatggcaaa tcatccttgg cttatgtgtg 840
 gtgcccagca aaaaaaaatc tgactgaacc tgtgtgtgtaa ctgatgggta tgggtgggtt 900
 ttgtgcaact gtaactaggg tgcttgacat ctgtgtctgt tgttcctctg cctccttagt 960

ttggagacgg tgcagctgca gctggtacca gtaatctgat catgctagac ttgtgacaag 1020
 gacaaaacta gcaccccggt atgtttcctg gcttctgaat ttggtggtca ttcagtaagc 1080
 aagcactcga cgtcagcggg aggggggtgc ttcgattgat ctagttcttt cgcgataaac 1140
 ttattttaatt ttgaacaaag gttgggtttca aaaaaaaaaa aaaaaaa 1187

<210> 44

<211> 239

<212> PRT

<213> Oryza sativa

<400> 44

Met Leu Pro Pro His Leu Thr Glu Asn Gly Thr Val Met Ile Gln Phe
 1 5 10 15

Gly His Lys Met Pro Asp Tyr Glu Ser Ser Ala Thr Gln Ser Thr Ser
 20 25 30

Gly Ser Pro Arg Glu Val Ser Gly Met Ser Glu Gly Ser Leu Asn Glu
 35 40 45

Gln Asn Asp Gln Ser Gly Asn Leu Asp Gly Tyr Thr Lys Ser Asp Glu
 50 55 60

Gly Lys Met Met Ser Ala Leu Ser Leu Gly Lys Ser Glu Thr Val Tyr
 65 70 75 80

Ala His Ser Glu Pro Asp Arg Ser Gln Pro Phe Gly Ile Ser Tyr Pro
 85 90 95

Tyr Ala Asp Ser Phe Tyr Gly Gly Ala Val Ala Thr Tyr Gly Thr His
 100 105 110

Ala Ile Met His Pro Gln Ile Val Gly Val Met Ser Ser Ser Arg Val
 115 120 125

Pro Leu Pro Ile Glu Pro Ala Thr Glu Glu Pro Ile Tyr Val Asn Ala
 130 135 140

Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Leu Arg Ala Lys Leu
 145 150 155 160

Glu Ala Glu Asn Lys Leu Val Lys Asn Arg Lys Pro Tyr Leu His Glu
 165 170 175

Ser Arg His Gln His Ala Met Lys Arg Ala Arg Gly Thr Gly Gly Arg
 180 185 190

Phe Leu Asn Thr Lys Gln Gln Pro Glu Ala Ser Asp Gly Gly Thr Pro
 195 200 205

Arg Leu Val Ser Ala Asn Gly Val Val Phe Ser Lys His Glu His Ser
 210 215 220

Leu Ser Ser Ser Asp Leu His His Arg Arg Val Lys Glu Gly Ala
 225 230 235

<210> 45

<211> 1442

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<212> DNA

<213> Oryza sativa

<400> 45

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gcacgagtac agcgctccgc attagggctc gcctctcggt ggctagagcg cgagagccag 60
tagccgcagc tgcagcaagc agcagcagca gcgaagagcc tgagccccag aggaggcgtg 120
caccgcctcc gattggccgg cctctcggag agagagagag agagagagat cgatcgagtc 180
ctattggccg ccgcctccgc gccctggctg ctactggtg agcgagcatg gtagtcgaggc 240
cggggggaac caacctcgtg gagccgaggg ggcagggcgc gctgccgtcc ggcataccga 300
tccagcagcc gtggtggacg acctccgccc gggtcggggc ggtgtcgccc gccgtcgtgg 360
cgccggggag cgggtgcgggg atcagcctgt cgggcaggga tggcggcggc gacgacgcgg 420
cagaggagag cagcgatgac tcacgaagat caggggagac caaagatgga agcactgatc 480
aagaaaagca tcatgcaaca tcgcagatga ctgctttggc atcagactat ttaacaccat 540
tttcacagct ggaactaaac caaccaattg cttcggcagc ataccagtac cctgactctt 600
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aagatgggtg tcccagtgag aaagccgaac caaacaagg agagcagaac tccgggtatc 960
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gtgctccatc tttcaaataga tcttcatcga gcaaagtaat tatatgtaca ttcctctgaa 1140
tgatctatgc accaattgtt gatcctggca gggtaataat ctggatgtat tgagtccatc 1200
acagtgcgaa tgtcacgggt agatctgctg ttttcaggca attcattctt ggctttctat 1260
cccaccggtt gttgttgcaa gttaagctag cagtacttgt ctcagtgtcc gtgagacgtt 1320
tgtgtaagat taggttaaac tagaagttgt aatgctgtat taagtgtttg tattttcta 1380
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aa

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<210> 46

<211> 258

<212> PRT

<213> Oryza sativa

<400> 46

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Met Glu Ser Arg Pro Gly Gly Thr Asn Leu Val Glu Pro Arg Gly Gln
 1              5              10              15

Gly Ala Leu Pro Ser Gly Ile Pro Ile Gln Gln Pro Trp Trp Thr Thr
          20              25              30

Ser Ala Gly Val Gly Ala Val Ser Pro Ala Val Val Ala Pro Gly Ser
          35              40              45

Gly Ala Gly Ile Ser Leu Ser Gly Arg Asp Gly Gly Gly Asp Asp Ala
          50              55              60

Ala Glu Glu Ser Ser Asp Asp Ser Arg Arg Ser Gly Glu Thr Lys Asp
          65              70              75              80

Gly Ser Thr Asp Gln Glu Lys His His Ala Thr Ser Gln Met Thr Ala
          85              90              95

Leu Ala Ser Asp Tyr Leu Thr Pro Phe Ser Gln Leu Glu Leu Asn Gln
          100             105             110

Pro Ile Ala Ser Ala Ala Tyr Gln Tyr Pro Asp Ser Tyr Tyr Met Gly
          115             120             125

```

Met Val Gly Pro Tyr Gly Pro Gln Ala Met Ser Ala Gln Thr His Phe
 130 135 140
 Gln Leu Pro Gly Leu Thr His Ser Arg Met Pro Leu Pro Leu Glu Ile
 145 150 155 160
 Ser Glu Glu Pro Val Tyr Val Asn Ala Lys Gln Tyr His Gly Ile Leu
 165 170 175
 Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Leu Glu Lys Lys Val Val
 180 185 190
 Lys Ser Arg Lys Pro Tyr Leu His Glu Ser Arg His Gln His Ala Met
 195 200 205
 Arg Arg Ala Arg Gly Thr Gly Gly Arg Phe Leu Asn Thr Lys Lys Asn
 210 215 220
 Glu Asp Gly Ala Pro Ser Glu Lys Ala Glu Pro Asn Lys Gly Glu Gln
 225 230 235 240
 Asn Ser Gly Tyr Arg Arg Ile Pro Pro Asp Leu Gln Leu Leu Gln Lys
 245 250 255

Glu Thr

<210> 47
 <211> 423
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (223)
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<220>
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 <222> (330)
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 <222> (369)
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 <222> (389)
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<220>
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<400> 47

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gtacagttct tgcagctgtc aagttctttg tacctatgtt tctgtatctt ctaaagattt 180
tgattcgtct gcaactgtgca gccatatctc catgagtcac ggnatcaaca tgccctgaaa 240
agggctaggg gagctggagg ccgatttctt aattcaaaat cggatgacaa ggaaagagca 300
ttctgattcc aagttccaag agataaacan gatggagttg caccctcgtg ataatgggca 360
aacgtctanc tctccgtctt caaaggggng gatcatcagc tnaacaaaat aaagaagtca 420
aaa                                              423

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<210> 48

<211> 34

<212> PRT

<213> Oryza sativa

<220>

<221> UNSURE

<222> (9)

<223> Xaa = any amino acid

<400> 48

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Gln Pro Tyr Leu His Glu Ser Arg Xaa Gln His Ala Leu Lys Arg Ala
 1              5              10              15

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Arg Gly Ala Gly Gly Arg Phe Leu Asn Ser Lys Ser Asp Asp Lys Glu
              20              25              30

```

Arg Ala

<210> 49

<211> 479

<212> DNA

<213> Oryza sativa

<400> 49

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ctcttctcat ctcattctccc tctcctctcc tctcgccgtc gccgtcgccg tcgcccgcgc 60
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cccgcacctc cgctcgcttg gcctcttctt cccggaagtg tgggtgtgctg caagctcctg 180
tctctcctac aaggtttcaa aaccaaata tgcctgaagc acacggaaag ctgggggtgat 240
taacgtctgt ttcttttgac tacaatcatc ctgattctgc ttctgtctgc aaaaacaacc 300
aagccatgac gtctgtagtt catgatgttt caggcaacca tggagctgat gagcggcaaa 360
aacagcaaag gcaaggtgaa cctgaggacc aagcaagaag cctcagttac tagtacagat 420
agccatacaa tggtaagcaa caccttcaac agattatgcg acaacctatg cccatcacg 479

```

<210> 50

<211> 35

<212> PRT

<213> Oryza sativa

<400> 50

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Met Thr Ser Val Val His Asp Val Ser Gly Asn His Gly Ala Asp Glu
 1              5              10              15

```

```

Arg Gln Lys Gln Gln Arg Gln Gly Glu Pro Glu Asp Gln Ala Arg Ser
              20              25              30

```

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Leu Ser Tyr
35

<210> 51
<211> 1107
<212> DNA
<213> Oryza sativa

<400> 51
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atgtcaacgc gaagcagtac gaaggcatcc tccgccgtcg ccgtgcccgc gccaaaggccc 180
agagggagaa caggctggtc aaaggcagga agccctacct ccacgagtcg cgccaccgcc 240
acgccatgcg ccggggccaga ggctccggcg gccgcttcct caacaccaag aaagaagcca 300
ccgccgccgg atgcggcggc agcagcaaga cgccctcgcg gtccctcgtc agccccgccg 360
acgtagccca tcgtccaggc tccggcgggc gcgcgtccag cctctccggc tccgacgtgt 420
cgtcgccggg aggcgtcatg tacgaccacc accgccacga cgacgccgac gcggcggacc 480
actacaacag catcgaccac cacctccgca cgccgttctt caccctcgtc ccgatcatca 540
tgacacagcg cggcgggcggc ggcgaccacg cctcacactc cgccgccgcc gtcgccgccc 600
ccttcagggtg ggcgacggcg gccggcgacg gctgctgcga gctcctcaag gcgtgacagc 660
cttgaggcgg ggatctccag gcgtgcccag agctgctgct gatcgatcac catcagcttt 720
ggctgcctgt aggcaaatca ttcttggtc tttacttgca ttgggggttct tgcaagcaac 780
tctcctcgtc acctaccaa actgtccctg aaacttctct agtgctgggg tctcgatcag 840
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tgattaagca actagtagta cttggtaatt actggctatg aattagtagt atggactctg 960
gtgtcagggtt gctctttgtc tgaataaact ggagtcgttt gaagctttgc aaaaaaaaaa 1020
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<210> 52
<211> 217
<212> PRT
<213> Oryza sativa

<400> 52
Thr Ser Asn Tyr Pro Cys Ile Asp Gln Cys Tyr Gly Leu Met Thr Thr
1 5 10 15
Tyr Ala Met Lys Ser Met Ser Gly Gly Arg Met Leu Leu Pro Leu Asn
20 25 30
Ala Pro Ala Asp Ala Pro Ile Tyr Val Asn Ala Lys Gln Tyr Glu Gly
35 40 45
Ile Leu Arg Arg Arg Arg Ala Arg Ala Lys Ala Gln Arg Glu Asn Arg
50 55 60
Leu Val Lys Gly Arg Lys Pro Tyr Leu His Glu Ser Arg His Arg His
65 70 75 80
Ala Met Arg Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys
85 90 95
Lys Glu Ala Thr Ala Ala Gly Cys Gly Gly Ser Ser Lys Thr Pro Leu
100 105 110
Ala Ser Leu Val Ser Pro Ala Asp Val Ala His Arg Pro Gly Ser Gly
115 120 125

Gly Arg Ala Ser Ser Leu Ser Gly Ser Asp Val Ser Ser Pro Gly Gly
 130 135 140

Val Met Tyr Asp His His Arg His Asp Asp Ala Asp Ala Ala Asp His
 145 150 155 160

Tyr Asn Ser Ile Asp His His Leu Arg Thr Pro Phe Phe Thr Pro Leu
 165 170 175

Pro Ile Ile Met Asp Ser Gly Gly Gly Gly Gly Asp His Ala Ser His
 180 185 190

Ser Ala Ala Ala Val Ala Ala Pro Phe Arg Trp Ala Thr Ala Ala Gly
 195 200 205

Asp Gly Cys Cys Glu Leu Leu Lys Ala
 210 215

<210> 53
 <211> 977
 <212> DNA
 <213> Oryza sativa

<400> 53
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 ggcccaaat aaggcgggtga aaggctcgaa gccttacctc catgaatctc gacatcatca 180
 tgctatgaag cgagcccgtg gatcagggtg tcggttcctt accaaaaagg agctgctgga 240
 acagcagcag cagcagcagc agcagaagcc accaccggca tcagctcagt ctccaacagg 300
 tagagccaga acgagcggcg gtgccgttgt ccttggcaag aacctgtgcc cagagaacag 360
 cacatcctgc tcgccatcga caccgacagg ctccgagatc tccagcatct catttggggg 420
 cggcatgctg gctcaccaag agcacatcag cttcgcatcc gctgatcgcc accccacaat 480
 gaaccagaac caccgtgtcc ccgtcatgag gtgaaaacct cgggatcgcg ggacacgggc 540
 ggttctggtt taccctcact ggcgcactcc ggtgtgcccg tggcaattca tccttggcctt 600
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 ataaactctt atagtttggt ttattgtaag ctatgactga acgaactgtc gagcagatgg 720
 ctaatttgta tgttggtgggt acagaaatcc tgaagctttt gatgtaccta attgcctttt 780
 gcttatactc ttgggtgtata cccattacca agttgcctta aaaaccctcc aattatgtaa 840
 tcagtcatgg ttttatagaa ccttgccaca tgtaatcaat cacctgtttt tgtaaattga 900
 tctataaacg ctataggctg ctgtgttatc tgcattttaa aaaaaaaaaa aaaaaaaaaa 960
 aaaaaaaaaa aaaaaaa 977

<210> 54
 <211> 168
 <212> PRT
 <213> Oryza sativa

<400> 54
 Ala Asn Ser Arg Met Pro Leu Pro Val Asp Pro Ser Val Glu Glu Pro
 1 5 10 15

Ile Phe Val Asn Ala Lys Gln Tyr Asn Ala Ile Leu Arg Arg Arg Gln
 20 25 30

Thr Arg Ala Lys Leu Glu Ala Gln Asn Lys Ala Val Lys Gly Arg Lys
 35 40 45

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Pro Tyr Leu His Glu Ser Arg His His His Ala Met Lys Arg Ala Arg
 50 55 60
 Gly Ser Gly Gly Arg Phe Leu Thr Lys Lys Glu Leu Leu Glu Gln Gln
 65 70 75 80
 Gln Gln Gln Gln Gln Gln Lys Pro Pro Pro Ala Ser Ala Gln Ser Pro
 85 90 95
 Thr Gly Arg Ala Arg Thr Ser Gly Gly Ala Val Val Leu Gly Lys Asn
 100 105 110
 Leu Cys Pro Glu Asn Ser Thr Ser Cys Ser Pro Ser Thr Pro Thr Gly
 115 120 125
 Ser Glu Ile Ser Ser Ile Ser Phe Gly Gly Gly Met Leu Ala His Gln
 130 135 140
 Glu His Ile Ser Phe Ala Ser Ala Asp Arg His Pro Thr Met Asn Gln
 145 150 155 160
 Asn His Arg Val Pro Val Met Arg
 165

<210> 55
 <211> 465
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (280)
 <223> n = A, C, G, or T

<220>
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 <222> (325)
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 <222> (349)
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<220>
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<220>
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<220>
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 ctccaccaag accaccacag acagccaaaa ttcttcaggt tcaagtcatc tacggctagg 180
 tgggtggcgca atcggagatc aaactccatt tccgttcaaa gcaatggatt cacaagctaa 240
 catcaagaga gctgcagctt ctgcttccac cttcactgtn acttctgcgg gacaaaaaga 300
 cgacgccttc ttcgaccgcc atggnaaaca tctcaataac ttctccggnc attttggna 360
 agcaagcnca caaaggggng tcggnaagca tgcataaccg gtcaaaagca agaggggtcc 420
 tgctnatgnn gatganatga aagagcagct tggaaatcna acant 465

<210> 56
 <211> 131
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (123)
 <223> Xaa = any amino acid

<400> 56
 Leu Gln Gln Pro Tyr Leu His Glu Ser Arg His Arg His Ala Met Lys
 1 5 10 15
 Arg Ala Arg Gly Thr Gly Gly Arg Phe Leu Asn Thr Lys Gln Leu Gln
 20 25 30
 Leu Gln Gln Gln Ser His Thr Thr Ser Thr Lys Thr Thr Thr Asp Ser
 35 40 45

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Gln Asn Ser Ser Gly Ser Ser His Leu Arg Leu Gly Gly Gly Ala Ile
 50 55 60
 Gly Asp Gln Thr Pro Phe Pro Phe Lys Ala Met Asp Ser Gln Ala Asn
 65 70 75 80
 Ile Lys Arg Ala Ala Ala Ser Ala Ser Thr Phe Thr Val Thr Ser Ala
 85 90 95
 Gly Gln Lys Asp Asp Ala Phe Phe Asp Arg His Gly Gln His Leu Asn
 100 105 110
 Asn Phe Ser Gly His Phe Gly Gln Ala Ser Xaa Gln Arg Gly Val Gly
 115 120 125
 Lys His Ala
 130

<210> 57
 <211> 1482
 <212> DNA
 <213> Glycine max

<400> 57
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 tgagatcaga tcctcattcc tttcaacctg gcagtgttta ttctgagcct tgggtggcgtg 120
 gtattgggta caatcctgtg gcccaaacia tggctggggc aaatgcatcc aattcatcgt 180
 ctcttgaatg ccctaattgt gattctgaat ccaatgaaga aggtcaatct ttgtccaata 240
 gcgggatgaa tgaggaagat gatgatgcca ctaaggattc acagcctgct gttcctaata 300
 gaacaggaaa ttatgggcaa gaacagcaag ggatgcagca tactgcatca tctgcaccct 360
 ccatgcgtga agaatgcctt actcagacac cacagctgga acttgctcgtt cattcaattg 420
 catgtgctac aaatccttat caggatccgt attatggggg catgatggca gcttatggtc 480
 accaacagtt gggatatgct ctttttatag gaatgcctca tgccagaatg cttttgcccc 540
 ttgagatggc tcaagaacct gtgtatgtga atgccaaaca gtaccaagga attctgaggc 600
 gaagacaggc tcgtgctaaa gcagagcttg aaaggaagct cataaaatct agaaagccat 660
 atcttcatga atctaggcat cagcatgcta tgagaagggc aaggggtact ggaggacgat 720
 ttgcaaagaa aactgacggg gaggggtcaa accactcagg caaggaaaag gataatggta 780
 ctgattctgt cctatcatca caatcaatta gttcatctgg ttctgaacct ttacattctg 840
 actctgccga aacctggaat tctcctaaca tgcaacaaga tgcaagagca tcaaaagtgc 900
 acaacagggt caaagcacc tgttaccaa atggcagtgg ctctaccat aatcataatg 960
 gattgcaatc ttcagtgtac cattcatcct cagggtgaaag actggaggaa agggattggt 1020
 cgggtcagca actgaaccac aattgatggg ggggttagagg ccgagggttg tttgtatcca 1080
 agtgacatat ttggtgaata ccttggttat ctgtaaacac tcttggaat atatatgcca 1140
 agcggcaaat cattcttggc tttgttcttg tgtttgtggg gttaatgata ctatgggggg 1200
 ggtggggggg gggggaatga ttggtatttg agatttctgt tgaagtcagt caatcaatcc 1260
 ttcgttcttt tctcattttt gcattttgta aagttttata gtgggttagga tggtcacttc 1320
 agaagattat ggagtatggg gagaaacaaa ctcttgatgt gccaacactc gtttgactgg 1380
 tttatctttg tgtagttcaa ccggttggtta atgttaacat aagacatcat aggataatga 1440
 acatgctgtt agttacatta catcaaaaaa aaaaaaaaaa aa 1482

<210> 58
 <211> 338
 <212> PRT
 <213> Glycine max

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<400> 58

Met	Gln	Ser	Lys	Ser	Glu	Thr	Ala	Asn	Arg	Leu	Arg	Ser	Asp	Pro	His
1				5				10						15	
Ser	Phe	Gln	Pro	Gly	Ser	Val	Tyr	Ser	Glu	Pro	Trp	Trp	Arg	Gly	Ile
			20					25					30		
Gly	Tyr	Asn	Pro	Val	Ala	Gln	Thr	Met	Ala	Gly	Ala	Asn	Ala	Ser	Asn
		35					40					45			
Ser	Ser	Ser	Leu	Glu	Cys	Pro	Asn	Gly	Asp	Ser	Glu	Ser	Asn	Glu	Glu
	50					55					60				
Gly	Gln	Ser	Leu	Ser	Asn	Ser	Gly	Met	Asn	Glu	Glu	Asp	Asp	Asp	Ala
65					70					75					80
Thr	Lys	Asp	Ser	Gln	Pro	Ala	Val	Pro	Asn	Gly	Thr	Gly	Asn	Tyr	Gly
				85					90					95	
Gln	Glu	Gln	Gln	Gly	Met	Gln	His	Thr	Ala	Ser	Ser	Ala	Pro	Ser	Met
			100					105					110		
Arg	Glu	Glu	Cys	Leu	Thr	Gln	Thr	Pro	Gln	Leu	Glu	Leu	Val	Gly	His
			115				120					125			
Ser	Ile	Ala	Cys	Ala	Thr	Asn	Pro	Tyr	Gln	Asp	Pro	Tyr	Tyr	Gly	Gly
	130					135					140				
Met	Met	Ala	Ala	Tyr	Gly	His	Gln	Gln	Leu	Gly	Tyr	Ala	Pro	Phe	Ile
145					150					155					160
Gly	Met	Pro	His	Ala	Arg	Met	Pro	Leu	Pro	Leu	Glu	Met	Ala	Gln	Glu
				165				170						175	
Pro	Val	Tyr	Val	Asn	Ala	Lys	Gln	Tyr	Gln	Gly	Ile	Leu	Arg	Arg	Arg
			180					185					190		
Gln	Ala	Arg	Ala	Lys	Ala	Glu	Leu	Glu	Arg	Lys	Leu	Ile	Lys	Ser	Arg
		195					200					205			
Lys	Pro	Tyr	Leu	His	Glu	Ser	Arg	His	Gln	His	Ala	Met	Arg	Arg	Ala
	210					215					220				
Arg	Gly	Thr	Gly	Gly	Arg	Phe	Ala	Lys	Lys	Thr	Asp	Gly	Glu	Gly	Ser
225					230					235					240
Asn	His	Ser	Gly	Lys	Glu	Lys	Asp	Asn	Gly	Thr	Asp	Ser	Val	Leu	Ser
			245					250						255	
Ser	Gln	Ser	Ile	Ser	Ser	Ser	Gly	Ser	Glu	Pro	Leu	His	Ser	Asp	Ser
			260				265						270		
Ala	Glu	Thr	Trp	Asn	Ser	Pro	Asn	Met	Gln	Gln	Asp	Ala	Arg	Ala	Ser
		275					280					285			
Lys	Val	His	Asn	Arg	Phe	Lys	Ala	Pro	Cys	Tyr	Gln	Asn	Gly	Ser	Gly
	290					295					300				
Ser	Tyr	His	Asn	His	Asn	Gly	Leu	Gln	Ser	Ser	Val	Tyr	His	Ser	Ser
305					310					315					320

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Ser Gly Glu Arg Leu Glu Glu Arg Asp Cys Ser Gly Gln Gln Leu Asn
 325 330 335

His Asn

<210> 59
 <211> 1385
 <212> DNA
 <213> Glycine max

<400> 59
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 ctgatgattg gcgagtagag cggggtgagc agattcagtt tcagtcttcc atttactctc 120
 atcatcagcc ttggtggtgt ggagtggggg aaaatgcctc taaatcatct tcagctgatc 180
 agttaaatgg ttcaatcgtg aatggtatca cgcggtctga gaccaatgat aagtcaggtg 240
 aaggtgttgc caaagaatac caaaacatca aacatgccgt gttgtcaacc ccatttacca 300
 tggacaaaca tcttgctcca aatccccaga tggaaacttg tggtcattca gttgttttaa 360
 catctcctta ttcagatgca cagcatggtc aaatcttgac tacttacggg caacaagtta 420
 tgataaacc tcaattgtac ggaatgtatc atgctagaat gcctttgcca cctgaaatgg 480
 aagaggagcc tgtttatgtc aatgcaaagc agtatcatgg tattttgagg cgaagacagt 540
 cacgtgctaa ggctgagctt gaaaagaaag taatcaaaaa caggaagcca tacctccatg 600
 aatcccgtca ctttcatgcc atgagaaggg ctagaggcaa tgggtggtcgc tttctcaaca 660
 aaaagaagct cgaaaattac aattctgatg ccacttcaga cattgggcaa aatactgggtg 720
 caaaccctc aacaaactca cctaacactc aacatttggt caccaacaat gagaatctag 780
 gctcatcaaa tgcgtcacia gccacgggtc aggacatgca cagagtggag agtttcaata 840
 ttggttacca taatggaaat ggtcttgag aactgtacca ttcacaagca aatggaaaaa 900
 aggagggaaa ctgctttggg aaagagaggg accctaataa tggggctttc aaatgacact 960
 tcgcccagcc atacagcaac agttaggtga agatgaaggg tttttatctc atccaacttg 1020
 tgatgctgta ttgaaggcaa ttcattcttg gcttagttaa gtggtgagac cagtgcacatg 1080
 gagtacactc tgccttggtt ggtctctccc cttgcatttg tttctcttta caagtccata 1140
 tgtaaaaatg gataacggaa agaaaaagaa aaatcacttt tgtttgagaa ctttttttaag 1200
 tttgttttta actgtgtgaa ggtttcataa aattgtggac tgacttgtgt gacatatgct 1260
 ccacaaaacc ttaaaacttt cgtctatttt gtccaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
 aaaaaaaaaa aaagggaata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
 aaaaaa 1385

<210> 60
 <211> 304
 <212> PRT
 <213> Glycine max

<400> 60
 Met Pro Gly Lys Ala Asp Thr Asp Asp Trp Arg Val Glu Arg Gly Glu
 1 5 10 15
 Gln Ile Gln Phe Gln Ser Ser Ile Tyr Ser His His Gln Pro Trp Trp
 20 25 30
 Cys Gly Val Gly Glu Asn Ala Ser Lys Ser Ser Ser Ala Asp Gln Leu
 35 40 45
 Asn Gly Ser Ile Val Asn Gly Ile Thr Arg Ser Glu Thr Asn Asp Lys
 50 55 60
 Ser Gly Glu Gly Val Ala Lys Glu Tyr Gln Asn Ile Lys His Ala Val
 65 70 75 80

Leu Ser Thr Pro Phe Thr Met Asp Lys His Leu Ala Pro Asn Pro Gln
 85 90 95
 Met Glu Leu Val Gly His Ser Val Val Leu Thr Ser Pro Tyr Ser Asp
 100 105 110
 Ala Gln His Gly Gln Ile Leu Thr Thr Tyr Gly Gln Gln Val Met Ile
 115 120 125
 Asn Pro Gln Leu Tyr Gly Met Tyr His Ala Arg Met Pro Leu Pro Pro
 130 135 140
 Glu Met Glu Glu Glu Pro Val Tyr Val Asn Ala Lys Gln Tyr His Gly
 145 150 155 160
 Ile Leu Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Leu Glu Lys Lys
 165 170 175
 Val Ile Lys Asn Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His
 180 185 190
 Ala Met Arg Arg Ala Arg Gly Asn Gly Gly Arg Phe Leu Asn Lys Lys
 195 200 205
 Lys Leu Glu Asn Tyr Asn Ser Asp Ala Thr Ser Asp Ile Gly Gln Asn
 210 215 220
 Thr Gly Ala Asn Pro Ser Thr Asn Ser Pro Asn Thr Gln His Leu Phe
 225 230 235 240
 Thr Asn Asn Glu Asn Leu Gly Ser Ser Asn Ala Ser Gln Ala Thr Val
 245 250 255
 Gln Asp Met His Arg Val Glu Ser Phe Asn Ile Gly Tyr His Asn Gly
 260 265 270
 Asn Gly Leu Ala Glu Leu Tyr His Ser Gln Ala Asn Gly Lys Lys Glu
 275 280 285
 Gly Asn Cys Phe Gly Lys Glu Arg Asp Pro Asn Asn Gly Ala Phe Lys
 290 295 300

<210> 61

<211> 1401

<212> DNA

<213> Glycine max

<400> 61

gaagtcttta tgtgacctgg gtggaatgat tctgtgtctg catgtgtgaa ttctggcaag 60
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 gtctgatcca cattccttta cacctaacaa tgcttattct gaaccctggg ggcgagggtat 180
 tcagtacaat cctgtccccc aagcaatgtt aggagtgaat gcatctaatt catcttcact 240
 tgaacgccct aatgggtgatt cggaatccag tgaagaggat gatgatgcca ctaaagaatc 300
 acaaccact gctcctaatac aatcaggaaa ttatggacag gaccaccaag cgatgcaaca 360
 ttcttcatca tctgcacctt tggtacgtga tgattgcctt acacaggctc cacaagtgga 420
 acttgttggc cactcaattg gatacactcc ttttatagga atgccccatg ccagaatggc 480
 tttgcccctt gagatggctc aagagcctgt ttatgtgaat gccaaacaat accaaggaat 540
 tctgagacga agacaggctc gtgctaaagc agagcttgaa aagaaattaa taaaagtcag 600

```

aaagccatat cttcatgaat cccggcatca gcatgctata agaagagcac gaggtaatgg 660
agggcgtttt gcaaagaaaa ctgaagttga ggcttcaaac cacatgaaca aggaaaagga 720
tatgggtact ggccagggtcc cattgtcacg gtcaattagt tcatctgggt ttggatcact 780
accctctgac tctgctgaga cctggaattc tcctagtgtg caacaagatg caagaggatc 840
tcaagtgcac gagagatttg aagaacgcaa ctatgcaaat gttttgcagt catcatctac 900
tttttgtttg cactcgggtg aaagagtgga ggaagggggac tgttcagggtc aacaacgggg 960
aagcatcttg tcagagcaca cctcacagag gcgtcttgct attcagtaaa ccactgcatg 1020
tgttgatgct gaggttggtg tatataattg agtgaactag taggttgagt accttggcta 1080
tctatctgta aacattggca atttgcatgc atgtcaagcg gcaaatcatt cttggctggg 1140
tttcagctgt tcatgatatg gggagaagaa tgattgattg ggccatcata cttgtgttgt 1200
tgaagtctac cagtccttca ttatatcctc tttttcattt tttctgtttt tgtacagaga 1260
tagtagttag caaagtcaag ccaacggatt agaagacttg atgaaacaaa ctactgactc 1320
actttcctct ggcggcttta ttttatgtta ctcaccgggt attaatgctt aatatgagac 1380
atcatatgag agatttgctg c 1401

```

<210> 62

<211> 307

<212> PRT

<213> Glycine max

<400> 62

```

Met Gln Ser Lys Ser Glu Thr Ala Asn Gln Leu Arg Ser Asp Pro His
  1              5              10              15

```

```

Ser Phe Thr Pro Asn Asn Ala Tyr Ser Glu Pro Trp Trp Arg Gly Ile
              20              25              30

```

```

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

```

```

Ser Ser Ser Leu Glu Arg Pro Asn Gly Asp Ser Glu Ser Ser Glu Glu
  50              55              60

```

```

Asp Asp Asp Ala Thr Lys Glu Ser Gln Pro Thr Ala Pro Asn Gln Ser
  65              70              75              80

```

```

Gly Asn Tyr Gly Gln Asp His Gln Ala Met Gln His Ser Ser Ser Ser
              85              90              95

```

```

Ala Pro Leu Val Arg Asp Asp Cys Leu Thr Gln Ala Pro Gln Val Glu
  100              105              110

```

```

Leu Val Gly His Ser Ile Gly Tyr Thr Pro Phe Ile Gly Met Pro His
  115              120              125

```

```

Ala Arg Met Ala Leu Pro Leu Glu Met Ala Gln Glu Pro Val Tyr Val
  130              135              140

```

```

Asn Ala Lys Gln Tyr Gln Gly Ile Leu Arg Arg Arg Gln Ala Arg Ala
  145              150              155              160

```

```

Lys Ala Glu Leu Glu Lys Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu
  165              170              175

```

```

His Glu Ser Arg His Gln His Ala Ile Arg Arg Ala Arg Gly Asn Gly
  180              185              190

```

```

Gly Arg Phe Ala Lys Lys Thr Glu Val Glu Ala Ser Asn His Met Asn
  195              200              205

```

Lys Glu Lys Asp Met Gly Thr Gly Gln Val Pro Leu Ser Arg Ser Ile
210 215 220

Ser Ser Ser Gly Phe Gly Ser Leu Pro Ser Asp Ser Ala Glu Thr Trp
225 230 235 240

Asn Ser Pro Ser Val Gln Gln Asp Ala Arg Gly Ser Gln Val His Glu
245 250 255

Arg Phe Glu Glu Arg Asn Tyr Ala Asn Val Leu Gln Ser Ser Ser Thr
260 265 270

Phe Cys Leu His Ser Gly Glu Arg Val Glu Glu Gly Asp Cys Ser Gly
275 280 285

Gln Gln Arg Gly Ser Ile Leu Ser Glu His Thr Ser Gln Arg Arg Leu
290 295 300

Ala Ile Gln
305

<210> 63
<211> 1241
<212> DNA
<213> Glycine max

<400> 63
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tgttttttgc agcaacactt cagttcaatt aacgaactac accactttct ttctcttctt 120
cgactgctct gtaaccgaaa acctcccttt cccagtttcg aatcttttgt ttctgccttt 180
ggttactgtt tttccgagcc atgctattca ttattgtcct tcgaatcgga ttgattggga 240
cactgtattg catgtaaate aggaaatcat gacttctact catgacctct cagataatga 300
agctgatgac cagcagcagt cggaaatcaca aatggagcct ttatctgcaa atggaatttc 360
ttatgcaggt attgctactc agaatgttca gtatgcaaca ccttcacagc ttggaactgg 420
gcatgctgtg gtaccgcccc cttaccata tccagatcca tactacagaa gtatctttgc 480
tccctatgat gcacaaactt atccccca accctatggg ggaaatccaa tgggtccacct 540
tcagttaatg ggaattcaac aagcaggtgt tcctttgcca actgatacag ttgaggagcc 600
tgtgtttgtc aatgcaaaaac agtatcatgg tatattaaga cgcagacagt cccgtgctaa 660
agctgaatca gaaaaaaagg ctgcaaggaa tcggaagcca tacttgcatg aatctcgaca 720
tttgcatgca ctgagaagag caagaggatg tggagggtcg tttttgaatt caaagaaaga 780
tgagaatcaa caggatgagg ttgcatcaac tgacgaatca cagtccacta tcaatctcaa 840
ttctgataaa aatgagcttg caccatcaga tagaacatcc taaaactaca gaaatggtga 900
tgctgtagat tgcagggatc tgttgtgtat atctatatgt ggagatgaat ctccaaccaa 960
cagtatcctc agatatctcc ctattattca ttctgtcgta caacgccata ggtataagta 1020
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agtgattcaa ctaagtctat cccaatgtg gtcctttctt gccttttttag gtatttttat 1140
tgtgtgggct tttctttgta ttatttggtg cctctgaggg aaagagaaga gattatccga 1200
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1241

<210> 64
<211> 204
<212> PRT
<213> Glycine max

<400> 64
Met Thr Ser Thr His Asp Leu Ser Asp Asn Glu Ala Asp Asp Gln Gln
1 5 10 15

Gln Ser Glu Ser Gln Met Glu Pro Leu Ser Ala Asn Gly Ile Ser Tyr
 20 25 30
 Ala Gly Ile Ala Thr Gln Asn Val Gln Tyr Ala Thr Pro Ser Gln Leu
 35 40 45
 Gly Thr Gly His Ala Val Val Pro Pro Thr Tyr Pro Tyr Pro Asp Pro
 50 55 60
 Tyr Tyr Arg Ser Ile Phe Ala Pro Tyr Asp Ala Gln Thr Tyr Pro Pro
 65 70 75 80
 Gln Pro Tyr Gly Gly Asn Pro Met Val His Leu Gln Leu Met Gly Ile
 85 90 95
 Gln Gln Ala Gly Val Pro Leu Pro Thr Asp Thr Val Glu Glu Pro Val
 100 105 110
 Phe Val Asn Ala Lys Gln Tyr His Gly Ile Leu Arg Arg Arg Gln Ser
 115 120 125
 Arg Ala Lys Ala Glu Ser Glu Lys Lys Ala Ala Arg Asn Arg Lys Pro
 130 135 140
 Tyr Leu His Glu Ser Arg His Leu His Ala Leu Arg Arg Ala Arg Gly
 145 150 155 160
 Cys Gly Gly Arg Phe Leu Asn Ser Lys Lys Asp Glu Asn Gln Gln Asp
 165 170 175
 Glu Val Ala Ser Thr Asp Glu Ser Gln Ser Thr Ile Asn Leu Asn Ser
 180 185 190
 Asp Lys Asn Glu Leu Ala Pro Ser Asp Arg Thr Ser
 195 200

<210> 65

<211> 1716

<212> DNA

<213> Glycine max

<400> 65

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gcacgaggta cgtaccgaca tgactccaac ctgatgggggt taaacactgc ttctgcgtag      60
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tgatgtttat gctgaagact gaataaaagt ctgagaaagc tgcttactac aaaccaacaa     180
gattaactaa gaaatcatct tttgggacga tgcaaaactgt ttatcttaaa gagcacgaag     240
gaaatgcgca caattttgtg ggcacgttgt cttctgcagc ttcagcacc cccaggagtg     300
cttttggatc tcaatctgtt catcagggag agtcttgtgg ccaagtga aa cctttttcat    360
tgagagctgcc aaactgcata gaccaacttg ctgccactaa gccactagca agaggagctg     420
accaagtgtt gggtaaaggg cacataactc agtttacaat ctttccagat gattgtaaaa     480
tgtcagatga tgcgcaaaag cttcagacaa ccatgtcact gcagtcacgc cttactgac     540
cacagtctcg ttttgagata gggtttagtc tgcccacgat atgtgcaaaa tacccttata     600
cggatcaatt ttatggactc ttctcagctt atgcacctca aatttcggga cgtataatgc     660
tgccacttaa catgacatct gatgatgaac caatttacgt aaatgctaag cagtaccatg     720
gaatcattag acgtcggcag tcccgtgcc aagctgtact tgatcacaaa ttgactaaac     780
gtcgcaagcc ctatatgcac gaatcacgcc atctccatgc aatgcggcga ccaagaggat     840
gtgggggtcg cttcttgaac actaagaatt ctgttgacgg aaatggtaaa attggaaatg     900
aagtgcataa aactgttggt gaacaattgc agtctagtgg ctctcagagt tctgaattcc     960

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ttcaatctga ggttggaact tttaattcat caaaagagac taatggaagc agtccaaata 1020
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atcatcttgg atctgctgtc cactcttttg cagacatgat agatgggtgg cgcggtatga 1140
tcatacccac caaatggggt gcagcagcag gtaactgctg caaccttaaa gtttgatttg 1200
caaagaatca aggggtgggt tgctgtagca ttgcaccagg cccatcctcg atgaggccag 1260
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aactatgttt ctgtctttgt gtgaaaatga aagcatgaaa ctctagttat gtgtgcttcg 1560
aataatgtct aaacgtggtg ttgtattttg tatttctgac ttcgaggaac aatgtattat 1620
agaaccttgt tctgtggtct ttgttagaaa aaataaagca ttggtgtgtt tttctccaaa 1680
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaag 1716

```

<210> 66

<211> 328

<212> PRT

<213> Glycine max

<400> 66

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Met Gln Thr Val Tyr Leu Lys Glu His Glu Gly Asn Ala His Asn Phe
  1              5              10              15

Val Gly Thr Leu Ser Ser Ala Ala Ser Ala Pro Trp Trp Ser Ala Phe
          20              25              30

Gly Ser Gln Ser Val His Gln Gly Glu Ser Cys Gly Gln Val Lys Pro
          35              40              45

Phe Ser Leu Glu Leu Pro Asn Cys Ile Asp Gln Leu Ala Ala Thr Lys
          50              55              60

Pro Leu Ala Arg Gly Ala Asp Gln Val Leu Gly Lys Gly His Ile Thr
          65              70              75              80

Gln Phe Thr Ile Phe Pro Asp Asp Cys Lys Met Ser Asp Asp Ala Gln
          85              90              95

Lys Leu Gln Thr Thr Met Ser Leu Gln Ser Ser Leu Thr Asp Pro Gln
          100              105              110

Ser Arg Phe Glu Ile Gly Phe Ser Leu Pro Thr Ile Cys Ala Lys Tyr
          115              120              125

Pro Tyr Thr Asp Gln Phe Tyr Gly Leu Phe Ser Ala Tyr Ala Pro Gln
          130              135              140

Ile Ser Gly Arg Ile Met Leu Pro Leu Asn Met Thr Ser Asp Asp Glu
          145              150              155              160

Pro Ile Tyr Val Asn Ala Lys Gln Tyr His Gly Ile Ile Arg Arg Arg
          165              170              175

Gln Ser Arg Ala Lys Ala Val Leu Asp His Lys Leu Thr Lys Arg Arg
          180              185              190

Lys Pro Tyr Met His Glu Ser Arg His Leu His Ala Met Arg Arg Pro
          195              200              205

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Arg Gly Cys Gly Gly Arg Phe Leu Asn Thr Lys Asn Ser Val Asp Gly
 210 215 220
 Asn Gly Lys Ile Gly Asn Glu Val His Lys Thr Val Gly Glu Gln Leu
 225 230 235 240
 Gln Ser Ser Gly Ser Gln Ser Ser Glu Phe Leu Gln Ser Glu Val Gly
 245 250 255
 Thr Phe Asn Ser Ser Lys Glu Thr Asn Gly Ser Ser Pro Asn Ile Ser
 260 265 270
 Gly Ser Glu Val Thr Ser Met Tyr Ser Arg Gly Gly Leu Asp Ser Phe
 275 280 285
 Ser Leu Asn His Leu Gly Ser Ala Val His Ser Phe Ala Asp Met Ile
 290 295 300
 Asp Gly Gly Arg Gly Met Ile Ile Pro Thr Lys Trp Val Ala Ala Ala
 305 310 315 320
 Gly Asn Cys Cys Asn Leu Lys Val
 325

<210> 67
 <211> 1103
 <212> DNA
 <213> Glycine max

<400> 67
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 aatccagagt gagaaacatt aggcttatca gaggagacat gcccgagttg aaccgacaat 120
 tctattacta ctcttttgctt ctttcttcat gcctcatcaa atcccaaagg atataattga 180
 aggttttggg aactaaggct gcaatattgt atacattcta ctcaaggaat ggctcactact 240
 tcttatacct gtggtgatcc ttattttggg agttcaatag ttgcttatgg aacacaggct 300
 attactcaac aaatggtgcc ccagatgctg ggattagcat ccaccagaat tgcattacca 360
 gttgagcttg cagaagatgg gcccatthtat gtcaatgcca aacaatacca tggatatactg 420
 agaaggcgac agtcacgagc aaagcttaag gctcaaaaaca aactcatcaa aagtcgtaag 480
 ccatactctt atgagtctcg gcaccgccac gcattgaaaa gggttagggg aactggggggg 540
 cgctttctta gtgccaaaaca gcttcaacag tttaatgcag aacttggtcac cgatgcccac 600
 tcaggccccg gccctgtcaa tgtttatcaa aagaaagatg catctgaggc agaaagtcac 660
 ccctcaagaa ctggaaaaaa tgcacatctc acattcacag caatctctgg cttgacaagt 720
 atgtccggta acagtgtcag tttcaggcgg cctgagcaca acttcttggg gaactctcct 780
 aatatagggt gatcgtcgca atgcagtggg ggactcacct ttggtggtgg agctcggcaa 840
 tgtacttcag ttggccgggtg agaggtggaa ccaatcaaaa tcaagtccac tgggtctggca 900
 aatcatcctt ggcttagtca ctttactttc tgtgtttcat gtgttggttac ggaaatgttg 960
 tcttttggaa gactctgcat tagcactcag acttttgcta gtgctttccc atgtatatttg 1020
 aaagttgctc ttgtttctgt tgttgaactg gaccagaaag tttgtgcttg aaaatttaac 1080
 tttttaaaaa aaaaaaaaaa aaa 1103

<210> 68
 <211> 210
 <212> PRT
 <213> Glycine max

<400> 68
 Met Ala His Thr Ser Tyr Pro Cys Gly Asp Pro Tyr Phe Gly Ser Ser
 1 5 10 15

Ile Val Ala Tyr Gly Thr Gln Ala Ile Thr Gln Gln Met Val Pro Gln
 20 25 30
 Met Leu Gly Leu Ala Ser Thr Arg Ile Ala Leu Pro Val Glu Leu Ala
 35 40 45
 Glu Asp Gly Pro Ile Tyr Val Asn Ala Lys Gln Tyr His Gly Ile Leu
 50 55 60
 Arg Arg Arg Gln Ser Arg Ala Lys Leu Lys Ala Gln Asn Lys Leu Ile
 65 70 75 80
 Lys Ser Arg Lys Pro Tyr Leu His Glu Ser Arg His Arg His Ala Leu
 85 90 95
 Lys Arg Val Arg Gly Thr Gly Gly Arg Phe Leu Ser Ala Lys Gln Leu
 100 105 110
 Gln Gln Phe Asn Ala Glu Leu Val Thr Asp Ala His Ser Gly Pro Gly
 115 120 125
 Pro Val Asn Val Tyr Gln Lys Lys Asp Ala Ser Glu Ala Glu Ser His
 130 135 140
 Pro Ser Arg Thr Gly Lys Asn Ala Ser Ile Thr Phe Thr Ala Ile Ser
 145 150 155 160
 Gly Leu Thr Ser Met Ser Gly Asn Ser Val Ser Phe Arg Arg Pro Glu
 165 170 175
 His Asn Phe Leu Gly Asn Ser Pro Asn Ile Gly Gly Ser Ser Gln Cys
 180 185 190
 Ser Gly Gly Leu Thr Phe Gly Gly Gly Ala Arg Gln Cys Thr Ser Val
 195 200 205
 Gly Arg
 210

<210> 69

<211> 1128

<212> DNA

<213> Glycine max

<400> 69

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 gtctgatgag catttttgaag gttacatgaa gcaattttctc ttttttgaatc ttcctgacac 180
 cgagatcaat tggtcacaag ttgattgcaa tcactcaatg gctcattctt cttatcccta 240
 cggcgatcca attcttgctt atggaccaca agctattagt catccccaaa tggtagccca 300
 gatgctggga ctagcatcca ccagagtggc attaccactt gatcttgctg aagatggacc 360
 gatttatgtc aacgcgaaac aataccatgg tatactgaga aggcgacagt cacgagcaaa 420
 acttgaggct cagaacaaac ttatcaaaaag tcgtaagcca tatcttcatg agtctcggca 480
 ccgccatgct ttgaataggg ttaggggatc tgggggtcga tttctgagta ccaaacagct 540
 tgcacagtct aatgcagaat ttgtcaccgg tgcacattct ggttctgacc ctaccaacat 600
 atatcagaaa gaacatccat tagaggtgga aagtcattcc tcaaaaagatg gagataatgc 660
 atcattcata acaacctact ccgaccggcc atgtttatct ggcaacaacc tcaattttcg 720
 gcagcaggag tgcattgtttc tggggaattc tgcaaacatg agtggagcac cacagtgcag 780

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tggggggactc acctttggcg gagcaaagca acgcacttca gttgtccggt gagagaagaa 840
actgatcgaa accgacttca ccggtcaggc aaatcatcct tggcttagtc acttttgtct 900
gtgtcttaat gtgttcgtac taaatgatca ttttgagaga ctcttcagtc tgcattagca 960
ctaataagac ctttccaatt gctttggcat gtattttaaa gttgctattg tactggattc 1020
tgaactggat tggaatagtc tgtgcatgga actagtatgt ttgtgttagt tactgttgaa 1080
tttccttctt taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1128

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<210> 70

<211> 228

<212> PRT

<213> Glycine max

<400> 70

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Met Lys Gln Phe Leu Phe Leu Asn Leu Pro Asp Thr Glu Ile Asn Cys
  1                      5                      10                      15

Ser Gln Val Asp Cys Asn His Ser Met Ala His Ser Ser Tyr Pro Tyr
                20                      25                      30

Gly Asp Pro Ile Leu Ala Tyr Gly Pro Gln Ala Ile Ser His Pro Gln
                35                      40                      45

Met Val Pro Gln Met Leu Gly Leu Ala Ser Thr Arg Val Ala Leu Pro
  50                      55                      60

Leu Asp Leu Ala Glu Asp Gly Pro Ile Tyr Val Asn Ala Lys Gln Tyr
  65                      70                      75                      80

His Gly Ile Leu Arg Arg Arg Gln Ser Arg Ala Lys Leu Glu Ala Gln
                85                      90                      95

Asn Lys Leu Ile Lys Ser Arg Lys Pro Tyr Leu His Glu Ser Arg His
                100                      105                      110

Arg His Ala Leu Asn Arg Val Arg Gly Ser Gly Gly Arg Phe Leu Ser
                115                      120                      125

Thr Lys Gln Leu Ala Gln Ser Asn Ala Glu Phe Val Thr Gly Ala His
                130                      135                      140

Ser Gly Ser Asp Pro Thr Asn Ile Tyr Gln Lys Glu His Pro Leu Glu
  145                      150                      155                      160

Val Glu Ser His Ser Ser Lys Asp Gly Asp Asn Ala Ser Phe Ile Thr
                165                      170                      175

Thr Tyr Ser Asp Arg Pro Cys Leu Ser Gly Asn Asn Leu Asn Phe Arg
                180                      185                      190

Gln Gln Glu Cys Met Phe Leu Gly Asn Ser Ala Asn Met Ser Gly Ala
                195                      200                      205

Pro Gln Cys Ser Gly Gly Leu Thr Phe Gly Gly Ala Lys Gln Arg Thr
  210                      215                      220

Ser Val Val Arg
  225

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<210> 71
 <211> 1286
 <212> DNA
 <213> Helianthus sp.

<400> 71
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 cgtcctctat actcgtagat cttgggtgtaa cagtattgca taagtttcat gtcctcttct 120
 gccatgcgag cgaattcatc tgattcgtct cctccagaac agtcgtaga cagggaatca 180
 cagtctgatg aagttcttag tgaggaagaa gatgatgcaa gcaaagaaac acaaaatgct 240
 tcgtcttttc gttcagataa aagttatcag cagcagggag taccaaatat ctttccaaat 300
 aatggcgaaa ccgtaggggca ggtcccacaa ctagaacttg tcggtcacac tattgcctgt 360
 gctccaaatc cttattgtga tccatattat ggtggaatga tggcagctta tggtcagcct 420
 tttgttcatc ctcagtttct tgagcaagca aggatgcctt tgccacttga aatggcgcaa 480
 gagcctgttt acgtgaatgc caaacaatac catgcgatat taaggcgaag gcaatcccgt 540
 gcaaaagcag agcttgagaa gaaacttata aaagacagaa agccttatct tcatgaatca 600
 cggcatcagc atgctttgag aagggttaagg ggcaccggtg gtcgttttgc aaagaaaact 660
 gacgttaata agaacacaac aggttcgggt tcagggttctg ccatgtcatc atcccagtcg 720
 gtgaattcaa accgggtgca ctcagaatct gccgagagct tggacacacc aaggggtgga 780
 ttggtaaatt cacacaatac tcgcacgtat cttgataacg gaggttcttt aggccagcag 840
 tggataaaca tttcatctaa ccaatcttca cagagggctg ttgccatgaa gtgatgtcga 900
 gtgtttaaca ccctttgtgt ctatccgtgg cttctaagct ggccggcaaa tcattcttgg 960
 ctcatgttaa tatgagggac aaacaggtaa atgtaccttt tgggtgtcctc tttggtttta 1020
 ctttcaggat ttctttcttc ggaactgatg ttatgtacaa agtttgcttt tggggataga 1080
 agaattggtt ggggttgggtt tgtgtgttct tttctgaatg tttggtatat ttggaggtga 1140
 agcatggagt ttaagatgtg cttatgtcta tcgtctaatt gtaggggcat atagtgtcct 1200
 acagcctcca gcacatgtgt aatgtcgtgg ctgttgaaaa ttggagcttc atatttactg 1260
 ttttgcaaaa aaaaaaaaaa aaaaaa 1286

<210> 72
 <211> 261
 <212> PRT
 <213> Helianthus sp.

<400> 72
 Met Ser Ser Ser Ala Met Arg Ala Asn Ser Ser Asp Ser Ser Pro Pro
 1 5 10 15
 Glu Gln Ser Leu Asp Arg Glu Ser Gln Ser Asp Glu Val Leu Ser Glu
 20 25 30
 Glu Glu Asp Asp Ala Ser Lys Glu Thr Gln Asn Ala Ser Ser Phe Arg
 35 40 45
 Ser Asp Lys Ser Tyr Gln Gln Gln Gly Val Pro Asn Ile Leu Pro Asn
 50 55 60
 Asn Gly Glu Thr Val Gly Gln Val Pro Gln Leu Glu Leu Val Gly His
 65 70 75 80
 Thr Ile Ala Cys Ala Pro Asn Pro Tyr Cys Asp Pro Tyr Tyr Gly Gly
 85 90 95
 Met Met Ala Ala Tyr Gly Gln Pro Phe Val His Pro Gln Phe Leu Glu
 100 105 110
 Gln Ala Arg Met Pro Leu Pro Leu Glu Met Ala Gln Glu Pro Val Tyr
 115 120 125

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Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Ser Arg
 130 135 140
 Ala Lys Ala Glu Leu Glu Lys Lys Leu Ile Lys Asp Arg Lys Pro Tyr
 145 150 155 160
 Leu His Glu Ser Arg His Gln His Ala Leu Arg Arg Val Arg Gly Thr
 165 170 175
 Gly Gly Arg Phe Ala Lys Lys Thr Asp Val Asn Lys Asn Thr Thr Gly
 180 185 190
 Ser Gly Ser Gly Ser Ala Met Ser Ser Ser Gln Ser Val Asn Ser Asn
 195 200 205
 Arg Val His Ser Glu Ser Ala Glu Ser Leu Asp Thr Pro Arg Gly Gly
 210 215 220
 Leu Val Asn Ser His Asn Thr Arg Thr Tyr Leu Asp Asn Gly Gly Ser
 225 230 235 240
 Leu Gly Gln Gln Trp Ile Asn Ile Ser Ser Asn Gln Ser Ser Gln Arg
 245 250 255
 Ala Val Ala Met Lys
 260

<210> 73
 <211> 1306
 <212> DNA
 <213> Triticum aestivum

<400> 73
 ggagaaacgg aaacagagac agaggggagag gagacttgca gaggagagga gagaagaggc 60
 ggaacaaggg aggagggagg ggtcgccgga aggggggacat gctccctccg catctcacat 120
 ctcgcagctt gaactgagag caagagcaga agcccatgag atgagacgca agcaaaatat 180
 gcaagaaaat ggcacaatca tgattcagtt tggtcagcaa gtgcctaact gcgagtcctc 240
 agctagcgat tctcctcaag aagtgtccgg aatgagcgaa gggagcttta atgagcagaa 300
 tgatcaatct ggtaatcgcg atggctatac gaagagtagt gatgaaggca agatgatgtc 360
 ggctttgtct ctgggcaatt cagaaatggc atacacaccg ccaaaacctg accgcactca 420
 tccctttgcc atatcatacc catatgctga tccttactat ggtggtgcag tggcagccta 480
 tggcgcacat gctattatgc acccccagat ggtgggcatg gtaccatcct ctcgagtgcc 540
 actaccgatt gaaccagctg ccgccgaaga gcccattht atggaatgcga agcaatacca 600
 tgccattctc cgaaggagac agctccgcgc aaaattagag gctgaaaata agctggtcaa 660
 aagccgtaag ccgtacctgc atgagtcctg gcaccagcac gcgatgaagc gggctcgggg 720
 aacaggcggg cggttcctca acgcaaagga gaagtctgaa gcttcaggcg gcggcaatgc 780
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 cgcagttgcc ccctggcaaa tcctccttgg cttatgtgtg tggcgaatga ccgtcaactc 960
 ggtccagtga tattgtaaaa ctgaatttag agtctgtgca attgtgttac ttggggggttt 1020
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 ttggagtaag taataaccat tcccggcgtg atgcatttgc gcccggtggtg gtgtttctgt 1260
 tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1306

<210> 74
 <211> 243

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<212> PRT

<213> Triticum aestivum

<400> 74

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Met Arg Arg Lys Gln Asn Met Gln Glu Asn Gly Thr Ile Met Ile Gln
 1           5           10           15

Phe Gly Gln Gln Val Pro Asn Cys Glu Ser Ser Ala Ser Asp Ser Pro
          20           25           30

Gln Glu Val Ser Gly Met Ser Glu Gly Ser Phe Asn Glu Gln Asn Asp
          35           40           45

Gln Ser Gly Asn Arg Asp Gly Tyr Thr Lys Ser Ser Asp Glu Gly Lys
          50           55           60

Met Met Ser Ala Leu Ser Leu Gly Asn Ser Glu Met Ala Tyr Thr Pro
 65           70           75           80

Pro Lys Pro Asp Arg Thr His Pro Phe Ala Ile Ser Tyr Pro Tyr Ala
          85           90           95

Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Tyr Gly Ala His Ala Ile
          100          105          110

Met His Pro Gln Met Val Gly Met Val Pro Ser Ser Arg Val Pro Leu
          115          120          125

Pro Ile Glu Pro Ala Ala Ala Glu Glu Pro Ile Tyr Val Asn Ala Lys
          130          135          140

Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Leu Arg Ala Lys Leu Glu
          145          150          155          160

Ala Glu Asn Lys Leu Val Lys Ser Arg Lys Pro Tyr Leu His Glu Ser
          165          170          175

Arg His Gln His Ala Met Lys Arg Ala Arg Gly Thr Gly Gly Arg Phe
          180          185          190

Leu Asn Ala Lys Glu Lys Ser Glu Ala Ser Gly Gly Gly Asn Ala Ser
          195          200          205

Ala Arg Ser Gly His Ala Gly Val Pro Pro Asp Gly Gly Met Phe Ser
          210          215          220

Lys His Asp His Thr Leu Pro Ser Gly Asp Phe His Tyr Arg Ala Arg
          225          230          235          240

Gly Gly Ala

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<210> 75

<211> 1077

<212> DNA

<213> Triticum aestivum

<400> 75

gcacgaggtt ggaaagtaac aaaccatgac ttctgtcacc gacggtgttt caggtgatca 60

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tagagctgat gagcagcaga agcaagctgc tgctcaaggg aaccaggaag aggccccagc 120
tactagtata ggtagtcagg caatggtggc aacaccttcc acagattatg tcacacccta 180
tgccaccag gaagcttgcc atgcaatggg tcaaattgct taccactg tcgatccatt 240
ctatggaagc ctttatgcag cctacggtgg acaacctatg atgcatccac caatggtcgg 300
aatgcatgca gccgcaatac cgttgcctac tgatgcaatt gaagagcctg tgtatgtgaa 360
tgcaaagcaa tataatgcca tattaaggcg gcgccaatct cgggctaaag cagagtcaga 420
aaggaagctt atcaagggcc gcaagccata tctccatgag tcgcggcatc aacatgcctt 480
gaaaagggcc aggggagccg gagggcggtt tcttaacgca aagtcagacg acaatgaaga 540
gcattctgat tccagctcca aagataagca gaatggcggt gcaccccgca gcagtggcca 600
atcctcccaa tctcccaaag gcgcgacttc ggctgataag tcagcaaacc atgaatgaga 660
tgctagaagg tccgccggac gcgacgatcc atgccaacag ttttgtacag tatatatatg 720
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gcgggtttgg tcaggaggct tttgtagctt ataaaagaag tataattagt gctacattgt 960
tttctttggt gtggatttgg tctcttagct gtgctgcac ctcattcgtg gtgcagaaaa 1020
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<210> 76

<211> 210

<212> PRT

<213> Triticum aestivum

<400> 76

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Met Thr Ser Val Thr Asp Gly Val Ser Gly Asp His Arg Ala Asp Glu
 1              5              10              15

Gln Gln Lys Gln Ala Ala Ala Gln Gly Asn Gln Glu Glu Ala Pro Ala
      20              25              30

Thr Ser Ile Gly Ser Gln Ala Met Val Ala Thr Pro Ser Thr Asp Tyr
      35              40              45

Val Thr Pro Tyr Gly His Gln Glu Ala Cys His Ala Met Gly Gln Ile
      50              55              60

Ala Tyr Pro Thr Val Asp Pro Phe Tyr Gly Ser Leu Tyr Ala Ala Tyr
      65              70              75              80

Gly Gly Gln Pro Met Met His Pro Pro Met Val Gly Met His Ala Ala
      85              90              95

Ala Ile Pro Leu Pro Thr Asp Ala Ile Glu Glu Pro Val Tyr Val Asn
      100             105             110

Ala Lys Gln Tyr Asn Ala Ile Leu Arg Arg Arg Gln Ser Arg Ala Lys
      115             120             125

Ala Glu Ser Glu Arg Lys Leu Ile Lys Gly Arg Lys Pro Tyr Leu His
      130             135             140

Glu Ser Arg His Gln His Ala Leu Lys Arg Ala Arg Gly Ala Gly Gly
      145             150             155             160

Arg Phe Leu Asn Ala Lys Ser Asp Asp Asn Glu Glu His Ser Asp Ser
      165             170             175

Ser Ser Lys Asp Lys Gln Asn Gly Val Ala Pro Arg Ser Ser Gly Gln
      180             185             190

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Ser Ser Gln Ser Pro Lys Gly Ala Thr Ser Ala Asp Lys Ser Ala Asn
 195 200 205

His Glu
 210

<210> 77
 <211> 1378
 <212> DNA
 <213> Triticum aestivum

<400> 77
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 gctctgctag gcagcgatga tgagcttcaa gggccacgac ggattcgggc aggcctccaa 120
 tgggtgggtg ggtgggtggag cctccgtgcc atggtggacg gtgtcccaga tgctgtacgg 180
 ggagccgggg gccgccttgt cgtcgtcgcc ggaggcggag cctcgccggg acgcccagtt 240
 ccaggctcgtg ccagagagctc agggcatcct ggatccactg ccggcgccca agagcggggc 300
 tcctgaggtc ctcaagttct cgggtgttcca agggaatttg gagtcgggag gcaacaaagg 360
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 cagtcgcttc gaatttggcc cgggtccttc catgatgtct tctggttatc cttcagccga 480
 gcagtgctat ggcctgctta ccacttacgc gatgaaatct acgcctgggtg gccgattgct 540
 cttgccactg aatgcaacag ctgacgcgcc gatttacgtg aatgcgaagc agtatgaagg 600
 catccttcgc cgccgccgtg ctcggtgcaa ggtggagcga gagaatcagc tggtgaaagg 660
 aagaaagccg tatcttcacg aatcacgcca ccgccacgcg atgcgccggg cgagggggcac 720
 gggagggggc ttcctcaaca ccaagaagga ggggaatggc aaggacgctg gaggaggagg 780
 caagagggca gagtgcgccc cgcccacgcg cttcgccacg tctccgagct ccgtcatccc 840
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 gtacgaccac gacgacgtgg accactacaa cagcatcgag cacctccgga cgcccttctt 960
 caccgccgtg ccgatcatca tggacggcga gcacggggca tccgccccct tcaagtgggc 1020
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 gcaccagat caagagccgg ccatggccgg ctctggctcc gtctggttgt ctgcaggcaa 1140
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 aactccggtg ctggtttctca gggatcttgt gatgatgggg ctcccatat gcctgtaaaa 1260
 tagtatcgga agcactagca gtgtactacg ggtatgaact ctgtggtact atcaggtatc 1320
 tgtgtcagaa ctcagaataa gtatcaaact tcagggtcta aaaaaaaaaa aaaaaaaa 1378

<210> 78
 <211> 327
 <212> PRT
 <213> Triticum aestivum

<400> 78
 Met Met Ser Phe Lys Gly His Asp Gly Phe Gly Gln Ala Ser Asn Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Ala Ser Val Pro Trp Trp Thr Val Ser Gln Met
 20 25 30
 Leu Tyr Gly Glu Pro Gly Ala Ala Leu Ser Ser Ser Pro Glu Ala Glu
 35 40 45
 Pro Arg Arg Asp Ala Gln Phe Gln Val Val Pro Arg Ala Gln Gly Ile
 50 55 60
 Leu Asp Pro Leu Pro Ala Pro Lys Ser Gly Ala Pro Glu Val Leu Lys
 65 70 75 80

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

<210> 79

<211> 1192

<212> DNA

<213> Triticum aestivum

<400> 79

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 agggaggagg cgcgtgggag ccatgcttct cccctcttct tegtcttctt cctacgatcc 180
 caaaggtgac tcctttggga aatcggttga cgatcatatg aggtcaactt tgacttttgg 240
 tgataagcat tctgtatatg cagggtcaaaa cactgactat ggccacccaa tggcttgcat 300

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ttcatacccg ttcaacgatt ctgggttctgg agtttgggcg gcctatgggt cacgggctat 360
gttccagccc ctcatggcgg gcggaggggc atctgcaacg gcaagagttc cattgcccgt 420
cgaactagca gcggatgagc ccataattgt caatcccaaa caatataatg ggattctccg 480
gcgaaggcag ctgcgcgcta agtttagaggc ccagaataaa ctcacaaaaa acagaaagcc 540
ctacctccac gagtcgcgcc atcttcacgc gatgaagcgg gcaagagggt ccggggggacg 600
tttcctcaat tccaaacagc tgaagcagca gcagcagtct ggcagtgcct gcaccaaggc 660
cattgcggat ggcgcggaatt ccctgggttc gacctatcta cggctaggca gcggcgcagc 720
cggagaccga accaactcgg tgtccaaggc gatgtcctcc caagagaaca gcaagagagt 780
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tacgtaataa ggggtcctcc gcgccccggg gtggtcaggc aactcatcct tggctttatt 960
tctggcgtgt taggacttca gagatagttt atctcacagt gctttgcagc ccatagttct 1020
cggcttgatg ttcggtatgc aaatgttggt gtactgggtg gttggaacaa aagtttgatg 1080
tggtcacatg acgattgggt gcggaactca tcttggtgtt tgctcgacct taaaaaaaaa 1140
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```

<210> 80

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 80

```

Met Leu Leu Pro Ser Ser Ser Ser Ser Ser Tyr Asp Pro Lys Gly Asp
  1                      5                      10                      15

Ser Phe Gly Lys Ser Val Asp Asp His Met Arg Ser Thr Leu Thr Phe
                      20                      25                      30

Gly Asp Lys His Ser Val Tyr Ala Gly Gln Asn Thr Asp Tyr Gly His
                      35                      40                      45

Pro Met Ala Cys Ile Ser Tyr Pro Phe Asn Asp Ser Gly Ser Gly Val
                      50                      55                      60

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

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

Ala Asp Glu Pro Ile Phe Val Asn Pro Lys Gln Tyr Asn Gly Ile Leu
                      100                     105                     110

Arg Arg Arg Gln Leu Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Thr
                      115                     120                     125

Lys Asn Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Met
                      130                     135                     140

Lys Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Ser Lys Gln Leu
                      145                     150                     155                     160

Lys Gln Gln Gln Gln Ser Gly Ser Ala Cys Thr Lys Ala Ile Ala Asp
                      165                     170                     175

Gly Ala Asn Ser Leu Gly Ser Thr His Leu Arg Leu Gly Ser Gly Ala
                      180                     185                     190

```

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Ala Gly Asp Arg Thr Asn Ser Val Ser Lys Ala Met Ser Ser Gln Glu
195 200 205

Asn Ser Lys Arg Val Ala Ala Pro Ala Pro Ala Phe Thr Met Ile Gln
210 215 220

Ala Ala Arg Lys Asp Asp Asp Phe Phe His His His Ala His His Leu
225 230 235 240

Ser Phe Ser Gly His Phe Gly Gln Ser Ser Asp Arg Tyr Thr
245 250

<210> 81

<211> 1260

<212> DNA

<213> Triticum aestivum

<400> 81

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cgattatatc ttcattgctaa cagtaacacc ctttttggtt cagacaatga caatgatcat 180
gggaagcccc atcagcacat ggtaaagccg ctttttatctt tggggaaccc agagactgtt 240
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gcttatgctg ggatctttcc aggatatgcc tcgcacgcta ttgttcatcc ccaattgaat 360
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gttaatgcaa agcagtagca tgcaattctt aggaggaggc agatacgtgc taaattggag 480
gccccaaata agctggtgaa agcccgaag ccataccttc atgaatctcg gcaccgccat 540
gccatgaagc gagctcgtgg aacaggaggg cggttcctca acacaaagca actcgaggag 600
cagaagcaga agcaggcttc aggtggtgca agctgtacaa aggtccttgg caagaataca 660
ctccttcaga gtagccccgc cttcgcacct tcggcatcag ctccctccaa catgtcaagc 720
ttttcaacaa ccggcatgtt ggctaataca gagcgcacct gcttcccctc ggttggcttc 780
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acattgttat gagtcctttt gagtttcatt tagttgaaag cactggtgtg ctgatgcaga 1020
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gtgaatgtat ctggtaatgt acttaagaga tggttgagcc tcgagctttg atgaatgctg 1200
ttgcagttca tcaactttgc aacctgggtt gcctgatttc aaaaaaaaaa aaaaaaaaaa 1260
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<210> 82

<211> 249

<212> PRT

<213> Triticum aestivum

<400> 82

Met Arg Leu Tyr Leu His Ala Asn Ser Asn Thr Leu Phe Val Ser Asp
1 5 10 15

Asn Asp Asn Asp His Gly Lys Pro Asp Gln His Met Val Lys Pro Leu
20 25 30

Leu Ser Leu Gly Asn Pro Glu Thr Val Ala Pro Pro Pro Met Leu Asp
35 40 45

Cys Ser Gln Ser Phe Ala Tyr Ile Pro Tyr Thr Ala Asp Ala Tyr Ala
50 55 60

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

<210> 83

<211> 887

<212> DNA

<213> *Canna edulis*

<400> 83

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cggatgatgg cgctgccgct ggagtgcctt atgcaactgc cgctgccgcc ggaccctatc 180
aggcctacca gaacctctac caccagcagc aacagcagca gcagcaacaa ctccagatgt 240
tctggggcca ccagtaccgt gagatcgagc aaactaccga cttccggaac cacagcctgc 300
cgctcgcgcg gatcaagaag atcatgaagg ccgacgagga cgtgcgtatg atcgctgccg 360
aggcgcctgt ggtgttcgcc cgcgccctgc agatgttcat cctggaactc acccaccggt 420
cgtggggtca cgccgaggag aacaagcgcc ggacactgca gaagaacgat atagccgcgg 480
ccatcagccg caccgacgtg ttcgattttc tcattgatat cgtgcccaagg gaggagggga 540
aggaagatgt tgcccacgcc ctccgacccc cagctggtgg tgacccctc gcttactatt 600
atgtccagaa gtagaagctg ctgctgtgtg agtctttaat taaatgtctc catgtttctc 660
atttcataaa tgccttagtg tgattataaa catagggcat ggggttttgt ttgttacctg 720
aagtgcactg aatttaatct ctagtgaact tgctttgcat agctggatgat gtgttcttgt 780
tagtaagttt atattgtttg ggtattgtcc atctaactac atgtatgctt atggcaagca 840
tcattacatt gatatggatg ggcatttacg ctgctctcat tcgcgcc 887

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<210> 84
 <211> 175
 <212> PRT
 <213> Canna edulis

<400> 84
 Met Asp Gln Pro Pro Gly His Pro Ala Val Pro Pro Val Met Gly Val
 1 5 10 15
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 20 25 30
 Ala Tyr Gln Asn Leu Tyr His Gln Gln Gln Gln Gln Gln Gln Gln
 35 40 45
 Leu Gln Met Phe Trp Ala Asp Gln Tyr Arg Glu Ile Glu Gln Thr Thr
 50 55 60
 Asp Phe Arg Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
 65 70 75 80
 Lys Ala Asp Glu Asp Val Arg Met Ile Ala Ala Glu Ala Pro Val Val
 85 90 95
 Phe Ala Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr His Arg Ser
 100 105 110
 Trp Ala His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp
 115 120 125
 Ile Ala Ala Ala Ile Ser Arg Thr Asp Val Phe Asp Phe Leu Ile Asp
 130 135 140
 Ile Val Pro Arg Glu Glu Gly Lys Glu Asp Val Ala His Ala Leu Gly
 145 150 155 160
 Pro Pro Ala Gly Gly Asp Pro Leu Ala Tyr Tyr Tyr Val Gln Lys
 165 170 175

<210> 85
 <211> 988
 <212> DNA
 <213> Vitis sp.

<400> 85
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 aatggagAAC aaccagcagg cccaatcctc cccataccca ccacagcaac cctttcacca 120
 tcttctgcag cagcaacagc agcagcttca gatgttttgg tcctaccaac gccaagagat 180
 cgagcaggtg aacgacttca agaaccacca actgcctctg gcccgcatca agaagattat 240
 gaaggcggat gaggatgtcc ggatgatctc ggcggaggcc ccaatcctct tcgccaaggc 300
 ctgcgagctc ttcattctgg agctgacgat aaggtcgtgg ttgcacgcgg aggagaacaa 360
 gaggaggaca ctgcagaaga atgatatcgc cgcggcgatt actaggacgg atatatattga 420
 ttttttgggtg gatattgtgc cgagggatga gatcaaggac gaggggggct tggggatggt 480
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 agtaatgatg ggaaggccgg cggttccggg ggtggatccg ggggtgtacg tgcagccgcc 600
 gtcgcaggca tggcagtcgg tgtggcagac ggcagaggac gggtcgtacg ggagcggagg 660
 gagcagtgga caggggaatc ttgatggcca aggttaagca aacgcccatt gtggatgttg 720
 tggtgcttcc cggcatgatg gaaactatcg agctcgtgga cagaacttgg attttccttg 780
 gctatgaatt gctctgttat tatttgtgaa aactagttgg tttttaatgt aatggcttca 840

WO 03/001902

PCT/US02/22086

attagaaact tgttaaaaac cgtgatttgg accagtgcag tgatatgact caactaatcc 900
 tatgtgcagt tctaaatgta aggtccatgt ttttcatttt aactgaatga ttctagttat 960
 ctgattaaaa aaaaaaaaaa aaaaaaaaaa 988

<210> 86
 <211> 211
 <212> PRT
 <213> Vitis sp.

<400> 86
 Met Glu Asn Asn Gln Gln Ala Gln Ser Ser Pro Tyr Pro Pro Gln Gln
 1 5 10 15
 Pro Phe His His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Met Phe
 20 25 30
 Trp Ser Tyr Gln Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn
 35 40 45
 His Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu
 50 55 60
 Asp Val Arg Met Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala
 65 70 75 80
 Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala
 85 90 95
 Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala
 100 105 110
 Ile Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg
 115 120 125
 Asp Glu Ile Lys Asp Glu Gly Gly Leu Gly Met Val Gly Ser Thr Ala
 130 135 140
 Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro Ala Pro Gly
 145 150 155 160
 Val Met Met Gly Arg Pro Ala Val Pro Gly Val Asp Pro Gly Val Tyr
 165 170 175
 Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln Thr Ala Glu
 180 185 190
 Asp Gly Ser Tyr Gly Ser Gly Gly Ser Ser Gly Gln Gly Asn Leu Asp
 195 200 205
 Gly Gln Gly
 210

<210> 87
 <211> 1572
 <212> DNA
 <213> Zea mays

<400> 87

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tcctgtcttc atacgtatcc atagccggca ggcggcagta cctgtatgtg gtttttagcta 180
tacgcgacct cagttcggggc gcaagctaca accccgacca ggcgagaaga agcatcgata 240
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ccctactcca caggccagcc ccctgcccc ccaggagccc cgggtggcggg catgcctggc 360
gcggccggcc tcccacccgt gccgcaccac cacctgctcc agcagcagca ggcccagctg 420
caggcgcttc gggcgtagca gcgcaggag gcggagcgcg cgtccgcgtc ggacttcaag 480
aaccaccagc tgcctctggc ccggatcaag aagatcatga aggccgacga ggacgtgcgc 540
atgatctccg ccgaggcgcc cgtgctgttc gccaaaggcct gcgagctctt catcctcgag 600
ctcactatcc gctcctggct ccacgccgag gagaacaagc gccgcaccct gcagcgcaac 660
gacgtcgccg cggccatcgc gcgcaccgac gtcttcgatt tcctcgtcga catcgtgccc 720
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aaaaaaaaaa ag 1572

```

<210> 88

<211> 245

<212> PRT

<213> Zea mays

<400> 88

```

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

Gly Gly Ala Pro Val Ala Gly Met Pro Gly Ala Ala Gly Leu Pro Pro
      20              25              30

Val Pro His His His Leu Leu Gln Gln Gln Ala Gln Leu Gln Ala
 35              40              45

Phe Trp Ala Tyr Gln Arg Gln Glu Ala Glu Arg Ala Ser Ala Ser Asp
 50              55              60

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

Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Leu Phe
      85              90              95

Ala Lys Ala Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp
      100             105             110

Leu His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Arg Asn Asp Val
      115             120             125

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Ala Ala Ala Ile Ala Arg Thr Asp Val Phe Asp Phe Leu Val Asp Ile
 130 135 140

Val Pro Arg Glu Glu Ala Lys Glu Glu Pro Gly Ser Ala Leu Gly Phe
 145 150 155 160

Ala Ala Pro Gly Thr Gly Val Val Gly Ala Gly Ala Pro Gly Gly Ala
 165 170 175

Pro Ala Ala Gly Met Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro Ala
 180 185 190

Pro Met Met Pro Ala Trp His Val Pro Ala Trp Asp Pro Ala Trp Gln
 195 200 205

Gln Gly Ala Ala Asp Val Asp Gln Ser Gly Ser Phe Ser Glu Glu Gly
 210 215 220

Gln Gly Phe Gly Ala Gly His Gly Gly Ala Ala Ser Phe Pro Pro Ala
 225 230 235 240

Pro Pro Thr Ser Glu
 245

<210> 89
 <211> 1164
 <212> DNA
 <213> Zea mays

<400> 89
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 gatcatagat ttttgggcaa tagcaagtgg acatggaacc atcctctcag cctcagcctg 180
 cgatgggtgt cgccgccggt gggtcacaag tgtatcctgc gtctgcctac ccgcctgcag 240
 caacagtagc tcctcctgct gttgcatctg ctggtttaca gtcagtgcaa ccattcccag 300
 ccaaccctgc ccatatgagt gctcagcacc agattgtcta ccaacaagct caacagttcc 360
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 agatcatgaa ggccgacgaa gatgtccgca tgatctcagc cgaagctccc gtggtcttcg 540
 caaaagcttg cgagatatc atactggagc tgacgctgag gtcgtggatg cacaccgagg 600
 agaacaagcg ccgcaccttg cagaagaacg acattgccgc agccatcacc aggaccgaca 660
 tttacgactt cttggtcgac attgttccca gggatgagat gaaggacgac ggaatcgggc 720
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 tgccacagca gcaggtgcct ggtcctggga tggtttatgg cgcccagcaa ggccacccgg 840
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 atgattagcg gctagtggat taaagttacc cataccgttt cctttcgttc caaaaaaaaaa 1140
 aaaaaaaaaa aaaaaaaaaa aaaa 1164

<210> 90
 <211> 255
 <212> PRT
 <213> Zea mays

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<400> 90

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Met Glu Pro Ser Ser Gln Pro Gln Pro Ala Met Gly Val Ala Ala Gly
 1             5             10             15

Gly Ser Gln Val Tyr Pro Ala Ser Ala Tyr Pro Pro Ala Ala Thr Val
          20             25             30

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

Pro Ala Asn Pro Ala His Met Ser Ala Gln His Gln Ile Val Tyr Gln
          50             55             60

Gln Ala Gln Gln Phe His Gln Gln Leu Gln Gln Gln Gln Gln Gln
65             70             75             80

Leu Gln Gln Phe Trp Val Glu Arg Met Thr Glu Ile Glu Ala Thr Ala
          85             90             95

Asp Phe Arg Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
          100            105            110

Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val
          115            120            125

Phe Ala Lys Ala Cys Glu Ile Phe Ile Leu Glu Leu Thr Leu Arg Ser
          130            135            140

Trp Met His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp
145            150            155            160

Ile Ala Ala Ala Ile Thr Arg Thr Asp Ile Tyr Asp Phe Leu Val Asp
          165            170            175

Ile Val Pro Arg Asp Glu Met Lys Asp Asp Gly Ile Gly Leu Pro Arg
          180            185            190

Pro Gly Leu Pro Pro Met Gly Ala Pro Ala Asp Ala Tyr Pro Tyr Tyr
          195            200            205

Tyr Met Pro Gln Gln Gln Val Pro Gly Pro Gly Met Val Tyr Gly Ala
          210            215            220

Gln Gln Gly His Pro Val Thr Tyr Leu Trp Gln Asp Pro Gln Glu Gln
225            230            235            240

Gln Glu Gln Ala Pro Glu Glu Gln Gln Ser Leu His Glu Arg Asp
          245            250            255

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<210> 91

<211> 1270

<212> DNA

<213> Zea mays

<400> 91

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ccgtcggccg accttctgcc gcagcttcca attgtaaaaa gatcatagat ttttgtgcaa 180
gagcgagtgg atatggaacc atcccctcag cctatgggtg tcgctgccgg tgggtcacaa 240

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gtgtatcctg cctctgccta tccgcctgca gcaacagtag ctccctgcttc tgttgtatct 300
gctggtttac agtcagggca gccattccca gccaatcctg gtcatatgag tgctcagcac 360
cagattgtct accaacaagc tcaacaattc caccaacagc tccagcagca acaacaacag 420
cagcttcagc agttctgggt tgaacgcatg actgaaattg aggcgacgac tgatttcaag 480
aaccacaact tgccacttgc gaggataaag aagatcatga aggccgatga agatgttcgc 540
atgatctcag ctgaagctcc tgtagtcttt gcaaaagctt gtgagatatt catactggag 600
ctgacactta ggtcgtggat gcacactgag gagaacaagc gccgcacctt gcaaaagaat 660
gacattgcag cagcgatcac taggactgac atttatgact tcttggtcga cattgttccc 720
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gtaatatcgt tggttatcaa actgaaacag gcgattctaa gtaggggtga gcatcatggt 1080
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agttaccata ccatttcctt ctattccgaa agtttgcctc catgaggcct ctgatatgac 1200
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<210> 92

<211> 248

<212> PRT

<213> Zea mays

<400> 92

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Met Glu Pro Ser Pro Gln Pro Met Gly Val Ala Ala Gly Gly Ser Gln
  1              5              10              15

Val Tyr Pro Ala Ser Ala Tyr Pro Pro Ala Ala Thr Val Ala Pro Ala
          20              25              30

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

Pro Gly His Met Ser Ala Gln His Gln Ile Val Tyr Gln Gln Ala Gln
          50              55              60

Gln Phe His Gln Gln Leu Gln Gln Gln Gln Gln Gln Gln Leu Gln Gln
          65              70              75              80

Phe Trp Val Glu Arg Met Thr Glu Ile Glu Ala Thr Thr Asp Phe Lys
          85              90              95

Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp
          100              105              110

Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe Ala Lys
          115              120              125

Ala Cys Glu Ile Phe Ile Leu Glu Leu Thr Leu Arg Ser Trp Met His
          130              135              140

Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala
          145              150              155              160

Ala Ile Thr Arg Thr Asp Ile Tyr Asp Phe Leu Val Asp Ile Val Pro
          165              170              175

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Arg Asp Glu Met Lys Glu Asp Gly Ile Gly Leu Pro Arg Ala Gly Leu
 180 185 190

Pro Pro Met Gly Ala Pro Ala Asp Ala Tyr Pro Tyr Tyr Tyr Met Pro
 195 200 205

Gln Gln Gln Val Pro Gly Ser Gly Met Val Tyr Gly Ala Gln Gln Gly
 210 215 220

His Pro Val Thr Tyr Leu Trp Gln Glu Pro Gln Gln Gln Gln Glu Gln
 225 230 235 240

Ala Pro Glu Glu Gln Gln Ser Ala
 245

<210> 93
 <211> 511
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (442)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (452)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (474)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (497)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (504)
 <223> n = A, C, G, or T

<400> 93
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 caagcaagca aatgacttca agatccacac cttgccactt gcaaggataa agaagataat 180
 gaaggctgat gaggatgtgc ggatgatctc tgcagaagct cctgttgtgt ttgcgaaggc 240
 atgcgaggta ttcataattag agctgacatt gaggtcatgg atgcacacag aggagaacaa 300
 gcgcccggacc ttgcagaaga acgacattgc agctgccatc accaggactg atatatatga 360
 cttcttggtg gacataatcc cgagggatga aatgaaagag gaagggcttc ggacataatc 420
 ccatagttgg cctgccgcct gntatggggg cntccagctt gatcatgggt cttnatccat 480
 tattactatg tggccantta acangtgcca a 511

<210> 94
 <211> 135

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<212> PRT

<213> Zea mays

<400> 94

Thr	Gln	Leu	Ser	Ala	Gln	His	Gln	Met	Val	Tyr	Gln	Gln	Ala	Gln	Gln
1				5					10					15	

Phe	His	Gln	Gln	Leu	Gln	Gln	Gln	Gln	Glu	Gln	Gln	Leu	Arg	Glu	Phe
		20					25						30		

Trp	Thr	Thr	Gln	Met	Asp	Glu	Ile	Lys	Gln	Ala	Asn	Asp	Phe	Lys	Ile
		35					40					45			

His	Thr	Leu	Pro	Leu	Ala	Arg	Ile	Lys	Lys	Ile	Met	Lys	Ala	Asp	Glu
	50					55					60				

Asp	Val	Arg	Met	Ile	Ser	Ala	Glu	Ala	Pro	Val	Val	Phe	Ala	Lys	Ala
65					70					75					80

Cys	Glu	Val	Phe	Ile	Leu	Glu	Leu	Thr	Leu	Arg	Ser	Trp	Met	His	Thr
				85					90					95	

Glu	Glu	Asn	Lys	Arg	Arg	Thr	Leu	Gln	Lys	Asn	Asp	Ile	Cys	Ser	Cys
			100					105					110		

His	His	Pro	Gly	Leu	Ile	Tyr	Met	Thr	Ser	Leu	Val	Asp	Ile	Ile	Pro
		115					120					125			

Arg	Asp	Glu	Met	Lys	Glu	Glu
130						135

<210> 95

<211> 499

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (278)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (368)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (390)..(391)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (452)

<223> n = A, C, G, or T

<220>

<221> unsure

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<222> (468)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (474)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (480)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (486)

<223> n = A, C, G, or T

<400> 95

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cccccggtga tgggcgcggc ggtggcggtac cctccggcgg ccggcgccgc gtactccgcc 180
gggcccgtacg cgcacgcgca cgcggcggtg ggcgcgctgt accgcctcc cccggcgccg 240
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gagcagtacc gcgagatcga ggcgacgacg gacttcaaga accacaacct gccgctgggc 360
cgcatacanga agatcatgaa ggcggacgan ngactgcgca tgatcgccgc cgaggcgccg 420
gtggtgttcg cccgcgcctg cgagatgttc ancctggagc tgaccaancg cggntgggcn 480
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<210> 96

<211> 134

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (61)

<223> Xaa = any amino acid

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<222> (91)

<223> Xaa = any amino acid

<220>

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<222> (98)..(99)

<223> Xaa = any amino acid

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<221> UNSURE

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<222> (124)

<223> Xaa = any amino acid

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<400> 96

Met Asp Pro Asn Ser Ser Ile Pro Pro Pro Val Met Gly Ala Ala Val
 1 5 10 15

Ala Tyr Pro Pro Ala Ala Gly Ala Ala Tyr Ser Ala Gly Pro Tyr Ala
 20 25 30

His Ala His Ala Ala Leu Gly Ala Leu Tyr Pro Pro Pro Pro Ala Pro
 35 40 45

Gly Pro Pro Ser Ser His Gln Gly Gly Ala Ala Ala Xaa Gln Leu Gln
 50 55 60

Leu Phe Trp Ala Glu Gln Tyr Arg Glu Ile Glu Ala Thr Thr Asp Phe
 65 70 75 80

Lys Asn His Asn Leu Pro Leu Gly Arg Ile Xaa Lys Ile Met Lys Ala
 85 90 95

Asp Xaa Xaa Leu Arg Met Ile Ala Ala Glu Ala Pro Val Val Phe Ala
 100 105 110

Arg Ala Cys Glu Met Phe Xaa Leu Glu Leu Thr Xaa Arg Gly Trp Ala
 115 120 125

His Ala Glu Glu Lys Lys
 130

<210> 97

<211> 1060

<212> DNA

<213> Zea mays

<400> 97

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 catgggtgcc cccgttgccct accctccgcc ggcgtaccct cccggtgtgg ccgccggcgc 180
 cggcgcctac ccgccgcagc tctacgcgcc gccggctgct gccgcggccc agcaggcggc 240
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 cactaccgac ttcaagaatc acaacctccc gctcgcccgc atcaagaaga tcatgaaagc 360
 cgacgaggac gtccgcatga tcgccgccga ggctcccgtg gtgttcgccc gggcctgcga 420
 gatgttcatc ctcgagctca cccatcgccg ctgggcgcac gccgaagaga acaagcgcgc 480
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 tgtggacatc gttccgcgcg acgacggtaa agacgctgat gcggcggccg ccgcagctgc 600
 cgcggctgcc gggatcccgc gcccgcgcgc cggagtacca gccaccgacc ctctcgccta 660
 ctactacgtg cctcagcagt aatgtatcat catcacgtta ttgttccgtc tatgtgcctg 720
 agcaataatg tatcatcatt gccttattgt tccggggcag ttgtgttatt tgtgtctgtt 780
 tagttgctgc tgctgttacc gcgtaatagc atatgtgtta tctgtgtctg tttagttgct 840
 gctgctgttg ccgcgtaata aaacttggtc gtttacgggg ctccctcaag attaagaatt 900
 gagttgtttg atggtagaat cctggtaagg ttgttgtaac tggggggcgc ctttgtttgg 960
 gctggtagtg tatgcctagg cctcacttat ctgatgctgt aatgcgacaa gtattatgtg 1020
 gttgtctggt aattattgtg caaaaaaaaa aaaaaaaaaa 1060

<210> 98

<211> 200

<212> PRT

<213> Zea mays

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<400> 98

Met Asp Pro Asn Lys Ser Ser Thr Pro Pro Pro Pro Pro Val Met Gly
 1 5 10 15

Ala Pro Val Ala Tyr Pro Pro Pro Ala Tyr Pro Pro Gly Val Ala Ala
 20 25 30

Gly Ala Gly Ala Tyr Pro Pro Gln Leu Tyr Ala Pro Pro Ala Ala Ala
 35 40 45

Ala Ala Gln Gln Ala Ala Ala Ala Gln Gln Gln Gln Leu Gln Ile Phe
 50 55 60

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

His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu
 85 90 95

Asp Val Arg Met Ile Ala Ala Glu Ala Pro Val Val Phe Ala Arg Ala
 100 105 110

Cys Glu Met Phe Ile Leu Glu Leu Thr His Arg Gly Trp Ala His Ala
 115 120 125

Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Ser Asp Ile Ala Ala Ala
 130 135 140

Ile Ala Arg Thr Glu Val Phe Asp Phe Leu Val Asp Ile Val Pro Arg
 145 150 155 160

Asp Asp Gly Lys Asp Ala Asp Ala Ala Ala Ala Ala Ala Ala Ala Ala
 165 170 175

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

Ala Tyr Tyr Tyr Val Pro Gln Gln
 195 200

<210> 99

<211> 901

<212> DNA

<213> Zea mays

<400> 99

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 gggccgtacg tgcacgcgcc ggcggccgcg ctctaccctc ctctccctc gccgcggcg 180
 cccccctcct cgcagcaggg cgcgcggcg gcgcaccagc agcagctatt ctgggcggag 240
 caataccgcg agatcgaggc caccaccgac ttcaagaacc acaacctgcc gctcgcccgc 300
 atcaagaaga tcatgaaggc cgacgaggac gtgcgcatga tcgcccgcga ggcgcccgtc 360
 gtcttctccc gcgcctgcga gatgttcac ctcgagctca cccaccgcgg ctgggcacac 420
 gccgaggaga acaagcgccg cacgctgcag aagtccgaca tcgcccgcgc cgtcgcgcg 480
 accgaggtct tcgacttcct cgtcgacatc gtgcccgcgg acgaggccaa ggacgccgac 540
 tccgccgcca tgggagcagc cgggatcccg caccgcccg ccggcctgcc cgccgccgat 600
 cccatgggct actactacgt ccagccgcag taacgaattt gcttccttat catggtttcg 660
 cttccatgca gcctttgcgg gtttttagta aactattatt attactgaga gtgccctgtt 720
 gttacccatg ctctgttggt gccacccaat aactcgatga cctgatgatc atctgatgtg 780

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cctcccgttc cgtaacaagt gattccattht ctgattaaaa aaaaaaaaaa aaaaaaaaaa 840
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 a 901

<210> 100
 <211> 200
 <212> PRT
 <213> Zea mays

<400> 100
 Met Glu Pro Lys Ser Thr Thr Pro Pro Pro Pro Val Met Gly Ala
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 20 25 30
 Tyr Val His Ala Pro Ala Ala Ala Leu Tyr Pro Pro Pro Pro Leu Pro
 35 40 45
 Pro Ala Pro Pro Ser Ser Gln Gln Gly Ala Ala Ala Ala His Gln Gln
 50 55 60
 Gln Leu Phe Trp Ala Glu Gln Tyr Arg Glu Ile Glu Ala Thr Thr Asp
 65 70 75 80
 Phe Lys Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys
 85 90 95
 Ala Asp Glu Asp Val Arg Met Ile Ala Ala Glu Ala Pro Val Val Phe
 100 105 110
 Ser Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr His Arg Gly Trp
 115 120 125
 Ala His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Ser Asp Ile
 130 135 140
 Ala Ala Ala Val Ala Arg Thr Glu Val Phe Asp Phe Leu Val Asp Ile
 145 150 155 160
 Val Pro Arg Asp Glu Ala Lys Asp Ala Asp Ser Ala Ala Met Gly Ala
 165 170 175
 Ala Gly Ile Pro His Pro Ala Ala Gly Leu Pro Ala Ala Asp Pro Met
 180 185 190
 Gly Tyr Tyr Tyr Val Gln Pro Gln
 195 200

<210> 101
 <211> 1118
 <212> DNA
 <213> Oryza sativa

<400> 101
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 cagcagctac cctacgccgg tcagccggcg gccgcaggcg ccggagcccc ggtgccgggc 120
 gtgcctggcg cgggcggggc gccggcggtg ccgcaccacc acctgctcca gcagcagcag 180

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gcgagctgc aggcgttctg ggcgtaccag cggcaggagg cggagcgcgc gtcggcgctcg 240
gacttcaaga accaccagct gccgctggcg cggatcaaga agatcatgaa ggcggacgag 300
gacgtgcgca tgatctcggc ggaggcgccc gtgctgttcg ccaaggcgtg cgagctcttc 360
atcctggagc tcaccatccg ctgctggctg cagcccgagg agaacaagcg ccgcaccctg 420
cagcgcaacg acgtcgccgc cgccatcgcg cgcaccgacg tgttcgactt cctcgtcgac 480
atcgtgccgc gggaggaggc caaggaggag cccggcagcg cgctcgggtt cgcggcgagg 540
gggcccgcgc gcgccgttgg agcggccggc cccgccgcgc ggctgccgta ctactaccgc 600
ccgatggggc agccggcgcc gatgatgccg gcgtggcatg ttccggcgtg ggaccggcg 660
tggcagcaag gagcagcgcc ggatgtggac cagggcgccg ccggcagctt cagcgaggaa 720
gggcagcaag gttttgcagg ccatggcggt gcggcagcta gcttccctcc tgcacctcca 780
agctccgaat agtgatgatc catatgggtc catgcatgca tcgctgaggt gctagctagc 840
tactatagct gctcaaatca aatgctcaat gtgtcggtaa ttaattaatg tggtagctat 900
taacttaacc gatgtacgta atggacgctc aagctaatta agggatgtac aatttactaa 960
ttaatttaat ttgtaatata tagccgatta actagcaagg tgaccagta ctatttgtaa 1020
tttcttttcc cgttatgcta ctaattgtgg acgcacaaac cattaccgga acagaaatta 1080
ctactgatga attactataa aaaaaaaaaa aaaaaaaaaa 1118

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<210> 102

<211> 246

<212> PRT

<213> Oryza sativa

<400> 102

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Met Asp Asn Gln Gln Leu Pro Tyr Ala Gly Gln Pro Ala Ala Ala Gly
  1             5             10             15

```

```

Ala Gly Ala Pro Val Pro Gly Val Pro Gly Ala Gly Gly Pro Pro Ala
          20             25             30

```

```

Val Pro His His His Leu Leu Gln Gln Gln Gln Ala Gln Leu Gln Ala
          35             40             45

```

```

Phe Trp Ala Tyr Gln Arg Gln Glu Ala Glu Arg Ala Ser Ala Ser Asp
          50             55             60

```

```

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

```

```

Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Leu Phe
          85             90             95

```

```

Ala Lys Ala Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp
          100            105            110

```

```

Leu His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Arg Asn Asp Val
          115            120            125

```

```

Ala Ala Ala Ile Ala Arg Thr Asp Val Phe Asp Phe Leu Val Asp Ile
          130            135            140

```

```

Val Pro Arg Glu Glu Ala Lys Glu Glu Pro Gly Ser Ala Leu Gly Phe
          145            150            155            160

```

```

Ala Ala Gly Gly Pro Ala Gly Ala Val Gly Ala Ala Gly Pro Ala Ala
          165            170            175

```

```

Gly Leu Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro Ala Pro Met Met
          180            185            190

```

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Pro Ala Trp His Val Pro Ala Trp Asp Pro Ala Trp Gln Gln Gly Ala
 195 200 205

Ala Pro Asp Val Asp Gln Gly Ala Ala Gly Ser Phe Ser Glu Glu Gly
 210 215 220

Gln Gln Gly Phe Ala Gly His Gly Gly Ala Ala Ala Ser Phe Pro Pro
 225 230 235 240

Ala Pro Pro Ser Ser Glu
 245

<210> 103

<211> 1343

<212> DNA

<213> Oryza sativa

<400> 103

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gccgctccc	ctcccgccgg	cgcgggagat	ccgggcgctg	tctctcgggc	ctttggcttt	180
ggacggacaa	gagctgacat	ggaaccatcc	tcacagcctc	agcctgtgat	gggtgttgcc	240
actggtgggt	cacaagcata	tcctcctcct	gctgctgcat	atccacctca	agccatggtt	300
cctggagctc	ctgctgttgt	tcctcctggc	tcacagccat	cagcaccatt	ccccactaat	360
ccagctcaac	tcagtgtctc	gcaccagcta	gtctaccaac	aagcccagca	atttcatcag	420
cagctgcagc	aacagcaaca	gcagcaactc	cgtgagttct	gggctaacca	aatggaagag	480
attgagcaaa	caaccgactt	caagaaccac	agcttgccac	tcgcaaggat	aaagaagata	540
atgaaggctg	atgaggatgt	ccggatgatc	tcggcagaag	ccccggttgt	cttcgcaaag	600
gcatgcgagg	tattcatatt	agagttaaca	ttgaggtcgt	ggatgcacac	ggaggagaac	660
aagcgccgga	ccttgcagaa	gaatgacatt	gcagctgcca	tcaccaggac	tgatatctat	720
gacttcttgg	tggacatagt	tcccagggat	gaaatgaaag	aagaagggct	tgggcttccg	780
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ccagcgcagc	aggggcctgg	atcaggaatg	atgtacgggtg	gacagcaagg	tcacccggtg	900
acgtatgtgt	ggcagcagcc	tcaagagcaa	caggaagagg	cccctgaaga	gcagcactct	960
ctgccagaaa	gtagctaaag	atgatacagt	gaagtttgtga	cattgatata	cattgtcctg	1020
tgaacttagg	gcctctaaaa	ctcagtgtct	ttgtcaaaac	tattcccatg	attggttggt	1080
gaaacgggta	atctgattag	gtcttaggct	ttcctaattg	tagttctgct	ctgctatggc	1140
agcagtagaa	aaaaaaaaaga	ttgtgatttg	gtaggtgatt	tgcaactaat	gtagtaactg	1200
taccttacct	ttcatcagtt	tctaatacaa	tactcaaaag	tgctggcatg	tggagaccct	1260
tgtatgaatt	gagtgtttgt	tcatgtcatg	catcagtcctg	ttgcctcatt	tatcagtcct	1320
catgcctcct	gctttgcaaa	aaa				1343

<210> 104

<211> 259

<212> PRT

<213> Oryza sativa

<400> 104

Met Glu Pro Ser Ser Gln Pro Gln Pro Val Met Gly Val Ala Thr Gly
 1 5 10 15

Gly Ser Gln Ala Tyr Pro Pro Pro Ala Ala Ala Tyr Pro Pro Gln Ala
 20 25 30

Met Val Pro Gly Ala Pro Ala Val Val Pro Pro Gly Ser Gln Pro Ser
 35 40 45

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Ala Pro Phe Pro Thr Asn Pro Ala Gln Leu Ser Ala Gln His Gln Leu
50 55 60

Val Tyr Gln Gln Ala Gln Gln Phe His Gln Gln Leu Gln Gln Gln Gln
65 70 75 80

Gln Gln Gln Leu Arg Glu Phe Trp Ala Asn Gln Met Glu Glu Ile Glu
85 90 95

Gln Thr Thr Asp Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys
100 105 110

Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala
115 120 125

Pro Val Val Phe Ala Lys Ala Cys Glu Val Phe Ile Leu Glu Leu Thr
130 135 140

Leu Arg Ser Trp Met His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln
145 150 155 160

Lys Asn Asp Ile Ala Ala Ala Ile Thr Arg Thr Asp Ile Tyr Asp Phe
165 170 175

Leu Val Asp Ile Val Pro Arg Asp Glu Met Lys Glu Glu Gly Leu Gly
180 185 190

Leu Pro Arg Val Gly Leu Pro Pro Asn Val Gly Gly Ala Ala Asp Thr
195 200 205

Tyr Pro Tyr Tyr Tyr Val Pro Ala Gln Gln Gly Pro Gly Ser Gly Met
210 215 220

Met Tyr Gly Gly Gln Gln Gly His Pro Val Thr Tyr Val Trp Gln Gln
225 230 235 240

Pro Gln Glu Gln Gln Glu Glu Ala Pro Glu Glu Gln His Ser Leu Pro
245 250 255

Glu Ser Ser

<210> 105

<211> 1085

<212> DNA

<213> Oryza sativa

<400> 105

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tggtggatca caagtgtacc ctgcataccg gcctgcagca acagtgccta cagctcctgc 180
tgtcattcct gccggttcac agccagcacc gtcgttcctt gcccaaccctg atcaactgag 240
tgctcagcac cagctcgtct atcagcaagc ccagcaattt caccagcagc ttcagcagca 300
gcaacagcgt caactccagc agtttttgggc tgaacgtctg gtcgatattg aacaaactac 360
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ggacgttcgc atgatctccg cagaggctcc tgtgatcttt gcgaaagcat gtgagatatt 480
catactggag ctgaccctga gatcatggat gcacacggag gagaacaagc gccgtacctt 540
gcagaagaat gacatagcag ctgccatcac caggacggat atgtacgatt tcttggtaga 600
tatagttccc agggatgact tgaaggagga gggagttggg ctccctaggg ctggattgcc 660

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gcccttgggt gtccctgctg actcatatcc gtatggctac tatgtgccac agcagcaggt 720
cccaggtgca ggaatagcgt atgggtggca gcaaggcat cccgggtatc tgtggcagga 780
tcctcaggaa cagcaggaag agcctcctgc agagcagcaa agtgattaag aagagtaaata 840
gatccctgtg aattgtcaag aagcttacca cctgattcag aattttactt ttagccaggt 900
tgtcgtctat tctgaattta tgaataggat taggattctc tcatggtagt tgcatttctg 960
ctgtagtgga aaaggattta tgacatgaga gtatgagact aatgggtttc agttactata 1020
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aaaaa 1085

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<210> 106

<211> 250

<212> PRT

<213> Oryza sativa

<400> 106

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Met Glu Pro Ser Ser Gln Pro Gln Pro Ala Ile Gly Val Val Ala Gly
  1              5              10              15

```

```

Gly Ser Gln Val Tyr Pro Ala Tyr Arg Pro Ala Ala Thr Val Pro Thr
          20              25              30

```

```

Ala Pro Ala Val Ile Pro Ala Gly Ser Gln Pro Ala Pro Ser Phe Pro
          35              40              45

```

```

Ala Asn Pro Asp Gln Leu Ser Ala Gln His Gln Leu Val Tyr Gln Gln
          50              55              60

```

```

Ala Gln Gln Phe His Gln Gln Leu Gln Gln Gln Gln Gln Arg Gln Leu
          65              70              75              80

```

```

Gln Gln Phe Trp Ala Glu Arg Leu Val Asp Ile Glu Gln Thr Thr Asp
          85              90              95

```

```

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

```

```

Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Ile Phe
          115              120              125

```

```

Ala Lys Ala Cys Glu Ile Phe Ile Leu Glu Leu Thr Leu Arg Ser Trp
          130              135              140

```

```

Met His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile
          145              150              155              160

```

```

Ala Ala Ala Ile Thr Arg Thr Asp Met Tyr Asp Phe Leu Val Asp Ile
          165              170              175

```

```

Val Pro Arg Asp Asp Leu Lys Glu Glu Gly Val Gly Leu Pro Arg Ala
          180              185              190

```

```

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

```

```

Tyr Val Pro Gln Gln Gln Val Pro Gly Ala Gly Ile Ala Tyr Gly Gly
          210              215              220

```

```

Gln Gln Gly His Pro Gly Tyr Leu Trp Gln Asp Pro Gln Glu Gln Gln
          225              230              235              240

```

Glu Glu Pro Pro Ala Glu Gln Gln Ser Asp
 245 250

<210> 107
 <211> 893
 <212> DNA
 <213> Oryza sativa

<400> 107
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 aagctccgct cgcagcagcc atggatccca ccaaatccag cacgccgccg ccggtgatgg 120
 gcgcgcccgt cggcttcccc cctggcgcggt accctccgcc tccccccggc ggcgcagcag 180
 cagctgcaga tgttctgggc ggagcagtac cgcgagatcg aggccaccac cgacttcaag 240
 aaccacaacc tccccctggc ccgcatcaag aagatcatga aggccgacga ggacgtccgc 300
 atgatcgccg ccgaggcccc cgtcgtgttc gcccgcgctt gcgagatggt catcctcgag 360
 ctaccccacc gcggctgggc gcacgccgag gagaacaagc gccgtacgct gcagaagtcc 420
 gacattgccg ccgccatcgc gcgcaccgag gtgttcgact tcctcgtcga catcgtgcc 480
 cgcgacgacg ccaaggacgc cgacgccgcc gcggccgcgg cggcggccgg catccccgc 540
 cccgccgccg gtgtgccggc caccgatccg ctgcctact actatgtgcc ccagcagtaa 600
 tgtatctgat taaccctttt caagcctttt ctaagcgaag gatgtgttgt tgtttgttgt 660
 tgctgttgct gttcttggtg ttgttggtgc cgcgtaataa gatatgttga taatttatgg 720
 cttcccctga gcttaaagaa tttgagcttt tggttctaga atctgggtaa aattgttgta 780
 atggggaaga ctgtatgact gtattttagt tgcattgtctt aacttgtcgg atagtgtaat 840
 ccgataatta ttatgcggtt agctgggttac ctctcaaaaa aaaaaaaaaa aaa 893

<210> 108
 <211> 172
 <212> PRT
 <213> Oryza sativa

<400> 108
 Met Asp Pro Thr Lys Ser Ser Thr Pro Pro Pro Val Met Gly Ala Pro
 1 5 10 15
 Val Gly Phe Pro Pro Gly Ala Tyr Pro Pro Pro Pro Pro Ala Ala Gln
 20 25 30
 Gln Gln Leu Gln Met Phe Trp Ala Glu Gln Tyr Arg Glu Ile Glu Ala
 35 40 45
 Thr Thr Asp Phe Lys Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys
 50 55 60
 Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ala Ala Glu Ala Pro
 65 70 75 80
 Val Val Phe Ala Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr His
 85 90 95
 Arg Gly Trp Ala His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys
 100 105 110
 Ser Asp Ile Ala Ala Ala Ile Ala Arg Thr Glu Val Phe Asp Phe Leu
 115 120 125
 Val Asp Ile Val Pro Arg Asp Asp Ala Lys Asp Ala Asp Ala Ala Ala
 130 135 140

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Ala Ala Ala Ala Ala Gly Ile Pro Arg Pro Ala Ala Gly Val Pro Ala
 145 150 155 160

Thr Asp Pro Leu Ala Tyr Tyr Tyr Val Pro Gln Gln
 165 170

<210> 109

<211> 1054

<212> DNA

<213> Glycine max

<400> 109

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agaacaacca gcaacaaggc gctcaagccc aatcgggacc gtaccccggc ggcgcgggtg 120
gaagtgcagg tgcaggtgca ggtgcaggcg cggccccgtt ccagcacctg ctccagcagc 180
agcagcagca gctgcagatg ttctgggtcgt accagcggca agagatcgag cacgtgaacg 240
acttcaagaa ccaccagctc cccttggtccc gcatacaagaa gatcatgaag gccgacgagg 300
acgtccgcat gatctccgcc gagggcccca tcctcttcgc caaggcctgc gagctcttca 360
tcctcgagct caccatccgc tcctgggtcc acgccgacga gaacaagcgc cgcaccctcc 420
agaagaacga catcgccgcc gccatcactc gcaccgacat tttcgacttc ctcgtcgaca 480
tcgtcccccg cgacgagatc aaggacgacg ccgcgctcgt cggggcaacg gccagtgggg 540
tgccttacta ctacccgcc attggccagc ctgccgggat gatgattggc cgccccgccg 600
tcgatcccg caccggagtt tatgtccagc cgccctccca ggcctggcag tccgtctggc 660
agtccgccc cgaggacacg ccctacggca ccggtgcccc ggggaacctt gatggccaga 720
gctgagcgac aaccatgccg aaacggactg tcaggagtta tgaagattct gaacttgctt 780
ggaattttga ttgcttgcaa tttggaaatg gttttgttaa ctaaattttt atgggatgac 840
actatgaacc tggttaactc atgaacagca tgatttaact acttctgtac aaaaatttaa 900
aactaaacaa tgatccttct gtgtgaactt gtttgatcat ctgctaatac tatttatattc 960
ctcgtaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1054
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<210> 110

<211> 222

<212> PRT

<213> Glycine max

<400> 110

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Met Glu Asn Asn Gln Gln Gln Gly Ala Gln Ala Gln Ser Gly Pro Tyr
  1 5 10 15
Pro Gly Gly Ala Gly Gly Ser Ala Gly Ala Gly Ala Gly Ala Gly Ala
  20 25 30
Ala Pro Phe Gln His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Met
  35 40 45
Phe Trp Ser Tyr Gln Arg Gln Glu Ile Glu His Val Asn Asp Phe Lys
  50 55 60
Asn His Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp
  65 70 75 80
Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys
  85 90 95
Ala Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His
  100 105 110
```

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Ala Asp Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala
 115 120 125

Ala Ile Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro
 130 135 140

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

Gly Val Pro Tyr Tyr Tyr Pro Pro Ile Gly Gln Pro Ala Gly Met Met
 165 170 175

Ile Gly Arg Pro Ala Val Asp Pro Ala Thr Gly Val Tyr Val Gln Pro
 180 185 190

Pro Ser Gln Ala Trp Gln Ser Val Trp Gln Ser Ala Ala Glu Asp Thr
 195 200 205

Pro Tyr Gly Thr Gly Ala Gln Gly Asn Leu Asp Gly Gln Ser
 210 215 220

<210> 111
 <211> 1036
 <212> DNA
 <213> Glycine max

<400> 111
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 aattggggga atggagacca acaaccagca acaacaacaa caaggagctc aagcccaatc 120
 gggaccctac cccgtcgccg gcgcccggcg cagtgcaggt gcaggtgcag gcgctcctcc 180
 ccctttccag caccttctcc agcagcagca gcagcagctc cagatgttct ggtcttacca 240
 gcgtcaagaa atcgagcacg tgaacgactt taagaatcac cagctccctc ttgcccgcac 300
 caagaagatc atgaaggccg acgaggatgt ccgcatgatc tccgcccagg cccccatcct 360
 cttcgccaag gcctgcgagc tcttcacccct cgagctcacc atccgctcct ggctccacgc 420
 cgaggagAAC aagcgccgca ccctccagaa gaacgacatc gccgcccga tcacccgcac 480
 cgacattttc gacttcctcg ttgatattgt ccccgccgac gagatcaagg acgacgctgc 540
 tcttggtgggg gccaccgcca gtgggggtgcc ttactactac ccgcccattg gacagcctgc 600
 cgggatgatg attggccgcc ccgcccgtcga tcccgccacc ggggtttatg tccagccgcc 660
 ctcccaggca tggcagtcg tctggcagtc cgctgccgag gacgcttcct atggcaccgg 720
 cggggccggt gccagcgga gccttgatgg ccagagttga gtgacatcga tgccgatgat 780
 ggacagtcag gagttatgaa gattctgaac ttgctgcaat ttagaaatgg ttttgtttac 840
 taaattttta tgggatgaca ctgtgaacct gttaactcga tgaacagcat gatttaacta 900
 cttttgtaca aaaattttaa actaaacact gatccttctg tgtgaaacat gtatgatcat 960
 ctgccaatac tgtttatttc ctcataagtc atgataccac tcgtatactt tgctaaaaaa 1020
 aaaaaaaaaa aaaaaa 1036

<210> 112
 <211> 229
 <212> PRT
 <213> Glycine max

<400> 112
 Met Glu Thr Asn Asn Gln Gln Gln Gln Gln Gly Ala Gln Ala Gln
 1 5 10 15

Ser Gly Pro Tyr Pro Val Ala Gly Ala Gly Gly Ser Ala Gly Ala Gly
 20 25 30

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

<210> 113
 <211> 514
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (424)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (430)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (464)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (506)
 <223> n = A, C, G, or T

<400> 113
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 ccatgggtttg tagattaaat cttaaagcag taagtcatca tggataaatc agagcagact 120
 cagcagcaac atcagcatgg gatgggctgt gccacagggt ctagccaaat ggcctattct 180
 tctcactacc cgactgctcc catggtggct tctggcacgc ctgctgtagc tgttccttcc 240
 ccaactcagg ctccagctgc cttctctagt tctgctcacc agcttgcata ccagcaagca 300
 cagcatttcc accaccaaca gcagcaacac caacaacagc agcttcaaata gttctgggtca 360
 aaccaaattgc aagaaattga gcaaacaatt gacttttaaaa accacagtct tcctcttgct 420
 cggntaaaan agataatgaa agctgatgaa gatgtccgga tgantttctgc aagaagctcc 480
 aagtcaatat ttgcaaaagc atgtgnaatg gtca 514

<210> 114
 <211> 126
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (109)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (111)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (122)
 <223> Xaa = any amino acid

<400> 114
 Met Asp Lys Ser Glu Gln Thr Gln Gln Gln His Gln His Gly Met Gly
 1 5 10 15
 Val Ala Thr Gly Ala Ser Gln Met Ala Tyr Ser Ser His Tyr Pro Thr
 20 25 30
 Ala Pro Met Val Ala Ser Gly Thr Pro Ala Val Ala Val Pro Ser Pro
 35 40 45
 Thr Gln Ala Pro Ala Ala Phe Ser Ser Ser Ala His Gln Leu Ala Tyr
 50 55 60
 Gln Gln Ala Gln His Phe His His Gln Gln Gln Gln His Gln Gln Gln
 65 70 75 80
 Gln Leu Gln Met Phe Trp Ser Asn Gln Met Gln Glu Ile Glu Gln Thr
 85 90 95
 Ile Asp Phe Lys Asn His Ser Leu Pro Leu Ala Arg Xaa Lys Xaa Ile
 100 105 110

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Met Lys Ala Asp Glu Asp Val Arg Met Xaa Ser Ala Arg Ser
 115 120 125

<210> 115
 <211> 1363
 <212> DNA
 <213> Glycine max

<400> 115
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 tctctcttag ggttttctcc tccccattg acccaccgtc catcgcaaag gaagtcgcgc 120
 ccaatttcca tggaactgta aagagattat agtttgtaga ttaaattctta aagcagtaag 180
 tcatcatgga taaatcagag cagactcagc agcaacatca gcatgggatg ggcgttgcca 240
 caggtgctag ccaaattggcc tattcttctc actacccgac tgctcccatg gtggcttctg 300
 gcacgcctgc tgtagctggt ccttccccaa ctcaggctcc agctgccttc tctagttctg 360
 ctcaccagct tgcataccag caagcacagc atttccacca ccaacagcag caacaccaac 420
 aacagcagct tcaaatgttc tgggtcaaacc aaatgcaaga aattgagcaa acaattgact 480
 ttaaaaacca cagtcttcct cttgctcgga taaaaaagat aatgaaagct gatgaagatg 540
 tccggatgat ttctgcagaa gctccagtca tatttgcaaa agcatgtgaa atgttcatat 600
 tagagttgac gttgagatct tggatccaca cagaagagaa caaggaggaga actctacaaa 660
 agaatgatat agcagctgct atttcgagaa acgatgtttt tgatttcttg gttgatatta 720
 tcccaagaga tgagttgaaa gaggaaggac ttggaataac caaggctact attccattgg 780
 tgaattctcc agctgatatg ccatattact atgtccctcc acagcatcct gttgtaggac 840
 ctcttgggat gatcatgggc aagcccgttg gtgctgagca agcaacgctg tattctacac 900
 agcagcctcg acctcccatg gcgttcatgc catggcccca tacacaaccc cagcaacagc 960
 agccaccca acatcaacaa acagactcat gatgaccatg caattcaatt aggtcggaaa 1020
 gtagcatgca ctttatgatt attacaaatt tacttaatgc ctttaagtca gctgtagttt 1080
 agtgttttgc attgaaaaat gccaaagatt gtttgagggt tcttgactc atttatgatt 1140
 gtatgagctc ttatgctgag ttacttttgg ttgtgtttat ttgagggtact ggtgtggtag 1200
 ttaaattagt ttgtagctgt ccataagtaa acagcgtagc tgcttaatta ggaggtctga 1260
 aatgatgaaa tagtttgtat tgttattgca gaaggtaggt tttattcagt atttcattct 1320
 attgcaatgg ctgaatttaa tgctcaaaaa aaaaaaaaaa aaa 1363

<210> 116
 <211> 268
 <212> PRT
 <213> Glycine max

<400> 116
 Met Asp Lys Ser Glu Gln Thr Gln Gln Gln His Gln His Gly Met Gly
 1 5 10 15
 Val Ala Thr Gly Ala Ser Gln Met Ala Tyr Ser Ser His Tyr Pro Thr
 20 25 30
 Ala Pro Met Val Ala Ser Gly Thr Pro Ala Val Ala Val Pro Ser Pro
 35 40 45
 Thr Gln Ala Pro Ala Ala Phe Ser Ser Ser Ala His Gln Leu Ala Tyr
 50 55 60
 Gln Gln Ala Gln His Phe His His Gln Gln Gln Gln His Gln Gln Gln
 65 70 75 80
 Gln Leu Gln Met Phe Trp Ser Asn Gln Met Gln Glu Ile Glu Gln Thr
 85 90 95

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Ile Asp Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile
 100 105 110
 Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val
 115 120 125
 Ile Phe Ala Lys Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg
 130 135 140
 Ser Trp Ile His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn
 145 150 155 160
 Asp Ile Ala Ala Ala Ile Ser Arg Asn Asp Val Phe Asp Phe Leu Val
 165 170 175
 Asp Ile Ile Pro Arg Asp Glu Leu Lys Glu Glu Gly Leu Gly Ile Thr
 180 185 190
 Lys Ala Thr Ile Pro Leu Val Asn Ser Pro Ala Asp Met Pro Tyr Tyr
 195 200 205
 Tyr Val Pro Pro Gln His Pro Val Val Gly Pro Pro Gly Met Ile Met
 210 215 220
 Gly Lys Pro Val Gly Ala Glu Gln Ala Thr Leu Tyr Ser Thr Gln Gln
 225 230 235 240
 Pro Arg Pro Pro Met Ala Phe Met Pro Trp Pro His Thr Gln Pro Gln
 245 250 255
 Gln Gln Gln Pro Pro Gln His Gln Gln Thr Asp Ser
 260 265

<210> 117
 <211> 1505
 <212> DNA
 <213> Glycine max

<400> 117
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 aggatagtta gaagattaaa tcttaaagca gtaagtcatt atggataaat cagagcagac 120
 tcaacagcag cagcagcaac aacagcatgt gatgggaggt gccgcagggg ctagccaaat 180
 ggcctattct tctcactacc cgactgcttc catggtgggt tctggcagcg ccgctgtaac 240
 tgctccttcc ccaactcagg ctccagctgc cttctctagt tctgctcacc agcttgcata 300
 ccagcaagca cagcatttcc accaccaaca gcagcaaac caacaacagc agcttcaaat 360
 gttctgggtca aaccaaattgc aagaaattga gcaaacaatt gactttaaaa accatagcct 420
 tcctcttggt cggataaaaa agataatgaa agctgatgaa gatgtccgga tgatttcagc 480
 agaagctccg gtcataattg caaaagcttg tgaaatgttc atattagagt tgacgttgcg 540
 atcttggatc cacacagaag agaacaagag gagaactcta caaaagaatg atatagcagc 600
 tgctatttct agaaacgatg tttttgatct cttgggtgat attattccaa gagatgagtt 660
 gaaagaggaa ggacttggaa taaccaaggc tactattccg ttagtggggt ctccagctga 720
 tatgccatat tactatgtcc ctccacagca tcctgttgta ggaccacctg ggatgatcat 780
 gggcaagccc attggcgctg agcaagcaac actatattct acacagcagc ctgcacctcc 840
 tgtggcgctt atgccatggc ctcatcacaca acccctgcaa cagcagccac cccaacatca 900
 acaaacagac tcatgatgac tatgcaattc aattaggttg gaaagtagcc tgcacctttt 960
 gattattaca aatttactta atgcctttca gccagctgta gtttagtggt gtgcattgaa 1020
 aaaaagcaaa agattgtttt gaggtttctt gcactcattt atgattgtat gagctcttgt 1080
 gatgagttac ttttggttgt gtttactatt ggtgtagtgg ttaaattatt tggcagctgt 1140
 ccataaccag agagcgtagc tgcttaatta ggaggtttga tatgatgaaa tagtttgtat 1200

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tggtattgca gaaggtaggt ttaattcagt attccattct actgcaatgg ctgaatttat 1260
tgctcatctg catagtacta gttgatgttt tttcctgtga ctcggtatgt gttagagtgc 1320
gaagaagaat gagtgtgcc aattttattct tcccctgttc ttgcgccaca ctctcgga aa 1380
aacaatggt tccgatcatt tcaattattt ccaggaacat caatatagt gttgatgttt 1440
aatgctgtca ctgcaaaaaa aaatatgttt tttacagttg gaaaaaaaaa aaaaaaaaaa 1500
aaaaa                                           1505

```

<210> 118

<211> 271

<212> PRT

<213> Glycine max

<400> 118

```

Met Asp Lys Ser Glu Gln Thr Gln Gln Gln Gln Gln Gln Gln His
  1              5              10              15

```

```

Val Met Gly Val Ala Ala Gly Ala Ser Gln Met Ala Tyr Ser Ser His
              20              25              30

```

```

Tyr Pro Thr Ala Ser Met Val Ala Ser Gly Thr Pro Ala Val Thr Ala
              35              40              45

```

```

Pro Ser Pro Thr Gln Ala Pro Ala Ala Phe Ser Ser Ser Ala His Gln
  50              55              60

```

```

Leu Ala Tyr Gln Gln Ala Gln His Phe His His Gln Gln Gln Gln His
  65              70              75              80

```

```

Gln Gln Gln Gln Leu Gln Met Phe Trp Ser Asn Gln Met Gln Glu Ile
              85              90              95

```

```

Glu Gln Thr Ile Asp Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile
              100              105              110

```

```

Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu
              115              120              125

```

```

Ala Pro Val Ile Phe Ala Lys Ala Cys Glu Met Phe Ile Leu Glu Leu
              130              135              140

```

```

Thr Leu Arg Ser Trp Ile His Thr Glu Glu Asn Lys Arg Arg Thr Leu
              145              150              155              160

```

```

Gln Lys Asn Asp Ile Ala Ala Ala Ile Ser Arg Asn Asp Val Phe Asp
              165              170              175

```

```

Phe Leu Val Asp Ile Ile Pro Arg Asp Glu Leu Lys Glu Glu Gly Leu
              180              185              190

```

```

Gly Ile Thr Lys Ala Thr Ile Pro Leu Val Gly Ser Pro Ala Asp Met
              195              200              205

```

```

Pro Tyr Tyr Tyr Val Pro Pro Gln His Pro Val Val Gly Pro Pro Gly
              210              215              220

```

```

Met Ile Met Gly Lys Pro Ile Gly Ala Glu Gln Ala Thr Leu Tyr Ser
              225              230              235              240

```

```

<400> 120
Asp Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
  1                               5                      10                      15

Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Ile
                20                      25                      30

Phe Ala Lys Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg Ser
      35                               40                      45

Trp Ile His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp
  50                               55                      60

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

Ile Ile Pro Arg Asp Glu Leu Lys Glu Glu Gly Leu Gly Ile Thr Lys
                85                      90                      95

Ala Thr Ile Pro Leu Val Gly Ser Pro Ala Asp Met Pro Tyr Tyr Tyr
                100                      105                      110

Val Pro Pro Gln His Pro Val Val Gly Pro Pro Gly Met Ile Met Gly
      115                      120                      125

Lys Pro Ile Gly Ala Glu Gln Ala Thr Leu Tyr Ser Thr Gln Gln Pro
      130                      135                      140

```

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Arg Pro Pro Val Ala Phe Met Pro Trp Pro His Thr Gln Pro Leu Gln
 145 150 155 160

Gln Gln Pro Pro Gln His Gln Gln Thr Asp Ser
 165 170

<210> 121

<211> 1139

<212> DNA

<213> Glycine max

<400> 121

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atctatgggg gtggttggta gtggagctca attagcatat ggttctaacc catatcagcc 180
aggccaaata actgggccac cggggtctgt tgtgacatca gttggtacca ttcaatccac 240
acctgctgga gctcagctag gacagcatca acttgcttat cagcatattc atcagcaaca 300
acaacaccag cttcagcaac agctccaaca attttgggtca aaccagtacc aagaaattga 360
gaaggttact gatttcaaga accacagtct tcccctggca aggatcaaga agattatgaa 420
ggctgacgag gatgttagga tgatatcagc cgaagcacca gtcactcttg caagggcatg 480
tgaaatgttc atattagagt taaccctgcg ttcttggaat cactactgaag agaacaaaag 540
gcgaacactt caaaaaaatg atattgctgc tgcaatcaca aggactgaca tctttgattt 600
cttggttgac attgtgcctc gtgaggactt gaaagatgaa gtgcttgcat caatcccaag 660
aggaacaatg cctgttgacg ggcctgctga tgcccttcca tattgctaca tgccgcctca 720
gcatgcgtcc caagttggag ctgctgggtg tataatgggt aagcctgtga tggacccaaa 780
catgtatgct cagcagtctc acccctacat ggcaccacaa atgtggccac agccaccaga 840
ccaacgacag tcgtccccag aacattagct gatgtgtcgt ggaaattaag ataaccaggc 900
accggaatca gttgtgaatg tcaaactgaa tggttgggaa gatccatact acattgagag 960
cagaagctgt agctgatagt ttacatgcaa tgcagactat aaacatatgt agataatgtg 1020
ctagggaaaa cttaacctta tctttgattt agctggataa aatggtatatt ttcattgtta 1080
aatttacagg tcatcagatg ataatatatta tttactgggtg caaaaaaaaa aaaaaaaaaa 1139
```

<210> 122

<211> 258

<212> PRT

<213> Glycine max

<400> 122

```
Met Asp His Gln Gly His Ser Gln Asn Pro Ser Met Gly Val Val Gly
  1 5 10 15
Ser Gly Ala Gln Leu Ala Tyr Gly Ser Asn Pro Tyr Gln Pro Gly Gln
  20 25 30
Ile Thr Gly Pro Pro Gly Ser Val Val Thr Ser Val Gly Thr Ile Gln
  35 40 45
Ser Thr Pro Ala Gly Ala Gln Leu Gly Gln His Gln Leu Ala Tyr Gln
  50 55 60
His Ile His Gln Gln Gln Gln His Gln Leu Gln Gln Gln Leu Gln Gln
  65 70 75 80
Phe Trp Ser Asn Gln Tyr Gln Glu Ile Glu Lys Val Thr Asp Phe Lys
  85 90 95
```

Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp
 100 105 110
 Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Ile Phe Ala Arg
 115 120 125
 Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg Ser Trp Asn His
 130 135 140
 Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala
 145 150 155 160
 Ala Ile Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro
 165 170 175
 Arg Glu Asp Leu Lys Asp Glu Val Leu Ala Ser Ile Pro Arg Gly Thr
 180 185 190
 Met Pro Val Ala Gly Pro Ala Asp Ala Leu Pro Tyr Cys Tyr Met Pro
 195 200 205
 Pro Gln His Ala Ser Gln Val Gly Ala Ala Gly Val Ile Met Gly Lys
 210 215 220
 Pro Val Met Asp Pro Asn Met Tyr Ala Gln Gln Ser His Pro Tyr Met
 225 230 235 240
 Ala Pro Gln Met Trp Pro Gln Pro Pro Asp Gln Arg Gln Ser Ser Pro
 245 250 255

Glu His

<210> 123
 <211> 1493
 <212> DNA
 <213> Triticum aestivum

<400> 123
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 aaggggtgatg gggaccgagc aagggaagga aggaacggga gcgggggagg ggcgcggtgga 120
 ggtgcgcacg gggccgaggc cagcgcgtgcc ggcgccgcag cagcgggaggc tggacggggtt 180
 ctggaggggag cggcaggagg agatggaggc gacggcggac ttcaacgacc gcatactgcc 240
 catggcccgc ctcaagaggc tcatccgcgc cgaggaggac ggcattgatga tcgccgccga 300
 cacgccggcg tacctggcca agctctgcga gctcttcgtg caggagctcg ccgtgcgcgc 360
 ctgggcgtgc gcccaatccc accaccgccg catcatactg gaatcggaca tcgccgaggc 420
 catcgccttc acccagtcgt acgacttcct cgccaccgtg ctctctcagc accaacggga 480
 ggcgcggctg gccggccgtg ctgctatccc gacaacgggt cgggtgacgg cggcgagggc 540
 aaggctcatc accaggaagc gccacatgcc ggacccgaat cctccacggc cgggtgcatgg 600
 ggtgcggaga attcgtcctc gtgcgcttcc tatcccgcgc ccgtcggact ttgcgtacgt 660
 gccggttcca tttccggttca cctcggcgcc gataggagcc gcagcgatgg cggagggggt 720
 gatgattctc ccacccatca accacgcgac taccgagcgc gtgttcttcc tggacaggaa 780
 cagcggcact gacttcgcag gtgaaaactc tgctgctgaa actatagcat ctccgcctcc 840
 tccggcaggg cctgcaggag cagtggcgct gccactgtc catcctgctg cttactactt 900
 gtgcgcttac ccggtgacca acgacgttga ggcctttgcc gttggcaaca ctgatcctga 960
 tgtcatccca ccggagattg tagtgggaga cgtcgccatc ccaccggaga ttatagaggg 1020
 aaacgtcgcc gatggcaacg gcgacggcgg acagcagcag cagcagagcg aaaaccttgg 1080
 tggtaatggt gagagtgtgg tgggtgtcga aagcaatggt gtgcaggaag atggtgcaga 1140
 tgggatgttt ctgaaggaga tcctcatgga tgaagacctg atgtttcccg acgctgagct 1200

ttttccgttg gtgggcgctg cacctgggtcc agaggatttc atcgtcgacc aagatgttct 1260
 cgacgacgtc ttcgccaacc cgagcagcag cgcaagcagc gactgaaccg aaagaagatc 1320
 agagcgggac gcagcatcgg ttgattcatc tatcgtctct cgacctgcta ctctatgcta 1380
 gccgctatat cggttaataa atttgggaat aagtttgtgt tcgtgcgtgt gacatggact 1440
 gtatggttcg ccctgaattt atcgtattgc aatatatagc cgtgattgtg tgt 1493

<210> 124
 <211> 434
 <212> PRT
 <213> Triticum aestivum

<400> 124
 Ala Pro Ala Leu Ala Ser Lys Ser Ile His Asn Ile Gly Thr Glu Leu
 1 5 10 15
 Ala Val Leu Pro Arg Val Met Gly Thr Glu Gln Gly Lys Glu Gly Thr
 20 25 30
 Gly Ala Gly Glu Gly Arg Val Glu Val Arg Thr Gly Pro Arg Pro Ala
 35 40 45
 Leu Pro Ala Pro Gln Gln Arg Ala Val Asp Gly Phe Trp Arg Glu Arg
 50 55 60
 Gln Glu Glu Met Glu Ala Thr Ala Asp Phe Asn Asp Arg Ile Leu Pro
 65 70 75 80
 Met Ala Arg Leu Lys Arg Leu Ile Arg Ala Glu Glu Asp Gly Met Met
 85 90 95
 Ile Ala Ala Asp Thr Pro Ala Tyr Leu Ala Lys Leu Cys Glu Leu Phe
 100 105 110
 Val Gln Glu Leu Ala Val Arg Ala Trp Ala Cys Ala Gln Ser His His
 115 120 125
 Arg Arg Ile Ile Leu Glu Ser Asp Ile Ala Glu Ala Ile Ala Phe Thr
 130 135 140
 Gln Ser Tyr Asp Phe Leu Ala Thr Val Leu Leu Glu His Gln Arg Glu
 145 150 155 160
 Ala Arg Leu Ala Gly Arg Ala Ala Ile Pro Thr Thr Val Pro Val Thr
 165 170 175
 Ala Ala Arg Ala Arg Leu Ile Thr Arg Lys Arg His Met Pro Asp Pro
 180 185 190
 Asn Pro Pro Arg Pro Val His Gly Val Arg Arg Ile Arg Pro Arg Ala
 195 200 205
 Leu Pro Ile Pro Pro Pro Ser Asp Phe Arg Tyr Val Pro Val Pro Phe
 210 215 220
 Pro Phe Thr Ser Ala Pro Ile Gly Ala Ala Ala Met Ala Glu Gly Leu
 225 230 235 240
 Met Ile Leu Pro Pro Ile Asn His Ala Thr Thr Glu Arg Val Phe Phe
 245 250 255

Leu Asp Arg Asn Ser Gly Thr Asp Phe Ala Gly Glu Asn Ser Ala Ala
 260 265 270
 Glu Thr Ile Ala Ser Pro Pro Pro Pro Ala Gly Pro Ala Gly Ala Val
 275 280 285
 Ala Leu Pro Thr Val His Pro Ala Ala Tyr Tyr Leu Cys Ala Tyr Pro
 290 295 300
 Val Thr Asn Asp Val Glu Ala Phe Ala Val Gly Asn Thr Asp Pro Asp
 305 310 315 320
 Val Ile Pro Pro Glu Ile Val Val Gly Asp Val Ala Ile Pro Pro Glu
 325 330 335
 Ile Ile Glu Gly Asn Val Ala Asp Gly Asn Gly Asp Gly Gly Gln Gln
 340 345 350
 Gln Gln Gln Ser Glu Asn Leu Gly Gly Asn Gly Glu Ser Val Val Val
 355 360 365
 Ser Gln Ser Asn Gly Val Gln Glu Asp Gly Ala Asp Gly Met Phe Leu
 370 375 380
 Lys Glu Ile Leu Met Asp Glu Asp Leu Met Phe Pro Asp Ala Glu Leu
 385 390 395 400
 Phe Pro Leu Val Gly Ala Ala Pro Gly Pro Glu Asp Phe Ile Val Asp
 405 410 415
 Gln Asp Val Leu Asp Asp Val Phe Ala Asn Pro Ser Ser Ser Ala Ser
 420 425 430

Ser Asp

<210> 125
 <211> 660
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (483)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (614)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (630)
 <223> n = A, C, G, or T

<220>
 <221> unsure

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<222> (644)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (647)

<223> n = A, C, G, or T

<400> 125

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tgtgctgaag catctgacgc gcttgcgccg agcagcagga gctagccgtt catgctcttc 120
ttccctcccc ttggcatctg aagcagtaag agctcaagtt cacagagggc gttcgtccga 180
tctacaaagc ccagctgtac atcgccttag ctagcttgca gatcgcaagc tagatagtaa 240
tggagaacca ccagctgccc tacaccaccc agccgcccgc aacgggcgcg gccggaggag 300
ccccggtgcc tggcgtgcct gggccaccgc cgggtgccaca ccaccacctg ctccagcagc 360
agcaggccca gctgcaggcg ttctgggcgt accagcggca ggaggcggag cgcgcatcgg 420
cgtccgactt caagaaccac cagctgccgc tggctcggat caagaagatc atgaaggccg 480
acnaagacgt gcgcatgatc tccgcggagg cgcccgtgct cttcgccaag gcctgcgagc 540
tctttattct cgaagctcac cattccgctt cctggctgca cgcccgagga agaacaagcc 600
gccgcacaac ttgnagcgca aacgacgtn cccgcttgcc aatnggngcc gccacccgac 660

```

<210> 126

<211> 147

<212> PRT

<213> Triticum aestivum

<220>

<221> UNSURE

<222> (82)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (125)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (131)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (135)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (142)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (145)

<223> Xaa = any amino acid

<400> 126

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Met Glu Asn His Gln Leu Pro Tyr Thr Thr Gln Pro Pro Ala Thr Gly
  1                      5                      10                      15

```

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Ala Ala Gly Gly Ala Pro Val Pro Gly Val Pro Gly Pro Pro Pro Val
 20 25 30

Pro His His His Leu Leu Gln Gln Gln Gln Ala Gln Leu Gln Ala Phe
 35 40 45

Trp Ala Tyr Gln Arg Gln Glu Ala Glu Arg Ala Ser Ala Ser Asp Phe
 50 55 60

Lys Asn His Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala
 65 70 75 80

Asp Xaa Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Leu Phe Ala
 85 90 95

Lys Ala Cys Glu Leu Phe Ile Leu Glu Ala His His Ser Ala Ser Trp
 100 105 110

Leu His Ala Arg Gly Arg Thr Ser Arg Arg Thr Thr Xaa Ser Ala Asn
 115 120 125

Asp Val Xaa Arg Leu Pro Xaa Gly Ala Ala Thr Arg Arg Xaa Phe Glu
 130 135 140

Xaa Phe Leu
 145

<210> 127

<211> 1874

<212> DNA

<213> Triticum aestivum

<400> 127

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gcacgagccc acccacaacc ctagctcccc cgaacccatg gatcccacca aatccagcac      60
cccgccgccc cccccgtcc tgggcgcgcc cgctcggtac ccgcccgggg cgtaccctcc    120
tccgccgggc gccccgcgg ccgcctaccc gccgcagctc tacgcgcgcg cgggcgcgcg    180
cgccgcccag caggccgcgg cgcagcagca gcagcagctg caggtgttct gggcggagca    240
gtaccgcgag atcgaggcca ccaccgactt caagaaccac aacctcccgc tggcccggat    300
caagaagatc atgaaggccg acgaggacgt ccgcatgatc gccgcccagg cccccgtcgt    360
cttcgcccgc gcctgcgaga tgttcatcct cgagctcacc caccgcggct gggcgcacgc    420
cgaggagAAC aagcgccgca cgctccagaa gtccgacatt gcgcccgcca tcgcccgcac    480
cgaggtcttc gacttcctcg tggacatcgt gccccgggac gacgccaagg acgccgaggc    540
ggccgcccgc gcggccatgg ccacggcggc ggccgggatc ccgcgcccgg ccgcccggcg    600
gcctgccacc gaccgagta tggcatacta ctatgtcccc cagcagtaat gtatcatcga    660
tctaaacttg cgcatttcta atcgagagaat gtgttgttgt tctgtgactg tccttggtgc    720
tgttgttgct gcggcgtaat aagatttatg ggcctcccct gagcttatga attgagctgt    780
tcggttctag tattacagta ggattgttgt aatgggggag gccgtatgat tgcttccgta    840
gtgcatgact aactggccac ccagtgtaat ctgataacta ttatctggcg cctcccattg    900
ttactatgta tttatgttct tcacacagtc ctctttgtct ctaccacttc gaggagtctc    960
tcggaaggat gggctccaag atgcttctgg tcaccgctct cttggtgggc atagcctctc   1020
agagctatgc caccaggagc cttgacggaa accacttggc tgatcagaag tacggcggcg   1080
gcggctacgg aggtggcggg gggggctccg gaggtggtgg tggctacgga ggaggtggca   1140
gcggcggcgg ggggtggctat ggaggaggcg gcggcggtgg ctacggagga ggaggcggcg   1200
gttacacacc gatgccaaca ccgtcgaccc ccagccacag cggatcctgc gactactgga   1260
agggccaccc ggagaagatc atcgactgca tcggcagcct gggcagcatc ctgggctccc   1320
tcggagaggt gtgccactcc ttcttcggca gcaagatcca taccctgcag gacgcgctgt   1380
gcaacacccg gaccgactgc tacggcgacc tgctgcgcga gggcgccgcc gcctacatca   1440
acgccatcgc cgccaagaag gagaagttcg cctacaccgc ctaccaggtc aaggagtgcg   1500

```

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```

tcgccgctcgg gctcacctcc gagttcgccg ccgccgcgca ggccgccatg ttgaagaagg 1560
ccaactacgc ctgccactac taggaggcta ggctaccggc cggccgcccc agctggtggt 1620
cgtcggtggc taaataagtc catatatgca tgcacgtgtc gtgcatgttt tcatgcagtt 1680
tcccggatgc gcgcgcgcgt gtcctccgct atgcctttat gtgtttgctt gccgtttgat 1740
gatgcatgcc atgccgtctc atatatacgt agtgatgctt aatgctttgc ttgcttttct 1800
tatcttcggt ggtgatgtaa gaataatttg attgaggagt tattagttaa agacatagta 1860
tgcaaaaaaa aaaa                                     1874

```

<210> 128

<211> 203

<212> PRT

<213> Triticum aestivum

<400> 128

```

Met Asp Pro Thr Lys Ser Ser Thr Pro Pro Pro Pro Pro Val Leu Gly
  1              5              10              15

```

```

Ala Pro Val Gly Tyr Pro Pro Gly Ala Tyr Pro Pro Pro Pro Gly Ala
          20              25              30

```

```

Pro Ala Ala Ala Tyr Pro Pro Gln Leu Tyr Ala Pro Pro Gly Ala Ala
          35              40              45

```

```

Ala Ala Gln Gln Ala Ala Ala Gln Gln Gln Gln Gln Leu Gln Val Phe
          50              55              60

```

```

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

```

```

His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu
          85              90              95

```

```

Asp Val Arg Met Ile Ala Ala Glu Ala Pro Val Val Phe Ala Arg Ala
          100             105             110

```

```

Cys Glu Met Phe Ile Leu Glu Leu Thr His Arg Gly Trp Ala His Ala
          115             120             125

```

```

Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Ser Asp Ile Ala Ala Ala
          130             135             140

```

```

Ile Ala Arg Thr Glu Val Phe Asp Phe Leu Val Asp Ile Val Pro Arg
        145             150             155             160

```

```

Asp Asp Ala Lys Asp Ala Glu Ala Ala Ala Ala Ala Met Ala Thr
          165             170             175

```

```

Ala Ala Ala Gly Ile Pro Arg Pro Ala Ala Gly Val Pro Ala Thr Asp
          180             185             190

```

```

Pro Ser Met Ala Tyr Tyr Tyr Val Pro Gln Gln
          195             200

```

<210> 129

<211> 629

<212> DNA

<213> Amaranthus retroflexus

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PCT/US02/22086

<220>
 <221> unsure
 <222> (566)..(567)..(568)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (606)..(607)..(608)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (626)..(627)..(628)..(629)
 <223> n = A, C, G, or T

<400> 129
 gcacgaggat ggatcatcat catcgtggag ggttccatgg ttaccgcaaa caacatcccc 60
 tttctaagtc ctctctttct gaaatgagat tgacatcgga ggtgttaccg gctgagatga 120
 atcacatacg cccaactagc aatggaaaag gagtatcaca tgacatgaac aaccatacca 180
 ataaccatca tccctacaac aatagcaaca acaacaacaa tggtttcagc aacggaaata 240
 gtaatcactc agcatcaacc gatcaagata acaatgagtg cactgtacgc gagcaagatc 300
 gcttttatgcc catcgccaat gtcattagga tcatgcgcaa gattcttcct cctcatgcca 360
 aaatctccga tgatgctaag gaaactatcc aggagtgtgt atcagagtac atcagcttca 420
 taacaggtga agccaacgag aggtgccaaa gggaacaacg taagaccata actgctgaag 480
 atgttctttg ggcgatgagc aagttgggat tcgatgacta catcgaaccc ctcacactgt 540
 acttgcacgc atacagggaa ctcgannngg aacgtgggttc catccgcact tgtgagccac 600
 tcctcnnnct cagtcgtgct gccatnnnn 629

<210> 130
 <211> 198
 <212> PRT
 <213> Amaranthus retroflexus

<220>
 <221> UNSURE
 <222> (186)..(187)
 <223> Xaa = any amino acid

<400> 130
 Met Asp His His His Arg Gly Gly Phe His Gly Tyr Arg Lys Gln His
 1 5 10 15
 Pro Leu Ser Lys Ser Ser Ser Ser Glu Met Arg Leu Thr Ser Glu Val
 20 25 30
 Leu Pro Ala Glu Met Asn His Ile Arg Pro Thr Ser Asn Gly Lys Gly
 35 40 45
 Val Ser His Asp Met Asn Asn His Thr Asn Asn His His Pro Tyr Asn
 50 55 60
 Asn Ser Asn Asn Asn Asn Asn Gly Phe Ser Asn Gly Asn Ser Asn His
 65 70 75 80
 Ser Ala Ser Thr Asp Gln Asp Asn Asn Glu Cys Thr Val Arg Glu Gln
 85 90 95
 Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile
 100 105 110

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Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln
 115 120 125
 Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu
 130 135 140
 Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu
 145 150 155 160
 Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr
 165 170 175
 Leu Tyr Leu His Arg Tyr Arg Glu Leu Xaa Xaa Glu Arg Gly Ser Ile
 180 185 190
 Arg Thr Cys Glu Pro Leu
 195

<210> 131
 <211> 625
 <212> DNA
 <213> Momordica charantia

<220>
 <221> unsure
 <222> (597)..(598)..(599)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (620)..(621)..(622)..(623)
 <223> n = A, C, G, or T

<400> 131
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 aggggaagag agagagagag gcatggaata tggaggagga ggaggagatg ggttccatag 120
 ctacagaagg cagcagccaa acacaaaacc aagctctgct ttgaacatgt tgctgaccac 180
 aaacaagcca tccgccaaca accaccacca ccacttaaac ggccaaaacg ccaccaccac 240
 caccaactcc tctgctgctg ccgccccgac cctggccccg gccgctgctg ccaacaacaa 300
 cgagcagcag tgcgtcgtgc gggagcaaga ccaatacatg ccgatcgcca acgtgatacg 360
 catcatgcgg cggatcttac cctcccatgc aaagatatcc gacgatgcca aggagaccat 420
 ccaagagtgt gtgtcggagt acattagctt catcaccggc gaggccaacg agcggtgcca 480
 gcgagagcag cgcaagacgg tgacggcgga ggacgtcctt tggggccatgg ggaagcttgg 540
 cttcgacgac tacatcgagc cactcaccgt gttcctcaac cgctaccggg agtcagnnng 600
 cgatcgaatc cgaacggagn nnntc 625

<210> 132
 <211> 179
 <212> PRT
 <213> Momordica charantia

<220>
 <221> UNSURE
 <222> (172)..(173)
 <223> Xaa = any amino acid

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<400> 132

Met Glu Tyr Gly Gly Gly Gly Gly Asp Gly Phe His Ser Tyr Arg Arg
 1 5 10 15

Gln Gln Pro Asn Thr Lys Pro Ser Ser Ala Leu Asn Met Leu Leu Thr
 20 25 30

Thr Asn Lys Pro Ser Ala Asn Asn His His His His Leu Asn Gly Gln
 35 40 45

Asn Ala Thr Thr Thr Thr Asn Ser Ser Ala Ala Ala Ala Pro Thr Leu
 50 55 60

Ala Pro Ala Ala Ala Ala Asn Asn Asn Glu Gln Gln Cys Val Val Arg
 65 70 75 80

Glu Gln Asp Gln Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
 85 90 95

Arg Ile Leu Pro Ser His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
 100 105 110

Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala
 115 120 125

Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Val Thr Ala Glu Asp
 130 135 140

Val Leu Trp Ala Met Gly Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
 145 150 155 160

Leu Thr Val Phe Leu Asn Arg Tyr Arg Glu Ser Xaa Xaa Asp Arg Ile
 165 170 175

Arg Thr Glu

<210> 133

<211> 1173

<212> DNA

<213> Zea mays

<400> 133

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gagagccaat ggactccagc agcttcctcc ctgccgccgg cgcggagaat ggctcggcgg 120

cgggcggcgc caacaatggc ggcgctgctc agcagcatgc ggcgccggcg atccgcgagc 180

aggaccggct gatgccgatc gcgaacgtga tccgcacatc gcggcgcgctg ctgccggcgc 240

acgccaagat ctccggacgac gccaaggaga cgatccagga gtgcgtgtcg gagtacatca 300

gcttcacacac gggggaggcc aacgagcggg gccagcggga gcagcgcaag accatcaccg 360

ccgaggacgt gctgtgggcc atgagccgcc tcggcttcga cgactacgtc gagccgctcg 420

gcgcctacct ccaccgctac cgcgagttcg agggcgacgc gcgcggcgctc gggctcgtcc 480

cggggggcgc cccatcgcg cgcggcgacc accaccgcga ctccatgtcg ccagcggcga 540

tgctcaagtc ccgcgggcca gtctccggag ccgccatgct accgcaccac caccaccacc 600

acgacatgca gatgcacgcc gccatgtacg ggggaacggc cgtgcccccg ccggccgggc 660

ctcctcacca cggcgggttc ctcatgccac acccacagg tagtagccac tacctgcctt 720

acgcgtacga gccacgtac ggcggtgagc acgccatggc tgcatactat ggaggcgccg 780

cgtacgcgcc cggcaacggc gggagcggcg acggcagtg cagtggcggc ggtggcggga 840

gcgcgtcgca cacaccgcag ggcagcggcg gcttgagca cccgcaccg ttcgcgtaca 900

agtagctagt tcgtacgtcg ttcgacttga gcaagccatc gatctgctga tctgaacgta 960

cgctgtattg tacacgcatg cacgtacgta tcggcgggcta gctctcctgt ttaagttgta 1020
 ctgtgattct gtcccggccg gctagcaact tagtatcttc cttcagtctc tagtttctta 1080
 gcagtcgtag aagtgttcaa tgcttgccag tgtgttggtt tagggccggg gtaaaccatc 1140
 cgatgagatt atttcaaaaa aaaaaaaaaa aaa 1173

<210> 134
 <211> 278
 <212> PRT
 <213> Zea mays

<400> 134

Met	Asp	Ser	Ser	Ser	Phe	Leu	Pro	Ala	Ala	Gly	Ala	Glu	Asn	Gly	Ser
1				5					10					15	
Ala	Ala	Gly	Gly	Ala	Asn	Asn	Gly	Gly	Ala	Ala	Gln	Gln	His	Ala	Ala
			20					25					30		
Pro	Ala	Ile	Arg	Glu	Gln	Asp	Arg	Leu	Met	Pro	Ile	Ala	Asn	Val	Ile
		35					40					45			
Arg	Ile	Met	Arg	Arg	Val	Leu	Pro	Ala	His	Ala	Lys	Ile	Ser	Asp	Asp
	50					55					60				
Ala	Lys	Glu	Thr	Ile	Gln	Glu	Cys	Val	Ser	Glu	Tyr	Ile	Ser	Phe	Ile
65					70					75					80
Thr	Gly	Glu	Ala	Asn	Glu	Arg	Cys	Gln	Arg	Glu	Gln	Arg	Lys	Thr	Ile
				85					90					95	
Thr	Ala	Glu	Asp	Val	Leu	Trp	Ala	Met	Ser	Arg	Leu	Gly	Phe	Asp	Asp
			100					105					110		
Tyr	Val	Glu	Pro	Leu	Gly	Ala	Tyr	Leu	His	Arg	Tyr	Arg	Glu	Phe	Glu
	115						120					125			
Gly	Asp	Ala	Arg	Gly	Val	Gly	Leu	Val	Pro	Gly	Ala	Ala	Pro	Ser	Arg
	130					135					140				
Gly	Gly	Asp	His	His	Pro	His	Ser	Met	Ser	Pro	Ala	Ala	Met	Leu	Lys
145					150					155					160
Ser	Arg	Gly	Pro	Val	Ser	Gly	Ala	Ala	Met	Leu	Pro	His	His	His	His
				165					170					175	
His	His	Asp	Met	Gln	Met	His	Ala	Ala	Met	Tyr	Gly	Gly	Thr	Ala	Val
			180					185					190		
Pro	Pro	Pro	Ala	Gly	Pro	Pro	His	His	Gly	Gly	Phe	Leu	Met	Pro	His
			195				200					205			
Pro	Gln	Gly	Ser	Ser	His	Tyr	Leu	Pro	Tyr	Ala	Tyr	Glu	Pro	Thr	Tyr
	210					215					220				
Gly	Gly	Glu	His	Ala	Met	Ala	Ala	Tyr	Tyr	Gly	Gly	Ala	Ala	Tyr	Ala
225					230					235					240
Pro	Gly	Asn	Gly	Gly	Ser	Gly	Asp	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Gly
				245					250					255	

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Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro
 260 265 270

His Pro Phe Ala Tyr Lys
 275

<210> 135
 <211> 1269
 <212> DNA
 <213> Zea mays

<400> 135
 ccacgcgtcc gcatgaataa tccccaaaac cctaaagcca gtgctccttg caccttgcca 60
 ccggagcttc ccaaagaagc agtggcgacc gacgaagcac cgccgccaat gggcaacaac 120
 aacaacacgg aatcggcgac ggcgacgatg gtccgggagc aggaccggct gatgcccgctg 180
 gccaacgtgt cccgcatcat gcgccaagtg ctgcctccgt acgccaagat ctccgacgac 240
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 aacgagcggg gccacaccga gcgccgcaag accgtcacct ccgaggacat cgtgtggggc 360
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 cgcgacgaca gcgaccacgg cggtgaagag cgcggcggcc ctgcagggcg tgggtggctcg 480
 cgccgcggct cgtcgtcctt gccgctccac tgcccgcagc agatgcacca cctgcaccca 540
 gccgtctgcc ggcgtccgca ccagagcgtg tcgcctgctg caggatacgc cgtccggccc 600
 gttccccgcc cgatgccagc cagtgggtac cgcatgcagg gcggagacca ccgcagcgtg 660
 ggcggcgtgg ctccctgcag ctacggaggg gcgctcgtcc aggcgggtgg aaccaaacac 720
 gttgttggtg tccacgacga cgaggcaagc tcttcgagtg aaaatccgcc gccggagggg 780
 cgtgccgctg gctcgaacta gcctagcttc tcagttcccc gtgtacaata agagggggcg 840
 tcgcggcgcc gcgccgcgcc cttgggttgg gccgggcgct atgctgcagt ttggtttgta 900
 aactaacgag cctagggtag ctggtgcacg cgcgccacct cgccggacgt cgccgtcgtc 960
 gtcggcatgg acttaaccgg cgggccctgt tgttatttct caagtttgta gccaacgcac 1020
 tggttcggtg gttccataat ttaatttacc atgttgctct cgaaatgaaa aaaaaaaaaa 1080
 aaaaaagggc ggccgccctt tttttttttt tttttttttt tcctcttaag gcaaggcaac 1140
 tcctgtttgt aggggaatcg ttatggttct gcttctgatt gctcctagtt cttccatcat 1200
 tttcgtgttc aaagagaagg ctcccagaaa ataaaataac gattgctatg aaaaaaaaaa 1260
 aaaaaaaag 1269

<210> 136
 <211> 262
 <212> PRT
 <213> Zea mays

<400> 136
 Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu Pro
 1 5 10 15
 Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro Pro
 20 25 30
 Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val Arg
 35 40 45
 Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met Arg
 50 55 60
 Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Lys Glu Val
 65 70 75 80
 Ile Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly Glu Ala
 85 90 95

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Asn Glu Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser Glu Asp
 100 105 110
 Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro
 115 120 125
 Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Asp Ser Asp His Gly Gly
 130 135 140
 Glu Glu Arg Gly Gly Pro Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser
 145 150 155 160
 Ser Ser Leu Pro Leu His Cys Pro Gln Gln Met His His Leu His Pro
 165 170 175
 Ala Val Cys Arg Arg Pro His Gln Ser Val Ser Pro Ala Ala Gly Tyr
 180 185 190
 Ala Val Arg Pro Val Pro Arg Pro Met Pro Ala Ser Gly Tyr Arg Met
 195 200 205
 Gln Gly Gly Asp His Arg Ser Val Gly Gly Val Ala Pro Cys Ser Tyr
 210 215 220
 Gly Gly Ala Leu Val Gln Ala Gly Gly Thr Gln His Val Val Gly Phe
 225 230 235 240
 His Asp Asp Glu Ala Ser Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly
 245 250 255
 Arg Ala Ala Gly Ser Asn
 260

<210> 137
 <211> 481
 <212> DNA
 <213> Argemone mexicana

<220>
 <221> unsure
 <222> (410)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (471)
 <223> n = A, C, G, or T

<400> 137
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 tgggtggtggt agtggtggtg gtttccatgg atatcagaaa ctcccaaaat caaactccgc 120
 tggaatgatg ctctcggagc tatcgaataa caacaacaat attgacgtaa actctacatg 180
 tactgtacga gagcaagatc gatacatgcc aattgctaata gtgatcagga tcatgcgtaa 240
 ggtacttcct actcatgccca agatctctga cgatgccaaa gaaactatcc aagaatgtgt 300
 ctcagaatac atcagtttca tcacaagtga agccaatgat cgttgccaac gtgaacaaag 360
 aaagacaatc acagctgaag atgttttatg ggcatgagc aaactagggg ttgatgagta 420
 cattgaacct ctaactcttt accttcaacg ttatcgtgag tttgaagggtg nacgttggtc 480
 a 481

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<210> 138
 <211> 146
 <212> PRT
 <213> Argemone mexicana

<220>
 <221> UNSURE
 <222> (123)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (143)
 <223> Xaa = any amino acid

<400> 138
 Met Glu Arg Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly
 1 5 10 15
 Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu
 20 25 30
 Leu Ser Asn Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val
 35 40 45
 Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met
 50 55 60
 Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu
 65 70 75 80
 Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu
 85 90 95
 Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
 100 105 110
 Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu
 115 120 125
 Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg
 130 135 140
 Trp Ser
 145

<210> 139
 <211> 1154
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (3)
 <223> n = A, C, G, or T

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<400> 139

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atnacacaca cctaccttat aactatggaa actggagggt ttcattggcta ccgcaagctc   60
cccaacacaa cctctgggtt gaagctgtca gtgtcagaca tgaacatgaa catgaggcag   120
cagcaggtag catcatcaga tcagaactgc agcaaccaca gtgcagcagg agaggagaac   180
gaatgcacgg tgagggagca agacagggtc atgccaatcg ctaacgtgat acggatcatg   240
cgcaagattc tccctccaca cgcaaaaatc tccgatgatg caaaggagac aatccaagag   300
tgcgtgtcgg agtacatcag cttcatcacc ggggaggcca acgagcgttg ccagagggag   360
cagcgcaaga ccataaccgc agaggacgtg ctttgggcaa tgagtaagct tggattcgac   420
gactacatcg aaccgttaac catgtacctt caccgctacc gtgagctgga gggtgaccgc   480
acctctatga ggggtgaacc gctcgggaag aggactgtgg aatatgccac gcttgctact   540
gcttttgtgc cgccaccctt tcatcaccac aatggctact ttggtgctgc catgcccattg   600
gggacttacg ttagggaaac gccaccaaat gctgcgtcat ctcaccacca tcatggaatc   660
tccaatgctc atgaaccaa tgctcgctcc atataaaatt aatgaagagt actgttcagt   720
aggagaacaa gacttcttgg acttgattag cttaactctc agtgattggg gttagagtac   780
tggttggtgag gatggttaat ttataatta agggctggga attggggagt tagtatatat   840
tcctaatact aattatgtgc atctttaatt tatggaataa ctttgttttt tgttttaact   900
tctgataatt tggattttct gatgtttaat gtggttttgt ctatccctta ttaacagtgc   960
caagcttaag gttttagcca tgctccaaaa tggaataact gtactgttat gttgttctgg 1020
tagtgatggg gatgaaacct gcaagttatg tttatgtata aagccactat tgatcaaaat 1080
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actcgagacc ggca                                     1154

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<210> 140

<211> 223

<212> PRT

<213> Glycine max

<400> 140

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Met Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr
  1              5              10              15

Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met Arg Gln
          20              25              30

Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser Ala Ala
          35              40              45

Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met Pro
          50              55              60

Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His Ala
          65              70              75              80

Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu
          85              90              95

Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu
          100             105             110

Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Lys
          115             120             125

Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu His Arg
          130             135             140

Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Pro Leu
          145             150             155             160

```

```
<400> 142
Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met Glu
  1                               10                      15
Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala Gly
      20                               25                      30
Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala Ser
      35                               40                      45
Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val Arg
      50                               55                      60
Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
      65                               70                      75                      80
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Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
85 90 95

Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala
100 105 110

Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
115 120 125

Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
130 135 140

Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr
145 150 155 160

Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr
165 170 175

Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His Asn
180 185 190

Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu Ala
195 200 205

Pro Pro Asn Thr Ala Ser Ser His His His His His His His His
210 215 220

His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
225 230 235 240

<210> 143

<211> 796

<212> DNA

<213> Glycine max

<400> 143

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gcacgagcaa tggcgaggagt gaggaacag gaccagtaca tgccgatagc gaacgtgata 60
aggatcatgc gtcggattct gccagcgcac gcgaagatct cagacgacgc gaaggagacg 120
atccaggagt gcgtgtctga gtacatcagt ttcatcacgg cggaggcgaa cgagcgggtgc 180
cagcgggagc agcgggaagac ggtgaccgca gaggatgtgt tgtgggcat ggagaagctt 240
ggctttgaca actacgctca ccctctctct ctttaccttc accgctaccg cgagagttaa 300
ggagaacctg cttctgtcag acgcgcttct tctgcaatgg ggatcaataa taatatgggtg 360
caccacctt atattaattc tcatggcttt ggaatgtttg attttgacct atcatcgcaa 420
gggttttaca gggacgatca taacgctgct tctggatctg gtggttttgt tgcgcctttt 480
gatccttatg ctaacatcaa acgtgatgcc ctgtgatcat gtaagaacaa caactagtgc 540
atgctgcttt ttcacttggt tagttatatt caagcacaag cacatgcagg tgcagctgca 600
actattttagc ttcattctaca aatctttttt cctctcttct tctcatgctt taattattta 660
gagacaatac ttgttattca ttgttatgct caattgctag cttctattca tcgtcgactg 720
tctgtattgt tgatgttcat tacagtaaca gataagatgg taactgcttt actacttcaa 780
aaaaaaaaa aaaaaa 796
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<210> 144

<211> 171

<212> PRT

<213> Glycine max

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<400> 144

Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
 1 5 10 15

Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
 20 25 30

Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
 35 40 45

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

Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
 65 70 75 80

Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
 85 90 95

Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
 100 105 110

Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
 115 120 125

Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
 130 135 140

Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
 145 150 155 160

Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
 165 170

<210> 145

<211> 905

<212> DNA

<213> Vernonia mespilifolia

<400> 145

gcacgagcca atttctagag agagaacgag agagaattct ctaaagagga aaaatagatg 60
 gaacgtggag gaggtttcca tggctaccac aggctcccca tccaccctac atctggaatc 120
 caacaatcgg atatgaagct aaagctacca gaaatgacca acaataactc gtccactgat 180
 gacaatgagt gcaccgttcg agaacaggac cgcttcatgc cgatagcaaa cgtgatccgc 240
 atcatgcgga agatccttcc tccacatgcc aagatctctg atgatgccaa agagacgatc 300
 caagaatgtg tttcagagta cattagcttt gtcacaggcg aggcaaatga ccgctgccag 360
 cgtgagcaaa ggaagaccat cacagctgaa gatgtgctct gggctatgag caaactggga 420
 tttgatgatt atatcgagcc cttgactgtg tatctccatc gctacaggga gtttgatggg 480
 ggcgaacgtg gatccataag gggtagagccc cttgtgaaga ggagtacttc tgatcctggg 540
 cactttggga tggcttcttt tgtgcctgct tttcatatgg gtcatacataa cggcttcttt 600
 ggtcctgcaa gcattggtgg tttcctgaaa gacccatcga gtgctggccc ttcgggacct 660
 gcagtcgctg ggtttgagcc gtatgctcag tgtaaagagt aactgcaaaa agtaggggtt 720
 gggatgagat gatgatgatg gtggtggtgg tggtggtttg ttttggtttt ttctttcttt 780
 tttttttctt ctttcttttc ttggtcattg aggaacaaac ttacattggt tcactttggc 840
 taggcatgta aacggttaac atgcttatca agtagtagtt ttcgatcaaa aaaaaaaaaa 900
 aaaaaa 905

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<210> 146
 <211> 214
 <212> PRT
 <213> Vernonia mespilifolia

<400> 146
 Met Glu Arg Gly Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His
 1 5 10 15
 Pro Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu
 20 25 30
 Met Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg
 35 40 45
 Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
 50 55 60
 Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
 65 70 75 80
 Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala
 85 90 95
 Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
 100 105 110
 Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
 115 120 125
 Leu Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg
 130 135 140
 Gly Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro
 145 150 155 160
 Gly His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His
 165 170 175
 His Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp
 180 185 190
 Pro Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro
 195 200 205
 Tyr Ala Gln Cys Lys Glu
 210

<210> 147
 <211> 1098
 <212> DNA
 <213> Triticum aestivum

<400> 147
 gcacgagcaa gtgcgagtgc gactacctgc attgcacctt ggctagccct agacatggag 60
 aacgacggcg tccccaacgg accagcggcg ccggcaccta cccaggggac gccggtggtg 120
 cgggagcagg accggctgat gccgatcgcg aacgtgatcc gcatcatgcg ccgtgcgctc 180
 cctgcccacg ccaagatctc cgacgacgcc aaggaggcga ttcaggaatg cgtgtccgag 240
 ttcatcagct tcgtcaccgg cgaggccaac gaacggtgcc gcatgcagca ccgcaagacc 300

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gtcaacgccg aagacatcgt gtggggcccta aaccgcctcg gcttcgacga ctacgtcgtg 360
cccctcagcg tcttcctgca ccgcatgcgc gaccccgagg cggggacagg tgggtgccgt 420
gcaggcgaca gccgcgccgt gacgagtgcg cctccccgcg cggccccgcc cgtgatccac 480
gccgtgccgc tgcaggctca gcgcccgatg tacgcgcccc cggctccgtt gcaggttgag 540
aatcagatgc agcggcctgt gtacgctccc ccggctccgg tgcaggttca gatgcagcgg 600
ggcatctatg ggccccgggc tccagtgcac gggtagcgcg tcggaatggc gcccgtgcgg 660
gccaacgtcg gcgggcagta ccagggtgtt ggccggagagg gtgtcatggc ccagcaatac 720
tacgggtacg ggtacgagga aggagcgtac ggcgcaggta gcagcaacgg aggagccgcc 780
attggcgacg aggagagctc gtccaacggc gtgccggcac cgggggaggg catgggggag 840
ccagagccag agccagcagc agaagaatcg catgacaagc ccgtccaatc tggctagtcg 900
cgtgcgcggc gcgcgttagc ttctgcgtcc tgtgtactgt aataatttgc cgtgtcgtac 960
cggccatggt ttgtgtgtgc gtagtgctta tctaattgtg gcttgtcctc tagtaattca 1020
tgtattgctt atctaattgt gacttgtcct ctagtaattc atgtactctt tgctgttgaa 1080
aaaaaaaaa aaaaaaaaaa

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<210> 148

<211> 280

<212> PRT

<213> Triticum aestivum

<400> 148

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

Gln Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala
                      20                      25                      30

Asn Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile
                      35                      40                      45

Ser Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile
                      50                      55                      60

Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg
                      65                      70                      75                      80

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

Phe Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg
                      100                      105                      110

Asp Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala
                      115                      120                      125

Val Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val
                      130                      135                      140

Pro Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln
                      145                      150                      155                      160

Val Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val
                      165                      170                      175

Gln Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His
                      180                      185                      190

Gly Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln
                      195                      200                      205

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Tyr Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly
 210 215 220

Tyr Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly
 225 230 235 240

Ala Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro
 245 250 255

Gly Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser
 260 265 270

His Asp Lys Pro Val Gln Ser Gly
 275 280

<210> 149

<211> 932

<212> DNA

<213> Canna edulis

<400> 149

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gcaccagctc aaatctccga attaggggtt ctgtgccttg tctccaatgg cggaatcggg 60
ggccccgggc acgcccgaga gcggacattc cggcggcgga tctggcgcg cggagcagga 120
ccgctgcctc cccattgcca acattgggcg gattatgagg aaggccgtac ccgagaacgg 180
caagatcgcc aaggacgcca aggaatccgt ccaggagtgc gtctccgagt tcatcagctt 240
cgtcaccagc gaggcgagcg ataagtgccg ccgcgagaaa aggaagacga tcaacggcga 300
tgatcttctg tgggctatgc ggatgcttgg ctctgaagag tacgtcgagc ctcttaagct 360
ctacttgcag ctctacagag agatggaggg aaacgtcatg gtttcacgtc ccgctgatca 420
atgatcaacc aggaaaaaga gatggagcaa ttaacaggca gccacagat tcgttcaatg 480
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ttgttagtgt agttaataag ttatagttgc tgcaggttat ttttgttctt atttgtactc 600
ttgtccaata ccttttcctc taagtgaaca acattcagag aatggctctt ctctaggact 660
tggacgaagg cacgaagcac tgatctgaag ttatgatcca ttcaaccatc taaaattaat 720
tttaaatttt aaattgagac aatgttttga cccttgtttc gacatttccc gacagcccta 780
ctgtaatgta aagatgactt ggatagcaaa attgttaaaa aggtacaatt cctgcaatgt 840
tttacaagtc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 932
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<210> 150

<211> 121

<212> PRT

<213> Canna edulis

<400> 150

Met Ala Glu Ser Gly Ala Pro Gly Thr Pro Glu Ser Gly His Ser Gly
 1 5 10 15

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

Ile Gly Arg Ile Met Arg Lys Ala Val Pro Glu Asn Gly Lys Ile Ala
 35 40 45

Lys Asp Ala Lys Glu Ser Val Gln Glu Cys Val Ser Glu Phe Ile Ser
 50 55 60

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Phe Val Thr Ser Glu Ala Ser Asp Lys Cys Arg Arg Glu Lys Arg Lys
 65 70 75 80

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Arg Met Leu Gly Phe
 85 90 95

Glu Glu Tyr Val Glu Pro Leu Lys Leu Tyr Leu Gln Leu Tyr Arg Glu
 100 105 110

Met Glu Gly Asn Val Met Val Ser Arg
 115 120

<210> 151
 <211> 863
 <212> DNA
 <213> Momordica charantia

<400> 151
 gcacgagcag gatctcgctc acatggcgga ggctccgacg agtccagccg gcggcagcca 60
 cgagagcggc ggcgagcaga gcccataac cggtgggggt cgaggagcagg accgatacct 120
 cccgatcgct aacattagcc ggatcatgaa gaaggccttg cccgctaata gcaagatcgc 180
 caaggacgcc aaggacaccg tccaggaatg cgtctccgaa ttcatacagct tcatcactag 240
 cgaggcgagc gataagtgcc agaaggagaa gagaaagacc attaatgggg atgatttgct 300
 gtgggcaatg gcgacattgg gtttcgagga ctatatatgat ccgcttaagt cgtatctaac 360
 taggtacaga gagttggagt gtgatgctaa gggatcttct aggggtggtg atgagtctgc 420
 taaaagagat gcagttgggg ccttgccctgg ccaaaattcc cagcagtaca tgcagccggg 480
 agcaatgacc tacattaaca cccaaggaca gcatttgatc attccttcaa tgcagaataa 540
 tgaataggag actcctgcat tccctcttgg attgtctgaa atctgaggct ggtagaagcg 600
 ttcaacacct atatagcatc tttacaatcg atttggctaa tttattatga aatgatgata 660
 ttatatatat ttctgggggt tctgtgttgg ttctggattt gattttgggt tgggctttta 720
 aggtgggctt cgattttatt gatgctctcg tcatctaaag ttattgtaaa tttgggacct 780
 tcaatttagt atagttgctt tggtaatttg gaaactggaa aaaaaaaaaa aaaaaaaaaa 840
 aaaaaaaaaa aaaaaaaaaa aaa 863

<210> 152
 <211> 174
 <212> PRT
 <213> Momordica charantia

<400> 152
 Met Ala Glu Ala Pro Thr Ser Pro Ala Gly Gly Ser His Glu Ser Gly
 1 5 10 15

Gly Glu Gln Ser Pro Asn Thr Gly Gly Val Arg Glu Gln Asp Arg Tyr
 20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Ala
 35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Val Gln Glu Cys Val
 50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln
 65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met
 85 90 95

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

Thr Arg Tyr Arg Glu Leu Glu Cys Asp Ala Lys Gly Ser Ser Arg Gly
115 120 125

Gly Asp Glu Ser Ala Lys Arg Asp Ala Val Gly Ala Leu Pro Gly Gln
130 135 140

Asn Ser Gln Gln Tyr Met Gln Pro Gly Ala Met Thr Tyr Ile Asn Thr
145 150 155 160

Gln Gly Gln His Leu Ile Ile Pro Ser Met Gln Asn Asn Glu
165 170

<210> 153

<211> 1179

<212> DNA

<213> Eucalyptus grandis

<400> 153

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tcttctatgt tttttttttt gcagctgctc ggcttgccctg ccctctcggg cgacgacgcg 180
atggcgaggg ctccggcgag tcccggcggc ggcggcagcc acgagagcgg cgagcacagc 240
ccccggtcgg gcggcgccgt ccgcgagcag gacaggtacc tccccatcgc caacatcagc 300
cgcatcatga agaaggccct ccccgccaac ggcaagatcg ccaaggacgc caaggagacc 360
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cagagggaga agaggaagac gatcaacggc gacgacttgc tctggcccat ggcgacctta 480
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ggggatacca aggggtcagc taaagtgggg gaagcatcta ctaaaagaga tggcgccgca 600
gttcagtcag ttcctaattgc acagattgct catcaagggt ctttctctca cggcaccaac 660
tattcgcatc ctcaagttca ccatcctgcg cttccgatgc atggctcaga atgacatgtt 720
ccagcccttg ttgcatgaga tgaagaagtc atcacacttg ttccaggcgt ttgactcatc 780
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tgttcatatt gagttgtttt ccagtgggct gtatatattta gcattctgcat catatttgct 900
ttcagcctta catatgtctg gtttagattt acttgataat gtagaaagggt aagccccctt 960
gcgagtattt atcttattgt catttagatt cgacacccaa ggaggacgag aatgaagttt 1020
cttttttagct ctctgtttcg ttggagttgt cttgtgtatt cttgagttag aaacttgtga 1080
acaaattggg atgcacagtc catgtttatg tgacaatgtc gaggtctgag tgtataatcc 1140
agagtccaat tcagatcgta aaaaaaaaaa aaaaaaaaaa 1179
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<210> 154

<211> 177

<212> PRT

<213> Eucalyptus grandis

<400> 154

Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Ser His Glu Ser
1 5 10 15

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

Tyr Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro
35 40 45

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Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys
50 55 60

Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys
65 70 75 80

Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Pro
85 90 95

Met Ala Thr Leu Gly Phe Glu Asp Tyr Leu Asp Pro Leu Lys Ile Tyr
100 105 110

Leu Ala Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Ala Lys
115 120 125

Val Gly Glu Ala Ser Thr Lys Arg Asp Gly Ala Ala Val Gln Ser Val
130 135 140

Pro Asn Ala Gln Ile Ala His Gln Gly Ser Phe Ser His Gly Thr Asn
145 150 155 160

Tyr Ser His Ser Gln Val His His Pro Ala Leu Pro Met His Gly Ser
165 170 175

Glu

<210> 155
<211> 983
<212> DNA
<213> Zea mays

<400> 155
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ataaggggttt cggcgagggc gcccggtcgc tggcgatggc cgacgacggc gggagccacg 180
agggcagcgg cggcgggcga ggcgtccggg agcaggaccg gttcctgccc atcgccaaca 240
tcagccggat catgaagaag gccgtcccgg ccaacggcaa gatcgccaag gacgctaagg 300
agaccctgca ggagtgcgtc tccgagttca tatcattcgt gaccagcgag gccagcgaca 360
aatgccagaa ggagaaacga aagacaatca acggggacga tttgctctgg gcgatggcca 420
ctttaggatt cgaggagtac gtcgagcctc tcaagattta cctacaaaag tacaaagaga 480
tgaggagggtga tagcaagctg tctacaaagg ctggcgaggg ctctgtaaag aaggatgcaa 540
ttagtcccca tgggtggcacc agtagctcaa gtaatcagtt gggttcagcat ggagtctaca 600
accaagggat gggctatatg cagccacagt accacaatgg ggaaacctaa taaagggcta 660
atacagcagc aatttatgct aggggaagtct ctgcattgct taccatgtgt attggcagaa 720
aacaggaggc acttacaaag ggtgttaatc tctgcgatgg ctgcctctca ggtgtaaatt 780
ggcttcgggt tagcgctgct tttgtccgta tatttaggat gatctgactg ttgctacttt 840
tggaacctt ttacatttac agatatgtat tattcagcat aaatataata tagtagtcct 900
aggcctaaat aatggtgatt aacataccaa gtctttttatc aggctactcg ttttctggaa 960
caaaaaaaaa aaaaaaaaaaaa aaa 983

<210> 156
<211> 164
<212> PRT
<213> Zea mays

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<400> 156

Met Ala Asp Asp Gly Gly Ser His Glu Gly Ser Gly Gly Gly Gly Gly
 1 5 10 15

Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
 20 25 30

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
 35 40 45

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
 50 55 60

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
 65 70 75 80

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

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp
 100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala
 115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln
 130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
 145 150 155 160

Asn Gly Glu Thr

<210> 157

<211> 1021

<212> DNA

<213> Zea mays

<400> 157

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ggcacgagcg ctcctgttct tctcgcaccc ccagcccagg tgggtgtcccc tgctcgcgttg 60
atgcatgctc cctcggcggt ggccttgagc tgaggcgggc gagcgatgcc ggactcggac 120
aacgactccg gcggggccgag caacgccggg ggcgagctgt cgtcgccgcg ggagcaggac 180
cggttcctgc ccatcgccaa cgtgagccgg atcatgaaga aggcgctccc ggccaacgcc 240
aagatcagca aggacgcaa ggagacggtg caggagtgcg tgtccgagtt catctccttc 300
atcaccggcg aggcctccga caagtgccag cgcgagaagc gcaagaccat caacggcgac 360
gacctgctgt gggccatgac cacgctcggc ttcgaggact acgtcgagcc gctcaagcac 420
tacctgcaca agttccgcga gatcgagggc gagagggccg ccgcgtccgc cggcgccctcg 480
ggctcgcagc agcagcagca gcagggcgag ctgcccagag gcgccgcaa tgccgcccgg 540
tacgccgggt acggcgcgcc tggctccggc ggcatgatga tgatgatgat ggggcagccc 600
atgtacggcg gctcgcagcc gcagcaacag ccgccgccgc ctcagccgcc acagcagcag 660
cagcaacatc aacagcatca catggcaata ggaggcagag gaggattcgg ccaacaaggc 720
ggcggcgggc gctcctcgtc gtcgtcaggg cttggccggc aagacagggc gtgagttgcg 780
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ctgcctgtat gtaaataaaa atctgaggct cccatttcga aacggacggg gaactactct 960
tcccgcttcg tttcatacga gaatcgaact cgttttcaat taacaaaaaa aaaaaaaa 1020
a 1021

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<210> 158
 <211> 222
 <212> PRT
 <213> Zea mays

<400> 158
 Met Pro Asp Ser Asp Asn Asp Ser Gly Gly Pro Ser Asn Ala Gly Gly
 1 5 10 15
 Glu Leu Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn
 20 25 30
 Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser
 35 40 45
 Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser
 50 55 60
 Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
 65 70 75 80
 Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe
 85 90 95
 Glu Asp Tyr Val Glu Pro Leu Lys His Tyr Leu His Lys Phe Arg Glu
 100 105 110
 Ile Glu Gly Glu Arg Ala Ala Ala Ser Ala Gly Ala Ser Gly Ser Gln
 115 120 125
 Gln Gln Gln Gln Gln Gly Glu Leu Pro Arg Gly Ala Ala Asn Ala Ala
 130 135 140
 Gly Tyr Ala Gly Tyr Gly Ala Pro Gly Ser Gly Gly Met Met Met Met
 145 150 155 160
 Met Met Gly Gln Pro Met Tyr Gly Gly Ser Gln Pro Gln Gln Gln Pro
 165 170 175
 Pro Pro Pro Gln Pro Pro Gln Gln Gln Gln Gln His Gln Gln His His
 180 185 190
 Met Ala Ile Gly Gly Arg Gly Gly Phe Gly Gln Gln Gly Gly Gly Gly
 195 200 205
 Gly Ser Ser Ser Ser Ser Gly Leu Gly Arg Gln Asp Arg Ala
 210 215 220

<210> 159
 <211> 1055
 <212> DNA
 <213> Oryza sativa

<400> 159
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 ctccaagaa caccactcc tctagtctct ctctcgagag agagaaaatt gatgattctt 120
 gggatgattt tgaggcgtct gatttgctga agaggaggag gaggatgccg gactcggaca 180
 acgactccgg cgggccgagc aactacgcgg gaggggagct gtcgtcgccg cgggagcagg 240

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acaggttcct gccgatcgcg aacgtgagca ggatcatgaa gaaggcgctg ccggcgaacg 300
ccaagatcag caaggacgcc aaggagacgg tgcaggagtg cgtctccgag ttcattctct 360
tcatcaccgg cgaggcctcc gacaagtgcc agcgcgagaa gcgcaagacc atcaacggcg 420
acgacctgct ctggggccatg accaccctcg gcttcgagga ctacgtcgac cccctcaagc 480
actacctcca caagttccgc gagatcgagg gcgagcgcgc cgccgcctcc accaccggcg 540
ccggcaccag cgccgcctcc accacgccgc cgacagcagca gcacaccgcc aatgccgccg 600
gcggctacgc cgggtacgcc gccccgggag ccggcccccg cgccatgatg atgatgatgg 660
ggcagcccat gtacggctcg ccgccaccgc cgccacagca gcagcagcag caacaccacc 720
acatggcaat gggaggaaga ggcggcttcg gtcattcatc cggcggcggc ggcggcgggg 780
cgtcgtcgtc gtcggggcac ggtcggcaaa acagggggcg ttgacatcg tccgagacga 840
gtagcatgca ccatggtaca tatatacagt aatcagcagc tgtttatatt tctatgatta 900
ctagttgact taagcttgca aatttgctaa tctgagctcc tgagtttttt tttttgggtc 960
gcaatttcaa gatggtcaga agctaaattt gtctatttgt tactgataaa ttatttggtc 1020
tctcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1055

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<210> 160

<211> 219

<212> PRT

<213> Oryza sativa

<400> 160

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Met Pro Asp Ser Asp Asn Asp Ser Gly Gly Pro Ser Asn Tyr Ala Gly
  1              5              10              15

Gly Glu Leu Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
      20              25              30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
      35              40              45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
      50              55              60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
      65              70              75              80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
      85              90              95

Phe Glu Asp Tyr Val Asp Pro Leu Lys His Tyr Leu His Lys Phe Arg
      100             105             110

Glu Ile Glu Gly Glu Arg Ala Ala Ala Ser Thr Thr Gly Ala Gly Thr
      115             120             125

Ser Ala Ala Ser Thr Thr Pro Pro Gln Gln Gln His Thr Ala Asn Ala
      130             135             140

Ala Gly Gly Tyr Ala Gly Tyr Ala Ala Pro Gly Ala Gly Pro Gly Gly
      145             150             155             160

Met Met Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Pro Pro
      165             170             175

Pro Gln Gln Gln Gln Gln Gln His His His Met Ala Met Gly Gly Arg
      180             185             190

Gly Gly Phe Gly His His Pro Gly Gly Gly Gly Gly Gly Ser Ser Ser
      195             200             205

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Ser Ser Gly His Gly Arg Gln Asn Arg Gly Ala
 210 215

<210> 161
 <211> 873
 <212> DNA
 <213> Oryza sativa

<400> 161
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 gaggagcggc ggggtgaggg agcaggacag gttcctgccc atcgccaaca tcagccgcat 120
 catgaagaag gccgtcccgg cgaacggcaa gatcgccaag gacgccaagg agaccctgca 180
 ggagtgcgtc tcggagttca tctccttcgt caccagcgag gcgagcgaca aatgtcagaa 240
 ggagaagcgc aagaccatca acggggaaga tctcctcttt gcgatgggta cgcttggctt 300
 tgaggagtac gttgatccgt tgaagatcta ttacacaaag tacagagaga tggagggtga 360
 tagtaagctg tcctcaaagg ctggtgatgg ttcagtaaag aaggatacaa ttggtccgca 420
 cagtggcgct agtagctcaa gtgcgcaagg gatgggttggg gcttacaccc aagggatggg 480
 ttatatgcaa cctcagtatc ataattggga cacctaaaga tgaggacagt gaaaattttc 540
 agtaactggt gtcctctgtg agttattatc catctgttaa ggaagaaccc acattagggc 600
 catatttatt agtagaagac taaagcactt gaagggtggt ggtttagaaa ggggtgtaac 660
 agttggctgt ggcgattgct tcacagatgt aaattgcttc ataagtgggt taatgcttgt 720
 ttttgcctgt atattcagag caattttcac atattggtag ttctgcaatc ttttgcattc 780
 ccatacatgt atcaggtggc acaaattctat tgcaagtacc ctagcattga ataattgctg 840
 ttaacatata aaaaaaaaaa aaaaaaaaaa aaa 873

<210> 162
 <211> 164
 <212> PRT
 <213> Oryza sativa

<400> 162
 Met Ala Asp Ala Gly His Asp Glu Ser Gly Ser Pro Pro Arg Ser Gly
 1 5 10 15
 Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg
 20 25 30
 Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala
 35 40 45
 Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
 50 55 60
 Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn
 65 70 75 80
 Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr
 85 90 95
 Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly
 100 105 110
 Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp
 115 120 125
 Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met
 130 135 140

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Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
 145 150 155 160

Asn Gly Asp Thr

<210> 163
 <211> 799
 <212> DNA
 <213> Glycine max

<400> 163
 gcacgagacg aaagcaacgg tgaagatgaa taatgagtga ggcaatccaa tgggtgagaaa 60
 ggagtccgtg aaagcagaga cttatcgaga aacaacggca cagaagggttc cacgtgggaa 120
 gcagataaag gaatattaag cagagagatc caacggacac tgctagtga ggcagaagaa 180
 gaagattcct ggattgattg tgaagatggc tgagtcggac aacgactcgg gaggggcgca 240
 gaacgcggga aacagtggaa acttgagcga gttgtcgcct cgggaacagg accggtttct 300
 ccccatagcg aacgtgagca ggatcatgaa gaaggccttg ccggcgaacg cgaagatctc 360
 gaaggacgag aaggagacgg tgcaggaatg cgtgtcggag ttcatacagct tcataacggg 420
 tgaggcgtcg gacaagtgcc agaggagaaa gcgcaagacc atcaacggcg acgatcttct 480
 ctggggccatg acaaccctgg gattcgaaga gtacgtggag cctctgaaga tttacctcca 540
 gcgcttccgc gagatggagg gagagaagac cgtggccgcc cgcgactctt ctaaggactc 600
 ggcctccgcc tcctcctatc atcagggaca cgtgtacggc tcccctgcct accatcatca 660
 agtgcctggg ccactttatc ctgcccctgg tagaccaga tgacgtgctc ctctattcgc 720
 cactccctag actttttata ttatattatt taattaaact ctcttctcca ctcaaccttt 780
 gcaaaaaaaaa aaaaaaaaaa 799

<210> 164
 <211> 165
 <212> PRT
 <213> Glycine max

<400> 164
 Met Ala Glu Ser Asp Asn Asp Ser Gly Gly Ala Gln Asn Ala Gly Asn
 1 5 10 15
 Ser Gly Asn Leu Ser Glu Leu Ser Pro Arg Glu Gln Asp Arg Phe Leu
 20 25 30
 Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
 35 40 45
 Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser
 50 55 60
 Glu Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg
 65 70 75 80
 Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
 85 90 95
 Thr Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Ile Tyr Leu Gln
 100 105 110
 Arg Phe Arg Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Ser
 115 120 125

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Ser Lys Asp Ser Ala Ser Ala Ser Ser Tyr His Gln Gly His Val Tyr
 130 135 140

Gly Ser Pro Ala Tyr His His Gln Val Pro Gly Pro Thr Tyr Pro Ala
 145 150 155 160

Pro Gly Arg Pro Arg
 165

<210> 165

<211> 644

<212> DNA

<213> Glycine max

<400> 165

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acgacaacaa caacaatggg ggcattcatca aggaacagga ccggttgctg ccaatagcca 120
atgttggtcg gctcatgaag cggattcttc ctcagaacgc caaatctctg aaggaggcga 180
aggagacgat gcaggaatgt gtgtcggagt tcataagctt cgtgacgagt gaggcttcgg 240
agaagtgcag gaaggagagg aggaagacag tgaatgggtga tgacatttgt tgggccttgg 300
caacactagg ctttgataac tatgctgaac caatgagaag gtacttgcac agatatagag 360
aggttgaggt agatcataat aaggtcaatc ttcaagaaaa agggaaatagt cctgaagaga 420
aagacgatga attattttaa ttgagcaata gaggggttgg gctttgacca attattatgc 480
ttatagtaga caggaactcg ttaatccatt catactcatc actgattact gattagatga 540
attagtaatt ttaagggttt tgtgaggatg agataatata tgtaataatt ttcttgtctt 600
aattggaatt tatcgagctt agaacaaaaa aaaaaaaaaa aaaa 644
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<210> 166

<211> 152

<212> PRT

<213> Glycine max

<400> 166

Ser Phe Trp Gly Ile Ser Lys Ser Met Glu Asp Ile Gly Gly Ser Ser
 1 5 10 15

Ser Asn Asp Asn Asn Asn Asn Gly Gly Ile Ile Lys Glu Gln Asp Arg
 20 25 30

Leu Leu Pro Ile Ala Asn Val Gly Arg Leu Met Lys Arg Ile Leu Pro
 35 40 45

Gln Asn Ala Lys Ile Ser Lys Glu Ala Lys Glu Thr Met Gln Glu Cys
 50 55 60

Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Glu Lys Cys
 65 70 75 80

Arg Lys Glu Arg Arg Lys Thr Val Asn Gly Asp Asp Ile Cys Trp Ala
 85 90 95

Leu Ala Thr Leu Gly Phe Asp Asn Tyr Ala Glu Pro Met Arg Arg Tyr
 100 105 110

Leu His Arg Tyr Arg Glu Val Glu Val Asp His Asn Lys Val Asn Leu
 115 120 125

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Gln Glu Lys Gly Asn Ser Pro Glu Glu Lys Asp Asp Glu Leu Phe Lys
 130 135 140

Leu Ser Asn Arg Gly Val Gly Leu
 145 150

<210> 167
 <211> 879
 <212> DNA
 <213> Glycine max

<400> 167
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 acatcacaaac agggttccgg cgaccatgtc cgatgctccg gcgagtccat gcggcggcgg 180
 cggcggaggc agccacgaga gcggcgagca cagtccccgc tccaatttcc gcgagcagga 240
 ccgcttcctc cccatcgcca acatcagccg catcatgaag aaagcgcttc ctcccaacgg 300
 gaaaatcgcc aaggacgcca aggaaaccgt gcaggaatgc gtctccgagt tcatcagctt 360
 cgtcaccagc gaagcgagcg ataagtgtca gagagagaag aggaagacca tcaacggcga 420
 cgatttgctt tgggctatga ccactttagg ttctgaggag tatattgatc cgctcaaggt 480
 ttacctcgcc gcttacagag agattgaggg tgattcaaag gggttcggcca aggggtggaga 540
 tgcattctgct aagagagatg tttatcagag tcctaattggc cagggttgctc atcaagggtc 600
 tttctcacaa ggtgttaatt atacgaattc ttagccccag gctcaacata tgatagttcc 660
 gatgcaaggc caagagtaga tattgatcct ctctttcagt gtttgacatg tgtgatctaa 720
 atgccagtgg aacttttatg tcaatatgtg cccttggtat aatgaatgca ttttatgtta 780
 tgtaaacact acatgcgggg atgttggttc ttgtgaccag atattattta ttaagactta 840
 catttatctt tggaaaaaaa aaaaaaaaaa aaaaaaaaaa 879

<210> 168
 <211> 162
 <212> PRT
 <213> Glycine max

<400> 168
 Met Ser Asp Ala Pro Ala Ser Pro Cys Gly Gly Gly Gly Gly Gly Ser
 1 5 10 15
 His Glu Ser Gly Glu His Ser Pro Arg Ser Asn Phe Arg Glu Gln Asp
 20 25 30
 Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu
 35 40 45
 Pro Pro Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu
 50 55 60
 Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys
 65 70 75 80
 Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp
 85 90 95
 Ala Met Thr Thr Leu Gly Phe Glu Glu Tyr Ile Asp Pro Leu Lys Val
 100 105 110
 Tyr Leu Ala Ala Tyr Arg Glu Ile Glu Gly Asp Ser Lys Gly Ser Ala
 115 120 125

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Lys Gly Gly Asp Ala Ser Ala Lys Arg Asp Val Tyr Gln Ser Pro Asn
 130 135 140

Gly Gln Val Ala His Gln Gly Ser Phe Ser Gln Gly Val Asn Tyr Thr
 145 150 155 160

Asn Ser

<210> 169

<211> 771

<212> DNA

<213> Glycine max

<400> 169

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acggggaacg cgagcgggag caacgagttg tccggttgca gggagcaaga caggttcctc 120
ccaatagcaa acgtgagcag gatcatgaag aaggcggttg cggcgaacgc gaagatatcg 180
aaggaggcga aggagacggt gcaggagtgc gtgtcggagt tcatcagctt cataacagga 240
gaggcttccg ataagtgccga gaaggagaag aggaagacga tcaacggcga cgatcttctc 300
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gagggttatg gccatggcca tggatcatga actcctatga tgacgatgat gatggggcat 480
cagccccagc accagcacca gcaccagcac cagcaccagc accagggaca cgtgtatgga 540
tctggatcag catcttctgc aagaactaga tagcatgtgt catctgttta agcttaattg 600
atattattat gaggatgata tgatataaga tttatatctg tatatgtttg gtttttagaaa 660
tacaccagct ccagcttgta attgcttgaa acttccttgt tgagagaata tagacattat 720
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<210> 170

<211> 181

<212> PRT

<213> Glycine max

<400> 170

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  1 5 10 15

Gly Ser Asn Glu Leu Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro
  20 25 30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
  35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
  50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu
  65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
  85 90 95

Leu Gly Phe Glu Asp Tyr Val Asp Pro Leu Lys Ile Tyr Leu His Lys
  100 105 110

Tyr Arg Glu Met Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
  115 120 125
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Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
 20 25 30
 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
 35 40 45
 Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
 50 55 60
 Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
 65 70 75 80
 Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
 85 90 95
 Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
 100 105 110
 Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr
 115 120 125
 Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val
 130 135 140
 Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly Gln Gln Gly Ala Tyr
 145 150 155 160
 Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile
 165 170 175

Ser Asn

<210> 198
 <211> 228
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222>
 <223> gi 6729485

<400> 198
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 Gly Gly Asp Gln Ser Pro Arg Ser Leu Asn Val Arg Glu Gln Asp Arg
 20 25 30
 Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu Pro
 35 40 45
 Leu Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Met Gln Glu Cys
 50 55 60
 Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys Cys
 65 70 75 80

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Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala
 85 90 95
 Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Asp Pro Leu Lys Val Tyr
 100 105 110
 Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Gly Lys
 115 120 125
 Gly Gly Glu Ser Ser Ala Lys Arg Asp Gly Gln Pro Ser Gln Val Ser
 130 135 140
 Gln Phe Ser Gln Val Pro Gln Gln Gly Ser Phe Ser Gln Gly Pro Tyr
 145 150 155 160
 Gly Asn Ser Gln Ser Leu Arg Phe Gly Asn Ser Ile Glu His Leu Glu
 165 170 175
 Val Leu Met Ser Ser Thr Arg Thr Leu Phe Ile Thr Ile Phe Arg Asp
 180 185 190
 Ser Thr Met Pro Val Val Ser Glu Asn Leu Ser Asp Pro Leu Ser Ile
 195 200 205
 Asp Met Asp Cys Glu Ala Ile Tyr His His Phe Ile Gly Leu Leu Ile
 210 215 220
 Leu Ser Cys Lys
 225

<210> 199

<211> 161

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222>

<223> gi 2244810

<400> 199

Met Ala Asp Ser Asp Asn Asp Ser Gly Gly His Lys Asp Gly Gly Asn
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 Ala Ser Thr Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser
 20 25 30
 Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp
 35 40 45
 Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
 50 55 60
 Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile
 65 70 75 80
 Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp
 85 90 95

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Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Val Glu
 100 105 110
 Gly Glu Lys Thr Thr Thr Ala Gly Arg Gln Gly Asp Lys Glu Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Ala Gly Ser Gly Ser Gly Gly Ala Pro Met Tyr
 130 135 140
 Gly Gly Gly Met Val Thr Thr Met Gly His Gln Phe Ser His His Phe
 145 150 155 160

Ser

<210> 200

<211> 187

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222>

<223> gi 2398529

<400> 200

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 20 25 30
 Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
 35 40 45
 Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys Val Ser Glu Phe Ile
 50 55 60
 Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg
 65 70 75 80
 Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
 85 90 95
 Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Arg Phe Arg
 100 105 110
 Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln Thr Gly Gly
 115 120 125
 Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly Gly Gly Phe
 130 135 140
 Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His Gln Phe Leu
 145 150 155 160
 His Gln Gln Asn His Met Tyr Gly Ala Thr Gly Gly Gly Ser Asp Ser
 165 170 175

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Gly Gly Gly Ala Ala Ser Gly Arg Thr Arg Thr
 180 185

<210> 201
 <211> 160
 <212> PRT
 <213> Arabidopsis thaliana

<220>
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 <222>
 <223> gi 3738293

<400> 201
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 20 25 30
 Gly Leu Val Val Val Val Glu Asp Gln Gln Gln Glu Glu Ser Met Met
 35 40 45
 Val Lys Glu Gln Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Ile
 50 55 60
 Met Lys Asn Ile Leu Pro Ala Asn Ala Lys Val Ser Lys Glu Ala Lys
 65 70 75 80
 Glu Thr Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly
 85 90 95
 Glu Ala Ser Asp Lys Cys His Lys Glu Lys Arg Lys Thr Val Asn Gly
 100 105 110
 Asp Asp Ile Cys Trp Ala Met Ala Asn Leu Gly Phe Asp Asp Tyr Ala
 115 120 125
 Ala Gln Leu Lys Lys Tyr Leu His Arg Tyr Arg Val Leu Glu Gly Glu
 130 135 140
 Lys Pro Asn His His Gly Lys Gly Gly Pro Lys Ser Ser Pro Asp Asn
 145 150 155 160

<210> 202
 <211> 308
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222>
 <223> gi 4587559

<400> 202
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 1 5 10 15

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Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr
 20 25 30
 Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser
 35 40 45
 Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu
 50 55 60
 Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg
 65 70 75 80
 Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn
 85 90 95
 Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser
 100 105 110
 Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile
 115 120 125
 Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu
 130 135 140
 Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met
 145 150 155 160
 Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu
 165 170 175
 Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg
 180 185 190
 Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys
 195 200 205
 Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys
 210 215 220
 Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln
 225 230 235 240
 Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn
 245 250 255
 Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser
 260 265 270
 Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro
 275 280 285
 Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu
 290 295 300
 Met Ser Gly Thr
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<210> 203

<211> 25

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<212> DNA

<213> synthetic construct

<400> 203

acagtacagt acagtacagt acagt

25

<210> 204

<211> 25

<212> DNA

<213> synthetic construct

<400> 204

actgtactgt actgtacgtg actgt

25

<210> 205

<211> 765

<212> DNA

<213> Oryza sativa

<400> 205

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aacgtgatcc	gcatcatgcg	ccgcgtgctc	ccggcgcacg	ccaagatctc	ggacgacgcc	180
aaggagacga	tccaggagtg	cgtgtcggag	tacatcagct	tcatcaccgg	ggaggccaac	240
gagcggtgcc	agcgcgagca	gcgcaagacc	atcaccgccg	aggacgtgct	ctggggccatg	300
agccgcctcg	gcttcgacga	ctacgtcgag	cccctcggcg	tctacctcca	ccgctaccgc	360
gagttcgagg	gggagtcccg	cggcgtcggc	gtcggcgctcg	gcgccgcgcg	cggcgaccac	420
caccatgggtc	acgtcgggtg	gatgctcaag	tcccgcgcgc	agggctccat	ggtgacgcac	480
cacgacatgc	agatgcacgc	ggccatgtac	ggtggcgggc	cggtgccgcc	gccgccgcat	540
cctcctccgc	accaccacgc	gttccaccag	ctcatgccgc	cgcaccacgg	ccagtacgcg	600
ccgccgtacg	acatgtacgg	cggcgagcac	gggatggcgg	cgtactacgg	cgggatgtac	660
gcgcccggca	gcggcggcga	cgggagcggc	agcagcggca	gcggtggcgc	cggcacgccg	720
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<210> 206

<211> 254

<212> PRT

<213> Oryza sativa

<400> 206

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			20				25						30		
Gln	Asp	Arg	Leu	Met	Pro	Ile	Ala	Asn	Val	Ile	Arg	Ile	Met	Arg	Arg
		35					40					45			
Val	Leu	Pro	Ala	His	Ala	Lys	Ile	Ser	Asp	Asp	Ala	Lys	Glu	Thr	Ile
	50					55					60				
Gln	Glu	Cys	Val	Ser	Glu	Tyr	Ile	Ser	Phe	Ile	Thr	Gly	Glu	Ala	Asn
65					70					75					80

Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val
 85 90 95
 Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val Glu Pro Leu
 100 105 110
 Gly Val Tyr Leu His Arg Tyr Arg Glu Phe Glu Gly Glu Ser Arg Gly
 115 120 125
 Val Gly Val Gly Val Gly Ala Ala Arg Gly Asp His His His Gly His
 130 135 140
 Val Gly Gly Met Leu Lys Ser Arg Ala Gln Gly Ser Met Val Thr His
 145 150 155 160
 His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Gly Ala Val Pro
 165 170 175
 Pro Pro Pro His Pro Pro Pro His His His Ala Phe His Gln Leu Met
 180 185 190
 Pro Pro His His Gly Gln Tyr Ala Pro Pro Tyr Asp Met Tyr Gly Gly
 195 200 205
 Glu His Gly Met Ala Ala Tyr Tyr Gly Gly Met Tyr Ala Pro Gly Ser
 210 215 220
 Gly Gly Asp Gly Ser Gly Ser Ser Gly Ser Gly Gly Ala Gly Thr Pro
 225 230 235 240
 Gln Thr Val Asn Phe Glu His Gln His Pro Phe Gly Tyr Lys
 245 250

<210> 207

<211> 1499

<212> DNA

<213> *Catalpa speciosa*

<400> 207

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 atcagatttc gccttaacag gacacattgg ttgatttctt tggagaaatt aggggagcat 180
 gcaatccaag tcccagagcg gcaaccaagg agaatccaac ctttataatg ttcctaactc 240
 caaagtaaat ccggattctt ggtggaataa tactggatat aattcctttt cctcaacaat 300
 gatgggtgga aatgcatcag attcatcatc cctagaacaa tctgtggatg gacagtcgca 360
 gtctaaaggt ggtataaatg aggaagatga tgatactacc aaacgatcac caagtagtac 420
 acctctgctg ccagatagaa actataggca ggagggtccg agtctccagc aagctccacc 480
 taccatacat ccaagaaaca atgggatcgt taatcaggcc ccacagcttg agcttggtgg 540
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 ttatggccag ccattggttc ctctcattt atatgatatg catcatgcaa ggatggcact 660
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 gcggaggcgg cagtctcgtg ctaaagctga gcttgaaaag aagttaataa aagttcggaa 780
 gccttatctc catgagtctc gacaccaaca tgccttaagg agggcaaggg ggactggagg 840
 acgatttgca aagaagtccg atgcagatac ttccaagggg actggaccgg gctcatccat 900
 cccatcgcag cttattagct catcacgagg ttctgagcca gtgcctgagg ctcagaattt 960
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 gagtcgcatg catgtgtttg ctacttacat ttgttgcact ttcgaattgt gaacccaaaa 1440
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<210> 208

<211> 307

<212> PRT

<213> *Catalpa speciosa*

<400> 208

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Asn Val Pro Asn Ser Lys Val Asn Pro Asp Ser Trp Trp Asn Asn Thr
 20 25 30

Gly Tyr Asn Ser Phe Ser Ser Thr Met Met Gly Gly Asn Ala Ser Asp
 35 40 45

Ser Ser Ser Leu Glu Gln Ser Val Asp Gly Gln Ser Gln Ser Lys Gly
 50 55 60

Gly Ile Asn Glu Glu Asp Asp Asp Thr Thr Lys Arg Ser Pro Ser Ser
 65 70 75 80

Thr Pro Leu Leu Pro Asp Arg Asn Tyr Arg Gln Glu Gly Pro Ser Leu
 85 90 95

Gln Gln Ala Pro Pro Thr Ile His Pro Arg Asn Asn Gly Ile Val Asn
 100 105 110

Gln Ala Pro Gln Leu Glu Leu Gly Gly His Ser Val Ala Cys Gly Ser
 115 120 125

Asn Pro Tyr Asp Pro Tyr Tyr Gly Gly Met Met Ala Ala Tyr Gly Gln
 130 135 140

Pro Leu Val Pro Pro His Leu Tyr Asp Met His His Ala Arg Met Ala
 145 150 155 160

Leu Pro Leu Glu Met Thr Gln Glu Pro Val Tyr Val Asn Ala Lys Gln
 165 170 175

Tyr His Gly Ile Leu Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Leu
 180 185 190

Glu Lys Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His Glu Ser Arg
 195 200 205

His Gln His Ala Leu Arg Arg Ala Arg Gly Thr Gly Gly Arg Phe Ala
 210 215 220

Lys Lys Ser Asp Ala Asp Thr Ser Lys Gly Thr Gly Pro Gly Ser Ser
 225 230 235 240

Ile Pro Ser Gln Leu Ile Ser Ser Ser Arg Gly Ser Glu Pro Val Pro
 245 250 255

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Glu Ala Gln Asn Leu Tyr Asn Ala Asp Asp Gly Asn Phe Arg Arg Gln
 260 265 270

Thr Asn Leu Gln Glu Pro Ala Leu Gln Leu Gly Lys Thr Gly Glu Gly
 275 280 285

Pro Thr Ser Ser His Lys Trp Gly Asn Thr Thr Ser Asn His Ala Leu
 290 295 300

Ala Met Gln
 305

<210> 209
 <211> 1626
 <212> DNA
 <213> Zea mays

<400> 209
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 gacccctccc ctccctactt cccatgctga tctcggcgcg cttctcttcc tcctccccc 120
 gagccgggca ctgatttccc ttggctgctg ctgctggatt ctttggtgtt ccatcaggcc 180
 aaggatcccg caaagagctc cggagccaag cctgctgcag ccgtcgcgtc gggtgaggca 240
 ggcttcagct tcagtctcct actcgacgag gcaagcggat cggagcgggc ctccgctccg 300
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 gccaggctgc ctcccatggg ggagcaggcc cgctgccatg gtgggcgggg cccagctgc 420
 tgttcggcga gccggcgccc ccgtcaccgg aggagacgcg ccgggacgcc cagttccagg 480
 tcgtgccggg ggttcagggc acgccggatc cagcgccgcc caagacaggg acacctgagg 540
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 caaagaactc taccactatt gctcttcagt caccgttccc agaatacaat ggccgtttcg 660
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 gccgtcgccg tgctcgcgcc aaggcggaga gcgagaacag gctcgccaaa ggcagaaagc 900
 cctatctcca cgagtcgcgc cacctccacg cgatgcgtcg ggtaagaggc accggcgggc 960
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 acataatagt gtacccaaac cactgcttcg gactatcatt gtctgtctcg gtatggattc 1560
 tctgttgtca cagtgtctga ataattgagg cgtcagactt caaagttaaa aaaaaaaaaa 1620
 aaaaaa 1626

<210> 210
 <211> 322
 <212> PRT
 <213> Zea mays

<400> 210
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Gly Ala Gly Ser Gln Ala Ala Ser His Gly Gly Ala Gly Pro Leu Pro
 20 25 30

I

Trp Trp Ala Gly Pro Gln Leu Leu Phe Gly Glu Pro Ala Pro Pro Ser
 35 40 45
 Pro Glu Glu Thr Arg Arg Asp Ala Gln Phe Gln Val Val Pro Gly Val
 50 55 60
 Gln Gly Thr Pro Asp Pro Ala Pro Pro Lys Thr Gly Thr Pro Glu Val
 65 70 75 80
 Leu Lys Phe Ser Val Phe Gln Gly Asn Leu Glu Ser Gly Gly Lys Gly
 85 90 95
 Glu Lys Thr Pro Lys Asn Ser Thr Thr Ile Ala Leu Gln Ser Pro Phe
 100 105 110
 Pro Glu Tyr Asn Gly Arg Phe Glu Ile Gly Leu Gly Gln Ser Met Leu
 115 120 125
 Ala Pro Ser Asn Tyr Pro Cys Ala Asp Gln Cys Tyr Gly Met Leu Ala
 130 135 140
 Ala Tyr Gly Met Arg Ser Met Ser Gly Gly Arg Met Leu Leu Pro Leu
 145 150 155 160
 Asn Ala Thr Ala Asp Ala Pro Ile Tyr Val Asn Pro Lys Gln Tyr Glu
 165 170 175
 Gly Ile Leu Arg Arg Arg Arg Ala Arg Ala Lys Ala Glu Ser Glu Asn
 180 185 190
 Arg Leu Ala Lys Gly Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu
 195 200 205
 His Ala Met Arg Arg Val Arg Gly Thr Gly Gly Arg Phe Val Asn Thr
 210 215 220
 Lys Lys Glu Gly Arg Gly Thr Gly Val Ala Ser Asn Gly Gly Ser Lys
 225 230 235 240
 Thr Ala Ala Ala Ala Pro Ser Arg Leu Ala Met Pro Pro Ser Phe Gln
 245 250 255
 Ser Ser Val Ala Ser Leu Ser Gly Ser Asp Val Ser Asn Met Tyr Ser
 260 265 270
 Gly Gly Leu Glu Gln His Leu Arg Ala Pro His Phe Phe Thr Pro Leu
 275 280 285
 Pro Pro Ile Met Glu Asp Gly Asp His Gly Gly Pro Pro Thr Arg Ile
 290 295 300
 Ser Ser Ser Phe Lys Trp Ala Ala Ser Asp Gly Cys Cys Glu Leu Leu
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 Lys Ala

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<210> 211
 <211> 1569
 <212> DNA
 <213> Oryza sativa

<400> 211
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 cttctaataa tgataatgct gttgcaagaa atggagaatc atcctgtcca atgcatggcc 180
 aagaccaact atgattttct tgccaggaat aactatccaa tgaaacagtt agttcagagg 240
 aactctgatg gtgactcgtc accaacaag tctggggagt ctcaccaaga agcatctgca 300
 gtaagtgaca gcagtctcaa cggacaacac acctcaccac aatcagtgtt tgtcccctca 360
 gatattaaca acaatgatag ttgtggggag cgggaccatg gcactaagtc ggtattgtct 420
 ttggggaaca cagaagctgc ctttcctcct tcaaagttcg attacaacca gccttttgca 480
 tgtgtttctt atccatatgg tactgatcca tattatgggt gagtattaac aggatacact 540
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 cagttttatat gcaatgcaac ctctgtcaga taaactctta tagtttggtt tattgtaagc 1260
 tatgactgaa cgaactgtcg agcagatggc taatttgtat gttgtgggta cagaaatcct 1320
 gaagcttttg atgtacctaa ttgccttttg cttatactct tgggtgtatac ccattacca 1380
 gttgccttaa aaacctcca attatgtaat cagtcatggt tttatagaac cttgccacat 1440
 gtaatcaatc acctgttttt gtaaattgat ctataaacgc taaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1560
 aaaaaaaaaa 1569

<210> 212
 <211> 317
 <212> PRT
 <213> Oryza sativa

<400> 212
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 Ala Lys Thr Asn Tyr Asp Phe Leu Ala Arg Asn Asn Tyr Pro Met Lys
 20 25 30
 Gln Leu Val Gln Arg Asn Ser Asp Gly Asp Ser Ser Pro Thr Lys Ser
 35 40 45
 Gly Glu Ser His Gln Glu Ala Ser Ala Val Ser Asp Ser Ser Leu Asn
 50 55 60
 Gly Gln His Thr Ser Pro Gln Ser Val Phe Val Pro Ser Asp Ile Asn
 65 70 75 80
 Asn Asn Asp Ser Cys Gly Glu Arg Asp His Gly Thr Lys Ser Val Leu
 85 90 95

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Ser Leu Gly Asn Thr Glu Ala Ala Phe Pro Pro Ser Lys Phe Asp Tyr
 100 105 110
 Asn Gln Pro Phe Ala Cys Val Ser Tyr Pro Tyr Gly Thr Asp Pro Tyr
 115 120 125
 Tyr Gly Gly Val Leu Thr Gly Tyr Thr Ser His Ala Phe Val His Pro
 130 135 140
 Gln Ile Thr Gly Ala Ala Asn Ser Arg Met Pro Leu Pro Val Asp Pro
 145 150 155 160
 Ser Val Glu Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr Asn Ala Ile
 165 170 175
 Leu Arg Arg Arg Gln Thr Arg Ala Lys Leu Glu Ala Gln Asn Lys Ala
 180 185 190
 Val Lys Gly Arg Lys Pro Tyr Leu His Glu Ser Arg His His His Ala
 195 200 205
 Met Lys Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Thr Lys Lys Glu
 210 215 220
 Leu Leu Glu Gln Gln Gln Gln Gln Gln Gln Lys Pro Pro Pro Ala
 225 230 235 240
 Ser Ala Gln Ser Pro Thr Gly Arg Ala Arg Thr Ser Gly Gly Ala Val
 245 250 255
 Val Leu Gly Lys Asn Leu Cys Pro Glu Asn Ser Thr Ser Cys Ser Pro
 260 265 270
 Ser Thr Pro Thr Gly Ser Glu Ile Ser Ser Ile Ser Phe Gly Gly Gly
 275 280 285
 Met Leu Ala His Gln Glu His Ile Ser Phe Ala Ser Ala Asp Arg His
 290 295 300
 Pro Thr Met Asn Gln Asn His Arg Val Pro Val Met Arg
 305 310 315

<210> 213

<211> 1375

<212> DNA

<213> Glycine max

<400> 213

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 aacctgacac tgatgattgg cgtgtagagc gtggggagca gattcagttt cagtcttcca 180
 tttactctca tcatcagcct tgggtggcgcg gagtggggga aaatgcctcc aaatcatctt 240
 cagatgatca gttaaattgg tcaatcgtga atggtatcac gcggtctgag accaatgata 300
 agtcaggcgg aggtgttgcc aaagaatacc aaaacatcaa acatgccatg ttgtcaaccc 360
 catttaccat ggagaaacat cttgctccaa atccccagat ggaacttggt ggtcattcag 420
 ttgttttaac atctccttat tcagatgcac agtatggtca aatcttgact acttacgggc 480
 aacaagttat gataaatcct cagttgtatg gaatgcatca tgctagaatg cttttgccac 540
 ttgaaatgga agaggagcct gtttatgtca atgcgaagca gtatcatggt attttgaggc 600
 gaagacagtc acgtgctaag gctgagattg aaaagaaagt aatcaaaaac aggaagccat 660

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ttctcaacac aaagaagctt gaaaataaca attctaattc cacttcagac aaaggcaaca 780
atactcgtgc aaacgcctca acaaactcgc ctaacactca acttttggtc accaacaatt 840
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gtgtacacta tggccttggt tggctctctcc cttgcttttg tttctctcta caagtccata 1200
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ttatatatac tgtgttaagg ttcataaaac tgtagactga tttgtgtgac atgctccaca 1320
gaaccttaaa ttttcctcta ttttgccta aaaaaaaaaa aaaaaaaaaa aaaaa 1375

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<210> 214

<211> 303

<212> PRT

<213> Glycine max

<400> 214

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Met Pro Gly Lys Pro Asp Thr Asp Asp Trp Arg Val Glu Arg Gly Glu
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Gln Ile Gln Phe Gln Ser Ser Ile Tyr Ser His His Gln Pro Trp Trp
      20              25              30

Arg Gly Val Gly Glu Asn Ala Ser Lys Ser Ser Ser Asp Asp Gln Leu
      35              40              45

Asn Gly Ser Ile Val Asn Gly Ile Thr Arg Ser Glu Thr Asn Asp Lys
      50              55              60

Ser Gly Gly Gly Val Ala Lys Glu Tyr Gln Asn Ile Lys His Ala Met
      65              70              75              80

Leu Ser Thr Pro Phe Thr Met Glu Lys His Leu Ala Pro Asn Pro Gln
      85              90              95

Met Glu Leu Val Gly His Ser Val Val Leu Thr Ser Pro Tyr Ser Asp
      100             105             110

Ala Gln Tyr Gly Gln Ile Leu Thr Thr Tyr Gly Gln Gln Val Met Ile
      115             120             125

Asn Pro Gln Leu Tyr Gly Met His His Ala Arg Met Pro Leu Pro Leu
      130             135             140

Glu Met Glu Glu Glu Pro Val Tyr Val Asn Ala Lys Gln Tyr His Gly
      145             150             155             160

Ile Leu Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Ile Glu Lys Lys
      165             170             175

Val Ile Lys Asn Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His
      180             185             190

Ala Met Arg Arg Ala Arg Gly Asn Gly Gly Arg Phe Leu Asn Thr Lys
      195             200             205

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Lys Leu Glu Asn Asn Asn Ser Asn Ser Thr Ser Asp Lys Gly Asn Asn
 210 215 220
 Thr Arg Ala Asn Ala Ser Thr Asn Ser Pro Asn Thr Gln Leu Leu Phe
 225 230 235 240
 Thr Asn Asn Leu Asn Leu Gly Ser Ser Asn Val Ser Gln Ala Thr Val
 245 250 255
 Gln His Met His Thr Glu Gln Ser Phe Thr Ile Gly Tyr His Asn Gly
 260 265 270
 Asn Gly Leu Thr Ala Leu Tyr Arg Ser Gln Ala Asn Gly Lys Lys Glu
 275 280 285
 Gly Asn Cys Phe Gly Lys Glu Arg Asp Pro Asn Gly Asp Phe Lys
 290 295 300

<210> 215
 <211> 1192
 <212> DNA
 <213> Triticum aestivum

<400> 215
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 aagggacggc ggaggcaagc tagcttcccg ggggcggacg caccgagaga gggcggcggg 120
 agggaggagg cgcgtgggag ccatgcttct cccctcttct tcgtcttctt cctacgatcc 180
 caaaggtgac tccttttgga aatcgggtga cgatcatatg aggtcaactt tgacttttgg 240
 tgataagcat tctgtatttg caagtcaaaa cactgactat ggccacccaa tggcttgcat 300
 ttcataccca ttcaatgatt ctgggttctgt ttgggcggcc tatgggtcac gggctatgtt 360
 ccagcccctc atggcggaag gaggggcatc tgcgaccgca agagttccat tgcctgtcga 420
 attagcagcg gatgagccca tatttgtcaa tcccaaacaa tataatggga ttctccggcg 480
 aaggcagctg cgcgccaagt tagaggccca gaataaactc acaaaaaaca gaaagcccta 540
 cctccacgag tctcgccatc ttcacgcgat gaagcgggca agaggttccg ggggacgttt 600
 cctcaatttc aaacagctga agcagcagca gcagcagtct ggcagtgcac gcacgaaggc 660
 cattgcggat ggcgcgaatt ccttgggttc aaccatctta cggctaggca gcggcgcagc 720
 cggagaccga agcaactcgg cgtccaaggc gatgtcctcc caagagaaca gcaagagagt 780
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 tctggcgtgt tagggtttca gagatagtgt atctcatagt actactgttg tactgctttg 1020
 caccacata gttctctgct tgatgttcgg catgcaaagt ttggtgtact ggtgcgttgg 1080
 gacaaaagtt tgatgtgttt acatgacaat tggtcgcgga actcatcttg tgttctgctc 1140
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<210> 216
 <211> 254
 <212> PRT
 <213> Triticum aestivum

<400> 216

Met Leu Leu Pro Ser Ser Ser Ser Ser Ser Tyr Asp Pro Lys Gly Asp
 1 5 10 15
 Ser Phe Gly Lys Ser Val Asp Asp His Met Arg Ser Thr Leu Thr Phe
 20 25 30

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

<210> 217

<211> 298

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222>

<223> gi 9293997

<400> 217

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His Gly Thr Val Ser Ser Ser Ile Asn Ser Leu Asn Pro Trp His Arg
 20 25 30

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Ala Ala Ala Ala Cys Asn Ala Asn Ser Ser Val Glu Ala Gly Asp Lys
 35 40 45
 Ser Ser Lys Ser Ile Ala Leu Ala Leu Glu Ser Asn Gly Ser Lys Ser
 50 55 60
 Pro Ser Asn Arg Asp Asn Thr Val Asn Lys Glu Ser Gln Val Thr Thr
 65 70 75 80
 Ser Pro Gln Ser Ala Gly Asp Tyr Ser Asp Lys Asn Gln Glu Ser Leu
 85 90 95
 His His Gly Ile Thr Gln Pro Pro Pro His Pro Gln Leu Val Gly His
 100 105 110
 Thr Val Gly Trp Ala Ser Ser Asn Pro Tyr Gln Asp Pro Tyr Tyr Ala
 115 120 125
 Gly Val Met Gly Ala Tyr Gly His His Pro Leu Gly Phe Val Pro Tyr
 130 135 140
 Gly Gly Met Pro His Ser Arg Met Pro Leu Pro Pro Glu Met Ala Gln
 145 150 155 160
 Glu Pro Val Phe Val Asn Ala Lys Gln Tyr Gln Ala Ile Leu Arg Arg
 165 170 175
 Arg Gln Ala Arg Ala Lys Ala Glu Leu Glu Lys Lys Leu Ile Lys Ser
 180 185 190
 Arg Lys Pro Tyr Leu His Glu Ser Arg His Gln His Ala Met Arg Arg
 195 200 205
 Pro Arg Gly Thr Gly Gly Arg Phe Ala Lys Lys Thr Asn Thr Glu Ala
 210 215 220
 Ser Lys Arg Lys Ala Glu Glu Lys Ser Asn Gly His Val Thr Gln Ser
 225 230 235 240
 Pro Ser Ser Ser Asn Ser Asp Gln Gly Glu Ala Trp Asn Gly Asp Tyr
 245 250 255
 Arg Thr Pro Gln Gly Asp Glu Met Gln Ser Ser Ala Tyr Lys Arg Arg
 260 265 270
 Glu Glu Gly Glu Cys Ser Gly Gln Gln Trp Asn Ser Leu Ser Ser Asn
 275 280 285
 His Pro Ser Gln Ala Arg Leu Ala Ile Lys
 290 295

<210> 218

<211> 238

<212> PRT

<213> Oryza sativa

WO 03/001902

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<220>

<221> misc_feature

<222>

<223> gi 7489565

<400> 218

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Met Leu Pro Pro His Leu Thr Glu Asn Gly Thr Val Met Ile Gln Phe
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          20          25          30

Gly Ser Pro Arg Glu Val Ser Gly Met Ser Glu Gly Ser Leu Asn Glu
          35          40          45

Gln Asn Asp Gln Ser Gly Asn Leu Asp Gly Tyr Thr Lys Ser Asp Glu
          50          55          60

Gly Lys Met Met Ser Ala Leu Ser Leu Gly Lys Ser Glu Thr Val Tyr
  65          70          75          80

Ala His Ser Glu Pro Asp Arg Ser Gln Pro Phe Gly Ile Ser Tyr Pro
          85          90          95

Tyr Ala Asp Ser Phe Tyr Gly Gly Ala Val Ala Thr Tyr Gly Thr His
          100          105          110

Ala Ile Met His Pro Gln Ile Val Gly Val Met Ser Ser Ser Arg Val
          115          120          125

Pro Leu Pro Ile Glu Pro Ala Thr Glu Glu Pro Ile Tyr Val Asn Ala
  130          135          140

Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Leu Arg Ala Lys Leu
  145          150          155          160

Glu Ala Glu Asn Lys Leu Val Lys Asn Arg Lys Pro Tyr Leu His Glu
          165          170          175

Ser Arg His Gln His Ala Met Lys Arg Ala Arg Gly Thr Gly Gly Arg
          180          185          190

Phe Leu Asn Thr Lys Gln Gln Pro Glu Ala Ser Asp Gly Gly Thr Pro
          195          200          205

Arg Leu Val Ser Ala Asn Gly Val Val Phe Ser Lys His Glu His Ser
  210          215          220

Leu Ser Ser Ser Asp Leu His His Arg Ala Lys Glu Gly Ala
  225          230          235

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<210> 219

<211> 215

<212> PRT

<213> Vitis riparia

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<220>

<221> misc_feature

<222>

<223> gi 7141243

<400> 219

Met Met Pro Met Thr Met Ala Glu Tyr His Leu Ala Pro Pro Ser Gln
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 20 25 30

Asn Val Ala Arg Met Ala Leu Pro Ile Glu Met Ala Glu Glu Pro Val
 35 40 45

Tyr Val Asn Ala Lys Gln Tyr His Gly Ile Leu Arg Arg Arg Gln Ser
 50 55 60

Arg Ala Lys Ala Glu Leu Glu Lys Lys Leu Ile Lys Val Arg Lys Pro
 65 70 75 80

Tyr Leu His Glu Ser Arg His Gln His Ala Met Arg Arg Ala Arg Gly
 85 90 95

Cys Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Asp Ser Asn Ala Ser
 100 105 110

Tyr Asp Met Pro Asp Lys Gly Ser Asp Pro Asp Val Asn Leu Ser Thr
 115 120 125

Arg Pro Ile Ser Ser Ser Val Ser Glu Ser Leu Pro Phe Asn Ser Ser
 130 135 140

Arg Asn Glu Asp Ser Pro Thr Ser His Leu Asp Ala Arg Gly Pro Ser
 145 150 155 160

Val Gln Glu Leu His Asn Arg Gln Thr Ser Ser Met Glu Met Ala Thr
 165 170 175

Ser Leu Leu Ser Thr Gln Pro Gly Ile Ser Val Gly Arg Thr Tyr His
 180 185 190

Ser Leu Lys Met Met Ile Gly Val Glu Arg Arg Arg Pro Arg Lys Ala
 195 200 205

Ala Ser Ile Arg Glu Phe Trp
 210 215

<210> 220

<211> 1329

<212> DNA

<213> Glycine max

<400> 220

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 ctattcttct cactaccga ctgctcccat ggtggcttct ggcacgctg ctgtagctgt 240
 tccttcccca actcaggctc cagctgcctt ctctagttct gctcaccagc ttgcatacca 300

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tcttgctcgg ataaaaaaga taatgaaagc tgatgaagat gtccggatga tttctgcaga 480
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<210> 221

<211> 268

<212> PRT

<213> Glycine max

<400> 221

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Met Asp Lys Ser Glu Gln Thr Gln Gln Gln His Gln His Gly Met Gly
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Val Ala Thr Gly Ala Ser Gln Met Ala Tyr Ser Ser His Tyr Pro Thr
                20                      25                      30

Ala Pro Met Val Ala Ser Gly Thr Pro Ala Val Ala Val Pro Ser Pro
                35                      40                      45

Thr Gln Ala Pro Ala Ala Phe Ser Ser Ser Ala His Gln Leu Ala Tyr
  50                      55                      60

Gln Gln Ala Gln His Phe His His Gln Gln Gln Gln His Gln Gln Gln
  65                      70                      75                      80

Gln Leu Gln Met Phe Trp Ser Asn Gln Met Gln Glu Ile Glu Gln Thr
                85                      90                      95

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

Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val
                115                      120                      125

Ile Phe Ala Lys Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg
                130                      135                      140

Ser Trp Ile His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn
  145                      150                      155                      160

Asp Ile Ala Ala Ala Ile Ser Arg Asn Asp Val Phe Asp Phe Leu Val
                165                      170                      175

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Asp Ile Ile Pro Arg Asp Glu Leu Lys Glu Glu Gly Leu Gly Ile Thr
 180 185 190
 Lys Ala Thr Ile Pro Leu Val Asn Ser Pro Ala Asp Met Pro Tyr Tyr
 195 200 205
 Tyr Val Pro Pro Gln His Pro Val Val Gly Pro Pro Gly Met Ile Met
 210 215 220
 Gly Lys Pro Val Gly Ala Glu Gln Ala Thr Leu Tyr Ser Thr Gln Gln
 225 230 235 240
 Pro Arg Pro Pro Met Ala Phe Met Pro Trp Pro His Thr Gln Pro Gln
 245 250 255
 Gln Gln Gln Pro Pro Gln His Gln Gln Thr Asp Ser
 260 265

<210> 222

<211> 199

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222>

<223> gi 15223482

<400> 222

Met Glu Gln Ser Glu Glu Gly Gln Gln Gln Gln Gln Gln Gly Val Met
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 20 25 30
 Ser His Met Ala Phe Gln Gln Ala His His Phe His His His His Gln
 35 40 45
 Gln Gln Gln Gln Gln Gln Leu Gln Met Phe Trp Ala Asn Gln Met Gln
 50 55 60
 Glu Ile Glu His Thr Thr Asp Phe Lys Asn His Thr Leu Pro Leu Ala
 65 70 75 80
 Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser
 85 90 95
 Ala Glu Ala Pro Val Ile Phe Ala Lys Ala Cys Glu Met Phe Ile Leu
 100 105 110
 Glu Leu Thr Leu Arg Ala Trp Ile His Thr Glu Glu Asn Lys Arg Arg
 115 120 125
 Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile Ser Arg Thr Asp Val
 130 135 140
 Phe Asp Phe Leu Val Asp Ile Ile Pro Arg Asp Glu Leu Lys Glu Glu
 145 150 155 160

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PCT/US02/22086

Gly Leu Gly Val Thr Pys Gly Thr Ile Pro Ser Val Val Gly Ser Pro
165 170 175

Pro Tyr Tyr Tyr Leu Gln Gln Gln Gly Met Met Gln His Trp Pro Gln
180 185 190

Glu Gln His Pro Asp Glu Ser
195

CLAIMS

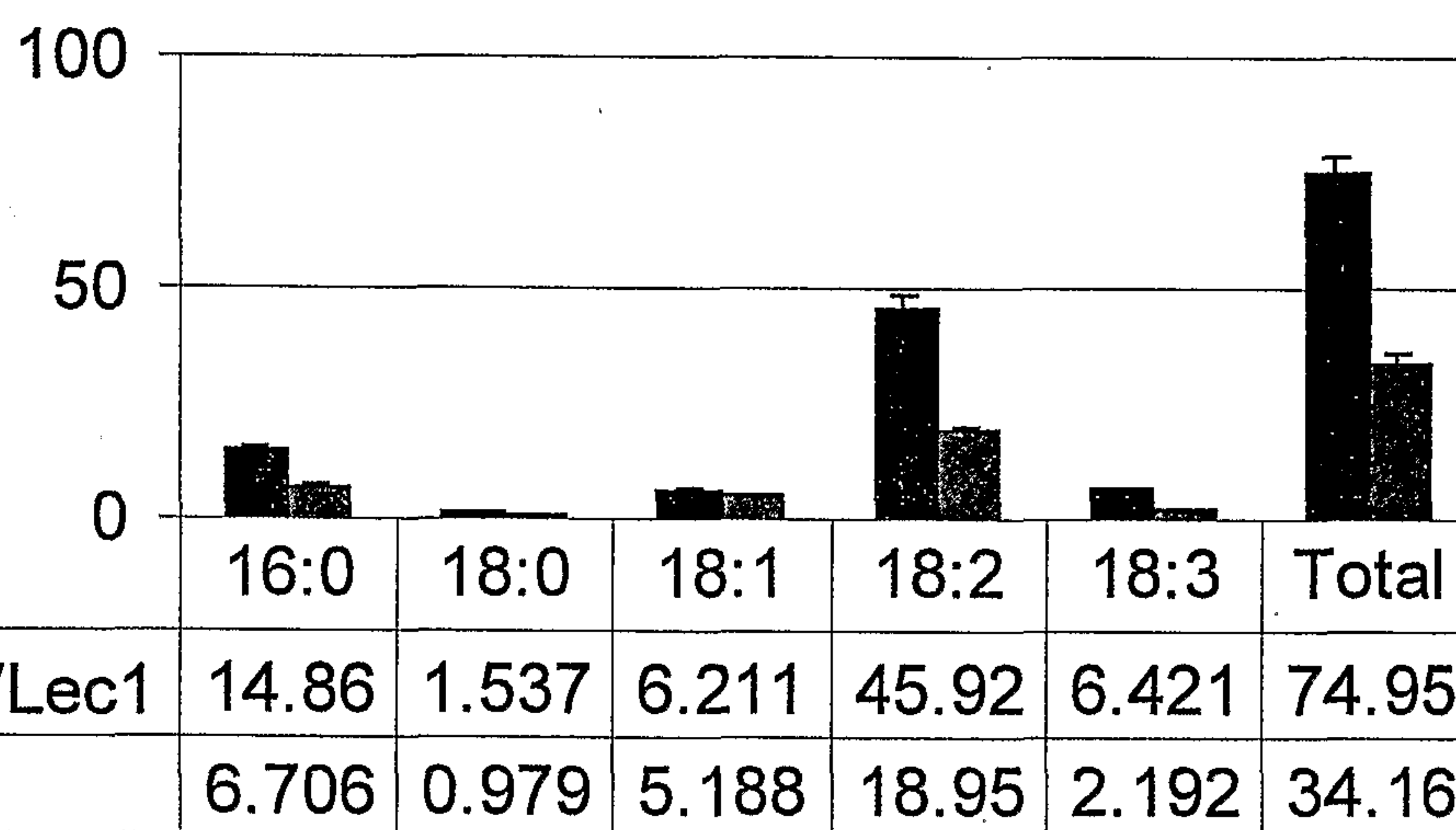
WHAT IS CLAIMED IS

1. A method for altering oil phenotype in a plant which comprises:
 - (a) transforming a plant with a recombinant DNA construct comprising an isolated nucleotide sequence encoding a plant Hap3/Lec1 transcription factor comprising SEQ ID 134, wherein said isolated nucleic acid sequence is operably linked to at least one regulatory sequence;
 - (b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and
 - (c) selecting transformed plants having an altered oil phenotype as compared to the oil phenotype of an untransformed plant.
2. A method for altering oil phenotype in a plant which comprises:
 - (a) transforming a plant with a recombinant DNA construct comprising an isolated nucleotide fragment encoding a plant Hap3/Lec1 transcription factor having at least 80% sequence identity based on the Clustal method of alignment when compared to the amino acid sequence set forth in SEQ ID NO:134; wherein said nucleic acid sequence is operably linked to at least one regulatory sequence;
 - (b) growing the transformed plant under conditions suitable for expression of the recombinant DNA construct; and
 - (c) selecting transformed plants having an altered oil phenotype as compared to the oil phenotype of an untransformed plant.
3. The method of Claim 1 or 2 wherein the plant is selected from the group consisting of corn, soybean, wheat, rice, canola, *Brassica*, sorghum, sunflower, and coconut.

1/2

**Fatty acid content/composition in corn somatic embryos
overexpressing HAP3/Lec1**

fatty acid (mg/gDW)



■ HAP3/Lec1
▨ Con

Co-segregation of Embryo-specific Expression of Lec1 and Oil Phenotype

