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(54) Title: ENCAPSULATION OF POLYPEPTIDES WITHIN THE STARCH MATRIX (57) Abstract Hybrid polypeptides are provided formed with encapsulating regions from genes that encode for anabolic proteins. More particularly, the present invention relates to recombinant nucleic acid molecules that code for genes which encapsulate an attached protein within a matrix; preferably, these genes encapsulate a desired ("payload") polypeptide within starch, and more specifically within the starch granule matrix. Expression vectors comprising these recombinant nucleic acid molecules, and hosts therefor, and more specifically the starch-bearing portions of such hosts, transformed with such vectors, are also provided. Preferably, grain containing a foreign protein encapsulated within the starch is provided, useful to produce mammalian, fish and avian food. The invention also encompasses methods of producing purified protein from starch and particularly from starch granules, and industrial uses of such protein.		

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ENCAPSULATION OF POLYPEPTIDES WITHIN THE STARCH MATRIX

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to provisional patent application serial No. 60/026,855 filed September 30, 1996. Said provisional application is incorporated herein
5 by reference to the extent not inconsistent herewith.

BACKGROUND OF THE INVENTION**Polysaccharide Enzymes**

Both prokaryotic and eukaryotic cells use polysaccharide enzymes as a storage reserve. In the prokaryotic cell the primary reserve polysaccharide is glycogen. Although
10 glycogen is similar to the starch found in most vascular plants it exhibits different chain lengths and degrees of polymerization. In many plants, starch is used as the primary reserve polysaccharide. Starch is stored in the various tissues of the starch bearing plant. Starch is made of two components in most instances; one is amylose and one is amylopectin. Amylose is formed as linear glucans and amylopectin is formed as branched
15 chains of glucans. Typical starch has a ratio of 25% amylose to 75% amylopectin. Variations in the amylose to amylopectin ratio in a plant can effect the properties of the starch. Additionally starches from different plants often have different properties. Maize starch and potato starch appear to differ due to the presence or absence of phosphate groups. Certain plants' starch properties differ because of mutations that have been
20 introduced into the plant genome. Mutant starches are well known in maize, rice and peas and the like.

The changes in starch branching or in the ratios of the starch components result in different starch characteristic. One characteristic of starch is the formation of starch granules which are formed particularly in leaves, roots, tubers and seeds. These granules
25 are formed during the starch synthesis process. Certain synthases of starch, particularly

granule-bound starch synthase, soluble starch synthases and branching enzymes are proteins that are "encapsulated" within the starch granule when it is formed.

The use of cDNA clones of animal and bacterial glycogen synthases are described in International patent application publication number GB92/01881. The nucleotide and amino acid sequences of glycogen synthase are known from the literature. For example, the nucleotide sequence for the *E. coli* glgA gene encoding glycogen synthase can be retrieved from the GenBank/EMBL (SWISSPROT) database, accession number J02616 (Kumar et al., 1986, J. Biol. Chem., 261:16256-16259). *E. coli* glycogen biosynthetic enzyme structural genes were also cloned by Okita et al. (1981, J. Biol. Chem., 256(13):6944-6952). The glycogen synthase glgA structural gene was cloned from *Salmonella typhimurium* LT2 by Leung et al. (1987, J. Bacteriol., 169(9):4349-4354). The sequences of glycogen synthase from rabbit skeletal muscle (Zhang et al., 1989, FASEB J., 3:2532-2536) and human muscle (Browner et al., 1989, Proc. Natl. Acad. Sci., 86:1443-1447) are also known.

The use of cDNA clones of plant soluble starch synthases has been reported. The amino acid sequences of pea soluble starch synthase isoforms I and II were published by Dry et al. (1991, Plant Journal, 2:193202). The amino acid sequence of rice soluble starch synthase was described by Baba et al. (1993, Plant Physiology,). This last sequence (rice SSTS) incorrectly cites the N-terminal sequence and hence is misleading. Presumably this is because of some extraction error involving a protease degradation or other inherent instability in the extracted enzyme. The correct N-terminal sequence (starting with AELSR) is present in what they refer to as the transit peptide sequence of the rice SSTS.

The sequence of maize branching enzyme I was investigated by Baba et al., 1991, BBRC, 181:8794. Starch branching enzyme II from maize endosperm was investigated by Fisher and Shrable (1993, Plant Physiol., 102:10451046). The use of cDNA clones of plant, bacterial and animal branching enzymes have been reported. The nucleotide and amino acid sequences for bacterial branching enzymes (BE) are known from the literature. For example, Kiel et al. cloned the branching enzyme gene glgB from *Cyanobacterium synechococcus* PCC7942 (1989, Gene (Amst), 78(1):918) and from *Bacillus*

stearothermophilus (Kiel et al., 1991, Mol. Gen. Genet., 230(12):136-144). The genes *glc3* and *ghal* of *S. cerevisiae* are allelic and encode the glycogen branching enzyme (Rowen et al., 1992, Mol. Cell Biol., 12(1):22-29). Matsumomoto et al. investigated glycogen branching enzyme from *Neurospora crassa* (1990, J. Biochem., 107:118-122).

5 The GenBank/EMBL database also contains sequences for the *E. coli* *glgB* gene encoding branching enzyme.

Starch synthase (EC 2.4.1.11) elongates starch molecules and is thought to act on both amylose and amylopectin. Starch synthase (STS) activity can be found associated both with the granule and in the stroma of the plastid. The capacity for starch association
10 of the bound starch synthase enzyme is well known. Various enzymes involved in starch biosynthesis are now known to have differing propensities for binding as described by Mu-Forster et al. (1996, Plant Phys. 111: 821-829). Granule-bound starch synthase (GBSTS) activity is strongly correlated with the product of the *waxy* gene (Shure et al., 1983, Cell 35: 225-233). The synthesis of amylose in a number of species such as maize, rice and
15 potato has been shown to depend on the expression of this gene (Tsai, 1974, Biochem Gen 11: 83-96; Hovenkamp-Hermelink et al., 1987, Theor. Appl. Gen. 75: 217-221). Visser et al. described the molecular cloning and partial characterization of the gene for granule-bound starch synthase from potato (1989, Plant Sci. 64(2):185192). Visser et al. have also described the inhibition of the expression of the gene for granule-bound starch
20 synthase in potato by antisense constructs (1991, Mol. Gen. Genet. 225(2):289296).

The other STS enzymes have become known as soluble starch synthases, following the pioneering work of Frydman and Cardini (Frydman and Cardini, 1964, Biochem. Biophys. Res. Communications 17: 407-411). Recently, the appropriateness of the term "soluble" has become questionable in light of discoveries that these enzymes are
25 associated with the granule as well as being present in the soluble phase (Denyer et al., 1993, Plant J. 4: 191-198; Denyer et al., 1995, Planta 97: 57-62; Mu-Forster et al., 1996, Plant Physiol. 111: 821-829). It is generally believed that the biosynthesis of amylopectin involves the interaction of soluble starch synthases and starch branching enzymes. Different isoforms of soluble starch synthase have been identified and cloned in pea
30 (Denyer and Smith, 1992, Planta 186: 609-617; Dry et al., 1992, Plant Journal, 2: 193-

202), potato (Edwards et al., 1995, Plant Physiol 112: 89-97; Marshall et al., 1996, Plant Cell 8: 1121-1135) and in rice (Baba et al., 1993, Plant Physiol. 103: 565-573), while barley appears to contain multiple isoforms, some of which are associated with starch branching enzyme (Tyynela and Schulman, 1994, Physiol. Plantarum 89: 835-841). A
5 common characteristic of STS clones is the presence of a KXGGLGDV consensus sequence which is believed to be the ADP-Glc binding site of the enzyme (Furukawa et al., 1990, J Biol Chem 265: 2086-2090; Furukawa et al., 1993, J. Biol. Chem. 268: 23837-23842).

In maize, two soluble forms of STS, known as isoforms I and II, have been
10 identified (Macdonald and Preiss, 1983, Plant Physiol. 73: 175-178; Boyer and Preiss, 1978, Carb. Res. 61: 321-334; Pollock and Preiss, 1980, Arch Biochem. Biophys. 204: 578-588; Macdonald and Preiss, 1985 Plant Physiol. 78: 849-852; Dang and Boyer, 1988, Phytochemistry 27: 1255-1259; Mu et al., 1994, Plant J. 6: 151-159), but neither of these has been cloned. STSI activity of maize endosperm was recently correlated with a 76-kDa
15 polypeptide found in both soluble and granule-associated fractions (Mu et al., 1994, Plant J. 6: 151-159). The polypeptide identity of STSII remains unknown. STSI and II exhibit different enzymological characteristics. STSI exhibits primer-independent activity whereas STSII requires glycogen primer to catalyze glucosyl transfer. Soluble starch synthases have been reported to have a high flux control coefficient for starch deposition (Jenner et al., 1993, Aust. J. Plant Physiol. 22: 703-709; Keeling et al., 1993, Planta 191: 342-348)
20 and to have unusual kinetic properties at elevated temperatures (Keeling et al., 1995, Aust. J. Plant Physiol. 21 807-827). The respective isoforms in maize exhibit significant differences in both temperature optima and stability.

Plant starch synthase (and *E. coli* glycogen synthase) sequences include the
25 sequence KTGGL which is known to be the ADPG binding domain. The genes for any such starch synthase protein may be used in constructs according to this invention.

Branching enzyme [α 1,4Dglucan: α 1,4Dglucan 6D(α 1,4Dglucano) transferase (E.C. 2.4.1.18)], sometimes called Q-enzyme, converts amylose to amylopectin. A segment of a α 1,4Dglucan chain is transferred to a primary hydroxyl group in a similar glucan chain.

Bacterial branching enzyme genes and plant sequences have been reported (rice endosperm: Nakamura et al., 1992, *Physiologia Plantarum*, 84:329-335 and Nakamura and Yamanouchi, 1992, *Plant Physiol.*, 99:1265-1266; pea: Smith, 1988, *Planta*, 175:270-279 and Bhattacharyya et al., 1989, *J. Cell Biochem., Suppl.* 13D:331; maize endosperm: Singh and Preiss, 1985, *Plant Physiology*, 79:34-40; VosScherperkeuter et al., 1989, *Plant Physiology*, 90:75-84; potato: Kossmann et al., 1991, *Mol. Gen. Genet.*, 230(12):39-44; cassava: Salehuzzaman and Visser, 1992, *Plant Mol Biol*, 20:809-819).

In the area of polysaccharide enzymes there are reports of vectors for engineering modification in the starch pathway of plants by use of a number of starch synthesis genes in various plant species. That some of these polysaccharide enzymes bind to cellulose or starch or glycogen is well known. One specific patent example of the use of a polysaccharide enzyme shows the use of glycogen biosynthesis enzymes to modify plant starch. In U.S. patent 5,349,123 to Shewmaker a vector containing DNA to form glycogen biosynthetic enzymes within plant cells is taught. Specifically, this patent refers to the changes in potato starch due to the introduction of these enzymes. Other starch synthesis genes and their use have also been reported.

Hybrid (fusion) Peptides

Hybrid proteins (also called "fusion proteins") are polypeptide chains that consist of two or more proteins fused together into a single polypeptide. Often one of the proteins is a ligand which binds to a specific receptor cell. Vectors encoding fusion peptides are primarily used to produce foreign proteins through fermentation of microbes. The fusion proteins produced can then be purified by affinity chromatography. The binding portion of one of the polypeptides is used to attach the hybrid polypeptide to an affinity matrix. For example, fusion proteins can be formed with beta galactosidase which can be bound to a column. This method has been used to form viral antigens.

Another use is to recover one of the polypeptides of the hybrid polypeptide. Chemical and biological methods are known for cleaving the fused peptide. Low pH can be used to cleave the peptides if an acid-labile aspartyl-proline linkage is employed between the peptides and the peptides are not affected by the acid. Hormones have been

cleaved with cyanobromide. Additionally, cleavage by site-specific proteolysis has been reported. Other methods of protein purification such as ion chromatography have been enhanced with the use of polyarginine tails which increase overall basicity of the protein thus enhancing binding to ion exchange columns.

5 A number of patents have outlined improvements in methods of making hybrid peptides or specific hybrid peptides targeted for specific uses. US patent 5,635,599 to Pastan et al. outlines an improvement of hybrid proteins. This patent reports a circularly permuted ligand as part of the hybrid peptide. This ligand possesses specificity and good binding affinity. Another improvement in hybrid proteins is reported in U.S. patent
10 5,648,244 to Kuliopulos. This patent describes a method for producing a hybrid peptide with a carrier peptide. This nucleic acid region, when recognized by a restriction endonuclease, creates a nonpalindromic 3-base overhang. This allows the vector to be cleaved.

15 An example of a specifically targeted hybrid protein is reported in U.S. patent 5,643,756. This patent reports a vector for expression of glycosylated proteins in cells. This hybrid protein is adapted for use in proper immunoreactivity of HIV gp120. The isolation of gp120 domains which are highly glycosylated is enhanced by this reported vector.

20 U.S. patent 5,202,247 and 5,137,819 discuss hybrid proteins having polysaccharide binding domains and methods and compositions for preparation of hybrid proteins which are capable of binding to a polysaccharide matrix. U.S. patent 5,202,247 specifically teaches a hybrid protein linking a cellulase binding region to a peptide of interest. The patent specifies that the hybrid protein can be purified after expression in a bacterial host by affinity chromatography on cellulose.

25 The development of genetic engineering techniques has made it possible to transfer genes from various organisms and plants into other organisms or plants. Although starch has been altered by transformation and mutagenesis in the past there is still a need for further starch modification. To this end vectors that provide for encapsulation of desired

amino acids or peptides within the starch and specifically within the starch granule are desirable. The resultant starch is modified and the tissue from the plant carrying the vector is modified.

SUMMARY OF THE INVENTION

5 This invention provides a hybrid polypeptide comprising a starch-encapsulating region (SER) from a starch-binding enzyme fused to a payload polypeptide which is not endogenous to said starch-encapsulating region, i.e. does not naturally occur linked to the starch-encapsulating region. The hybrid polypeptide is useful to make modified starches comprising the payload polypeptide. Such modified starches may be used to provide grain
10 feeds enriched in certain amino acids. Such modified starches are also useful for providing polypeptides such as hormones and other medicaments, e.g. insulin, in a starch-encapsulated form to resist degradation by stomach acids. The hybrid polypeptides are also useful for producing the payload polypeptides in easily-purified form. For example, such hybrid polypeptides produced by bacterial fermentation, or in grains or animals, may
15 be isolated and purified from the modified starches with which they are associated by art-known techniques.

The term "polypeptide" as used herein means a plurality of identical or different amino acids, and also encompasses proteins.

20 The term "hybrid polypeptide" means a polypeptide composed of peptides or polypeptides from at least two different sources, e.g. a starch-encapsulating region of a starch-binding enzyme, fused to another polypeptide such as a hormone, wherein at least two component parts of the hybrid polypeptide do not occur fused together in nature.

25 The term "payload polypeptide" means a polypeptide not endogenous to the starch-encapsulating region whose expression is desired in association with this region to express a modified starch containing the payload polypeptide.

When the payload polypeptide is to be used to enhance the amino acid content of particular amino acids in the modified starch, it preferably consists of not more than three different types of amino acids selected from the group consisting of: Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, and Val.

5 When the payload polypeptide is to be used to supply a biologically active polypeptide to either the host organism or another organism, the payload polypeptide may be a biologically active polypeptide such as a hormone, e.g., insulin, a growth factor, e.g. somatotropin, an antibody, enzyme, immunoglobulin, or dye, or may be a biologically active fragment thereof as is known to the art. So long as the polypeptide has biological
10 activity, it does not need to be a naturally-occurring polypeptide, but may be mutated, truncated, or otherwise modified. Such biologically active polypeptides may be modified polypeptides, containing only biologically-active portions of biologically-active polypeptides. They may also be amino acid sequences homologous to naturally-occurring biologically-active amino acid sequences (preferably at least about 75% homologous)
15 which retain biological activity.

The starch-encapsulating region of the hybrid polypeptide may be a starch-encapsulating region of any starch-binding enzyme known to the art, e.g. an enzyme selected from the group consisting of soluble starch synthase I, soluble starch synthase II, soluble starch synthase III, granule-bound starch synthase, branching enzyme I, branching
20 enzyme IIa, branching enzyme IIBb and glucoamylase polypeptides.

When the hybrid polypeptide is to be used to produce payload polypeptide in pure or partially purified form, the hybrid polypeptide preferably comprises a cleavage site between the starch-encapsulating region and the payload polypeptide. The method of isolating the purified payload polypeptide then includes the step of contacting the hybrid
25 polypeptide with a cleaving agent specific for that cleavage site.

This invention also provides recombinant nucleic acid (RNA or DNA) molecules encoding the hybrid polypeptides. Such recombinant nucleic acid molecules preferably comprise control sequences adapted for expression of the hybrid polypeptide in the

selected host. The term "control sequences" includes promoters, introns, preferred codon sequences for the particular host organism, and other sequences known to the art to affect expression of DNA or RNA in particular hosts. The nucleic acid sequences encoding the starch-encapsulating region and the payload polypeptide may be naturally-occurring
5 nucleic acid sequences, or biologically-active fragments thereof, or may be biologically-active sequences homologous to such sequences, preferably at least about 75% homologous to such sequences.

Host organisms include bacteria, plants, and animals. Preferred hosts are plants. Both monocotyledonous plants (monocots) and dicotyledonous plants (dicots) are useful
10 hosts for expressing the hybrid polypeptides of this invention.

This invention also provides expression vectors comprising the nucleic acids encoding the hybrid proteins of this invention. These expression vectors are used for transforming the nucleic acids into host organisms and may also comprise sequences aiding in the expression of the nucleic acids in the host organism. The expression vectors
15 may be plasmids, modified viruses, or DNA or RNA molecules, or other vectors useful in transformation systems known to the art.

By the methods of this invention, transformed cells are produced comprising the recombinant nucleic acid molecules capable of expressing the hybrid polypeptides of this invention. These may prokaryotic or eukaryotic cells from one-celled organisms, plants or
20 animals. They may be bacterial cells from which the hybrid polypeptide may be harvested. Or, they may be plant cells which may be regenerated into plants from which the hybrid polypeptide may be harvested, or, such plant cells may be regenerated into fertile plants with seeds containing the nucleic acids encoding the hybrid polypeptide. In a preferred embodiment, such seeds contain modified starch comprising the payload
25 polypeptide.

The term "modified starch" means the naturally-occurring starch has been modified to comprise the payload polypeptide.

A method of targeting digestion of a payload polypeptide to a particular phase of the digestive process, e.g., preventing degradation of a payload polypeptide in the stomach of an animal, is also provided comprising feeding the animal a modified starch of this invention comprising the payload polypeptide, whereby the polypeptide is protected by the starch from degradation in the stomach of the animal. Alternatively, the starch may be one known to be digested in the stomach to release the payload polypeptide there.

Preferred recombinant nucleic acid molecules of this invention comprise DNA encoding starch-encapsulating regions selected from the starch synthesizing gene sequences set forth in the tables hereof.

Preferred plasmids of this invention are adapted for use with specific hosts. Plasmids comprising a promoter, a plastid-targeting sequence, a nucleic acid sequence encoding a starch-encapsulating region, and a terminator sequence, are provided herein. Such plasmids are suitable for insertion of DNA sequences encoding payload polypeptides and starch-encapsulating regions for expression in selected hosts.

Plasmids of this invention can optionally include a spacer or a linker unit proximate the fusion site between nucleic acids encoding the SER and the nucleic acids encoding the payload polypeptide. This invention includes plasmids comprising promoters adapted for a prokaryotic or eukaryotic hosts. Such promoters may also be specifically adapted for expression in monocots or in dicots.

A method of forming peptide-modified starch of this invention includes the steps of: supplying a plasmid having a promoter associated with a nucleic acid sequence encoding a starch-encapsulating region, the nucleic acid sequence encoding the starch-encapsulating region being connected to a nucleic acid region encoding a payload polypeptide, and transforming a host with the plasmid whereby the host expresses peptide-modified starch.

This invention furthermore comprises starch-bearing grains comprising: an embryo, nutritive tissues; and, modified starch granules having encapsulated therein a protein that is

not endogenous to starch granules of said grain which are not modified. Such starch-bearing grains may be grains wherein the embryo is a maize embryo, a rice embryo, or a wheat embryo.

All publications referred to herein are incorporated by reference to the extent not inconsistent herewith.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1a shows the plasmid pEXS114 which contains the synthetic GFP (Green Fluorescent Protein) subcloned into pBSK from Stratagene.

FIG. 1b shows the plasmid pEXS115.

FIG. 2a. shows the *waxy* gene with restriction sites subcloned into a commercially available plasmid.

FIG. 2b shows the p ET-21A plasmid commercially available from Novagen having the GFP fragment from pEXS115 subcloned therein.

FIG. 3a shows pEXS114 subcloned into pEXSWX, and the GFP-FLWX map.

FIG. 3b shows the GFP-Bam HIWX plasmid.

FIG. 4 shows the SGFP fragment of pEXS115 subcloned into pEXSWX, and the GFP-NcoWX map.

FIG. 5 shows a linear depiction of a plasmid that is adapted for use in monocots.

FIG. 6 shows the plasmid pEXS52.

FIG. 7 shows the six introductory plasmids used to form pEXS51 and pEX560. **FIG. 7a** shows pEXS adh1. **FIG. 7b** shows pEXS adh1-nos3'. **FIG. 7c** shows pEXS33. **FIG. 7d** shows pEXS10zp. **FIG. 7e** shows pEXS10zp-adh1. **FIG. 7f** shows pEXS10zp-adh1-nos3'.

FIGS. 8a and **8b** show the plasmids pEXS50 and pEXS51, respectively, containing the MS-SIII gene which is a starch-soluble synthase gene.

FIG. 9a shows the plasmid pEXS60 which excludes the intron shown in pEXS50, and **FIG. 9b** shows the plasmid pEXS61 which excludes the intron shown in pEXS60.

DETAILED DESCRIPTION

The present invention provides, broadly, a hybrid polypeptide, a method for making a hybrid polypeptide, and nucleic acids encoding the hybrid polypeptide. A hybrid polypeptide consists of two or more subparts fused together into a single peptide chain. The subparts can be amino acids or peptides or polypeptides. One of the subparts is a starch-encapsulating region. Hybrid polypeptides may thus be targeted into starch granules produced by organisms expressing the hybrid polypeptides.

A method of making the hybrid polypeptides within cells involves the preparation of a DNA construct comprising at least a fragment of DNA encoding a sequence which functions to bind the expression product of attached DNA into a granule of starch, ligated to a DNA sequence encoding the polypeptide of interest (the payload polypeptide). This construct is expressed within a eukaryotic or prokaryotic cell. The hybrid polypeptide can be used to produce purified protein or to immobilize a protein of interest within the protection of a starch granule, or to produce grain that contains foreign amino acids or peptides.

The hybrid polypeptide according to the present invention has three regions.

Payload Peptide (X)	Central Site (CS)*	Starch-encapsulating region (SER)
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X is any amino acid or peptide of interest.

* optional component.

The gene for X can be placed in the 5' or 3' position within the DNA construct described below.

5 CS is a central site which may be a leaving site, a cleavage site, or a spacer, as is known to the art. A cleavage site is recognized by a cleaving enzyme. A cleaving enzyme is an enzyme that cleaves peptides at a particular site. Examples of chemicals and enzymes that have been employed to cleave polypeptides include thrombin, trypsin, cyanobromide, formic acid, hydroxyl amine, collagenase, and alacubtilisin. A spacer is a
10 peptide that joins the peptides comprising the hybrid polypeptide. Usually it does not have any specific activity other than to join the peptides or to preserve some minimum distance or to influence the folding, charge or water acceptance of the protein. Spacers may be any peptide sequences not interfering with the biological activity of the hybrid polypeptide.

The starch-encapsulating region (SER) is the region of the subject polypeptide that
15 has a binding affinity for starch. Usually the SER is selected from the group consisting of peptides comprising starch-binding regions of starch synthases and branching enzymes of plants, but can include starch binding domains from other sources such as glucoamylase and the like. In the preferred embodiments of the invention, the SER includes peptide products of genes that naturally occur in the starch synthesis pathway. This subset of
20 preferred SERs is defined as starch-forming encapsulating regions (SFER). A further subset of SERs preferred herein is the specific starch-encapsulating regions (SSER) from the specific enzymes starch synthase (STS), granule-bound starch synthase (GBSTS) and branching enzymes (BE) of starch-bearing plants. The most preferred gene product from this set is the GBSTS. Additionally, starch synthase I and branching enzyme II are useful
25 gene products. Preferably, the SER (and all the subsets discussed above) are truncated versions of the full length starch synthesizing enzyme gene such that the truncated portion includes the starch-encapsulating region.

The DNA construct for expressing the hybrid polypeptide within the host, broadly is as follows:

Promoter	Intron*	Transit Peptide Coding Region*	X	SER	Terminator
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* optional component. Other optional components can also be used.

5 As is known to the art, a promoter is a region of DNA controlling transcription. Different types of promoters are selected for different hosts. Lac and T7 promoters work well in prokaryotes, the 35S CaMV promoter works well in dicots, and the polyubiquitin promoter works well in many monocots. Any number of different promoters are known to the art and can be used within the scope of this invention.

10 Also as is known to the art, an intron is a nucleotide sequence in a gene that does not code for the gene product. One example of an intron that often increases expression in monocots is the Adh1 intron. This component of the construct is optional.

The transit peptide coding region is a nucleotide sequence that encodes for the translocation of the protein into organelles such as plastids. It is preferred to choose a transit peptide that is recognized and compatible with the host in which the transit peptide is employed. In this invention the plastid of choice is the amyloplast.

15 It is preferred that the hybrid polypeptide be located within the amyloplast in cells such as plant cells which synthesize and store starch in amyloplasts. If the host is a bacterial or other cell that does not contain an amyloplast, there need not be a transit peptide coding region.

20 A terminator is a DNA sequence that terminates the transcription.

X is the coding region for the payload polypeptide, which may be any polypeptide of interest, or chains of amino acids. It may have up to an entire sequence of a known polypeptide or comprise a useful fragment thereof. The payload polypeptide may be a

polypeptide, a fragment thereof, or biologically active protein which is an enzyme, hormone, growth factor, immunoglobulin, dye, etc. Examples of some of the payload polypeptides that can be employed in this invention include, but are not limited to, prolactin (PRL), serum albumin, growth factors and growth hormones, i.e., somatotropin.

5 Serum albumins include bovine, ovine, equine, avian and human serum albumin. Growth factors include epidermal growth factor (EGF), insulin-like growth factor I (IGF-I), insulin-like growth factor II (IGF-II), fibroblast growth factor (FGF), transforming growth factor alpha (TGF-alpha), transforming growth factor beta (TGF-beta), nerve growth factor (NGF), platelet-derived growth factor (PDGF), and recombinant human insulin-like growth
10 factors I (rHuIGF-I) and II (rHuIGF-II). Somatotropins which can be employed to practice this invention include, but are not limited to, bovine, porcine, ovine, equine, avian and human somatotropin. Porcine somatotropin includes delta-7 recombinant porcine somatotropin, as described and claimed in European Patent Application Publication No. 104,920 (Biogen). Preferred payload polypeptides are somatotropin, insulin A and B
15 chains, calcitonin, beta endorphin, urogastrone, beta globin, myoglobin, human growth hormone, angiotensin, proline, proteases, beta-galactosidase, and cellulases.

The hybrid polypeptide, the SER region and the payload polypeptides may also include post-translational modifications known to the art such as glycosylation, acylation, and other modifications not interfering with the desired activity of the polypeptide.

20 **Developing a Hybrid polypeptide**

The SER region is present in genes involved in starch synthesis. Methods for isolating such genes include screening from genomic DNA libraries and from cDNA libraries. Genes can be cut and changed by ligation, mutation agents, digestion, restriction and other such procedures, e.g., as outlined in Maniatis et al., Molecular Cloning, Cold
25 Spring Harbor Labs, Cold Spring Harbor, N.Y. Examples of excellent starting materials for accessing the SER region include, but are not limited to, the following: starch synthases I, II, III, IV, Branching Enzymes I, IIA and B and granule-bound starch synthase (GBSTS). These genes are present in starch-bearing plants such as rice, maize, peas, potatoes, wheat, and the like. Use of a probe of SER made from genomic DNA or cDNA
30 or mRNA or antibodies raised against the SER allows for the isolation and identification

of useful genes for cloning. The starch enzyme-encoding sequences may be modified as long as the modifications do not interfere with the ability of the SER region to encapsulate associated polypeptides.

When genes encoding proteins that are encapsulated into the starch granule are located, then several approaches to isolation of the SER can be employed, as is known to the art. One method is to cut the gene with restriction enzymes at various sites, deleting sections from the N-terminal end and allowing the resultant protein to express. The expressed truncated protein is then run on a starch gel to evaluate the association and dissociation constant of the remaining protein. Marker genes known to the art, e.g., green fluorescent protein gene, may be attached to the truncated protein and used to determine the presence of the marker gene in the starch granule.

Once the SER gene sequence region is isolated it can be used in making the gene fragment sequence that will express the payload polypeptide encapsulated in starch. The SER gene sequence and the gene sequence encoding the payload polypeptide can be ligated together. The resulting fused DNA can then be placed in a number of vector constructs for expression in a number of hosts. The preferred hosts form starch granules in plastids, but the testing of the SER can be readily performed in bacterial hosts such as *E.coli*.

The nucleic acid sequence coding for the payload polypeptide may be derived from DNA, RNA, genomic DNA, cDNA, mRNA or may be synthesized in whole or in part. The sequence of the payload polypeptide can be manipulated to contain mutations such that the protein produced is a novel, mutant protein, so long as biological function is maintained.

When the payload polypeptide-encoding nucleic acid sequence is ligated onto the SER-encoding sequence, the gene sequence for the payload polypeptide is preferably attached at the end of the SER sequence coding for the N-terminus. Although the N-terminus end is preferred, it does not appear critical to the invention whether the payload polypeptide is ligated onto the N-terminus end or the C-terminus end of the SER. Clearly,

the method of forming the recombinant nucleic acid molecules of this invention, whether synthetically, or by cloning and ligation, is not critical to the present invention.

The central region of the hybrid polypeptide is optional. For some applications of the present invention it can be very useful to introduce DNA coding for a convenient
5 protease cleavage site in this region into the recombinant nucleic acid molecule used to express the hybrid polypeptide. Alternatively, it can be useful to introduce DNA coding for an amino acid sequence that is pH-sensitive to form the central region. If the use of the present invention is to develop a pure protein that can be extracted and released from the starch granule by a protease or the like, then a protease cleavage site is useful.

10 Additionally, if the protein is to be digested in an animal then a protease cleavage site may be useful to assist the enzymes in the digestive tract of the animal to release the protein from the starch. In other applications and in many digestive uses the cleavage site would be superfluous.

The central region site may comprise a spacer. A spacer refers to a peptide that
15 joins the proteins comprising a hybrid polypeptide. Usually it does not have any specific activity other than to join the proteins, to preserve some minimum distance, to influence the folding, charge or hydrophobic or hydrophilic nature of the hybrid polypeptide.

Construct Development

Once the ligated DNA which encodes the hybrid polypeptide is formed, then
20 cloning vectors or plasmids are prepared which are capable of transferring the DNA to a host for expressing the hybrid polypeptides. The recombinant nucleic acid sequence of this invention is inserted into a convenient cloning vector or plasmid. For the present invention the preferred host is a starch granule-producing host. However, bacterial hosts can also be employed. Especially useful are bacterial hosts that have been transformed to
25 contain some or all of the starch-synthesizing genes of a plant. The ordinarily skilled person in the art understands that the plasmid is tailored to the host. For example, in a bacterial host transcriptional regulatory promoters include lac, TAC, trp and the like. Additionally, DNA coding for a transit peptide most likely would not be used and a secretory leader that is upstream from the structural gene may be used to get the

polypeptide into the medium. Alternatively, the product is retained in the host and the host is lysed and the product isolated and purified by starch extraction methods or by binding the material to a starch matrix (or a starch-like matrix such as amylose or amylopectin, glycogen or the like) to extract the product.

5 The preferred host is a plant and thus the preferred plasmid is adapted to be useful in a plant. The plasmid should contain a promoter, preferably a promoter adapted to target the expression of the protein in the starch-containing tissue of the plant. The promoter may be specific for various tissues such as seeds, roots, tubers and the like; or, it can be a constitutive promoter for gene expression throughout the tissues of the plant.
10 Well-known promoters include the 10 kD zein (maize) promoter, the CAB promoter, patastin, 35S and 19S cauliflower mosaic virus promoters (very useful in dicots), the polyubiquitin promoter (useful in monocots) and enhancements and modifications thereof known to the art.

15 The cloning vector may contain coding sequences for a transit peptide to direct the plasmid into the correct location. Examples of transit peptide-coding sequences are shown in the sequence tables. Coding sequences for other transit peptides can be used. Transit peptides naturally occurring in the host to be used are preferred. Preferred transit peptide coding regions for maize are shown in the tables and figures hereof. The purpose of the transit peptide is to target the vector to the correct intracellular area.

20 Attached to the transit peptide-encoding sequence is the DNA sequence encoding the N-terminal end of the payload polypeptide. The direction of the sequence encoding the payload polypeptide is varied depending on whether sense or antisense transcription is desired. DNA constructs of this invention specifically described herein have the sequence encoding the payload polypeptide at the N-terminus end but the SER coding region can
25 also be at the N-terminus end and the payload polypeptide sequence following. At the end of the DNA construct is the terminator sequence. Such sequences are well known in the art.

The cloning vector is transformed into a host. Introduction of the cloning vector, preferably a plasmid, into the host can be done by a number of transformation techniques known to the art. These techniques may vary by host but they include microparticle bombardment, micro injection, *Agrobacterium* transformation, "whiskers" technology (U.S. Patent Nos. 5,302,523 and 5,464,765), electroporation and the like. If the host is a plant, the cells can be regenerated to form plants. Methods of regenerating plants are known in the art. Once the host is transformed and the proteins expressed therein, the presence of the DNA encoding the payload polypeptide in the host is confirmable. The presence of expressed proteins may be confirmed by Western Blot or ELISA or as a result of a change in the plant or the cell.

Uses of Encapsulated Protein

There are a number of applications of this invention. The hybrid polypeptide can be cleaved in a pure state from the starch (cleavage sites can be included) and pure protein can be recovered. Alternatively, the encapsulated payload polypeptide within the starch can be used in raw form to deliver protein to various parts of the digestive tract of the consuming animal ("animal" shall include mammals, birds and fish). For example if the starch in which the material is encapsulated is resistant to digestion then the protein will be released slowly into the intestine of the animal, therefore avoiding degradation of the valuable protein in the stomach. Amino acids such as methionine and lysine may be encapsulated to be incorporated directly into the grain that the animal is fed thus eliminating the need for supplementing the diet with these amino acids in other forms.

The present invention allows hormones, enzymes, proteins, proteinaceous nutrients and proteinaceous medicines to be targeted to specific digestive areas in the digestive tracts of animals. Proteins that normally are digested in the upper digestive tract encapsulated in starch are able to pass through the stomach in a nondigested manner and be absorbed intact or in part by the intestine. If capable of passing through the intestinal wall, the payload polypeptides can be used for medicating an animal, or providing hormones such as growth factors, e.g., somatotropin, for vaccination of an animal or for enhancing the nutrients available to an animal.

If the starch used is not resistant to digestion in the stomach (for example the sugary 2 starch is highly digestible), then the added protein can be targeted to be absorbed in the upper digestive tract of the animal. This would require that the host used to produce the modified starch be mutated or transformed to make sugary 2 type starch. The present invention encompasses the use of mutant organisms that form modified starch as hosts. Some examples of these mutant hosts include rice and maize and the like having sugary 1, sugary 2, brittle, shrunken, waxy, amylose extender, dull, opaque, and floury mutations, and the like. These mutant starches and starches from different plant sources have different levels of digestibility. Thus by selection of the host for expression of the DNA and of the animal to which the modified starch is fed, the hybrid polypeptide can be digested where it is targeted. Different proteins are absorbed most efficiently by different parts of the body. By encapsulating the protein in starch that has the selected digestibility, the protein can be supplied anywhere throughout the digestive tract and at specific times during the digestive process.

Another of the advantages of the present invention is the ability to inhibit or express differing levels of glycosylation of the desired polypeptide. The encapsulating procedure may allow the protein to be expressed within the granule in a different glycosylation state than if expressed by other DNA molecules. The glycosylation will depend on the amount of encapsulation, the host employed and the sequence of the polypeptide.

Improved crops having the above-described characteristics may be produced by genetic manipulation of plants known to possess other favorable characteristics. By manipulating the nucleotide sequence of a starch-synthesizing enzyme gene, it is possible to alter the amount of key amino acids, proteins or peptides produced in a plant. One or more genetically engineered gene constructs, which may be of plant, fungal, bacterial or animal origin, may be incorporated into the plant genome by sexual crossing or by transformation. Engineered genes may comprise additional copies of wildtype genes or may encode modified or allelic or alternative enzymes with new properties. Incorporation of such gene construct(s) may have varying effects depending on the amount and type of

gene(s) introduced (in a sense or antisense orientation). It may increase the plant's capacity to produce a specific protein, peptide or provide an improved amino acid balance.

Cloning Enzymes Involved in Starch Biosynthesis

Known cloning techniques may be used to provide the DNA constructs of this invention. The source of the special forms of the SSTS, GBSTS, BE, glycogen synthase (GS), amylopectin, or other genes used herein may be any organism that can make starch or glycogen. Potential donor organisms are screened and identified. Thereafter there can be two approaches: (a) using enzyme purification and antibody/sequence generation following the protocols described herein; (b) using SSTS, GBSTS, BE, GS, amylopectin or other cDNAs as heterologous probes to identify the genomic DNAs for SSTS, GBSTS, BE, GS, amylopectin or other starch-encapsulating enzymes in libraries from the organism concerned. Gene transformation, plant regeneration and testing protocols are known to the art. In this instance it is necessary to make gene constructs for transformation which contain regulatory sequences that ensure expression during starch formation. These regulatory sequences are present in many small grains and in tubers and roots. For example these regulatory sequences are readily available in the maize endosperm in DNA encoding Granule Bound Starch Synthesis (GBSTS), Soluble Starch Synthases (SSTS) or Branching Enzymes (BE) or other maize endosperm starch synthesis pathway enzymes. These regulatory sequences from the endosperm ensure protein expression at the correct developmental time (e.g., ADPG pyrophosphorylase).

In this method we measure starch-binding constants of starch-binding proteins using native protein electrophoresis in the presence of suitable concentrations of carbohydrates such as glycogen or amylopectin. Starch-encapsulating regions can be elucidated using site-directed mutagenesis and other genetic engineering methods known to those skilled in the art. Novel genetically-engineered proteins carrying novel peptides or amino acid combinations can be evaluated using the methods described herein.

EXAMPLES

Example One:

Method for Identification of Starch-encapsulating Proteins

Starch-Granule Protein Isolation:

5 Homogenize 12.5 g grain in 25 ml Extraction buffer (50 mM Tris acetate, pH 7.5, 1 mM EDTA, 1 mM DTT for 3 x 20 seconds in Waring blender with 1 min intervals between blending). Keep samples on ice. Filter through mira cloth and centrifuge at 6,000 rpm for 30 min. Discard supernatant and scrape off discolored solids which overlay white starch pellet. Resuspend pellet in 25 ml buffer and recentrifuge. Repeat washes twice
10 more. Resuspend washed pellet in -20°C acetone, allow pellet to settle at -20°C. Repeat. Dry starch under stream of air. Store at -20°C.

Protein Extraction:

Mix 50 mg starch with 1 ml 2% SDS in eppendorf. Vortex, spin at 18,000 rpm, 5 min, 4°C. Pour off supernatant. Repeat twice. Add 1 ml sample buffer (4 ml distilled
15 water, 1 ml 0.5 M Tris-HCl, pH 6.8, 0.8 ml glycerol, 1.6 ml 10% SDS, 0.4 ml B-mercaptoethanol, 0.2 ml 0.5% bromphenol blue). Boil eppendorf for 10 min with hole in lid. Cool, centrifuge 10,000 rpm for 10 min. Decant supernatant into new eppendorf. Boil for 4 minutes with standards. Cool.

SDS-Page Gels: (non-denaturing)

20		10% Resolve	4% Stack
	Acryl/Bis 40% stock	2.5 ml	1.0 ml
	1.5 M Tris pH 8.8	2.5 ml	-
	0.5 M Tris pH 8.8	-	2.5 ml
	10% SDS	100 µl	100 µl
25	Water	4.845 ml	6.34 ml
	Degas 15 min add fresh		
	10% Ammonium Persulfate	50 µl	50 µl
	TEMED	5µl	10 µl

Mini-Protean II Dual Slab Cell; 3.5 ml of Resolve buffer per gel. 4% Stack is poured on top. The gel is run at 200V constant voltage. 10 x Running buffer (250 mM Tris, 1.92 M glycine, 1% SDS, pH 8.3).

Method of Measurement of Starch-Encapsulating Regions:

5

Solutions:

Extraction Buffer: 50 mM Tris-acetate pH 7.5, 10 mM EDTA, 10% sucrose, 2.5 mM DTT-fresh.

Stacking Buffer: 0.5 M Tris-HCl, pH 6.8

Resolve Buffer: 1.5 M Tris-HCl, pH 8.8

10 10 X Lower Electrode Buffer: 30.3 g Tris + 144 g Glycine qs to 1 L. (pH is ~8.3, no adjustment). Dilute for use.

Upper Electrode Buffer: Same as Lower

Sucrose Solution: 18.66 g sucrose + 100 ml dH₂O

15 30% Acryl/Bis Stock (2.67%C): 146 g acrylamide + 4 g bis + 350 ml dH₂O. Bring up to 500 ml. Filter and store at 4 C in the dark for up to 1 month.

15% Acryl/Bis Stock (20% C): 6 g acrylamide + 1.5 g bis + 25 ml dH₂O. Bring up to 50 ml. Filter and store at 4 C in the dark for up to 1 month.

20 Riboflavin Solution: 1.4 g riboflavin + 100 ml dH₂O. Store in dark for up to 1 month.

SS Assay mix: 25 mM Sodium Citrate, 25 mM Bicine-NaOH (pH 8.0), 2 mM EDTA, 1 mM DTT-fresh, 1 mM Adenosine 5' Diphosphoglucose-fresh, 10 mg/ml rabbit liver glycogen Type III-fresh.

25

Iodine Solution: 2 g iodine + 20 g KI, 0.1 N HCl up to 1 L.

Extract:

- 4 ml extraction buffer + 12 g endosperm. Homogenize.
- filter through mira cloth or 4 layers cheesecloth, spin 20,000 g (14,500 rpm, SM-24 rotor), 20 min., 4°C.
- 5 · remove supernatant using a glass pipette.
- 0.85 ml extract + 0.1 ml glycerol + 0.05 ml 0.5% bromophenol blue.
- vortex and spin 5 min. full speed microfuge. Use directly or freeze in liquid nitrogen and store at -80°C for up to 2 weeks.

Cast Gels:

- 10 Attach Gel Bond PAG film (FMC Industries, Rockland, ME) to (inside of) outer glass plate using two-sided scotch tape, hydrophilic side up. The tape and the film is lined up as closely and evenly as possible with the bottom of the plate. The film is slightly smaller than the plate. Squirt water between the film and the plate to adhere the film. Use a tissue to push out excess water. Set up plates as usual, then seal the bottom
- 15 of the plates with tacky adhesive. The cassette will fit into the casting stand if the gray rubber is removed from the casting stand. The gel polymerizes with the film, and stays attached during all subsequent manipulations.

Cast 4.5% T resolve mini-gel (0.75 mm):

- 20 2.25 ml dH₂O
- + 3.75 ml sucrose solution
- + 2.5 ml resolve buffer
- + 1.5 ml 30% Acryl/Bis stock
- + various amounts of glycogen for each gel (i.e., 0 - 1.0%)
- DEGAS 15 MIN.
- 25 + 50 µl 10% APS
- + 5 µl TEMED
- POLYMERIZE FOR 30 MIN. OR OVERNIGHT

Cast 3.125 % T stack:

1.59 ml dH₂O

+ 3.75 ml sucrose solution
+ 2.5 ml stack buffer
+ 2.083 ml 15% Acryl/Bis stock

DO NOT DEGAS

5 15 μ l 10% APS

+ 35 μ l riboflavin solution

+ 30 μ l TEMED

POLYMERIZE FOR 2.5 HOURS CLOSE TO A LIGHT BULB

cool in 4°C before pulling out combs. Can also not use combs, and just

10 cast a centimeter of stacker.

The foregoing procedure:

- Can run at different temperatures; preincubate gels and solutions.
- Pre-run for 15 min. at 200 V
- Load gel: 7 μ l per well, or 115 μ l if no comb.
- 15 · Run at 140 V until dye front is close to bottom. Various running temperatures are achieved by placing the whole gel rig into a water bath. Can occasionally stop the run to insert a temperature probe into the gel.
- Enzyme assay: Cut gels off at dye front. Incubate in SS. Assay mix overnight at room temperature with gentle shaking. Rinse gels with water. Flood with I2/KI
- 20 solution.
- Take pictures of the gels on a light box, and measure the pictures. R_m = mm from top of gel to the active band/mm from top of gel to the bottom of the gel where it was cut (where the dye front was). Plot % glycogen vs. $1/R_m$. The point where the line intersects the x axis is $-K$ (where $y=0$).

25 **Testing and evaluation protocol for SER region length:**

Following the procedure above for selection of the SER region requires four basic steps. First DNA encoding a protein having a starch-encapsulation region must be selected. This can be selected from known starch-synthesizing genes or starch-binding genes such as genes for amylases, for example. The protein must be extracted. A number

30 of protein extraction techniques are well known in the art. The protein may be treated

with proteases to form protein fragments of different lengths. The preferred fragments have deletions primarily from the N-terminus region of the protein. The SER region is located nearer to the C-terminus end than the N-terminus end. The protein is run on the gels described above and affinity for the gel matrix is evaluated. Higher affinity shows more preference of that region of the protein for the matrix. This method enables comparison of different proteins to identify the starch-encapsulating regions in natural or synthetic proteins.

Example Two:

SER Fusion Vector:

The following fusion vectors are adapted for use in *E.coli*. The fusion gene that was attached to the probable SER in these vectors encoded for the green fluorescent protein (GFP). Any number of different genes encoding for proteins and polypeptides could be ligated into the vectors. A fusion vector was constructed having the SER of *waxy* maize fused to a second gene or gene fragment, in this case GFP.

pEXS114 (see FIG. 1a): Synthetic GFP (SGFP) was PCR-amplified from the plasmid HBT-SGFP (from Jen Sheen; Dept. of Molecular Biology; Wellman 11, MGH; Boston, MA 02114) using the primers EXS73 (5'-GACTAGTCATATG GTG AGC AAG GGC GAG GAG-3') [SEQ ID NO:1] and EXS74 (5'-CTAGATCTTCATATG CTT GTA CAG CTC GTC CAT GCC-3') [SEQ ID NO:2]. The ends of the PCR product were polished off with T DNA polymerase to generate blunt ends; then the PCR product was digested with *Spe* I. This SGFP fragment was subcloned into the *EcoRV-Spe* I sites of pBSK (Stratagene at 11011 North Torrey Pines Rd. La Jolla, Ca.) to generate pEXS114.

pEXS115 [see FIG. 1b]: Synthetic GFP (SGFP) was PCR-amplified from the plasmid HBT-SGFP (from Jen Sheen) using the primers EXS73 (see above) and EXS75 (5'-CTAGATCTTGGCCATGGC CTT GTA CAG CTC GTC CAT GCC-3') [SEQ ID NO:3]. The ends of the PCR product were polished off with T DNA polymerase to generate blunt ends; then the PCR product was digested with *Spe* I. This SGFP fragment was subcloned into the *EcoRV-Spe* I sites of pBSK (Stratagene) generating pEXS115.

pEXSWX (see FIG. 2a): Maize WX subcloned *NdeI*-*Not I* into pET-21a (see FIG. 2b). The genomic DNA sequence and associated amino acids from which the mRNA sequence can be generated is shown in TABLES 1a and 1b below and alternatively the DNA listed in the following tables could be employed.

TABLE 1a
DNA Sequence and Deduced Amino Acid Sequence
of the waxy Gene in Maize
[SEQ ID NO:4 and SEQ ID NO:5]

	LOCUS	ZMWAXY	4800 bp	DNA	PLN
10	DEFINITION	Zea mays waxy (wx+) locus for UDP-glucose starch glycosyl transferase.			
	ACCESSION	X03935 M24258			
	KEYWORDS	glycosyl transferase; transit peptide; UDP-glucose starch glycosyl transferase; waxy locus.			
15	SOURCE	maize.			
	ORGANISM	Zea mays			
		Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida; Commelinidae; Cyperales; Poaceae.			
	REFERENCE	1 (bases 1 to 4800)			
20	AUTHORS	Kloesgen, R.B., Gierl, A., Schwarz-Sommer, Z. and Saedler, H.			
	TITLE	Molecular analysis of the waxy locus of Zea mays			
	JOURNAL	Mol. Gen. Genet. 203, 237-244 (1986)			
	STANDARD	full automatic			
	COMMENT	NCBI gi: 22509			
25	FEATURES	Location/Qualifiers			
	source	1..4800			
		/organism="Zea mays"			
	repeat_region	283..287			
		/note="direct repeat 1"			
30	repeat_region	288..292			
		/note="direct repeat 1"			
	repeat_region	293..297			
		/note="direct repeat 1"			
35	repeat_region	298..302			
		/note="direct repeat 1"			
	misc_feature	372..385			
		/note="GC stretch (pot. regulatory factor binding site)"			
	misc_feature	442..468			
40		/note="GC stretch (pot. regulatory factor binding site)"			
	misc_feature	768..782			
		/note="GC stretch (pot. regulatory factor binding site)"			
45	misc_feature	810..822			
		/note="GC stretch (pot. regulatory factor binding site)"			
	misc_feature	821..828			
		/note="target duplication site (Ac7)"			
50	CAAT_signal	821..828			
	TATA_signal	867..873			
	misc_feature	887..900			
		/note="GC stretch (pot. regulatory factor binding site)"			
55	misc_feature	901			
		/note="transcriptional start site"			
	exon	901..1080			
		/number=1			

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    intron          1081..1219
                    /number=1
    exon            1220..1553
                    /number=2
5    transit_peptide 1233..1448
    CDS             join(1449..1553,1685..1765,1860..1958,2055..2144,
2226..2289,2413..2513,2651..2760,2858..3101,3212..3394,
10    3490..3681,3793..3879,3977..4105,4227..4343)
                    /note="NCBI gi: 22510"
                    /codon_start=1
                    /product="glucosyl transferase"

15    /translation="ASAGMNVVVFVGAEMAPWSKTGGLGDLGGLPPAMAANGHRVMV
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KIYGPVAGTDYRDNQLRFSLLCQAALAPRILSLNNNPYFSGPYGEDVVFVVCNDWHTG
20    PLSCYLKSNIYQSHGIYRDAKTAFCIHNIYQGRFAFSYDPELNLPERFKSSFDFIDGY
EKPVEGRKINWMKAGILEADRVLTVSPYYAEELISGIARGCELDNIMRLTGITGIVNG
MDVSEWDPSRDKYIAVKYDVSTAVEAKALNKEALQAEVGLPVDRNIPLVAFIGRLEEQ
25    KGPDMMAAIPQLMEMVEDVQIVLLGTGKKKFERMLMSAEEKFPGKVRVAVVKFNAALA
HHIMAGADVLAVTSRFEPCLIQQLQGMRYGTPCACASTGGLVDTIIEGKTGFHMGRLS
30    VDCNVVEPADVKKVATTLQRAIKVVGTPAYEEMVRNCMIQDLSWKGPKNWENVLLSL
    GVAGGEPGVEGEEIAPLAKENVAAP"
    intron          1554..1684
                    /number=2
    exon            1685..1765
                    /number=3
35    intron          1766..1859
                    /number=3
    exon            1860..1958
                    /number=4
40    intron          1959..2054
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    exon            2055..2144
                    /number=5
45    intron          2145..2225
                    /number=5
    exon            2226..2289
                    /number=6
    intron          2290..2412
                    /number=6
50    exon            2413..2513
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    intron          2514..2650
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55    exon            2651..2760
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                    /number=8
    exon            2858..3101
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60    intron          3102..3211
                    /number=9
    exon            3212..3394
                    /number=10
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                    /note="target duplication site (Ac9)"
    intron          3395..3489
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    exon            3490..3681

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        /number=11
        exon 3793..3879
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        intron 3880..3976
        /number=12
    10      exon 3977..4105
        /number=13
        intron 4106..4226
        /number=13
        exon 4227..4595
        /number=14
    15      polyA_signal 4570..4575
        polyA_signal 4593..4598
        polyA_site 4595
        polyA_signal 4597..4602
    20      polyA_site 4618
        polyA_site 4625
BASE COUNT 935 A 1413 C 1447 G 1005 T
ORIGIN
    25      1 CAGCGACCTA TTACACAGCC CGCTCGGGCC CGCGACGTCG GGACACATCT TCTTCCCCCT
        61 TTTGGTGAAG CTCTGCTCGC AGCTGTCCGG CTCCTTGGAC GTTCGTGTGG CAGATTCATC
        121 TGTTGTCTCG TCTCCTGTGC TTCCTGGGTA GCTTGTGTAG TGGAGCTGAC ATGGTCTGAG
    30      181 CAGGCTTAAA ATTTGCTCGT AGACGAGGAG TACCAGCACA GCACGTTGCG GATTTCTCTG
        241 CCTGTGAAGT GCAACGTCTA GGATTGTCAC ACGCCTTGGT CGCGTCGCGT CGCGTCGCGT
        301 CGATGCGGTG GTGAGCAGAG CAGCAACAGC TGGGCGGCCC AACGTTGGCT TCCGTGTCTT
    35      361 CGTCGTACGT ACGCGCGCGC CGGGGACACG CAGCAGAGAG CGGAGAGCGA GCCGTGCACG
        421 GGGAGGTGGT GTGGAAGTGG AGCCGCGCGC CCGGCCGCCC GCGCCCGGTG GGCAACCCAA
    40      481 AAGTACCCAC GACAAGCGAA GGCGCCAAAG CGATCCAAGC TCCGGAACGC AACAGCATGC
        541 GTCGCGTCGG AGAGCCAGCC ACAAGCAGCC GAGAACCGAA CCGGTGGGCG AC GCGTCATG
        601 GGACGGACGC GGGCGACGCT TCCAAACGGG CCACGTACGC CGGCGTGTGC GTGCGTGCAG
    45      661 ACGACAAGCC AAGGCGAGGC AGCCCCGAT CGGGAAAGCG TTTTGGGCGC GAGCGCTGGC
        721 GTGCGGGTCA GTCGCTGGTG CGCAGTGCCG GGGGGAACGG GTATCGTGGG GGGCGCGGGC
    50      781 GGAGGAGAGC GTGGCGAGGG CCGAGAGCAG CGCGCGGCCG GGTCACGCAA CGCGCCCCAC
        841 GTACTGCCCT CCCCCTCCGC GCGCGCTAGA AATACCGAGG CCTGGACCGG GGGGGGGCCC
        901 CGTCACATCC ATCCATCGAC CGATCGATCG CCACAGCCAA CACCACCCGC CGAGGCGACG
    55      961 CGACAGCCGC CAGGAGGAAG GAATAAACTC ACTGCCAGCC AGTGAAGGGG GAGAAGTGTA
        1021 CTGCTCCGTC GACCAGTGCG CGCACC GCCAGGGCTG CTCATCTCGT CGACGACCAG
    60      1081 GTTCTGTTCC GTTCCGATCC GATCCGATCC TGTCCTTGAG TTTCGTCCAG ATCCTGGCGC
        1141 GTATCTGCGT GTTTGATGAT CCAGGTTCTT CGAACCTAAA TCTGTCCGTG CACACGTCTT
        1201 TTCTCTCTCT CCTACGCAGT GGATTAATCG GCATGGCGGC TCTGGCCACG TCGCAGCTCG
    65      1261 TCGCAACGCG CGCCGGCCTG GCGTCCCGG ACGCGTCCAC GTTCCGCCGC GCGCCGCGC

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5 1321 AGGGCCTGAG GGGGGCCCGG GCGTCGGCGG CGGCGGACAC GCTCAGCATG CGGACCAGCG
1381 CGCGCGCGGC GCCCAGGCAC CAGCAGCAGG CGCGCCGCGG GGGCAGGTTT CCGTCGCTCG
10 1441 TCGTGTGCGC CAGCGCCGCG ATGAACGTCG TCTTCGTCGG CGCCGAGATG GCGCCGTGGA
1501 GCAAGACCGG CGGCCTCGGC GACGTCCTCG GCGGCCTGCC GCCGGCCATG GCCGTAAGCG
1561 CGCGCACC GAACATGCATC CGTTGGATCG CGTCTTCTTC GTGCTCTTGC CGCGTGCATG
1621 ATGCATGTGT TTCCTCCTGG CTTGTGTTCG TGTATGTGAC GTGTTTGTTC GGGCATGCAT
1681 GCAGGCGAAC GGGCACCCTG TCATGGTTCG CTCTCCCCGC TACGACCAGT ACAAGGACGC
15 1741 CTGGGACACC AGCGTCGTGT CCGAGGTACG GCCACCGAGA CCAGATTCAG ATCACAGTCA
1801 CACACACCGT CATATGAACC TTTCTCTGCT CTGATGCCTG CAACTGCAAA TGCATGCAGA
20 1861 TCAAGATGGG AGACGGGTAC GAGACGGTCA GGTCTTCCA CTGCTACAAG CGCGGAGTGG
1921 ACCGCGTGTT CGTTGACCAC CCACTGTTCC TGGAGAGGGT GAGACGAGAT CTGATCACTC
1981 GATACGCAAT TACCACCCCA TTGTAAGCAG TTACAGTGAG CTTTTTTTCC CCCC GGCCCTG
25 2041 GTCGCTGGTT TCAGGTTTGG GGAAAGACCG AGGAGAAGAT CTACGGGCCT GTCGCTGGAA
2101 CGGACTACAG GGACAACCAG CTGCGGTTCA GCCTGCTATG CCAGGTCAGG ATGGCTTGGT
30 2161 ACTACAATT CATATCATCT GTATGCAGCA GTATACACTG ATGAGAAATG CATGCTGTTC
2221 TGCAGGCAGC ACTTGAAGCT CCAAGGATCC TGAGCCTCAA CAACAACCCA TACTTCTCCG
2281 GACCATACGG TAAGAGTTGC AGTCTTCGTA TATATATCTG TTGAGCTCGA GAATCTTCAC
35 2341 AGGAAGCGGC CCATCAGACG GACTGTCATT TTACACTGAC TACTGCTGCT GCTCTTCGTC
2401 CATCCATACA AGGGGAGGAC GTCGTGTTCG TCTGCAACGA CTGGCACACC GGCCCTCTCT
40 2461 CGTGCTACCT CAAGAGCAAC TACCAGTCCC ACGGCATCTA CAGGGACGCA AAGGTTGCCT
2521 TCTCTGAACT GAACAACGCC GTTTTCGTTT TCCATGCTCG TATATACCTC GTCTGGTAGT
2581 GGTGGTGCTT CTCTGAGAAA CTAAGTGAAG CTGACTGCAT GTCTGTCTGA CCATCTTCAC
45 2641 GTACTACCAG ACCGCTTTCT GCATCCACAA CATCTCCTAC CAGGGCCGGT TCGCCTTCTC
2701 CGACTACCCG GAGCTGAACC TCCCGGAGAG ATTCAAGTCG TCCTTCGATT TCATCGACGG
50 2761 GTCTGTTTTT CTGCGTGCAT GTGAACATTC ATGAATGGTA ACCCACTA GTTTCGCTCC
2821 TGCTGGTTCA TTATCTGACC TGATTGCATT ATTGCAGCTA CGAGAAGCCC GTGGAAGGCC
2881 GGAAGATCAA CTGGATGAAG GCCGGGATCC TCGAGGCCGA CAGGGTCTCT ACCGTCAGCC
55 2941 CCTACTACGC CGAGGAGCTC ATCTCCGGCA TCGCCAGGGG CTGCGAGCTC GACAACATCA
3001 TCGCCTCAC CGGCATCACC GGCATCGTCA ACGGCATGGA CGTCAGCGAG TGGGACCCCA
60 3061 GCAGGGACAA GTACATCGCC GTGAAGTACG ACGTGTGAC GGTGAGCTGG CTAGCTCTGA
3121 TTCTGCTGCC TGGTCTCCT GCTCATCATG CTGGTTCGGT ACTGACGCGG CAAGTGATACG
3181 TACGTGCGTG CGACGGTGGT GTCCGGTTCA GGCCGTGGAG GCCAAGGCGC TGAACAAGGA
65 3241 GCGCTGCAG GCGGAGGTCG GGCTCCCGGT GGACCGGAAC ATCCCGCTGG TGGCGTTCAT
3301 CGGCAGGCTG GAAGAGCAGA AGGGCCCGA CGTCATGGCG GCCGCCATCC CGCAGCTCAT

5 3361 GGAGATGGTG GAGGACGTGC AGATCGTTCT GCTGGTACGT GTGCGCCGGC CGCCACCCGG
3421 CTACTACATG CGTGTATCGT TCGTTCTACT GGAACATGCG TGTGAGCAAC GCGATGGATA
3481 ATGCTGCAGG GCACGGGCAA GAAGAAGTTC GAGCGCATGC TCATGAGCGC CGAGGAGAAG
10 3541 TTCCCAGGCA AGGTGCGCGC CGTGGTCAAG TTCAACGCGG CGCTGGCGCA CCACATCATG
3601 GCCGGCGCCG ACGTGCTCGC CGTCACCAGC CGCTTCGAGC CCTGCGGCCT CATCCAGCTG
3661 CAGGGGATGC GATACGGAAC GGTACGAGAG AAAAAAAAAA TCCTGAATCC TGACGAGAGG
3721 GACAGAGACA GATTATGAAT GCTTCATCGA TTTGAATTGA TTGATCGATG TCTCCCGCTG
15 3781 CCACTCTTGC AGCCCTGCGC CTGCGCGTCC ACCGGTGGAC TCGTCGACAC CATCATCGAA
3841 GGCAAGACCG GGTTCACAT GGGCCGCCCTC AGCGTCGACG TAAGCCTAGC TCTGCCATGT
20 3901 TCTTTCTTCT TTCTTTCTGT ATGTATGTAT GAATCAGCAC CGCCGTTCTT GTTTCGTCGT
3961 CGTCCTCTCT TCCCAGTGTA ACGTCGTGGA GCCGGCGGAC GTCAAGAAGG TGGCCACCAC
4021 ATTGCAGCGC GCCATCAAGG TGGTCGGCAC GCCGGCGTAC GAGGAGATGG TGAGGAACTG
25 4081 CATGATCCAG GATCTCTCCT GGAAGGTACG TACGCCCCGC CCGCCCCGCC CCGCCAGAGC
4141 AGAGCGCCAA GATCGACCGA TCGACCGACC ACACGTACGC GCCTCGCTCC TGTGCTGAC
30 4201 CGTGGTTTAA TTTGCGAAAT GCGCAGGGCC CTGCCAAGAA CTGGGAGAAC GTGCTGCTCA
4261 GCCTCGGGGT CGCCGGCGGC GAGCCAGGGG TCGAAGGCCA GGAGATCGCG CCGCTCGCCA
4321 AGGAGAACGT GGCCGCGCCC TGAAGAGTTC GGCTGCAGG GCGCTGATC TCGCGCGTGG
35 4381 TGCAAAGATG TTGGGACATC TTCTTATATA TGCTGTTTCG TTTATGTGAT ATGGACAAGT
4441 ATGTGTAGCT GCTTGCTTGT GCTAGTGTA TGTAGTGTAG TGGTGGCCAG TGGCACAACC
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40 4561 TTGCGAGTAA ATAAATGGAC CTGTAGTGGT GGAGTAAATA ATCCCTGCTG TTCGGTGTTC
4621 TTATCGCTCC TCGTATAGAT ATTATATAGA GTACATTTTT CTCTCTCTGA ATCCTACGTT
45 4681 TGTGAAATTT CTATATCATT ACTGTAAAAT TTCTGCGTTC CAAAAGAGAC CATAGCCTAT
4741 CTTTGGCCCT GTTTGTTTCG GCTTCTGGCA GCTTCTGGCC ACCAAAAGCT GCTGCGGACT

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TABLE 1b
DNA Sequence and Deduced Amino Acid Sequence in waxy Gene in Rice
[SEQ ID NO:6 and SEQ ID NO:7]

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5  LOCUS      OSWX      2542 bp      RNA      PLN
   DEFINITION O.sativa Waxy mRNA.
   ACCESSION  X62134 S39554
   KEYWORDS   glucosyltransferase; starch biosynthesis; waxy gene.
10  SOURCE     rice.
   ORGANISM   Oryza sativa
              Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
              Commelinidae; Cyperales; Poaceae.
   REFERENCE  1 (bases 1 to 2542)
   AUTHORS    Okayaki, R.J.
15  TITLE      Direct Submission
   JOURNAL     Submitted (12-SEP-1991) to the EMBL/GenBank/DDBJ databases.
   R.J.
              Okayaki, University of Florida, Dep of Vegetable Crops, 1255
              Fifield Hall, 514 IFAS, Gainesville, Florida 32611-0514, USA
20  STANDARD   full automatic
   REFERENCE  2 (bases 1 to 2542)
   AUTHORS    Okagaki, R.J.
   TITLE      Nucleotide sequence of a long cDNA from the rice waxy gene
   JOURNAL     Plant Mol. Biol. 19, 513-516 (1992)
25  STANDARD   full automatic
   COMMENT    NCBI gi: 20402
   FEATURES   Location/Qualifiers
              source          1..2542
              /organism="Oryza sativa"
              /dev_stage="immature seed"
              /tissue type="seed"
              CDS             453..2282
              /gene="Wx"
              /standard_name="Waxy gene"
              /EC_number="2.4.1.21"
              /note="NCBI gi: 20403"
              /codon_start=1
              /function="starch biosynthesis"
              /product="starch (bacterial glycogen) synthase"
40  /translation="MSALTTSQLATSATGFGIADRSAPSSLLRHGFQGLKPRSPAGGD
   ATSLSVTTSARATPKQQRSVQGRSRRFPSVVVYATGAGMNVVFVGAEMAPWSKTGGLG
45  DVLGGLPPAMAANGHRVMVISPRYDQYKDAWDTSVVAEIKVADRYERVFFHCYKRGV
   DRVFIDHPSFLEKVGKTGEKIYGPDTGVDYKDNQMRFSLLCQAALAPRILNLNNNP
   YFKGTYGEDVVVFCNDWHTGPLASYLKNNYQPNGIYRNAKVAFCIHNISYQGRFATED
50  YPELNLSEFRSSFDIDGYDTPVEGRKINWMKAGILEADRVLTVPYYAEELISGIA
   RGCELDNIMRLTGITGIVNGMDVSEWDPSKDKYITAKYDATTAEAKALNKEALQAEA
55  GLPVDRKIPLIAFIGRLEEQKGPDMMAAIPELMQEDVQIVLLGTGKKKFEKLLKSME
   EKYPGKVRVAVKFNAPLAHLIMAGADVLAVPSRFEPGLIQLQGMRYGTPCACASTGG
   LVDTVIEGKTGFHMGRLSVDCKVVEPSDVKKVAATLKRAIKVVGTPAYEEMVRNCMNQ
60  DLSWKGPAKNWENVLLGLGVAGSAPGIEGDEIAPLAKENVAAP"
   3'UTR      2283..2535
   polyA_site 2535
   BASE COUNT 610 A      665 C      693 G      574 T
   ORIGIN
65  1 GAATTCAGTG TGAAGGAATA GATTCTCTTC AAAACAATTT AATCATTCAT CTGATCTGCT

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61 CAAAGCTCTG TGCATCTCCG GGTGCAACGG CCAGGATATT TATTGTGCAG TAAAAAATG
121 TCATATCCCC TAGCCACCCA AGAAACTGCT CCTTAAGTCC TTATAAGCAC ATATGGCATT
181 GTAATATATA TGTTTGAGTT TTAGCGACAA TTTTTTTAAA AACTTTTGGT CCTTTTATG
241 AACGTTTTAA GTTTCACGT CTTTTTTTTT CGAATTTTAA ATGTAGCTTC AAATTCTAAT
301 CCCC AATCCA AATTGTAATA AACTTCAATT CTCCTAATTA ACATCTTAAT TCATTTATTT
361 GAAAACCAGT TCAAATTCTT TTTAGGCTCA CCAAACCTTA AACAAATCAA TTCAGTGCAG
421 AGATCTTCCA CAGCAACAGC TAGACAACCA CCATGTCGGC TCTCACCAGC TCCCAGCTCG
481 CCACCTCGGC CACCGGCTTC GGCATCGCCG ACAGGTCGGC GCCGTCGTCG CTGCTCCGCC
541 ACGGGTTCCA GGGCCTCAAG CCCCGCAGCC CCGCCGGCGG CGACGCGACG TCGCTCAGCG
601 TGACGACCAG CGCGCGCGCG ACGCCCAAGC AGCAGCGGTC GGTGCAGCGT GGCAGCCGGA
661 GGTTCCCCTC CGTCGTCGTG TACGCCACCG GCGCCGGCAT GAACGTCGTG TTCGTCGGCG
721 CCGAGATGGC CCCCTGGAGC AAGACCGGCG GCCTCGGTGA CGTCCTCGGT GGCCTCCCCC
781 CTGCCATGGC TGCGAATGGC CACAGGGTCA TGGTGATCTC TCCTCGGTAC GACCAGTACA
841 AGGACGCTTG GGATACCAGC GTTGTGGCTG AGATCAAGGT TGCAGACAGG TACGAGAGGG
901 TGAGGTTTTT CCATTGCTAC AAGCGTGGAG TCGACCGTGT GTTCATCGAC CATCCGTCAT
961 TCCTGGAGAA GGT TTGGGA AAGACCGGTG AGAAGATCTA CGGACCTGAC ACTGGAGTTG
1021 ATTACAAAGA CAACCAGATG CGTTTCAGCC TTCTTTGCCA GGCAGCACTC GAGGCTCCTA
1081 GGATCCTAAA CCTCAACAAC AACCATACT TCAAAGGAAC TTATGGTGAG GATGTTGTGT
1141 TCGTCTGCAA CGACTGGCAC ACTGGCCAC TGGCGAGCTA CCTGAAGAAC AACTACCAGC
1201 CCAATGGCAT CTACAGGAAT GCAAAGGTTG CTTTCTGCAT CCACAACATC TCCTACCAGG
1261 GCCGTTTCGC TTTCGAGGAT TACCCTGAGC TGAACCTCTC CGAGAGGTTT AGGTCATCCT
1321 TCGATTTTCA CGACGGGTAT GACACGCCGG TGGAGGGCAG GAAGATCAAC TGGATGAAGG
1381 CCGGAATCCT GGAAGCCGAC AGGGTGCTCA CCGTGAGCCC GTACTACGCC GAGGAGCTCA
1441 TCTCCGGCAT CGCCAGGGGA TGCGAGCTCG ACAACATCAT GCGGCTCACC GGCATCACC
1501 GCATCGTCAA CGGCATGGAC GTCAGCGAGT GGGATCCTAG CAAGGACAAG TACATCACC
1561 CCAAGTACGA CGCAACCACG GCAATCGAGG CGAAGGCGCT GAACAAGGAG GCGTTGCAGG
1621 CGGAGGCGGG TCTTCCGGTC GACAGGAAAA TCCCACTGAT CGCGTTCATC GGCAGGCTGG
1681 AGGAACAGAA GGGCCCTGAC GTCATGGCCG CCGCCATCCC GGAGCTCATG CAGGAGGACG
1741 TCCAGATCGT TCTTCTGGGT ACTGGAAAGA AGAAGTTCGA GAAGCTGCTC AAGAGCATGG
1801 AGGAGAAGTA TCCGGGCAAG GTGAGGGCGG TGGTGAAGTT CAACGCGCCG CTTGCTCATC
1861 TCATCATGGC CGGAGCCGAC GTGCTCGCCG TCCCCAGCCG CTTGAGCCC TGTGGACTCA
1921 TCCAGCTGCA GGGGATGAGA TACGGAACGC CCTGTGCTTG CGCGTCCACC GGTGGGCTCG
1981 TGGACACGGT CATCGAAGGC AAGACTGGTT TCCACATGGG CCGTCTCAGC GTCGACTGCA
2041 AGGTGGTGGA GCCAAGCGAC GTGAAGAAGG TGGCGGCCAC CCTGAAGCGC GCCATCAAGG

2101 TCGTCGGCAC GCCGGCGTAC GAGGAGATGG TCAGGAACTG CATGAACCAG GACCTCTCCT
 2161 GGAAGGGGCC TGCGAAGAAC TGGGAGAATG TGCTCCTGGG CCTGGGCGTC GCCGGCAGCG
 5 2221 CGCCGGGGAT CGAAGGCGAC GAGATCGCGC CGCTCGCCAA GGAGAACGTG GCTGCTCCTT
 2281 GAAGAGCCTG AGATCTACAT ATGGAGTGAT TAATTAATAT AGCAGTATAT GGATGAGAGA
 10 2341 CGAATGAACC AGTGGTTTGT TTGTTGTAGT GAATTTGTAG CTATAGCCAA TTATATAGGC
 2401 TAATAAGTTT GATGTTGTAC TCTTCTGGGT GTGCTTAAGT ATCTTATCGG ACCCTGAATT
 2461 TATGTGTGTG GCTTATTGCC AATAATATTA AGTAATAAAG GGTTTATTAT ATTATTATAT
 15 2521 ATGTTATATT ATACTAAAAA AA

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TABLE 2
DNA Sequence and Deduced Amino Acid Sequence of
the Soluble Starch Synthase IIa Gene in Maize
[SEQ ID NO:8 and SEQ ID NO:9]

FILE NAME : MSS2C.SEQ SEQUENCE : NORMAL 2007 BP

CODON TABLE : UNIV.TCN

SEQUENCE REGION : 1 - 2007

TRANSLATION REGION : 1 - 2007

*** DNA TRANSLATION ***

1	GCT GAG GCT GAG GCC GGG GGC AAG GAC GCG CCG CCG GAG AGG AGC GGC	48
1	A E A E A G G K D A P P E R S G	16
49	GAC GCC GCC AGG TTG CCC CGC GCT CGG CGC AAT GCG GTC TCC AAA CGG	96
17	D A A R L P R A R R N A V S K R	32
97	AGG GAT CCT CTT CAG CCG GTC GGC CGG TAC GGC TCC GCG ACG GGA AAC	144
33	R D P L Q P V G R Y G S A T G N	48
145	ACG GCC AGG ACC GGC GCC GCG TCC TGC CAG AAC GCC GCA TTG GCG GAC	192
49	T A R T G A A S C Q N A A L A D	64
193	GTT GAG ATC GTT GAG ATC AAG TCC ATC GTC GCC GCG CCG CCG ACG AGC	240
65	V E I V E I K S I V A A P P T S	80
241	ATA GTG AAG TTC CCA GGG CGC GGG CTA CAG GAT GAT CCT TCC CTC TGG	288
81	I V K F P G R G L Q D D P S L W	96
289	GAC ATA GCA CCG GAG ACT GTC CTC CCA GCC CCG AAG CCA CTG CAT GAA	336
97	D I A P E T V L P A P K P L H E	112
337	TCG CCT GCG GTT GAC GGA GAT TCA AAT GGA ATT GCA CCT CCT ACA GTT	384
113	S P A V D G D S N G I A P P T V	128
385	GAG CCA TTA GTA CAG GAG GCC ACT TGG GAT TTC AAG AAA TAC ATC GGT	432
129	E P L V Q E A T W D F K K Y I G	144
433	TTT GAC GAG CCT GAC GAA GCG AAG GAT GAT TCC AGG GTT GGT GCA GAT	480

	145	F	D	E	P	D	E	A	K	D	D	S	R	V	G	A	D	160
	481	GAT	GCT	GGT	TCT	TTT	GAA	CAT	TAT	GGG	ACA	ATG	ATT	CTG	GGC	CTT	TGT	528
	161	D	A	G	S	F	E	H	Y	G	T	M	I	L	G	L	C	176
5	529	GGG	GAG	AAT	GTT	ATG	AAC	GTG	ATC	GTG	GTG	GCT	GCT	GAA	TGT	TCT	CCA	576
	177	G	E	N	V	M	N	V	I	V	V	A	A	E	C	S	P	192
	577	TGG	TGC	AAA	ACA	GGT	GGT	CTT	GGA	GAT	GTT	GTG	GGA	GCT	TTA	CCC	AAG	624
	193	W	C	K	T	G	G	L	G	D	V	V	G	A	L	P	K	208
	625	GCT	TTA	GCG	AGA	AGA	GGA	CAT	CGT	GTT	ATG	GTT	GTG	GTA	CCA	AGG	TAT	672
	209	A	L	A	R	R	G	H	R	V	M	V	V	V	P	R	Y	224
10	673	GGG	GAC	TAT	GTG	GAA	GCC	TTT	GAT	ATG	GGA	ATC	CGG	AAA	TAC	TAC	AAA	720
	225	G	D	Y	V	E	A	F	D	M	G	I	R	K	Y	Y	K	240
	721	GCT	GCA	GGA	CAG	GAC	CTA	GAA	GTG	AAC	TAT	TTC	CAT	GCA	TTT	ATT	GAT	768
	241	A	A	G	Q	D	L	E	V	N	Y	F	H	A	F	I	D	256
15	769	GGA	GTC	GAC	TTT	GTG	TTC	ATT	GAT	GCC	TCT	TTC	CGG	CAC	CGT	CAA	GAT	816
	257	G	V	D	F	V	F	I	D	A	S	F	R	H	R	Q	D	272
	817	GAC	ATA	TAT	GGG	GGA	AGT	AGG	CAG	GAA	ATC	ATG	AAG	CGC	ATG	ATT	TTG	864
	273	D	I	Y	G	G	S	R	Q	E	I	M	K	R	M	I	L	288
	865	TTT	TGC	AAG	GTT	GCT	GTT	GAG	GTT	CCT	TGG	CAC	GTT	CCA	TGC	GGT	GGT	912
	289	F	C	K	V	A	V	E	V	P	W	H	V	P	C	G	G	304
20	913	GTG	TGC	TAC	GGA	GAT	GGA	AAT	TTG	GTG	TTC	ATT	GCC	ATG	AAT	TGG	CAC	960
	305	V	C	Y	G	D	G	N	L	V	F	I	A	M	N	W	H	320
	961	ACT	GCA	CTC	CTG	CCT	GTT	TAT	CTG	AAG	GCA	TAT	TAC	AGA	GAC	CAT	GGG	1008
	321	T	A	L	L	P	V	Y	L	K	A	Y	Y	R	D	H	G	336
25	1009	TTA	ATG	CAG	TAC	ACT	CGC	TCC	GTC	CTC	GTC	ATA	CAT	AAC	ATC	GGC	CAC	1056
	337	L	M	Q	Y	T	R	S	V	L	V	I	H	N	I	G	H	352
	1057	CAG	GGC	CGT	GGT	CCT	GTA	CAT	GAA	TTC	CCG	TAC	ATG	GAC	TTG	CTG	AAC	1104
	353	Q	G	R	G	P	V	H	E	F	P	Y	M	D	L	L	N	368
	1105	ACT	AAC	CTT	CAA	CAT	TTC	GAG	CTG	TAC	GAT	CCC	GTC	GGT	GGC	GAG	CAC	1152
	369	T	N	L	Q	H	F	E	L	Y	D	P	V	G	G	E	H	384
30	1153	GCC	AAC	ATC	TTT	GCC	GCG	TGT	GTT	CTG	AAG	ATG	GCA	GAC	CGG	GTG	GTG	1200
	385	A	N	I	F	A	A	C	V	L	K	M	A	D	R	V	V	400
	1201	ACT	GTC	AGC	CGC	GGC	TAC	CTG	TGG	GAG	CTG	AAG	ACA	GTG	GAA	GGC	GGC	1248
	401	T	V	S	R	G	Y	L	W	E	L	K	T	V	E	G	G	416
35	1249	TGG	GGC	CTC	CAC	GAC	ATC	ATC	CGT	TCT	AAC	GAC	TGG	AAG	ATC	AAT	GGC	1296
	417	W	G	L	H	D	I	I	R	S	N	D	W	K	I	N	G	432
	1297	ATT	CGT	GAA	CGC	ATC	GAC	CAC	CAG	GAG	TGG	AAC	CCC	AAG	GTG	GAC	GTG	1344
	433	I	R	E	R	I	D	H	Q	E	W	N	P	K	V	D	V	448
	1345	CAC	CTG	CGG	TCG	GAC	GGC	TAC	ACC	AAC	TAC	TCC	CTC	GAG	ACA	CTC	GAC	1392
	449	H	L	R	S	D	G	Y	T	N	Y	S	L	E	T	L	D	464
40	1393	GCT	GGA	AAG	CGG	CAG	TGC	AAG	GCG	GCC	CTG	CAG	CGG	GAC	GTG	GGC	CTG	1440
	465	A	G	K	R	Q	C	K	A	A	L	Q	R	D	V	G	L	480
	1441	GAA	GTG	CGC	GAC	GAC	GTG	CCG	CTG	CTC	GGC	TTC	ATC	GGG	CGT	CTG	GAT	1488
	481	E	V	R	D	D	V	P	L	L	G	F	I	G	R	L	D	496
45	1489	GGA	CAG	AAG	GGC	GTG	GAC	ATC	ATC	GGG	GAC	GCG	ATG	CCG	TGG	ATC	GCG	1536
	497	G	Q	K	G	V	D	I	I	G	D	A	M	P	W	I	A	512

	1537	GGG	CAG	GAC	GTG	CAG	CTG	GTG	ATG	CTG	GGC	ACC	GGC	CCA	CCT	GAC	CTG	1584
	513	G	Q	D	V	Q	L	V	M	L	G	T	G	P	P	D	L	528
	1585	GAA	CGA	ATG	CTG	CAG	CAC	TTG	GAG	CGG	GAG	CAT	CCC	AAC	AAG	GTG	CGC	1632
	529	E	R	M	L	Q	H	L	E	R	E	H	P	N	K	V	R	544
5	1633	GGG	TGG	GTC	GGG	TTC	TCG	GTC	CTA	ATG	GTG	CAT	CGC	ATC	ACG	CCG	GGC	1680
	545	G	W	V	G	F	S	V	L	M	V	H	R	I	T	P	G	560
	1681	GCC	AGC	GTG	CTG	GTG	ATG	CCC	TCC	CGC	TTC	GCC	GGC	GGG	CTG	AAC	CAG	1728
	561	A	S	V	L	V	M	P	S	R	F	A	G	G	L	N	Q	576
10	1729	CTC	TAC	GCG	ATG	GCA	TAC	GGC	ACC	GTC	CCT	GTG	GTG	CAC	GCC	GTG	GGC	1776
	577	L	Y	A	M	A	Y	G	T	V	P	V	V	H	A	V	G	592
	1777	GGG	CTC	AGG	GAC	ACC	GTG	GCG	CCG	TTC	GAC	CCG	TTC	GGC	GAC	GCC	GGG	1824
	593	G	L	R	D	T	V	A	P	F	D	P	F	G	D	A	G	608
	1825	CTC	GGG	TGG	ACT	TTT	GAC	CGC	GCC	GAG	GCC	AAC	AAG	CTG	ATC	GAG	GTG	1872
	609	L	G	W	T	F	D	R	A	E	A	N	K	L	I	E	V	624
15	1873	CTC	AGC	CAC	TGC	CTC	GAC	ACG	TAC	CGA	AAC	TAC	GAG	GAG	AGC	TGG	AAG	1920
	625	L	S	H	C	L	D	T	Y	R	N	Y	E	E	S	W	K	640
	1921	AGT	CTC	CAG	GCG	CGC	GGC	ATG	TCG	CAG	AAC	CTC	AGC	TGG	GAC	CAC	GCG	1968
	641	S	L	Q	A	R	G	M	S	Q	N	L	S	W	D	H	A	656
20	1969	GCT	GAG	CTC	TAC	GAG	GAC	GTC	CTT	GTC	AAG	TAC	CAG	TGG				2007
	657	A	E	L	Y	E	D	V	L	V	K	Y	Q	W				669

TABLE 3
DNA Sequence and Deduced Amino Acid Sequence of
The Soluble Starch Synthase IIb Gene in Maize
[SEQ ID NO:10 and SEQ ID NO: 11]

25	FILE NAME : MSS3FULL.DNA SEQUENCE : NORMAL 2097 BP																	
	CODON TABLE : UNIV.TCN																	
	SEQUENCE REGION : 1 - 2097																	
	TRANSLATION REGION : 1 - 2097																	
	*** DNA TRANSLATION ***																	
30	1	ATG	CCG	GGG	GCA	ATC	TCT	TCC	TCG	TCG	TCG	GCT	TTT	CTC	CTC	CCC	GTC	48
	1	M	P	G	A	I	S	S	S	S	S	A	F	L	L	P	V	16
	49	GCG	TCC	TCC	TCG	CCG	CGG	CGC	AGG	CGG	GGC	AGT	GTG	GGT	GCT	GCT	CTG	96
	17	A	S	S	S	P	R	R	R	R	G	S	V	G	A	A	L	32
35	97	CGC	TCG	TAC	GGC	TAC	AGC	GGC	GCG	GAG	CTG	CGG	TTG	CAT	TGG	GCG	CGG	144
	33	R	S	Y	G	Y	S	G	A	E	L	R	L	H	W	A	R	48
	145	CGG	GGC	CCG	CCT	CAG	GAT	GGA	GCG	GCG	TCG	GTA	CGC	GCC	GCA	GCG	GCA	192
	49	R	G	P	P	Q	D	G	A	A	S	V	R	A	A	A	A	64
	193	CCG	GCC	GGG	GGC	GAA	AGC	GAG	GAG	GCA	GCG	AAG	AGC	TCC	TCC	TCG	TCC	240
	65	P	A	G	G	E	S	E	E	A	A	K	S	S	S	S	S	80
40	241	CAG	GCG	GGC	GCT	GTT	CAG	GGC	AGC	ACG	GCC	AAG	GCT	GTG	GAT	TCT	GCT	288

	81	Q	A	G	A	V	Q	G	S	T	A	K	A	V	D	S	A	96
	289	TCA	CCT	CCC	AAT	CCT	TTG	ACA	TCT	GCT	CCG	AAG	CAA	AGT	CAG	AGC	GCT	336
	97	S	P	P	N	P	L	T	S	A	P	K	Q	S	Q	S	A	112
5	337	GCA	ATG	CAA	AAC	GGA	ACG	AGT	GGG	GGC	AGC	AGC	GCG	AGC	ACC	GCC	GCG	384
	113	A	M	Q	N	G	T	S	G	G	S	S	A	S	T	A	A	128
	385	CCG	GTG	TCC	GGA	CCC	AAA	GCT	GAT	CAT	CCA	TCA	GCT	CCT	GTC	ACC	AAG	432
	129	P	V	S	G	P	K	A	D	H	P	S	A	P	V	T	K	144
	433	AGA	GAA	ATC	GAT	GCC	AGT	GCG	GTG	AAG	CCA	GAG	CCC	GCA	GGT	GAT	GAT	480
	145	R	E	I	D	A	S	A	V	K	P	E	P	A	G	D	D	160
10	481	GCT	AGA	CCG	GTG	GAA	AGC	ATA	GGC	ATC	GCT	GAA	CCG	GTG	GAT	GCT	AAG	528
	161	A	R	P	V	E	S	I	G	I	A	E	P	V	D	A	K	176
	529	GCT	GAT	GCA	GCT	CCG	GCT	ACA	GAT	GCG	GCG	GCG	AGT	GCT	CCT	TAT	GAC	576
	177	A	D	A	A	P	A	T	D	A	A	A	S	A	P	Y	D	192
15	577	AGG	GAG	GAT	AAT	GAA	CCT	GGC	CCT	TTG	GCT	GGG	CCT	AAT	GTG	ATG	AAC	624
	193	R	E	D	N	E	P	G	P	L	A	G	P	N	V	M	N	208
	625	GTC	GTC	GTG	GTG	GCT	TCT	GAA	TGT	GCT	CCT	TTC	TGC	AAG	ACA	GGT	GGC	672
	209	V	V	V	V	A	S	E	C	A	P	F	C	K	T	G	G	224
	673	CTT	GGA	GAT	GTC	GTG	GGT	GCT	TTG	CCT	AAG	GCT	CTG	GCG	AGG	AGA	GGA	720
	225	L	G	D	V	V	G	A	L	P	K	A	L	A	R	R	G	240
20	721	CAC	CGT	GTT	ATG	GTC	GTG	ATA	CCA	AGA	TAT	GGA	GAG	TAT	GCC	GAA	GCC	768
	241	H	R	V	M	V	V	I	P	R	Y	G	E	Y	A	E	A	256
	769	CGG	GAT	TTA	GGT	GTA	AGG	AGA	CGT	TAC	AAG	GTA	GCT	GGA	CAG	GAT	TCA	816
	257	R	D	L	G	V	R	R	R	Y	K	V	A	G	Q	D	S	272
25	817	GAA	GTT	ACT	TAT	TTT	CAC	TCT	TAC	ATT	GAT	GGA	GTT	GAT	TTT	GTA	TTC	864
	273	E	V	T	Y	F	H	S	Y	I	D	G	V	D	F	V	F	288
	865	GTA	GAA	GCC	CCT	CCC	TTC	CGG	CAC	CGG	CAC	AAT	AAT	ATT	TAT	GGG	GGA	912
	289	V	E	A	P	P	F	R	H	R	H	N	N	I	Y	G	G	304
	913	GAA	AGA	TTG	GAT	ATT	TTG	AAG	CGC	ATG	ATT	TTG	TTC	TGC	AAG	GCC	GCT	960
	305	E	R	L	D	I	L	K	R	M	I	L	F	C	K	A	A	320
30	961	GTT	GAG	GTT	CCA	TGG	TAT	GCT	CCA	TGT	GGC	GGT	ACT	GTC	TAT	GGT	GAT	1008
	321	V	E	V	P	W	Y	A	P	C	G	G	T	V	Y	G	D	336
	1009	GGC	AAC	TTA	GTT	TTC	ATT	GCT	AAT	GAT	TGG	CAT	ACC	GCA	CTT	CTG	CCT	1056
	337	G	N	L	V	F	I	A	N	D	W	H	T	A	L	L	P	352
35	1057	GTC	TAT	CTA	AAG	GCC	TAT	TAC	CGG	GAC	AAT	GGT	TTG	ATG	CAG	TAT	GCT	1104
	353	V	Y	L	K	A	Y	Y	R	D	N	G	L	M	Q	Y	A	368
	1105	CGC	TCT	GTG	CTT	GTG	ATA	CAC	AAC	ATT	GCT	CAT	CAG	GGT	CGT	GGC	CCT	1152
	369	R	S	V	L	V	I	H	N	I	A	H	Q	G	R	G	P	384
	1153	GTA	GAC	GAC	TTC	GTC	AAT	TTT	GAC	TTG	CCT	GAA	CAC	TAC	ATC	GAC	CAC	1200
	385	V	D	D	F	V	N	F	D	L	P	E	H	Y	I	D	H	400
40	1201	TTC	AAA	CTG	TAT	GAC	AAC	ATT	GGT	GGG	GAT	CAC	AGC	AAC	GTT	TTT	GCT	1248
	401	F	K	L	Y	D	N	I	G	G	D	H	S	N	V	F	A	416
	1249	GCG	GGG	CTG	AAG	ACG	GCA	GAC	CGG	GTG	GTG	ACC	GTT	AGC	AAT	GGC	TAC	1296
	417	A	G	L	K	T	A	D	R	V	V	T	V	S	N	G	Y	432
45	1297	ATG	TGG	GAG	CTG	AAG	ACT	TCG	GAA	GGC	GGG	TGG	GGC	CTC	CAC	GAC	ATC	1344
	433	M	W	E	L	K	T	S	E	G	G	W	G	L	H	D	I	448

	1345	ATA	AAC	CAG	AAC	GAC	TGG	AAG	CTG	CAG	GGC	ATC	GTG	AAC	GGC	ATC	GAC	1392
	449	I	N	Q	N	D	W	K	L	Q	G	I	V	N	G	I	D	464
	1393	ATG	AGC	GAG	TGG	AAC	CCC	GCT	GTG	GAC	GTG	CAC	CTC	CAC	TCC	GAC	GAC	1440
	465	M	S	E	W	N	P	A	V	D	V	H	L	H	S	D	D	480
5	1441	TAC	ACC	AAC	TAC	ACG	TTC	GAG	ACG	CTG	GAC	ACC	GGC	AAG	CGG	CAG	TGC	1488
	481	Y	T	N	Y	T	F	E	T	L	D	T	G	K	R	Q	C	496
	1489	AAG	GCC	GCC	CTG	CAG	CGG	CAG	CTG	GGC	CTG	CAG	GTC	CGC	GAC	GAC	GTG	1536
	497	K	A	A	L	Q	R	Q	L	G	L	Q	V	R	D	D	V	512
10	1537	CCA	CTG	ATC	GGG	TTC	ATC	GGG	CGG	CTG	GAC	CAC	CAG	AAG	GGC	GTG	GAC	1584
	513	P	L	I	G	F	I	G	R	L	D	H	Q	K	G	V	D	528
	1585	ATC	ATC	GCC	GAC	GCG	ATC	CAC	TGG	ATC	GCG	GGG	CAG	GAC	GTG	CAG	CTC	632
	529	I	I	A	D	A	I	H	W	I	A	G	Q	D	V	Q	L	544
	1633	GTG	ATG	CTG	GGC	ACC	GGG	CGG	GCC	GAC	CTG	GAG	GAC	ATG	CTG	CGG	CGG	1680
	545	V	M	L	G	T	G	R	A	D	L	E	D	M	L	R	R	560
15	1681	TTC	GAG	TCG	GAG	CAC	AGC	GAC	AAG	GTG	CGC	GCG	TGG	GTG	GGG	TTC	TCG	1728
	561	F	E	S	E	H	S	D	K	V	R	A	W	V	G	F	S	576
	1729	GTG	CCC	CTG	GCG	CAC	CGC	ATC	ACG	GCG	GGC	GCG	GAC	ATC	CTG	CTG	ATG	1776
	577	V	P	L	A	H	R	I	T	A	G	A	D	I	L	L	M	592
20	1777	CCG	TCG	CGG	TTC	GAG	CCG	TGC	GGG	CTG	AAC	CAG	CTC	TAC	GCC	ATG	GCG	1824
	593	P	S	R	F	E	P	C	G	L	N	Q	L	Y	A	M	A	608
	1825	TAC	GGG	ACC	GTG	CCC	GTG	GTG	CAC	GCC	GTG	GGG	GGG	CTC	CGG	GAC	ACG	1872
	609	Y	G	T	V	P	V	V	H	A	V	G	G	L	R	D	T	624
	1873	GTG	GCG	CCG	TTC	GAC	CCG	TTC	AAC	GAC	ACC	GGG	CTC	GGG	TGG	ACG	TTC	1920
	625	V	A	P	F	D	P	F	N	D	T	G	L	G	W	T	F	640
25	1921	GAC	CGC	GCG	GAG	GCG	AAC	CGG	ATG	ATC	GAC	GCG	CTC	TCG	CAC	TGC	CTC	1968
	641	D	R	A	E	A	N	R	M	I	D	A	L	S	H	C	L	656
	1969	ACC	ACG	TAC	CGG	AAC	TAC	AAG	GAG	AGC	TGG	CGC	GCC	TGC	AGG	GCG	CGC	2016
	657	T	T	Y	R	N	Y	K	E	S	W	R	A	C	R	A	R	672
30	2017	GGC	ATG	GCC	GAG	GAC	CTC	AGC	TGG	GAC	CAC	GCC	GCC	GTG	CTG	TAT	GAG	2064
	673	G	M	A	E	D	L	S	W	D	H	A	A	V	L	Y	E	688
	2065	GAC	GTG	CTC	GTC	AAG	GCG	AAG	TAC	CAG	TGG	TGA						2097
	689	D	V	L	V	K	A	K	Y	Q	W	*						699

TABLE 4
DNA and Deduced Amino Acid Sequence of
The Soluble Starch Synthase I Gene in Maize
[SEQ ID NO:12; SEQ ID NO: 13]

FILE NAME : MSS1FULL.DNA SEQUENCE : NORMAL 1752 BP

CODON TABLE : UNIV.TCN

SEQUENCE REGION : 1 - 1752

TRANSLATION REGION : 1 - 1752

	TGC	GTC	GCG	GAG	CTG	AGC	AGG	GAG	GGG	CCC	GCG	CCG	CGC	CCG	CTG	CCA	48
	Cys	Val	Ala	Glu	Leu	Ser	Arg	Glu	Gly	Pro	Ala	Pro	Arg	Pro	Leu	Pro	
	700					705					710					715	
5	CCC	GCG	CTG	CTG	GCG	CCC	CCG	CTC	GTG	CCC	GGC	TTC	CTC	GCG	CCG	CCG	96
	Pro	Ala	Leu	Leu	Ala	Pro	Pro	Leu	Val	Pro	Gly	Phe	Leu	Ala	Pro	Pro	
					720					725					730		
	GCC	GAG	CCC	ACG	GGT	GAG	CCG	GCA	TCG	ACG	CCG	CCG	CCC	GTG	CCC	GAC	144
	Ala	Glu	Pro	Thr	Gly	Glu	Pro	Ala	Ser	Thr	Pro	Pro	Pro	Val	Pro	Asp	
				735					740					745			
10	GCC	GGC	CTG	GGG	GAC	CTC	GGT	CTC	GAA	CCT	GAA	GGG	ATT	GCT	GAA	GGT	192
	Ala	Gly	Leu	Gly	Asp	Leu	Gly	Leu	Glu	Pro	Glu	Gly	Ile	Ala	Glu	Gly	
			750					755					760				
	TCC	ATC	GAT	AAC	ACA	GTA	GTT	GTG	GCA	AGT	GAG	CAA	GAT	TCT	GAG	ATT	240
15	Ser	Ile	Asp	Asn	Thr	Val	Val	Val	Ala	Ser	Glu	Gln	Asp	Ser	Glu	Ile	
		765					770					775					
	GTG	GTT	GGA	AAG	GAG	CAA	GCT	CGA	GCT	AAA	GTA	ACA	CAA	AGC	ATT	GTC	288
	Val	Val	Gly	Lys	Glu	Gln	Ala	Arg	Ala	Lys	Val	Thr	Gln	Ser	Ile	Val	
	780					785					790					795	
20	TTT	GTA	ACC	GGC	GAA	GCT	TCT	CCT	TAT	GCA	AAG	TCT	GGG	GGT	CTA	GGA	336
	Phe	Val	Thr	Gly	Glu	Ala	Ser	Pro	Tyr	Ala	Lys	Ser	Gly	Gly	Leu	Gly	
					800					805					810		
	GAT	GTT	TGT	GGT	TCA	TTG	CCA	GTT	GCT	CTT	GCT	GCT	CGT	GGT	CAC	CGT	384
	Asp	Val	Cys	Gly	Ser	Leu	Pro	Val	Ala	Leu	Ala	Ala	Arg	Gly	His	Arg	
				815					820					825			
25	GTG	ATG	GTT	GTA	ATG	CCC	AGA	TAT	TTA	AAT	GGT	ACC	TCC	GAT	AAG	AAT	432
	Val	Met	Val	Val	Met	Pro	Arg	Tyr	Leu	Asn	Gly	Thr	Ser	Asp	Lys	Asn	
			830					835					840				
	TAT	GCA	AAT	GCA	TTT	TAC	ACA	GAA	AAA	CAC	ATT	CGG	ATT	CCA	TGC	TTT	480
30	Tyr	Ala	Asn	Ala	Phe	Tyr	Thr	Glu	Lys	His	Ile	Arg	Ile	Pro	Cys	Phe	
		845					850					855					
	GGC	GGT	GAA	CAT	GAA	GTT	ACC	TTC	TTC	CAT	GAG	TAT	AGA	GAT	TCA	GTT	528
	Gly	Gly	Glu	His	Glu	Val	Thr	Phe	Phe	His	Glu	Tyr	Arg	Asp	Ser	Val	
	860					865					870					875	
35	GAC	TGG	GTG	TTT	GTT	GAT	CAT	CCC	TCA	TAT	CAC	AGA	CCT	GGA	AAT	TTA	576
	Asp	Trp	Val	Phe	Val	Asp	His	Pro	Ser	Tyr	His	Arg	Pro	Gly	Asn	Leu	
					880					885					890		
	TAT	GGA	GAT	AAG	TTT	GGT	GCT	TTT	GGT	GAT	AAT	CAG	TTC	AGA	TAC	ACA	624
	Tyr	Gly	Asp	Lys	Phe	Gly	Ala	Phe	Gly	Asp	Asn	Gln	Phe	Arg	Tyr	Thr	
				895					900					905			
40	CTC	CTT	TGC	TAT	GCT	GCA	TGT	GAG	GCT	CCT	TTG	ATC	CTT	GAA	TTG	GGA	672
	Leu	Leu	Cys	Tyr	Ala	Ala	Cys	Glu	Ala	Pro	Leu	Ile	Leu	Glu	Leu	Gly	
			910					915					920				
	GGA	TAT	ATT	TAT	GGA	CAG	AAT	TGC	ATG	TTT	GTT	GTC	AAT	GAT	TGG	CAT	720
45	Gly	Tyr	Ile	Tyr	Gly	Gln	Asn	Cys	Met	Phe	Val	Val	Asn	Asp	Trp	His	
		925					930					935					
	GCC	AGT	CTA	GTG	CCA	GTC	CTT	CTT	GCT	GCA	AAA	TAT	AGA	CCA	TAT	GGT	768
	Ala	Ser	Leu	Val	Pro	Val	Leu	Leu	Ala	Ala	Lys	Tyr	Arg	Pro	Tyr	Gly	
	940					945					950					955	
50	GTT	TAT	AAA	GAC	TCC	CGC	AGC	ATT	CTT	GTA	ATA	CAT	AAT	TTA	GCA	CAT	816
	Val	Tyr	Lys	Asp	Ser	Arg	Ser	Ile	Leu	Val	Ile	His	Asn	Leu	Ala	His	
					960					965						970	

	CAG GGT GTA GAG CCT GCA AGC ACA TAT CCT GAC CTT GGG TTG CCA CCT	864
	Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro	
	975 980 985	
5	GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA TGG GCG AGG AGG	912
	Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg	
	990 995 1000	
	CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG AAA GGT GCA GTT	960
	His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val	
	1005 1010 1015	
10	GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT TAT TCG TGG GAG	1008
	Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly Tyr Ser Trp Glu	
	1020 1025 1030 1035	
15	GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG CTC TTA AGC TCC	1056
	Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser	
	1040 1045 1050	
	AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT GAC ATT AAT GAT	1104
	Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp	
	1055 1060 1065	
20	TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT TAT TCT GTT GAT	1152
	Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His Tyr Ser Val Asp	
	1070 1075 1080	
	GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG CAG AAG GAG CTG	1200
	Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu Gln Lys Glu Leu	
	1085 1090 1095	
25	GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC TTT ATT GGA AGG	1248
	Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg	
	1100 1105 1110 1115	
30	TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT ATC ATA CCA GAT	1296
	Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp	
	1120 1125 1130	
	CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA TCT GGT GAC CCA	1344
	Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro	
	1135 1140 1145	
35	GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC TTC AAG GAT AAA	1392
	Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys	
	1150 1155 1160	
	TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC CAC CGA ATA ACT	1440
	Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr	
	1165 1170 1175	
40	GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC GAA CCT TGT GGT	1488
	Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly	
	1180 1185 1190 1195	
45	CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT CCT GTT GTC CAT	1536
	Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His	
	1200 1205 1210	
	GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC AAC CCT TTC GGT	1584
	Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly	
	1215 1220 1225	
50	GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA CCC CTA ACC ACA	1632
	Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr	
	1230 1235 1240	

GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC TAC ATA CAG GGA 1680
 Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly
 1245 1250 1255

5 ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG CAT GTC AAA AGA 1728
 Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg
 1260 1265 1270 1275

CTT CAC GTG GGA CCA TGC CGC TGA 1752
 Leu His Val Gly Pro Cys Arg *
 1280

10 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 584 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

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

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

	Ala	Ser	Leu	Val	Pro	Val	Leu	Leu	Ala	Ala	Lys	Tyr	Arg	Pro	Tyr	Gly
					245					250					255	
	Val	Tyr	Lys	Asp	Ser	Arg	Ser	Ile	Leu	Val	Ile	His	Asn	Leu	Ala	His
				260					265					270		
5	Gln	Gly	Val	Glu	Pro	Ala	Ser	Thr	Tyr	Pro	Asp	Leu	Gly	Leu	Pro	Pro
			275					280					285			
	Glu	Trp	Tyr	Gly	Ala	Leu	Glu	Trp	Val	Phe	Pro	Glu	Trp	Ala	Arg	Arg
		290					295					300				
10	His	Ala	Leu	Asp	Lys	Gly	Glu	Ala	Val	Asn	Phe	Leu	Lys	Gly	Ala	Val
		305				310					315					320
	Val	Thr	Ala	Asp	Arg	Ile	Val	Thr	Val	Ser	Lys	Gly	Tyr	Ser	Trp	Glu
				325						330					335	
	Val	Thr	Thr	Ala	Glu	Gly	Gly	Gln	Gly	Leu	Asn	Glu	Leu	Leu	Ser	Ser
				340					345					350		
15	Arg	Lys	Ser	Val	Leu	Asn	Gly	Ile	Val	Asn	Gly	Ile	Asp	Ile	Asn	Asp
			355					360					365			
	Trp	Asn	Pro	Ala	Thr	Asp	Lys	Cys	Ile	Pro	Cys	His	Tyr	Ser	Val	Asp
		370					375					380				
20	Asp	Leu	Ser	Gly	Lys	Ala	Lys	Cys	Lys	Gly	Ala	Leu	Gln	Lys	Glu	Leu
		385				390					395					400
	Gly	Leu	Pro	Ile	Arg	Pro	Asp	Val	Pro	Leu	Ile	Gly	Phe	Ile	Gly	Arg
				405						410					415	
	Leu	Asp	Tyr	Gln	Lys	Gly	Ile	Asp	Leu	Ile	Gln	Leu	Ile	Ile	Pro	Asp
				420					425					430		
25	Leu	Met	Arg	Glu	Asp	Val	Gln	Phe	Val	Met	Leu	Gly	Ser	Gly	Asp	Pro
			435					440					445			
	Glu	Leu	Glu	Asp	Trp	Met	Arg	Ser	Thr	Glu	Ser	Ile	Phe	Lys	Asp	Lys
		450					455					460				
30	Phe	Arg	Gly	Trp	Val	Gly	Phe	Ser	Val	Pro	Val	Ser	His	Arg	Ile	Thr
		465				470					475					480
	Ala	Gly	Cys	Asp	Ile	Leu	Leu	Met	Pro	Ser	Arg	Phe	Glu	Pro	Cys	Gly
				485						490					495	
	Leu	Asn	Gln	Leu	Tyr	Ala	Met	Gln	Tyr	Gly	Thr	Val	Pro	Val	Val	His
				500					505					510		
35	Ala	Thr	Gly	Gly	Leu	Arg	Asp	Thr	Val	Glu	Asn	Phe	Asn	Pro	Phe	Gly
			515					520					525			
	Glu	Asn	Gly	Glu	Gln	Gly	Thr	Gly	Trp	Ala	Phe	Ala	Pro	Leu	Thr	Thr
		530					535					540				
40	Glu	Asn	Met	Phe	Val	Asp	Ile	Ala	Asn	Cys	Asn	Ile	Tyr	Ile	Gln	Gly
		545				550					555					560
	Thr	Gln	Val	Leu	Leu	Gly	Arg	Ala	Asn	Glu	Ala	Arg	His	Val	Lys	Arg
				565						570					575	

TABLE 5
mRNA Sequence and Deduced Amino Acid Sequence of
The Maize Branching Enzyme II Gene and the Transit Peptide
[SEQ ID NO:14 and SEQ ID NO:15]

5	LOCUS	MZEGLUCTRN 2725 bp ss-mRNA	PLN
	DEFINITION	Corn starch branching enzyme II mRNA, complete cds.	
	ACCESSION	L08065	
	KEYWORDS	1,4-alpha-glucan branching enzyme; amylo-transglycosylase; glucanotransferase; starch branching enzyme II.	
10	SOURCE	Zea mays cDNA to mRNA.	
	ORGANISM	Zea mays Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida; Commelinidae; Cyperales; Poaceae.	
	REFERENCE	1 (bases 1 to 2725)	
15	AUTHORS	Fisher,D.K., Boyer,C.D. and Hannah,L.C.	
	TITLE	Starch branching enzyme II from maize endosperm	
	JOURNAL	Plant Physiol. 102, 1045-1046 (1993)	
	STANDARD	full automatic	
	COMMENT	NCBI gi: 168482	
20	FEATURES	Location/Qualifiers	
	source	1..2725 /cultivar="W64Ax182E" /dev_stage="29 days post pollination" /tissue_type="endosperm" /organism="Zea mays"	
25	sig_peptide	91..264 /codon_start=1	
	CDS	91..2490 /EC_number="2.4.1.18" /note="NCBI gi: 168483" /codon_start=1 /product="starch branching enzyme II"	
30			
35		/translation="MAFRVSGAVLGGA VRAPRLTGGGEGSLVFRHTGLFLTRGARVGC SGTHGAMRAAAAARKAVMVPEGENDGLASRADSAQFQSDELEVDPDISEETTCGAGVAD AQALNRVRVPPPSDGQKIFQIDPMLQGYKYHLEYRYSLYRRIRSDIDEHEGGLEAFS RSYEKFGFNASAEGITYREWAPGAFSAALVGDVNNWDPNADRMSKNEFGVWEIFLPNN ADGTSPIPHGSRVKVRMDTPSGIKDSIPAWIKYSVQAPGEIPYDGIYYDPPEEVKYVF RHAQPKRPKSLRIYETHVGMSSPEPKINTYVNFREVLPRIKKLGYNVQIMAIQEH YYGSFGYHVTNFFAPSSRFPTPEDLKSLIDRAHELGLLVMDVVHSHASSNTLDGLNG FDGTDTHYFHSGPRGHHWWSRLFNYG NWEVLRFLLSNARWWLEEYKFDGFRFDGVT SMMYTHHGLQVTFGTGNFNEYFGFATD VDAVVYLMVNDLIHGLYPEAVTIGEDVSGMP TFALPVHDGGVGFDYRMHMAVADKWIDLLKQSDETWKMGDIVHTLTNRRWLEKCVTYA ESHQALVGDKTIAFWLMDKMDYDFMALDRPSTPTIDRGIALHKMIRLITMGLGGEY LNFMGNEFGHPEWIDFPRGPQRLPSGKFIPGNNNSYDKCRRRFDLGDADYLRHYGMQE FDQAMQHLEQKYEFMTSDHQYISRKHEEDKVIVFEKGD LVFVFNFHCNNSYFDYRIGC RKPGVYKVVLDS DAGLFGGFSRIHHAAEHFTADCSHDNRPYSF SVYTPSRTC VVYAPV E"	
40			
45			
50			
55			
60	mat_peptide	265..2487 /codon_start=1 /product="starch branching enzyme II"	
65	BASE COUNT	727 A 534 C 715 G 749 T	

ORIGIN

```

1  GGCCAGAGC AGACCCGGAT TTCGCTCTTG CGGTCGCTGG GGTTTTAGCA TTGGCTGATC
61 AGTTTCGATCC GATCCGGCTG CGAAGGCGAG ATGGCGTTCC GGGTTTCTGG GCGGGTGCTC
121 GGTGGGGCCG TAAGGGCTCC CCGACTCACC GCGGGCGGGG AGGGTAGTCT AGTCTTCCGG
181 CACACCGGCC TCTTCTTAAC TCGGGGTGCT CGAGTTGGAT GTTCGGGGAC GCACGGGGCC
241 ATGCGCGCGG CGGCCGCGGC CAGGAAGGCG GTCATGGTTC CTGAGGGCGA GAATGATGGC
301 CTCGCATCAA GGGCTGACTC GGCTCAATTC CAGTCGGATG AACTGGAGGT ACCAGACATT
361 TCTGAAGAGA CAACGTGCGG TGCTGGTGTG GCTGATGCTC AAGCCTTGAA CAGAGTTCTGA
421 GTGGTCCCCC CACCAAGCGA TGGACAAAAA ATATTCCAGA TTGACCCCAT GTTGCAAGGC
481 TATAAGTACC ATCTTGAGTA TCGGTACAGC CTCTATAGAA GAATCCGTTT AGACATTGAT
541 GAACATGAAG GAGGCTTGGA AGCCTTCTCC CGTAGTTATG AGAAGTTTGG ATTTAATGCC
601 AGCGCGGAAG GTATCACATA TCGAGAATGG GCTCCTGGAG CATTCTCTGC AGCATTTGGT
661 GGTGACGTCA ACAACTGGGA TCCAAATGCA GATCGTATGA GCAAAAATGA GTTTGGTGTG
721 TGGGAAATTT TTCTGCCTAA CAATGCAGAT GGTACATCAC CTATTCTCTA TGGATCTCGT
781 GTAAAGGTGA GAATGGATAC TCCATCAGGG ATAAAGGATT CAATTCCAGC CTGGATCAAG
841 TACTCAGTGC AGGCCCCAGG AGAAATACCA TATGATGGGA TTTATTATGA TCCTCCTGAA
901 GAGGTAAAGT ATGTGTTTCA GATGCGCAA CCTAAACGAC CAAAATCATT GCGGATATAT
961 GAAACACATG TCGGAATGAG TAGCCCGGAA CCGAAGATAA ACACATATGT AAACTTTAGG
1021 GATGAAGTCC TCCCAAGAAT AAAAAAACTT GGATACAATG CAGTGCAAAT AATGGCAATC
1081 CAAGAGCACT CATATTATGG AAGCTTTGGA TACCATGTAA CTAATTTTTT TGCGCCAAGT
1141 AGTCGTTTTG GTACCCCGA AGATTTGAAG TCTTTGATTG ATAGAGCACA TGAGCTTGGT
1201 TTGCTAGTTC TCATGGATGT GGTTCATAGT CATGCGTCAA GTAATACTCT GGTGGGTTG
1261 AATGGTTTTG ATGGTACAGA TACACATTAC TTTACAGTGT GTCCACGTGG CCATCACTGG
1321 ATGTGGGATT CTCGCCTATT TAACTATGGG AACTGGGAAG TTTAAGATT TCTTCTCTCC
1381 AATGCTAGAT GGTGGCTCGA GGAATATAAG TTTGATGGTT TCCGTTTTGA TGGTGTGACC
1441 TCCATGATGT ACACTACCA CGGATTACAA GTAACATTTA CGGGGAACCT CAATGAGTAT
1501 TTTGGCTTTG CCACCGATGT AGATGCAGTG GTTTACTTGA TGCTGGTAAA TGATCTAATT
1561 CATGGACTTT ATCCTGAGG TGTAAACATT GGTGAAGATG TTAGTGGAAAT GCCTACATTT
1621 GCCCTTCCTG TTCACGATGG TGGGGTAGGT TTTGACTATC GGATGCATAT GGCTGTGGCT
1681 GACAAATGGA TTGACCTTCT CAAGCAAAGT GATGAAACTT GGAAGATGGG TGATATTGTG
1741 CACACACTGA CAAATAGGAG GTGGTTAGAG AAGTGTGTAA CTTATGCTGA AAGTCATGAT
1801 CAAGCATTAG TCGGCGACAA GACTATTGCG TTTTGGTTGA TGGACAAGGA TATGTATGAT
1861 TTCATGGCCC TCGATAGACC TTCAACTCCT ACCATTGATC GTGGGATAGC ATTACATAAG
1921 ATGATTAGAC TTATCACAAT GGGTTTAGGA GGAGAGGGCT ATCTTAATTT CATGGGAAAT
1981 GAGTTTGGAC ATCCTGAATG GATAGATTTT CCAAGAGGTC CGCAAAGACT TCCAAGTGGT
2041 AAGTTTATTC CAGGGAATAA CAACAGTTAT GACAAATGTC GTCGAAGATT TGACCTGGGT
2101 GATGCAGACT ATCTTAGGTA TCATGGTATG CAAGAGTTTG ATCAGGCAAT GCAACATCTT
2161 GAGCAAAAAT ATGAATTCAT GACATCTGAT CACCAGTATA TTTCCCGGAA ACATGAGGAG
2221 GATAAGGTGA TTGTGTTCGA AAAGGGAGAT TTGGTATTTG TGTTCAACTT CCACTGCAAC
2281 AACAGCTATT TTGACTACCG TATTGGTTGT CGAAAGCCTG GGGTGTATAA GGTGGTCTTG
2341 GACTCCGACG CTGGACTATT TGGTGGATTT AGCAGGATCC ATCACGCAGC CGAGCACTTC
2401 ACCGCCGACT GTTCGCATGA TAATAGGCCA TATTCATTCT CGGTTTATAC ACCAAGCAGA
2461 ACATGTGTCT TCTATGCTCC AGTGGAGTGA TAGCGGGGTA CTCGTTGCTG CCGGCATGT
2521 GTGGGGCTGT CGATGTGAGG AAAAACCTTC TTCCAAAACC GGCAGATGCA TGCATGCATG
2581 CTACAATAAG GTTCTGATAC TTTAATCGAT GCTGGAAAGC CCATGCATCT CGCTGCGTTG
2641 TCCTCTCTAT ATATATAAGA CCTTCAAGGT GTCAATTAAA CATAGAGTTT TCGTTTTTTCG
2701 CTTTCCTAAA AAAAAAAAAA AAAAA

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TABLE 6

mRNA Sequence and Deduced Amino Acid Sequence of the
Maize Branching Enzyme I and the Transit Peptide
[SEQ ID NO:16 and SEQ ID NO:17]

LOCUS	MZEBEI	2763 bp ss-mRNA	PLN
DEFINITION	Maize mRNA for branching enzyme-I (BE-I).		
ACCESSION	D11081		
KEYWORDS	branching enzyme-I.		
SOURCE	Zea mays L. (inbred Oh43), cDNA to mRNA.		
ORGANISM	Zea mays		
	Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;		
	Commelinidae; Liliopsida.		
REFERENCE	1 (bases 1 to 2763)		
AUTHORS	Baba,T., Kimura,K., Mizuno,K., Etoh,H., Ishida,Y., Shida,O. and Arai,Y.		

TITLE Sequence conservation of the catalytic regions of Amylolytic enzymes in maize branching enzyme-I
JOURNAL Biochem. Biophys. Res. Commun. 181, 87-94 (1991)
STANDARD full automatic
COMMENT Submitted (30-APR-1992) to DDBJ by: Tadashi Baba
Institute of Applied Biochemistry
University of Tsukuba
Tsukuba, Ibaraki 305
Japan
Phone: 0298-53-6632
Fax: 0298-53-6632.

NCBI gi: 217959
FEATURES Location/Qualifiers
source 1..2763
/organism="Zea mays"
CDS <1..2470
/note="NCBI gi: 217960"
/codon_start=2
/product="branching enzyme-I precursor"

/translation="LCLVSPSSSPTPLPPRRSRSHADRAAPPGIAGGGNVRLSVLSV
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KRFLEQKGSIEENEGSLESFSKGYLKFGINTNEDGTVYREWAPAAQEAELIGDFNDWN
GANHKMEKDKFGVWSIKIDHVGKKAIPHNSKVKFRFLHGGVWVDRI PALIRYATVDA
SKFGAPYDGVHWDPPASERYTFKHPRPSKPAAPRIYEAHVGMSEKPAVSTYREFADN
VLPRIRANNYNTVQLMAVMEHSYYASFGYHVTNFFAVSSRSRSGTPEDLKYLVDKAHSLG
LRVLMDVVHSHASNNVTDGLNGYDVGQSTQESYFHAGDRGYHKLWDSRLFNANWEVL
RFLLSNRLRYWLDEFMFDGFRFDGVTSMLYHHHGINVGFTGNYQEYFSLDTAVDAVVYM
MLANHLMHKLLPEATVVAEDVSGMPVLCRPVDEGGVGFYRLAMAIPDRWIDYLNKND
DSEWSMGEIAHTLTNRRYTEKCIAYAESHQDSIVGDKTIAFLMDKEMYTGMSDLQPA
SPTIDRGIALQKMIHFITMALGGDGYLNFMGNEFGHPEWIDFPREGNNWSYDKCRRQW
SLVDTDHLRYKYMNAFDQAMNALDERFSFLSSSKQIVSDMNDEEKVIVFERGDLVVFV
NFHPKKTIEGYKVGCDLPGKYRVALDS DALVFGGHGRVGHVDHFTSPEGVPVPETN
FNNRPNSFKVLSPPRTCVAYYRVDEAGAGRRRLHAKAETGKTSPAESIDVKASRASSKE
DKEATAGGKKGWK FARQPSDQDTK"

transit_peptide 2..190
mat_peptide 191..2467
/EC_number="2.4.1.18"
/codon_start=1
/product="branching enzyme-I precursor"
polyA_signal 2734..2739
BASE COUNT 719 A 585 C 737 G 722 T
ORIGIN

1 GCTGTGCCTC GTGTCCGCCCT CTTCCTCGCC GACTCCGCTT CCGCCGCCGC GCGCCTCTCG
61 CTCGCATGCT GATCGGGCGG CACCGCCGGG GATCGCGGGT GGCGGCAATG TGCGCCTGAG
121 TGTGTTGTCT GTCCAGTGCA AGGCTCGCCG GTCAGGGGTG CGGAAGGTCA AGAGCAAATT
60 181 CGCCACTGCA GCTACTGTGC AAGAAGATAA AACTATGGCA ACTGCCAAAG GCGATGTGCA
241 CCATCTCCCC ATATACGACC TGGACCCCAA GCTGGAGATA TTCAAGGACC ATTTCAAGGTA
301 CCGATGAAA AGATTCCTAG AGCAGAAAGG ATCAATTGAA GAAAATGAGG GAAGTCTTGA
361 ATCTTTTCT AAAGGCTATT TGA AATTG GATTAATACA AATGAGGATG GAACTGTATA
421 TCGTGAATGG GCACCTGCTG CGCAGGAGGC AGAGCTTATT GGTGACTTCA ATGACTGGAA
65 481 TGGTGCAAAC CATAAGATGG AGAAGGATAA ATTTGGTGTT TGGTCGATCA AAATTGACCA
541 TGTCAAAGGG AAACCTGCCA TCCCTCACAA TTCCAAGGTT AAATTTGCTT TTCTACATGG
601 TGGAGTATGG GTTGATCGTA TTCCAGCATT GATTGCTTAT GCGACTGTTG ATGCCTCTAA

661 ATTTGGAGCT CCCTATGATG GTGTTTCATTG GGATCCTCCT GCTTCTGAAA GGTACACATT
 721 TAAGCATCCT CGGCCTTCAA AGCCTGCTGC TCCACGTATC TATGAAGCCC ATGTAGGTAT
 781 GAGTGGTGAA AAGCCAGCAG TAAGCACATA TAGGGAATTT GCAGACAATG TGTGGCCACG
 841 CATACGAGCA AATAACTACA ACACAGTTCA GTTGATGGCA GTTATGGAGC ATTCGTACTA
 5 901 TGCTTCTTTC GGGTACCATG TGACAAATTT CTTTGCGGTT AGCAGCAGAT CAGGCACACC
 961 AGAGGACCTC AAATATCTTG TTGATAAGGC ACACAGTTTG GGTTTGCGAG TTCTGATGGA
 1021 TGTTGTCCAT AGCCATGCAA GTAATAATGT CACAGATGGT TTAAATGGCT ATGATGTTGG
 1081 ACAAAGCACC CAAGAGTCCT ATTTTCATGC GGGAGATAGA GGTTATCATA AACTTTGGGA
 1141 TAGTCGGCTG TTCAACTATG CTAAGTGGGA GGTATTAAGG TTTCTTCTTT CTAACCTGAG
 10 1201 ATATTGGTTG GATGAATTCA TGTTTGATGG CTTCCGATTT GATGGAGTTA CATCAATGCT
 1261 GTATCATCAC CATGGTATCA ATGTGGGGTT TACTGGAAAC TACCAGGAAT ATTTTCAGTTT
 1321 GGACACAGCT GTGGATGCAG TTGTTTACAT GATGCTTGCA AACCATTAA TGCACAAACT
 1381 CTTGCCAGAA GCAACTGTTG TTGCTGAAGA TGTTTCAGGC ATGCCGGTCC TTTGCCGGCC
 1441 AGTTGATGAA GGTGGGGTTG GGTTTGACTA TCGCCTGGCA ATGGCTATCC CTGATAGATG
 15 1501 GATTGACTAC CTGAAGAATA AAGATGACTC TGAGTGGTCG ATGGGTGAAA TAGCGCATAC
 1561 TTTGACTAAC AGGAGATATA CTGAAAAATG CATCGCATAT GCTGAGAGCC ATGATCAGTC
 1621 TATTGTTGGC GACAAAACTA TTGCATTTCT CCTGATGGAC AAGGAAATGT ACCTGGCAT
 1681 GTCAGACTTG CAGCCTGCTT CACCTACAAT TGATCGAGGG ATGCACTCC AAAAGATGAT
 1741 TCACTTCATC ACAATGGCCC TTGGAGGTGA TGGCTACTTG AATTTTATGG GAAATGAGTT
 20 1801 TGGTCACCCA GAATGGATTG ACTTTCCAAG AGAAGGGAAC AACTGGAGCT ATGATAAATG
 1861 CAGACGACAG TGGAGCCTTG TGGACACTGA TCACTTGCGG TACAAGTACA TGAATGCGTT
 1921 TGACCAAGCG ATGAATGCGC TCGATGAGAG ATTTTCCTTC CTTTCGTCGT CAAAGCAGAT
 1981 CGTCAGCGAC ATGAACGATG AGGAAAAGGT TATTGTCTTT GAACGTGGAG ATTTAGTTTT
 2041 TGTTTTCAAT TTCCATCCCA AGAAAACCTA CGAGGGCTAC AAAGTGGGAT GCGATTTGCC
 25 2101 TGGGAAATAC AGAGTAGCCC TGGACTCTGA TGCTCTGGTC TTCGGTGGAC ATGGAAGAGT
 2161 TGGCCACGAC GTGGATCACT TCACGTGCGC TGAAGGGGTG CCAGGGGTGC CCGAAACGAA
 2221 CTTCAACAAC CGGCCGAAC CGTTCAAAGT CCTTCTCCG CCCCACCTT GTGTGGCTTA
 2281 TTACCGTGTA GACGAAGCAG GGGCTGGACG ACGTCTTCAC GCGAAAGCAG AGACAGGAAA
 2341 GACGTCTCCA GCAGAGAGCA TCGACGTCAA AGCTTCCAGA GCTAGTAGCA AAGAAGACAA
 30 2401 GGAGGCAACG GCTGGTGGCA AGAAGGGATG GAAGTTTGGC CGGCAGCCAT CCGATCAAGA
 2461 TACCAATGA AGCCACGAGT CCTTGGTGAG GACTGGACTG GCTGCCGGCG CCCTGTTAGT
 2521 AGTCTGCTC TACTGGACTA GCCGCCGTG GCGCCCTTG AACGTCCTT TCCTGTAGCT
 2581 TGCAGGCGAC TGGTGTCTCA TCACCGAGCA GGCAGGCACT GCTTGATAG CTTTTCTAGA
 2641 ATAATAATCA GGGATGGATG GATGGTGTGT ATTGGCTATC TGGCTAGACG TGCATGTGCC
 35 2701 CAGTTTGTAT GTACAGGAGC AGTTCCCCTC CAGAATAAAA AAAAATTGT TGGGGGGTTT
 2761 TTC

//

TABLE 7
 Coding Sequence and Deduced Amino Acid Sequence for
 Transit Peptide Region of the
 Soluble Starch Synthase I Maize Gene (153 bp)
 [SEQ ID NO:18 and SEQ ID NO:19]

FILE NAME : MSS1TRPT.DNA SEQUENCE : NORMAL 153 BP

CODON TABLE : UNIV.TCN

SEQUENCE REGION : 1 - 153

TRANSLATION REGION : 1 - 153

*** DNA TRANSLATION ***

1 ATG GCG ACG CCC TCG GCC GTG GGC GCC GCG TGC CTC CTC CTC GCG CGG 48
 1 M A T P S A V G A A C L L L A R 16
 50 49 GCC GCC TGG CCG GCC GCC GTC GGC GAC CGG GCG CGC CCG CGG AGG CTC 96
 17 A A W P A A V G D R A R P R R L 32
 97 CAG CGC GTG CTG CGC CGC CGG TGC GTC GCG GAG CTG AGC AGG GAG GGG 144
 33 Q R V L R R R C V A E L S R E G 48
 55 145 CCC CAT ATG 153
 49 P H M 51

GFP constructs:

1. GFP only in pET-21a:

pEXS115 is digested with *Nde* I and *Xho* I and the 740 bp fragment containing the SGFP coding sequence is subcloned into the *Nde* I and *Xho* I sites of pET-21a (Novagen 601 Science Dr. Madison WI). (See FIG. 2b GFP-21a map.)

2. GFP subcloned in-frame at the 5' end of full-length mature WX:

The 740 bp *Nde* I fragment containing SGFP from pEXS114 is subcloned into the *Nde* I site of pEXSWX. (See FIG.3a GFP-FLWX map.)

3. GFP subcloned in-frame at the 5' end of N-terminally truncated WX:

WX truncated by 700 bp at N-terminus.

The 1 kb *Bam*H I fragment encoding the C-terminus of WX from pEXSWX is subcloned into the *Bgl* II site of pEXS115. Then the entire SGFP-truncated WX fragment is subcloned into pET21a as a *Nde* I-*Hind*III fragment. (See FIG. 3b GFP-BamHIWX map.)

4. GFP subcloned in-frame at the 5' end of truncated WX: WX truncated by 100 bp at N-terminus.

The 740 bp *Nde* I-*Nco* I fragment containing SGFP from pEXS115 is subcloned into pEXSWX at the *Nde* I and *Nco* I sites. (See Fig. 4 GFP-NcoWX map.)

Example Three:**Plasmid Transformation into Bacteria:**

Escherichia coli competent cell preparation:

1. Inoculate 2.5 ml LB media with a single colony of desired *E. coli* strain : selected strain was XLIBLUE DL2IDE3 from (Stratagene); included appropriate antibiotics. Grow at 37°C, 250 rpm overnight.

2. Inoculate 100 ml of LB media with a 1:50 dilution of the overnight culture, including appropriate antibiotics. Grow at 37°C, 250 rpm until OD₆₀₀=0.3-0.5.

3. Transfer culture to sterile centrifuge bottle and chill on ice for 15 minutes.

4. Centrifuge 5 minutes at 3,000x g (4°C).
5. Resuspend pellet in 8 ml ice-cold Transformation buffer. Incubate on ice for 15 minutes.
6. Centrifuge 5 minutes at 3,000x g (4°C).
- 5 7. Resuspend pellet in 8 ml ice-cold Transformation buffer 2. Aliquot, flash-freeze in liquid nitrogen, and stored at -70°C.

	<u>Transformation Buffer 1</u>	<u>Transformation Buffer 2</u>
	RbCl 1.2 g	MOPS (10 mM) 0.209 g
	MnCl ₂ 4H ₂ O 0.99g	RbCl 0.12 g
10	K-Acetate 0.294 g	CaCl ₂ 2H ₂ O 1.1 g
	CaCl ₂ 2H ₂ O 0.15 g	Glycerol 15 g
	Glycerol 15 g	dH ₂ O 100 ml
	dH ₂ O 100 ml	pH to 6.8 with NaOH
	pH to 5.8 with 0.2 M acetic acid	Filter sterilize
15	Filter sterilize	

Escherichia coli transformation by rubidium chloride heat shock method: Hanahan, D. (1985) in DNA cloning: a practical approach (Glover, D.M. ed.), pp. 109-135, IRL Press.

1. Incubate 1-5 µl of DNA on ice with 150 µl *E. coli* competent cells for 30 minutes.
- 20 2. Heat shock at 42°C for 45 seconds.
3. Immediately place on ice for 2 minutes.
4. Add 600 µl LB media and incubate at 37°C for 1 hour.

5. Plate on LB agar including the appropriate antibiotics.

This plasmid will express the hybrid polypeptide containing the green fluorescent protein within the bacteria.

Example Four:

5 Expression of Construct in *E. coli*:

1. Inoculate 3 ml LB with *E. coli* containing plasmid of interest. Include appropriate antibiotics. 37°C, 250 rpm, overnight.
2. Inoculate 100 ml LB with 2 ml of overnight culture. Include appropriate antibiotics. Grow at 37°C, 250 rpm.
- 10 3. At OD₆₀₀ about 0.4-0.5, place at room temperature, 200 rpm.
4. At OD₆₀₀ about 0.6-0.8, induce with 100 µl 1M IPTG. Final IPTG concentration is 1 mM.
5. Grow at room temperature, 200 rpm, 4-5 hours.
6. Collect cells by centrifugation.
- 15 7. Flash freeze in liquid nitrogen and store at -70°C until use.

Cells can be resuspended in dH₂O and viewed under UV light ($\lambda_{\text{max}} = 395 \text{ nm}$) for intrinsic fluorescence. Alternatively, the cells can be sonicated and an aliquot of the cell extract can be separated by SDS-PAGE and viewed under UV light to detect GFP fluorescence. When the protein employed is a green fluorescent protein, the presence of the protein in the lysed material can be evaluated under UV at 395 nm in a light box and the signature green glow can be identified.

20

Example Five:**Plasmid Extraction from Bacteria:**

The following is one of many common alkaline lysis plasmid purification protocols useful in practicing this invention.

- 5 1. Inoculate 100-200 ml LB media with a single colony of *E. coli* transformed with the one of the plasmids described above. Include appropriate antibiotics. Grow at 37°C, 250 rpm overnight.
2. Centrifuge 10 minutes at 5,000x g (4°C).
- 10 3. Resuspend cells in 10 ml water, transfer to a 15 ml centrifuge tube, and repeat centrifugation.
4. Resuspend pellet in 5 ml 0.1 M NaOH, 0.5% SDS. Incubate on ice for 10 minutes.
5. Add 2.5 ml of 3 M sodium acetate (pH 5.2), invert gently, and incubate 10 minutes on ice.
6. Centrifuge 5 minutes at 15,000-20,000x g (4°C).
- 15 7. Extract supernatant with an equal volume of phenol:chloroform:isoamyl alcohol (25:24:1).
8. Centrifuge 10 minutes at 6,000-10,000x g (4°C).
9. Transfer aqueous phase to clean tube and precipitate with 1 volume of isopropanol.
10. Centrifuge 15 minutes at 12,000x g (4°C).
- 20 11. Dissolve pellet in 0.5 ml TE, add 20 µl of 10 mg/ml Rnase, and incubate 1 hour at 37°C.

12. Extract twice with phenol:chloroform:isoamyl alcohol (25:24:1).
13. Extract once with chloroform.
14. Precipitate aqueous phase with 1 volume of isopropanol and 0.1 volume of 3 M sodium acetate.
15. Wash pellet once with 70% ethanol.
16. Dry pellet in SpeedVac and resuspend pellet in TE.

This plasmid can then be inserted into other hosts.

TABLE 8
DNA Sequence and Deduced Amino Acid Sequence of
Starch Synthase Coding Region from pEXS52 [SEQ ID NO:20; SEQ ID NO:21]

FILE NAME : MSS1DELN.DNA SEQUENCE : NORMAL 1626 BP
CODON TABLE : UNIV.TCN
SEQUENCE REGION : 1 - 1626
TRANSLATION REGION : 1 - 1626

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

15	TGC GTC GCG GAG CTG AGC AGG GAG GAC CTC GGT CTC GAA CCT GAA GGG Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly 55 60 65	48
20	ATT GCT GAA GGT TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln 70 75 80	96
	GAT TCT GAG ATT GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr 85 90 95	144
25	CAA AGC ATT GTC TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA AAG TCT Gln Ser Ile Val Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser 100 105 110 115	192
30	GGG GGT CTA GGA GAT GTT TGT GGT TCA TTG CCA GTT GCT CTT GCT GCT Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala 120 125 130	240
	CGT GGT CAC CGT GTG ATG GTT GTA ATG CCC AGA TAT TTA AAT GGT ACC Arg Gly His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr	288

			135					140					145					
		TCC Ser	GAT Asp	AAG Lys 150	AAT Asn	TAT Tyr	GCA Ala	AAT Asn	GCA Ala 155	TTT Phe	TAC Tyr	ACA Thr	GAA Glu	AAA Lys 160	CAC His	ATT Ile	CGG Arg	336
5		ATT Ile	CCA Pro 165	TGC Cys	TTT Phe	GGC Gly	GGT Gly	GAA Glu 170	CAT His	GAA Glu	GTT Val	ACC Thr	TTC Phe 175	TTC Phe	CAT His	GAG Glu	TAT Tyr	384
		AGA Arg 180	GAT Asp	TCA Ser	GTT Val	GAC Asp	TGG Trp 185	GTG Val	TTT Phe	GTT Val	GAT Asp	CAT His 190	CCC Pro	TCA Ser	TAT Tyr	CAC His	AGA Arg 195	432
10		CCT Pro	GGA Gly	AAT Asn	TTA Leu	TAT Tyr 200	GGA Gly	GAT Asp	AAG Lys	TTT Phe	GGT Gly 205	GCT Ala	TTT Phe	GGT Gly	GAT Asp	AAT Asn 210	CAG Gln	480
		TTC Phe	AGA Arg	TAC Tyr	ACA Thr 215	CTC Leu	CTT Leu	TGC Cys	TAT Tyr	GCT Ala 220	GCA Ala	TGT Cys	GAG Glu	GCT Ala 225	CCT Pro	TTG Leu	ATC Ile	528
15		CTT Leu	GAA Glu	TTG Leu 230	GGA Gly	GGA Gly	TAT Tyr	ATT Ile	TAT Tyr 235	GGA Gly	CAG Gln	AAT Asn	TGC Cys	ATG Met 240	TTT Phe	GTT Val	GTC Val	576
		AAT Asn 245	GAT Asp	TGG Trp	CAT His	GCC Ala	AGT Ser 250	CTA Leu	GTG Val	CCA Pro	GTC Val	CTT Leu 255	CTT Leu	GCT Ala	GCA Ala	AAA Lys	TAT Tyr	624
20		AGA Arg 260	CCA Pro	TAT Tyr	GGT Gly	GTT Val	TAT Tyr 265	AAA Lys	GAC Asp	TCC Ser	CGC Arg	AGC Ser 270	ATT Ile	CTT Leu	GTA Val	ATA Ile	CAT His 275	672
25		AAT Asn	TTA Leu	GCA Ala	CAT His	CAG Gln 280	GGT Gly	GTA Val	GAG Glu	CCT Pro	GCA Ala 285	AGC Ser	ACA Thr	TAT Tyr	CCT Pro	GAC Asp 290	CTT Leu	720
		GGG Gly	TTG Leu	CCA Pro	CCT Pro 295	GAA Glu	TGG Trp	TAT Tyr	GGA Gly	GCT Ala 300	CTG Leu	GAG Glu	TGG Trp	GTA Val	TTC Phe 305	CCT Pro	GAA Glu	768
		TGG Trp	GCG Ala	AGG Arg 310	AGG Arg	CAT His	GCC Ala	CTT Leu	GAC Asp 315	AAG Lys	GGT Gly	GAG Glu	GCA Ala	GTT Val 320	AAT Asn	TTT Phe	TTG Leu	816
30		AAA Lys 325	GGT Gly	GCA Ala	GTT Val	GTG Val	ACA Thr 330	GCA Ala	GAT Asp	CGA Arg	ATC Ile	GTG Val	ACT Thr 335	GTC Val	AGT Ser	AAG Lys	GGT Gly	864
		TAT Tyr 340	TCG Ser	TGG Trp	GAG Glu	GTC Val	ACA Thr 345	ACT Thr	GCT Ala	GAA Glu	GGT Gly	GGA Gly 350	CAG Gln	GGC Gly	CTC Leu	AAT Asn	GAG Glu 355	912
40		CTC Leu	TTA Leu	AGC Ser	TCC Ser	AGA Arg 360	AAG Lys	AGT Ser	GTA Val	TTA Leu	AAC Asn 365	GGA Gly	ATT Ile	GTA Val	AAT Asn	GGA Gly 370	ATT Ile	960
		GAC Asp	ATT Ile	AAT Asn	GAT Asp 375	TGG Trp	AAC Asn	CCT Pro	GCC Ala	ACA Thr 380	GAC Asp	AAA Lys	TGT Cys	ATC Ile	CCC Pro 385	TGT Cys	CAT His	1008
45		TAT Tyr	TCT Ser	GTT Val 390	GAT Asp	GAC Asp	CTC Leu	TCT Ser	GGA Gly 395	AAG Lys	GCC Ala	AAA Lys	TGT Cys	AAA Lys 400	GGT Gly	GCA Ala	TTG Leu	1056

	CAG AAG GAG CTG GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC	1104
	Gln Lys Glu Leu Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly	
	405 410 415	
5	TTT ATT GGA AGG TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT	1152
	Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu	
	420 425 430 435	
	ATC ATA CCA GAT CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA	1200
	Ile Ile Pro Asp Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly	
	440 445 450	
10	TCT GGT GAC CCA GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC	1248
	Ser Gly Asp Pro Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile	
	455 460 465	
15	TTC AAG GAT AAA TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC	1296
	Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser	
	470 475 480	
	CAC CGA ATA ACT GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC	1344
	His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe	
	485 490 495	
20	GAA CCT TGT GGT CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT	1392
	Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val	
	500 505 510 515	
	CCT GTT GTC CAT GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC	1440
	Pro Val Val His Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe	
	520 525 530	
25	AAC CCT TTC GGT GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA	1488
	Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala	
	535 540 545	
30	CCC CTA ACC ACA GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC	1536
	Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile	
	550 555 560	
	TAC ATA CAG GGA ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG	1584
	Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg	
	565 570 575	
35	CAT GTC AAA AGA CTT CAC GTG GGA CCA TGC CGC TGA	1620
	His Val Lys Arg Leu His Val Gly Pro Cys Arg *	
	580 585 590	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

- 45 Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly
1 5 10 15
Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln
20 25 30
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr
35 40 45

	Gln	Ser	Ile	Val	Phe	Val	Thr	Gly	Glu	Ala	Ser	Pro	Tyr	Ala	Lys	Ser	
	50						55					60					
	Gly	Gly	Leu	Gly	Asp	Val	Cys	Gly	Ser	Leu	Pro	Val	Ala	Leu	Ala	Ala	
	65					70					75					80	
5	Arg	Gly	His	Arg	Val	Met	Val	Val	Met	Pro	Arg	Tyr	Leu	Asn	Gly	Thr	
					85					90					95		
	Ser	Asp	Lys	Asn	Tyr	Ala	Asn	Ala	Phe	Tyr	Thr	Glu	Lys	His	Ile	Arg	
				100					105					110			
10	Ile	Pro	Cys	Phe	Gly	Gly	Glu	His	Glu	Val	Thr	Phe	Phe	His	Glu	Tyr	
			115					120					125				
	Arg	Asp	Ser	Val	Asp	Trp	Val	Phe	Val	Asp	His	Pro	Ser	Tyr	His	Arg	
	130						135					140					
	Pro	Gly	Asn	Leu	Tyr	Gly	Asp	Lys	Phe	Gly	Ala	Phe	Gly	Asp	Asn	Gln	
	145					150					155					160	
15	Phe	Arg	Tyr	Thr	Leu	Leu	Cys	Tyr	Ala	Ala	Cys	Glu	Ala	Pro	Leu	Ile	
					165					170					175		
	Leu	Glu	Leu	Gly	Gly	Tyr	Ile	Tyr	Gly	Gln	Asn	Cys	Met	Phe	Val	Val	
				180					185					190			
20	Asn	Asp	Trp	His	Ala	Ser	Leu	Val	Pro	Val	Leu	Leu	Ala	Ala	Lys	Tyr	
			195					200					205				
	Arg	Pro	Tyr	Gly	Val	Tyr	Lys	Asp	Ser	Arg	Ser	Ile	Leu	Val	Ile	His	
	210						215					220					
	Asn	Leu	Ala	His	Gln	Gly	Val	Glu	Pro	Ala	Ser	Thr	Tyr	Pro	Asp	Leu	
	225					230					235					240	
25	Gly	Leu	Pro	Pro	Glu	Trp	Tyr	Gly	Ala	Leu	Glu	Trp	Val	Phe	Pro	Glu	
					245					250					255		
	Trp	Ala	Arg	Arg	His	Ala	Leu	Asp	Lys	Gly	Glu	Ala	Val	Asn	Phe	Leu	
				260					265					270			
30	Lys	Gly	Ala	Val	Val	Thr	Ala	Asp	Arg	Ile	Val	Thr	Val	Ser	Lys	Gly	
			275					280					285				
	Tyr	Ser	Trp	Glu	Val	Thr	Thr	Ala	Glu	Gly	Gly	Gln	Gly	Leu	Asn	Glu	
	290						295					300					
	Leu	Leu	Ser	Ser	Arg	Lys	Ser	Val	Leu	Asn	Gly	Ile	Val	Asn	Gly	Ile	
	305					310					315					320	
35	Asp	Ile	Asn	Asp	Trp	Asn	Pro	Ala	Thr	Asp	Lys	Cys	Ile	Pro	Cys	His	
					325					330					335		
	Tyr	Ser	Val	Asp	Asp	Leu	Ser	Gly	Lys	Ala	Lys	Cys	Lys	Gly	Ala	Leu	
				340					345					350			
40	Gln	Lys	Glu	Leu	Gly	Leu	Pro	Ile	Arg	Pro	Asp	Val	Pro	Leu	Ile	Gly	
			355					360					365				
	Phe	Ile	Gly	Arg	Leu	Asp	Tyr	Gln	Lys	Gly	Ile	Asp	Leu	Ile	Gln	Leu	
	370						375					380					
	Ile	Ile	Pro	Asp	Leu	Met	Arg	Glu	Asp	Val	Gln	Phe	Val	Met	Leu	Gly	
	385					390					395					400	
45	Ser	Gly	Asp	Pro	Glu	Leu	Glu	Asp	Trp	Met	Arg	Ser	Thr	Glu	Ser	Ile	
					405					410					415		

Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser
 420 425 430
 His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe
 435 440 445
 5 Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val
 450 455 460
 Pro Val Val His Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe
 465 470 475 480
 10 Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala
 485 490 495
 Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile
 500 505 510
 Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg
 515 520 525
 15 His Val Lys Arg Leu His Val Gly Pro Cys Arg *
 530 535 540

Example Six:

This experiment employs a plasmid having a maize promoter, a maize transit peptide,
 a starch-encapsulating region from the starch synthase I gene, and a ligated gene fragment
 20 attached thereto. The plasmid shown in FIG. 6 contains the DNA sequence listed in Table 8.

Plasmid pEXS52 was constructed according to the following protocol:

Materials used to construct transgenic plasmids are as follows:

Plasmid pBluescript SK-

Plasmid pMF6 (contain nos3' terminator)

25 Plasmid pKH1 (contain maize adh1 intron)

Plasmid MstSI(6-4) (contain maize stSI transit peptide, use as a template for PCT stSI transit
peptide out)

Plasmid MstSIII in pBluescript SK-

Primers EXS29 (GTGGATCCATGGCGACGCCCTCGGCCGTGG) [SEQ ID NO:22]

30 EXS35 (CTGAATTCCATATGGGGCCCCTCCCTGCTCAGCTC) [SEQ ID NO:23]
 both used for PCT stSI transit peptide

Primers EXS31 (CTCTGAGCTCAAGCTTGCTACTTTCTTTCTTAATG) [SEQ ID NO:24]

EXS32 (GTCTCCGCGGTGGTGGTGCCTTGCTTCCTAG) [SEQ ID NO:25]

both used for PCR maize 10KD zein promoter (Journal: Gene 71:359-370 [1988])

Maize A632 genomic DNA (used as a template for PCR maize 10KD zein promoter).

Step 1: Clone maize 10KD zein promoter in pBluescriptSK-(named as pEXS10zp).

- 5
1. PCR 1.1Kb maize 10KD zein promoter
primers: EXS31, EXS32
template: maize A632 genomic DNA
 2. Clone 1.1Kb maize, 10KD zein promoter PCR product into pBluescript SK-
plasmid at SacI and SacII site (See FIG. 7).

10 Step 2: Delete NdeI site in pEXS10zp (named as pEXS10zp-NdeI).

NdeI is removed by fill in and blunt end ligation from maize 10KD zein promoter in pBluescriptSK.

Step 3: Clone maize adh1 intron in pBluescriptSK- (named as pEXSadh1).

15 Maize adh1 intron is released from plasmid pHKH1 at XbaI and BamHI sites. Maize adh1 intron (XbaI/BamHI fragment) is cloned into pBluescriptSK- at XbaI and BamHI sites (see FIG. 7).

Step 4: Clone maize 10KD zein promoter and maize adh1 intron into pBluescriptSK-
(named as pEXS10zp-adh1).

20 Maize 10KD zein promoter is released from plasmid pEXS 10zp-NdeI at SacI and SacII sites. Maize 10KD zein promoter (SacI/SacII fragment) is cloned into plasmid pEXSadh1 (contain maize adh1 intron) at SacI and SacII sites (see FIG. 7).

Step 5: Clone maize nos3' terminator into plasmid pEXSadhl (named as pEXSadhl-nos3').

Maize nos3' terminator is released from plasmid pMF6 at EcoRI and HindIII sites. Maize nos3' terminator (EcoRI/HindIII fragment) is cloned into plasmid pEXSadhl at EcoRI and HindIII (see FIG. 7).

Step 6: Clone maize nos3' terminator into plasmid pEXS10zp-adhl (named as pEXS10zp-adhl-nos3').

Maize nos3' terminator is released from plasmid pEXSadhl-nos3' at EcoRI and ApaI sites. Maize nos3' terminator (EcoRI/ApaI fragment) is cloned into plasmid pEXS10zp-adhl at EcoRI and ApaI sites (see FIG. 7).

Step 7: Clone maize STSI transit peptide into plasmid pEXS10zp-adhl-nos3' (named as pEXS33).

1. PCR 150bp maize STSI transit peptide
primer: EXS29, EXS35
template: MSTSI(6-4) plasmid

2. Clone 150bp maize STSI transit peptide PCR product into plasmid pEXS10zp-adhl-nos3' at EcoRI and BamHI sites (see FIG. 7).

Step 8: Site-directed mutagenesis on maize STSI transit peptide in pEXS33 (named as pEXS33(m)).

There is a mutation (stop codon) on maize STSI transit peptide in plasmid pEXS33. Site-directed mutagenesis is carried out to change stop codon to non-stop codon. New plasmid (containing maize 10KD zein promoter, maize STSI transit peptide, maize adh1 intron, maize nos3' terminator) is named as pEXS33(m).

Step 9: NotI site in pEXS33(m) deleted (named as pEXS50).

NotI site is removed from pEXS33 by NotI fillin, blunt end ligation to form pEXS50 (see FIG. 8).

Step 10: Maize adh1 intron deleted in pEXS33(m) (named as pEXS60).

5 Maize adh1 intron is removed by NotI/BamHI digestion, filled in with Klenow fragment, blunt end ligation to form pEXS60 (see FIG. 9).

Step 11: Clone maize STSIII into pEXS50, pEXS60.

10 Maize STSIII is released from plasmid maize STSIII in pBluescript SK- at NdeI and EcoRI sites. Maize STSIII (NdeI-EcoRI fragment) is cloned into pEXS50, pEXS60 separately, named as pEXS51, pEXS61 (see FIGS. 8 and 9, respectively).

Step 12: Clone the gene in Table 8 into pEXS51 at NdeI/NotI site to form pEXS52. Other similar plasmids can be made by cloning other genes (STS1, II, WX, glgA, glgB, glgC, BEI, BEII, etc.) into pEXS51, pEXS61 at NdeI/NotI site.

15 Plasmid EXS52 was transformed into rice. The regenerated rice plants transformed with pEXS52 were marked and placed in a magenta box.

20 Two siblings of each line were chosen from the magenta box and transferred into 2.5 inch pots filled with soil mix (topsoil mixed with peat-vermiculite 50/50). The pots were placed in an aquarium (fish tank) with half an inch of water. The top was covered to maintain high humidity (some holes were made to help heat escape). A thermometer monitored the temperature. The fish tank was placed under fluorescent lights. No fertilizer was used on the plants in the first week. Light period was 6 a.m.-8 p.m., minimum 14 hours light. Temperature was minimum 68°F at night, 80°-90°F during the day. A heating mat was used under the fish tank to help root growth when necessary. The plants stayed in the

above condition for a week. (Note: the seedlings began to grow tall because of low light intensity.)

After the first week, the top of the aquarium was opened and rice transformants were transferred to growth chambers for three weeks with high humidity and high light intensity.

5 Alternatively, water mix in the greenhouse can be used to maintain high humidity. The plants grew for three weeks. Then the plants were transferred to 6-inch pots (minimum 5-inch pots) with soil mix (topsoil and peat-Vet, 50/50). The pots were in a tray filled with half an inch of water. 15-16-17 (N-K-P) was used to fertilize the plants (250 ppm) once a week or according to the plants' needs by their appearances. The plants remained in 14 hours
10 light (minimum) 6 a.m.-8 p.m. high light intensity, temperature 85°-90°/70°F day/night.

The plants formed rice grains and the rice grains were harvested. These harvested seeds can have the starch extracted and analyzed for the presence of the ligated amino acids C, V, A, E, L, S, R, E [SEQ ID NO:27] in the starch within the seed.

Example Seven:

SER Vector for Plants:

15 The plasmid shown in Figure 6 is adapted for use in monocots, i.e., maize. Plasmid pEXS52 (FIG. 6) has a promoter, a transit peptide (from maize), and a ligated gene fragment (TGC GTC GCG GAG CTG AGC AGG GAG) [SEQ ID NO:26] which encodes the amino acid sequence C V A E L S R E [SEQ ID NO:27].

20 This gene fragment naturally occurs close to the N-terminal end of the maize soluble starch synthase (MSTSI) gene. As is shown in TABLE 8, at about amino acid 292 the SER from the starch synthase begins. This vector is preferably transformed into a maize host. The transit peptide is adapted for maize so this is the preferred host. Clearly the transit peptide and the promoter, if necessary, can be altered to be appropriate for the host plant
25 desired. After transformation by "whiskers" technology (U.S. Patent Nos. 5,302,523 and 5,464,765), the transformed host cells are regenerated by methods known in the art, the

transformant is pollinated, and the resultant kernels can be collected and analyzed for the presence of the peptide in the starch and the starch granule.

The following preferred genes can be employed in maize to improve feeds: phytase gene, the somatotrophin gene, the following chained amino acids: AUG AUG AUG AUG
5 AUG AUG AUG AUG [SEQ ID NO:28]; and/or, AAG AAG AAG AAG AAG AAG AAG AAG
AAG AAG AAG AAG AAG {SEQ ID NO:29}; and/or AAA AAA AAA AAA AAA AAA AAA
[SEQ ID NO:30]; or a combination of the codons encoding the lysine amino acid in a chain
or a combination of the codons encoding both lysine and the methionine codon or any
combination of two or three of these amino acids. The length of the chains should not be
10 unduly long but the length of the chain does not appear to be critical. Thus the amino acids
will be encapsulated within the starch granule or bound within the starch formed in the starch-
bearing portion of the plant host.

This plasmid may be transformed into other cereals such as rice, wheat, barley, oats,
sorghum, or millet with little to no modification of the plasmid. The promoter may be the
15 *waxy* gene promoter whose sequence has been published, or other zein promoters known to
the art.

Additionally these plasmids, without undue experimentation, may be transformed into
dicots such as potatoes, sweet potato, taro, yam, lotus cassava, peanuts, peas, soybean, beans,
or chickpeas. The promoter may be selected to target the starch-storage area of particular
20 dicots or tubers, for example the patatin promoter may be used for potato tubers.

Various methods of transforming monocots and dicots are known in the industry and
the method of transforming the genes is not critical to the present invention. The plasmid can
be introduced into *Agrobacterium tumefaciens* by the freeze-thaw method of An et al. (1988)
Binary Vectors, in Plant Molecular Biology Manual A3, S.B. Gelvin and R.A. Schilperoot,
25 eds. (Dordrecht, The Netherlands: Kluwer Academic Publishers), pp. 1-19. Preparation of
Agrobacterium inoculum carrying the construct and inoculation of plant material, regeneration
of shoots, and rooting of shoots are described in Edwards et al., "Biochemical and molecular
characterization of a novel starch synthase from potatoes," Plant J. 8, 283-294 (1995).

A number of encapsulating regions are present in a number of different genes. Although it is preferred that the protein be encapsulated within the starch granule (granule encapsulation), encapsulation within non-granule starch is also encompassed within the scope of the present invention in the term "encapsulation." The following types of genes are useful for this purpose.

Use of Starch-Encapsulating Regions of Glycogen Synthase:

E. coli glycogen synthase is not a large protein: the structural gene is 1431 base pairs in length, specifying a protein of 477 amino acids with an estimated molecular weight of 49,000. It is known that problems of codon usage can occur with bacterial genes inserted into plant genomes but this is generally not so great with *E. coli* genes as with those from other bacteria such as those from *Bacillus*. Glycogen synthase from *E. coli* has a codon usage profile much in common with maize genes but it is preferred to alter, by known procedures, the sequence at the translation start point to be more compatible with a plant consensus sequence:

glgA G A T A A T G C A G [SEQ ID NO:31]

cons A A C A A T G G C T [SEQ ID NO:32]

Use of Starch-Encapsulating Regions of Soluble Starch Synthase:

cDNA clones of plant-soluble starch synthases are described in the background section above and can be used in the present invention. The genes for any such SSTS protein may be used in constructs according to this invention.

Use of Starch-Encapsulating Regions of Branching Enzyme:

cDNA clones of plant, bacterial and animal branching enzymes are described in the background section above and can be used in the present invention. Branching enzyme [1,4Dglucan: 1,4Dglucan 6D(1,4Dglucano) transferase (E.C. 2.4.1.18)] converts amylose to amylopectin, (a segment of a 1,4Dglucan chain is transferred to a primary hydroxyl group in a similar glucan chain) sometimes called Q-enzyme.

The sequence of maize branching enzyme I was investigated by Baba et al. (1991) BBRC, 181:87-94. Starch branching enzyme II from maize endosperm was investigated by

Fisher et al. (1993) Plant Physiol, 102:1045-1046. The BE gene construct may require the presence of an amyloplast transit peptide to ensure its correct localization in the amyloplast. The genes for any such branching enzyme of GBSTS protein may be used in constructs according to this invention.

5 **Use of Starch-Binding Domains of Granule-Bound Starch Synthase:**

The use of cDNA clones of plant granule-bound starch synthases are described in Shure et al. (1983) Cell 35:225-233, and Visser et al. (1989) Plant Sci. 64(2):185-192. Visser et al. have also described the inhibition of the expression of the gene for granule-bound starch synthase in potato by antisense constructs (1991) Mol. Gen. Genetic 225(2):289-296; (1994) The Plant Cell 6:43-52.) Shimada et al. show antisense in rice (1993) Theor. Appl. Genet. 86:665-672. Van der Leij et al. show restoration of amylose synthesis in low-amylose potato following transformation with the wild-type *waxy* potato gene (1991) Theor. Appl. Genet. 82:289-295.

15 The amino acid sequences and nucleotide sequences of granule starch synthases from, for example, maize, rice, wheat, potato, cassava, peas or barley are well known. The genes for any such GBSTS protein may be used in constructs according to this invention.

Construction of Plant Transformation Vectors:

Plant transformation vectors for use in the method of the invention may be constructed using standard techniques

20 .

Use of Transit Peptide Sequences:

Some gene constructs require the presence of an amyloplast transit peptide to ensure correct localization in the amyloplast. It is believed that chloroplast transit peptides have similar sequences (Heijne et al. describe a database of chloroplast transit peptides in (1991) Plant Mol. Biol. Reporter, 9(2):104-126). Other transit peptides useful in this invention are those of ADPG pyrophosphorylase (1991) Plant Mol. Biol. Reporter, 9:104-126), small subunit RUBISCO, acetolactate synthase, glyceraldehyde3Pdehydrogenase and nitrite reductase.

The consensus sequence of the transit peptide of small subunit RUBISCO from many genotypes has the sequence:

MASSMLSSAAVATRTNPAQASM VAPFTGLKSAAFPVSRKQNLDI TSIASNGGRVQC
[SEQ ID NO:33]

5 The corn small subunit RUBISCO has the sequence:

MAPTVMMASSATATRTNPAQAS AVAPFQGLKSTASLPVARRSSR SLGNVASNGGRIRC
[SEQ ID NO:34]

The transit peptide of leaf glyceraldehyde3Pdehydrogenase from corn has the sequence:

10 MAQILAPSTQWQMRITKTSPCA TPITSKMWSSLVMKQTKKVAHS
AKFRVMAVNSENGT [SEQ ID NO:35]

The transit peptide sequence of corn endosperm-bound starch synthase has the sequence:

MAALATSQLVATRAGHGVPDASTFRRGAAQGLRGARASAAADTL SMRTSARAAPRHQ
15 QQARRGGRFPFPSLVVC [SEQ ID NO:36]

The transit peptide sequence of corn endosperm soluble starch synthase has the sequence:

MATPSAVGAACLLLARXAWPAAVGDRLRPRRLQRLRRR [SEQ ID NO:37]

Engineering New Amino Acids or Peptides into Starch-Encapsulating Proteins:

20 The starch-binding proteins used in this invention may be modified by methods known to those skilled in the art to incorporate new amino acid combinations. For example,

sequences of starch-binding proteins may be modified to express higher-than-normal levels of lysine, methionine or tryptophan. Such levels can be usefully elevated above natural levels and such proteins provide nutritional enhancement in crops such as cereals.

5 In addition to altering amino acid balance, it is possible to engineer the starch-binding proteins so that valuable peptides can be incorporated into the starch-binding protein. Attaching the payload polypeptide to the starch-binding protein at the N-terminal end of the protein provides a known means of adding peptide fragments and still maintaining starch-binding capacity. Further improvements can be made by incorporating specific protease cleavage sites into the site of attachment of the payload polypeptide to the starch-encapsulating
10 region. It is well known to those skilled in the art that proteases have preferred specificities for different amino-acid linkages. Such specificities can be used to provide a vehicle for delivery of valuable peptides to different regions of the digestive tract of animals and man.

15 In yet another embodiment of this invention, the payload polypeptide can be released following purification and processing of the starch granules. Using amylolysis and/or gelatinization procedures it is known that the proteins bound to the starch granule can be released or become available for proteolysis. Thus recovery of commercial quantities of proteins and peptides from the starch granule matrix becomes possible.

20 In yet another embodiment of the invention it is possible to process the starch granules in a variety of different ways in order to provide a means of altering the digestibility of the starch. Using this methodology it is possible to change the bioavailability of the proteins, peptides or amino acids entrapped within the starch granules.

25 Although the foregoing invention has been described in detail by way of illustration and example for purposes of clarity and understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Keeling, Peter
Guan, Hanping
- (ii) TITLE OF INVENTION: Starch Encapsulation
- (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 - (B) STREET: 5370 Manhattan Circle
 - (C) CITY: Boulder
 - (D) STATE: CO
 - (E) COUNTRY: US
 - (F) ZIP: 80303
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 30-SEP-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/026,855
 - (B) FILING DATE: 30-SEP-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Winner, Ellen P
 - (B) REGISTRATION NUMBER: 28,547
 - (C) REFERENCE/DOCKET NUMBER: 89-97
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (303) 499-8080
 - (B) TELEFAX: (303) 499-8089

(2) INFORMATION FOR SEQ ID NO:1:

66

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTAGTCAT ATGGTGAGCA AGGGCGAGGA G

31

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

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

CTAGATCTTC ATATGCTTGT ACAGCTCGTC CATGCC

36

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

67

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

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

CTAGATCTTG GCCATGGCCT TGTACAGCTC GTCCATGCC

39

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055
..2144, 2226..2289, 2413..2513, 2651..2760, 2858
..3101, 3212..3394, 3490..3681, 3793..3879, 3977
..4105, 4227..4343)

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

CAGCGACCTA TTACACAGCC CGCTCGGGCC CGCGACGTCG GGACACATCT TCTTCCCCCT	60
TTTGGTGAAG CTCTGCTCGC AGCTGTCCGG CTCCTTGGAC GTTCGTGTGG CAGATTCATC	120
TGTTGTCTCG TCTCCTGTGC TTCCTGGGTA GCTTGTGTAG TGGAGCTGAC ATGGTCTGAG	180
CAGGCTTAAA ATTTGCTCGT AGACGAGGAG TACCAGCACA GCACGTTGCG GATTCTCTG	240

CCTGTGAAGT	GCAACGTCTA	GGATTGTCAC	ACGCCTTGGT	CGCGTCGCGT	CGCGTCGCGT	300
CGATGCGGTG	GTGAGCAGAG	CAGCAACAGC	TGGGCGGCCC	AACGTTGGCT	TCCGTGTCTT	360
CGTCGTACGT	ACGCGCGCGC	CGGGGACACG	CAGCAGAGAG	CGGAGAGCGA	GCCGTGCACG	420
GGGAGGTGGT	GTGGAAGTGG	AGCCGCGCGC	CCGGCCGCCC	GCGCCCGGTG	GGCAACCCAA	480
AAGTACCCAC	GACAAGCGAA	GGCGCCAAAG	CGATCCAAGC	TCCGGAACGC	AACAGCATGC	540
GTCGCGTCGG	AGAGCCAGCC	ACAAGCAGCC	GAGAACCGAA	CCGGTGGGCG	ACGCGTCATG	600
GGACGGACGC	GGGCGACGCT	TCCAAACGGG	CCACGTACGC	CGGCGTGTGC	GTGCGTGCAG	660
ACGACAAGCC	AAGGCGAGGC	AGCCCCCGAT	CGGGAAAGCG	TTTTGGGCGC	GAGCGCTGGC	720
GTGCGGGTCA	GTCGCTGGTG	CGCAGTGCCG	GGGGGAACGG	GTATCGTGGG	GGGCGCGGGC	780
GGAGGAGAGC	GTGGCGAGGG	CCGAGAGCAG	CGCGCGGCCG	GGTCACGCAA	CGCGCCCCAC	840
GTACTGCCCT	CCCCCTCCGC	GCGCGCTAGA	AATACCGAGG	CCTGGACCGG	GGGGGGGCCC	900
CGTCACATCC	ATCCATCGAC	CGATCGATCG	CCACAGCCAA	CACCACCCGC	CGAGGCGACG	960
CGACAGCCGC	CAGGAGGAAG	GAATAAACTC	ACTGCCAGCC	AGTGAAGGGG	GAGAAGTGTA	1020
CTGCTCCGTC	GACCAGTGCG	CGCACCGCCC	GGCAGGGCTG	CTCATCTCGT	CGACGACCAG	1080
GTTCTGTTCC	GTTCCGATCC	GATCCGATCC	TGTCCTTGAG	TTTCGTCCAG	ATCCTGGCGC	1140
GTATCTGCGT	GTTTGATGAT	CCAGGTTCTT	CGAACCTAAA	TCTGTCCGTG	CACACGTCTT	1200
TTCTCTCTCT	CCTACGCAGT	GGATTAATCG	GCATGGCGGC	TCTGGCCACG	TCGCAGCTCG	1260
TCGCAACGCG	CGCCGGCCTG	GGCGTCCCGG	ACGCGTCCAC	GTTCCGCCGC	GGCGCCGCGC	1320
AGGGCCTGAG	GGGGGCCCGG	GCGTCGGCGG	CGGCGGACAC	GCTCAGCATG	CGGACCAGCG	1380
CGCGCGCGGC	GCCCAGGCAC	CAGCAGCAGG	CGCGCCGCGG	GGGCAGGTTC	CCGTCGCTCG	1440
TCGTGTGC	GCC AGC GCC GGC ATG AAC	GTC GTC TTC GTC GGC GCC GAG ATG				1490
Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met						
1	5	10				
GCG CCG TGG AGC AAG ACC GGC GGC CTC GGC GAC GTC CTC GGC GGC CTG						1538

Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu
 15 20 25 30

CCG CCG GCC ATG GCC GTAAGCGCGC GCACCGAGAC ATGCATCCGT TGGATCGCGT 1593
 Pro Pro Ala Met Ala
 35

CTTCTTCGTG CTCTTGCCGC GTGCATGATG CATGTGTTTC CTCCTGGCTT GTGTTCGTGT 1653

ATGTGACGTG TTTGTTCGGG CATGCATGCA G GCG AAC GGG CAC CGT GTC ATG 1705
 Ala Asn Gly His Arg Val Met
 40

GTC GTC TCT CCC CGC TAC GAC CAG TAC AAG GAC GCC TGG GAC ACC AGC 1753
 Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser
 45 50 55

GTC GTG TCC GAG GTACGGCCAC CGAGACCAGA TTCAGATCAC AGTCACACAC 1805
 Val Val Ser Glu
 60

ACCGTCATAT GAACCTTTCT CTGCTCTGAT GCCTGCAACT GCAAATGCAT GCAG ATC 1862
 Ile

AAG ATG GGA GAC GGG TAC GAG ACG GTC AGG TTC TTC CAC TGC TAC AAG 1910
 Lys Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys
 65 70 75

CGC GGA GTG GAC CGC GTG TTC GTT GAC CAC CCA CTG TTC CTG GAG AGG 1958
 Arg Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg
 80 85 90 95

GTGAGACGAG ATCTGATCAC TCGATACGCA ATTACCACCC CATTGTAAGC AGTTACAGTG 2018

AGCTTTTTTTT CCCCCCGGCC TGGTCGCTGG TTTCAG GTT TGG GGA AAG ACC GAG 2072
 Val Trp Gly Lys Thr Glu
 100

GAG AAG ATC TAC GGG CCT GTC GCT GGA ACG GAC TAC AGG GAC AAC CAG 2120
 Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln
 105 110 115

CTG CGG TTC AGC CTG CTA TGC CAG GTCAGGATGG CTTGGTACTA CAACTTCATA 2174
 Leu Arg Phe Ser Leu Leu Cys Gln

120	125	
TCATCTGTAT GCAGCAGTAT ACACTGATGA GAAATGCATG CTGTTCTGCA G GCA GCA	2231	Ala Ala
CTT GAA GCT CCA AGG ATC CTG AGC CTC AAC AAC AAC CCA TAC TTC TCC	2279	
Leu Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser		
130 135 140		
GGA CCA TAC G GTAAGAGTTG CAGTCTTCGT ATATATATCT GTTGAGCTCG	2329	
Gly Pro Tyr		
145		
AGAATCTTCA CAGGAAGCGG CCCATCAGAC GGACTGTCAT TTTACACTGA CTACTGCTGC	2389	
TGCTCTTCGT CCATCCATAC AAG GG GAG GAC GTC GTG TTC GTC TGC AAC	2438	
Gly Glu Asp Val Val Phe Val Cys Asn		
150 155		
GAC TGG CAC ACC GGC CCT CTC TCG TGC TAC CTC AAG AGC AAC TAC CAG	2486	
Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln		
160 165 170		
TCC CAC GGC ATC TAC AGG GAC GCA AAG GTTGCCTTCT CTGAACTGAA	2533	
Ser His Gly Ile Tyr Arg Asp Ala Lys		
175 180		
CAACGCCGTT TTCGTTCTCC ATGCTCGTAT ATACCTCGTC TGGTAGTGGT GGTGCTTCTC	2593	
TGAGAAACTA ACTGAAACTG ACTGCATGTC TGTCTGACCA TCTTCACGTA CTACCAG	2650	
ACC GCT TTC TGC ATC CAC AAC ATC TCC TAC CAG GGC CGG TTC GCC TTC	2698	
Thr Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe		
185 190 195		
TCC GAC TAC CCG GAG CTG AAC CTC CCG GAG AGA TTC AAG TCG TCC TTC	2746	
Ser Asp Tyr Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe		
200 205 210		
GAT TTC ATC GAC GG GTCTGTTTTTCT CTGCGTGCAT GTGAACATTC ATGAATGGTA	2800	
Asp Phe Ile Asp Gly		
215		
ACCCACAACCT GTTCGCGTCC TGCTGGTTCA TTATCTGACC TGATTGCATT ATTGCAG C	2858	

TAC GAG AAG CCC GTG GAA GGC CGG AAG ATC AAC TGG ATG AAG GCC GGG Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly 220 225 230	2906
ATC CTC GAG GCC GAC AGG GTC CTC ACC GTC AGC CCC TAC TAC GCC GAG Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu 235 240 245	2954
GAG CTC ATC TCC GGC ATC GCC AGG GGC TGC GAG CTC GAC AAC ATC ATG Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met 250 255 260 265	3002
CGC CTC ACC GGC ATC ACC GGC ATC GTC AAC GGC ATG GAC GTC AGC GAG Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu 270 275 280	3050
TGG GAC CCC AGC AGG GAC AAG TAC ATC GCC GTG AAG TAC GAC GTG TCG Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp Val Ser 285 290 295	3098
ACG GTGAGCTGGC TAGCTCTGAT TCTGCTGCCT GGTCCCTCTG CTCATCATGC Thr	3151
TGGTTCGGTA CTGACGCGGC AAGTGACGT ACGTGCGTGC GACGGTGGTG TCCGGTTCAG	3211
GCC GTG GAG GCC AAG GCG CTG AAC AAG GAG GCG CTG CAG GCG GAG GTC Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu Val 300 305 310	3259
GGG CTC CCG GTG GAC CGG AAC ATC CCG CTG GTG GCG TTC ATC GGC AGG Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe Ile Gly Arg 315 320 325 330	3307
CTG GAA GAG CAG AAG GGC CCC GAC GTC ATG GCG GCC GCC ATC CCG CAG Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala Ile Pro Gln 335 340 345	3355
CTC ATG GAG ATG GTG GAG GAC GTG CAG ATC GTT CTG CTG GTACGTGTGC Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu 350 355	3404
GCCGGCCGCC ACCCGGCTAC TACATGCGTG TATCGTTCGT TCTACTGGAA CATGCGTGTG	3464
AGCAACGCGA TGGATAATGC TGCAG GGC ACG GGC AAG AAG AAG TTC GAG CGC	3516

	Gly Thr Gly Lys Lys Lys Phe Glu Arg	
	360	365
ATG CTC ATG AGC GCC GAG GAG AAG TTC CCA GGC AAG GTG CGC GCC GTG		3564
Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val		
370	375	380
GTC AAG TTC AAC GCG GCG CTG GCG CAC CAC ATC ATG GCC GGC GCC GAC		3612
Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp		
385	390	400
GTG CTC GCC GTC ACC AGC CGC TTC GAG CCC TGC GGC CTC ATC CAG CTG		3660
Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu		
	405	415
CAG GGG ATG CGA TAC GGA ACG GTACGAGAGA AAAAAAAAT CCTGAATCCT		3711
Gln Gly Met Arg Tyr Gly Thr		
420		
GACGAGAGGG ACAGAGACAG ATTATGAATG CTTTCATCGAT TTGAATTGAT TGATCGATGT		3771
CTCCCGCTGC GACTCTTGCA G CCC TGC GCC TGC GCG TCC ACC GGT GGA CTC		3822
Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu		
425	430	
GTC GAC ACC ATC ATC GAA GGC AAG ACC GGG TTC CAC ATG GGC CGC CTC		3870
Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu		
435	440	445
AGC GTC GAC GTAAGCCTAG CTCTGCCATG TTCTTTCTTC TTTCTTTCTG		3919
Ser Val Asp		
450		
TATGTATGTA TGAATCAGCA CCGCCGTTCT TGTTTCGTGC TCGTCCTCTC TTCCAG		3976
TGT AAC GTC GTG GAG CCG GCG GAC GTC AAG AAG GTG GCC ACC ACA TTG		4024
Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala Thr Thr Leu		
455	460	465
CAG CGC GCC ATC AAG GTG GTC GGC ACG CCG GCG TAC GAG GAG ATG GTG		4072
Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val		
470	475	480
AGG AAC TGC ATG ATC CAG GAT CTC TCC TGG AAG GTACGTACGC CCGCCCCGCC		4125
Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys		

485	490	495	
CCGCCCCGCC	AGAGCAGAGC	GCCAAGATCG	ACCGATCGAC CGACCACACG TACGCGCCTC 4185
GCTCCTGTCTG	CTGACCGTGG	TTTAATTTGC	GAAATGCGCA G GGC CCT GCC AAG 4238
			Gly Pro Ala Lys
AAC TGG GAG AAC GTG CTG CTC AGC CTC GGG GTC GCC GGC GGC GAG CCA			4286
Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly Glu Pro			
500	505	510	515
GGG GTC GAA GGC GAG GAG ATC GCG CCG CTC GCC AAG GAG AAC GTG GCC			4334
Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala			
	520	525	530
GCG CCC TGA AGAGTTCGGC CTGCAGGGCC CCTGATCTCG CGCGTGGTGC			4383
Ala Pro *			
AAAGATGTTG	GGACATCTTC	TTATATATGC	TGTTTCGTTT ATGTGATATG GACAAGTATG 4443
TGTAGCTGCT	TGCTTGTGCT	AGTGTAATGT	AGTGTAGTGG TGGCCAGTGG CACAACCTAA 4503
TAAGCGCATG	AACTAATTGC	TTGCGTGTGT	AGTTAAGTAC CGATCGGTAA TTTTATATTG 4563
CGAGTAAATA	AATGGACCTG	TAGTGGTGGA	GTAAATAATC CCTGCTGTTC GGTGTTCTTA 4623
TCGCTCCTCG	TATAGATATT	ATATAGAGTA	CATTTTCTC TCTCTGAATC CTACGTTTGT 4683
GAAATTTCTA	TATCATTACT	GTAAAATTTT	TGCGTTCCAA AAGAGACCAT AGCCTATCTT 4743
TGGCCCTGTT	TGTTTCGGCT	TCTGGCAGCT	TCTGGCCACC AAAAGCTGCT GCGGACT 4800

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

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

Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala
 245 250 255

Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
 260 265 270

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

Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
 290 295 300

Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
 305 310 315 320

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

Pro Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
 340 345 350

Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
 355 360 365

Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val
 370 375 380

Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
 385 390 395 400

Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
 405 410 415

Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
 420 425 430

Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
 435 440 445

Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
 450 455 460

Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
 465 470 475 480

76

Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
 485 490 495

Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
 500 505 510

Gly Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu
 515 520 525

Asn Val Ala Ala Pro *
 530

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Oryza sativa*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 453..2282

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

GAATTCAGTG TGAAGGAATA GATTCTCTTC AAAACAATTT AATCATTCAT CTGATCTGCT	60
CAAAGCTCTG TGCATCTCCG GGTGCAACGG CCAGGATATT TATTGTGCAG TAAAAAATG	120
TCATATCCCC TAGCCACCCA AGAAACTGCT CCTTAAGTCC TTATAAGCAC ATATGGCATT	180
GTAATATATA TGTTTGAGTT TTAGCGACAA TTTTTTTAAA AACTTTTGGT CCTTTTATG	240
AACGTTTTAA GTTTCAGTGT CTTTTTTTTT CGAATTTTAA ATGTAGCTTC AAATTCTAAT	300
CCCCAATCCA AATTGTAATA AACTTCAATT CTCCTAATTA ACATCTTAAT TCATTTATTT	360

GAAAACCAGT TCAAATTCTT TTTAGGCTCA CCAAACCTTA AACAAATTCAA TTCAGTGCAG	420
AGATCTTCCA CAGCAACAGC TAGACAACCA CC ATG TCG GCT CTC ACC ACG TCC	473
Met Ser Ala Leu Thr Thr Ser	
535 540	
CAG CTC GCC ACC TCG GCC ACC GGC TTC GGC ATC GCC GAC AGG TCG GCG	521
Gln Leu Ala Thr Ser Ala Thr Gly Phe Gly Ile Ala Asp Arg Ser Ala	
545 550 555	
CCG TCG TCG CTG CTC CGC CAC GGG TTC CAG GGC CTC AAG CCC CGC AGC	569
Pro Ser Ser Leu Leu Arg His Gly Phe Gln Gly Leu Lys Pro Arg Ser	
560 565 570	
CCC GCC GGC GGC GAC GCG ACG TCG CTC AGC GTG ACG ACC AGC GCG CGC	617
Pro Ala Gly Gly Asp Ala Thr Ser Leu Ser Val Thr Thr Ser Ala Arg	
575 580 585	
GCG ACG CCC AAG CAG CAG CGG TCG GTG CAG CGT GGC AGC CGG AGG TTC	665
Ala Thr Pro Lys Gln Gln Arg Ser Val Gln Arg Gly Ser Arg Arg Phe	
590 595 600 605	
CCC TCC GTC GTC GTG TAC GCC ACC GGC GCC GGC ATG AAC GTC GTG TTC	713
Pro Ser Val Val Val Tyr Ala Thr Gly Ala Gly Met Asn Val Val Phe	
610 615 620	
GTC GGC GCC GAG ATG GCC CCC TGG AGC AAG ACC GGC GGC CTC GGT GAC	761
Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp	
625 630 635	
GTC CTC GGT GGC CTC CCC CCT GCC ATG GCT GCG AAT GGC CAC AGG GTC	809
Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His Arg Val	
640 645 650	
ATG GTG ATC TCT CCT CGG TAC GAC CAG TAC AAG GAC GCT TGG GAT ACC	857
Met Val Ile Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr	
655 660 665	
AGC GTT GTG GCT GAG ATC AAG GTT GCA GAC AGG TAC GAG AGG GTG AGG	905
Ser Val Val Ala Glu Ile Lys Val Ala Asp Arg Tyr Glu Arg Val Arg	
670 675 680 685	
TTT TTC CAT TGC TAC AAG CGT GGA GTC GAC CGT GTG TTC ATC GAC CAT	953
Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Ile Asp His	
690 695 700	

CCG TCA TTC CTG GAG AAG GTT TGG GGA AAG ACC GGT GAG AAG ATC TAC	1001
Pro Ser Phe Leu Glu Lys Val Trp Gly Lys Thr Gly Glu Lys Ile Tyr	
705 710 715	
GGA CCT GAC ACT GGA GTT GAT TAC AAA GAC AAC CAG ATG CGT TTC AGC	1049
Gly Pro Asp Thr Gly Val Asp Tyr Lys Asp Asn Gln Met Arg Phe Ser	
720 725 730	
CTT CTT TGC CAG GCA GCA CTC GAG GCT CCT AGG ATC CTA AAC CTC AAC	1097
Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Asn Leu Asn	
735 740 745	
AAC AAC CCA TAC TTC AAA GGA ACT TAT GGT GAG GAT GTT GTG TTC GTC	1145
Asn Asn Pro Tyr Phe Lys Gly Thr Tyr Gly Glu Asp Val Val Phe Val	
750 755 760 765	
TGC AAC GAC TGG CAC ACT GGC CCA CTG GCG AGC TAC CTG AAG AAC AAC	1193
Cys Asn Asp Trp His Thr Gly Pro Leu Ala Ser Tyr Leu Lys Asn Asn	
770 775 780	
TAC CAG CCC AAT GGC ATC TAC AGG AAT GCA AAG GTT GCT TTC TGC ATC	1241
Tyr Gln Pro Asn Gly Ile Tyr Arg Asn Ala Lys Val Ala Phe Cys Ile	
785 790 795	
CAC AAC ATC TCC TAC CAG GGC CGT TTC GCT TTC GAG GAT TAC CCT GAG	1289
His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Glu Asp Tyr Pro Glu	
800 805 810	
CTG AAC CTC TCC GAG AGG TTC AGG TCA TCC TTC GAT TTC ATC GAC GGG	1337
Leu Asn Leu Ser Glu Arg Phe Arg Ser Ser Phe Asp Phe Ile Asp Gly	
815 820 825	
TAT GAC ACG CCG GTG GAG GGC AGG AAG ATC AAC TGG ATG AAG GCC GGA	1385
Tyr Asp Thr Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly	
830 835 840 845	
ATC CTG GAA GCC GAC AGG GTG CTC ACC GTG AGC CCG TAC TAC GCC GAG	1433
Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu	
850 855 860	
GAG CTC ATC TCC GGC ATC GCC AGG GGA TGC GAG CTC GAC AAC ATC ATG	1481
Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met	
865 870 875	
CGG CTC ACC GGC ATC ACC GGC ATC GTC AAC GGC ATG GAC GTC AGC GAG	1529

Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu	
880	885 890
TGG GAT CCT AGC AAG GAC AAG TAC ATC ACC GCC AAG TAC GAC GCA ACC	1577
Trp Asp Pro Ser Lys Asp Lys Tyr Ile Thr Ala Lys Tyr Asp Ala Thr	
895 900 905	
ACG GCA ATC GAG GCG AAG GCG CTG AAC AAG GAG GCG TTG CAG GCG GAG	1625
Thr Ala Ile Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu	
910 915 920 925	
GCG GGT CTT CCG GTC GAC AGG AAA ATC CCA CTG ATC GCG TTC ATC GGC	1673
Ala Gly Leu Pro Val Asp Arg Lys Ile Pro Leu Ile Ala Phe Ile Gly	
930 935 940	
AGG CTG GAG GAA CAG AAG GGC CCT GAC GTC ATG GCC GCC GCC ATC CCG	1721
Arg Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala Ile Pro	
945 950 955	
GAG CTC ATG CAG GAG GAC GTC CAG ATC GTT CTT CTG GGT ACT GGA AAG	1769
Glu Leu Met Gln Glu Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys	
960 965 970	
AAG AAG TTC GAG AAG CTG CTC AAG AGC ATG GAG GAG AAG TAT CCG GGC	1817
Lys Lys Phe Glu Lys Leu Leu Lys Ser Met Glu Glu Lys Tyr Pro Gly	
975 980 985	
AAG GTG AGG GCG GTG GTG AAG TTC AAC GCG CCG CTT GCT CAT CTC ATC	1865
Lys Val Arg Ala Val Val Lys Phe Asn Ala Pro Leu Ala His Leu Ile	
990 995 1000 1005	
ATG GCC GGA GCC GAC GTG CTC GCC GTC CCC AGC CGC TTC GAG CCC TGT	1913
Met Ala Gly Ala Asp Val Leu Ala Val Pro Ser Arg Phe Glu Pro Cys	
1010 1015 1020	
GGA CTC ATC CAG CTG CAG GGG ATG AGA TAC GGA ACG CCC TGT GCT TGC	1961
Gly Leu Ile Gln Leu Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys	
1025 1030 1035	
GCG TCC ACC GGT GGG CTC GTG GAC ACG GTC ATC GAA GGC AAG ACT GGT	2009
Ala Ser Thr Gly Gly Leu Val Asp Thr Val Ile Glu Gly Lys Thr Gly	
1040 1045 1050	
TTC CAC ATG GGC CGT CTC AGC GTC GAC TGC AAG GTG GTG GAG CCA AGC	2057
Phe His Met Gly Arg Leu Ser Val Asp Cys Lys Val Val Glu Pro Ser	

1055	1060	1065	
GAC GTG AAG AAG GTG GCG GCC ACC CTG AAG CGC GCC ATC AAG GTC GTC			2105
Asp Val Lys Lys Val Ala Ala Thr Leu Lys Arg Ala Ile Lys Val Val			
1070	1075	1080	1085
GGC ACG CCG GCG TAC GAG GAG ATG GTC AGG AAC TGC ATG AAC CAG GAC			2153
Gly Thr Pro Ala Tyr Glu Glu Met Val Arg Asn Cys Met Asn Gln Asp			
	1090	1095	1100
CTC TCC TGG AAG GGG CCT GCG AAG AAC TGG GAG AAT GTG CTC CTG GGC			2201
Leu Ser Trp Lys Gly Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Gly			
	1105	1110	1115
CTG GGC GTC GCC GGC AGC GCG CCG GGG ATC GAA GGC GAC GAG ATC GCG			2249
Leu Gly Val Ala Gly Ser Ala Pro Gly Ile Glu Gly Asp Glu Ile Ala			
	1120	1125	1130
CCG CTC GCC AAG GAG AAC GTG GCT GCT CCT TGA AGAGCCTGAG ATCTACATAT			2302
Pro Leu Ala Lys Glu Asn Val Ala Ala Pro *			
	1135	1140	
GGAGTGATTA ATTAATATAG CAGTATATGG ATGAGAGACG AATGAACCAG TGGTTTGT			2362
GTTGTAGTGA ATTTGTAGCT ATAGCCAATT ATATAGGCTA ATAAGTTTGA TGTGTACTC			2422
TTCTGGGTGT GCTTAAGTAT CTTATCGGAC CCTGAATTTA TGTGTGTGGC TTATTGCCAA			2482
TAATATTAAG TAATAAAGGG TTTATTATAT TATTATATAT GTTATATTAT ACTAAAAAA			2542

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met Ser Ala Leu Thr Thr Ser Gln Leu Ala Thr Ser Ala Thr Gly Phe
 1 5 10 15

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

Gln Gly Leu Lys Pro Arg Ser Pro Ala Gly Gly Asp Ala Thr Ser Leu
 35 40 45

Ser Val Thr Thr Ser Ala Arg Ala Thr Pro Lys Gln Gln Arg Ser Val
 50 55 60

Gln Arg Gly Ser Arg Arg Phe Pro Ser Val Val Val Tyr Ala Thr Gly
 65 70 75 80

Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser
 85 90 95

Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met
 100 105 110

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

Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ala Glu Ile Lys Val Ala
 130 135 140

Asp Arg Tyr Glu Arg Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val
 145 150 155 160

Asp Arg Val Phe Ile Asp His Pro Ser Phe Leu Glu Lys Val Trp Gly
 165 170 175

Lys Thr Gly Glu Lys Ile Tyr Gly Pro Asp Thr Gly Val Asp Tyr Lys
 180 185 190

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

Pro Arg Ile Leu Asn Leu Asn Asn Asn Pro Tyr Phe Lys Gly Thr Tyr
 210 215 220

Gly Glu Asp Val Val Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu
 225 230 235 240

Ala Ser Tyr Leu Lys Asn Asn Tyr Gln Pro Asn Gly Ile Tyr Arg Asn
 245 250 255

Ala Lys Val Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe
 260 265 270

Ala Phe Glu Asp Tyr Pro Glu Leu Asn Leu Ser Glu Arg Phe Arg Ser
 275 280 285

Ser Phe Asp Phe Ile Asp Gly Tyr Asp Thr Pro Val Glu Gly Arg Lys
 290 295 300

Ile Asn Trp Met Lys Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr
 305 310 315 320

Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly
 325 330 335

Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile Val
 340 345 350

Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Lys Asp Lys Tyr Ile
 355 360 365

Thr Ala Lys Tyr Asp Ala Thr Thr Ala Ile Glu Ala Lys Ala Leu Asn
 370 375 380

Lys Glu Ala Leu Gln Ala Glu Ala Gly Leu Pro Val Asp Arg Lys Ile
 385 390 395 400

Pro Leu Ile Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro Asp
 405 410 415

Val Met Ala Ala Ala Ile Pro Glu Leu Met Gln Glu Asp Val Gln Ile
 420 425 430

Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Lys Leu Leu Lys Ser
 435 440 445

Met Glu Glu Lys Tyr Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn
 450 455 460

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

Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln Gly Met Arg
 485 490 495

Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu Val Asp Thr
500 505 510

Val Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu Ser Val Asp
515 520 525

Cys Lys Val Val Glu Pro Ser Asp Val Lys Lys Val Ala Ala Thr Leu
530 535 540

Lys Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val
545 550 555 560

Arg Asn Cys Met Asn Gln Asp Leu Ser Trp Lys Gly Pro Ala Lys Asn
565 570 575

Trp Glu Asn Val Leu Leu Gly Leu Gly Val Ala Gly Ser Ala Pro Gly
580 585 590

Ile Glu Gly Asp Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala Ala
595 600 605

Pro *
610

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2007

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

GCT GAG GCT GAG GCC GGG GGC AAG GAC GCG CCG CCG GAG AGG AGC GGC	48
Ala Glu Ala Glu Ala Gly Gly Lys Asp Ala Pro Pro Glu Arg Ser Gly	
615 620 625	
GAC GCC GCC AGG TTG CCC CGC GCT CGG CGC AAT GCG GTC TCC AAA CGG	96
Asp Ala Ala Arg Leu Pro Arg Ala Arg Arg Asn Ala Val Ser Lys Arg	
630 635 640	
AGG GAT CCT CTT CAG CCG GTC GGC CGG TAC GGC TCC GCG ACG GGA AAC	144
Arg Asp Pro Leu Gln Pro Val Gly Arg Tyr Gly Ser Ala Thr Gly Asn	
645 650 655	
ACG GCC AGG ACC GGC GCC GCG TCC TGC CAG AAC GCC GCA TTG GCG GAC	192
Thr Ala Arg Thr Gly Ala Ala Ser Cys Gln Asn Ala Ala Leu Ala Asp	
660 665 670	
GTT GAG ATC GTT GAG ATC AAG TCC ATC GTC GCC GCG CCG CCG ACG AGC	240
Val Glu Ile Val Glu Ile Lys Ser Ile Val Ala Ala Pro Pro Thr Ser	
675 680 685 690	
ATA GTG AAG TTC CCA GGG CGC GGG CTA CAG GAT GAT CCT TCC CTC TGG	288
Ile Val Lys Phe Pro Gly Arg Gly Leu Gln Asp Asp Pro Ser Leu Trp	
695 700 705	
GAC ATA GCA CCG GAG ACT GTC CTC CCA GCC CCG AAG CCA CTG CAT GAA	336
Asp Ile Ala Pro Glu Thr Val Leu Pro Ala Pro Lys Pro Leu His Glu	
710 715 720	
TCG CCT GCG GTT GAC GGA GAT TCA AAT GGA ATT GCA CCT CCT ACA GTT	384
Ser Pro Ala Val Asp Gly Asp Ser Asn Gly Ile Ala Pro Pro Thr Val	
725 730 735	
GAG CCA TTA GTA CAG GAG GCC ACT TGG GAT TTC AAG AAA TAC ATC GGT	432
Glu Pro Leu Val Gln Glu Ala Thr Trp Asp Phe Lys Lys Tyr Ile Gly	
740 745 750	
TTT GAC GAG CCT GAC GAA GCG AAG GAT GAT TCC AGG GTT GGT GCA GAT	480
Phe Asp Glu Pro Asp Glu Ala Lys Asp Asp Ser Arg Val Gly Ala Asp	
755 760 765 770	
GAT GCT GGT TCT TTT GAA CAT TAT GGG ACA ATG ATT CTG GGC CTT TGT	528
Asp Ala Gly Ser Phe Glu His Tyr Gly Thr Met Ile Leu Gly Leu Cys	
775 780 785	
GGG GAG AAT GTT ATG AAC GTG ATC GTG GTG GCT GCT GAA TGT TCT CCA	576

Gly	Glu	Asn	Val	Met	Asn	Val	Ile	Val	Val	Ala	Ala	Glu	Cys	Ser	Pro	
			790					795					800			
TGG	TGC	AAA	ACA	GGT	GGT	CTT	GGA	GAT	GTT	GTG	GGA	GCT	TTA	CCC	AAG	624
Trp	Cys	Lys	Thr	Gly	Gly	Leu	Gly	Asp	Val	Val	Gly	Ala	Leu	Pro	Lys	
		805					810					815				
GCT	TTA	GCG	AGA	AGA	GGA	CAT	CGT	GTT	ATG	GTT	GTG	GTA	CCA	AGG	TAT	672
Ala	Leu	Ala	Arg	Arg	Gly	His	Arg	Val	Met	Val	Val	Val	Pro	Arg	Tyr	
		820				825					830					
GGG	GAC	TAT	GTG	GAA	GCC	TTT	GAT	ATG	GGA	ATC	CGG	AAA	TAC	TAC	AAA	720
Gly	Asp	Tyr	Val	Glu	Ala	Phe	Asp	Met	Gly	Ile	Arg	Lys	Tyr	Tyr	Lys	
835					840					845					850	
GCT	GCA	GGA	CAG	GAC	CTA	GAA	GTG	AAC	TAT	TTC	CAT	GCA	TTT	ATT	GAT	768
Ala	Ala	Gly	Gln	Asp	Leu	Glu	Val	Asn	Tyr	Phe	His	Ala	Phe	Ile	Asp	
			855					860					865			
GGA	GTC	GAC	TTT	GTG	TTC	ATT	GAT	GCC	TCT	TTC	CGG	CAC	CGT	CAA	GAT	816
Gly	Val	Asp	Phe	Val	Phe	Ile	Asp	Ala	Ser	Phe	Arg	His	Arg	Gln	Asp	
		870						875				880				
GAC	ATA	TAT	GGG	GGA	AGT	AGG	CAG	GAA	ATC	ATG	AAG	CGC	ATG	ATT	TTG	864
Asp	Ile	Tyr	Gly	Gly	Ser	Arg	Gln	Glu	Ile	Met	Lys	Arg	Met	Ile	Leu	
		885					890					895				
TTT	TGC	AAG	GTT	GCT	GTT	GAG	GTT	CCT	TGG	CAC	GTT	CCA	TGC	GGT	GGT	912
Phe	Cys	Lys	Val	Ala	Val	Glu	Val	Pro	Trp	His	Val	Pro	Cys	Gly	Gly	
		900					905				910					
GTG	TGC	TAC	GGA	GAT	GGA	AAT	TTG	GTG	TTC	ATT	GCC	ATG	AAT	TGG	CAC	960
Val	Cys	Tyr	Gly	Asp	Gly	Asn	Leu	Val	Phe	Ile	Ala	Met	Asn	Trp	His	
915						920				925				930		
ACT	GCA	CTC	CTG	CCT	GTT	TAT	CTG	AAG	GCA	TAT	TAC	AGA	GAC	CAT	GGG	1008
Thr	Ala	Leu	Leu	Pro	Val	Tyr	Leu	Lys	Ala	Tyr	Tyr	Arg	Asp	His	Gly	
			935					940				945				
TTA	ATG	CAG	TAC	ACT	CGC	TCC	GTC	CTC	GTC	ATA	CAT	AAC	ATC	GGC	CAC	1056
Leu	Met	Gln	Tyr	Thr	Arg	Ser	Val	Leu	Val	Ile	His	Asn	Ile	Gly	His	
		950						955				960				
CAG	GGC	CGT	GGT	CCT	GTA	CAT	GAA	TTC	CCG	TAC	ATG	GAC	TTG	CTG	AAC	1104
Gln	Gly	Arg	Gly	Pro	Val	His	Glu	Phe	Pro	Tyr	Met	Asp	Leu	Leu	Asn	

965	970	975	
ACT AAC CTT CAA CAT TTC GAG CTG TAC GAT CCC GTC GGT GGC GAG CAC			1152
Thr Asn Leu Gln His Phe Glu Leu Tyr Asp Pro Val Gly Gly Glu His			
980	985	990	
GCC AAC ATC TTT GCC GCG TGT GTT CTG AAG ATG GCA GAC CGG GTG GTG			1200
Ala Asn Ile Phe Ala Ala Cys Val Leu Lys Met Ala Asp Arg Val Val			
995	1000	1005	1010
ACT GTC AGC CGC GGC TAC CTG TGG GAG CTG AAG ACA GTG GAA GGC GGC			1248
Thr Val Ser Arg Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly			
	1015	1020	1025
TGG GGC CTC CAC GAC ATC ATC CGT TCT AAC GAC TGG AAG ATC AAT GGC			1296
Trp Gly Leu His Asp Ile Ile Arg Ser Asn Asp Trp Lys Ile Asn Gly			
	1030	1035	1040
ATT CGT GAA CGC ATC GAC CAC CAG GAG TGG AAC CCC AAG GTG GAC GTG			1344
Ile Arg Glu Arg Ile Asp His Gln Glu Trp Asn Pro Lys Val Asp Val			
	1045	1050	1055
CAC CTG CGG TCG GAC GGC TAC ACC AAC TAC TCC CTC GAG ACA CTC GAC			1392
His Leu Arg Ser Asp Gly Tyr Thr Asn Tyr Ser Leu Glu Thr Leu Asp			
	1060	1065	1070
GCT GGA AAG CGG CAG TGC AAG GCG GCC CTG CAG CGG GAC GTG GGC CTG			1440
Ala Gly Lys Arg Gln Cys Lys Ala Ala Leu Gln Arg Asp Val Gly Leu			
1075	1080	1085	1090
GAA GTG CGC GAC GAC GTG CCG CTG CTC GGC TTC ATC GGG CGT CTG GAT			1488
Glu Val Arg Asp Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp			
	1095	1100	1105
GGA CAG AAG GGC GTG GAC ATC ATC GGG GAC GCG ATG CCG TGG ATC GCG			1536
Gly Gln Lys Gly Val Asp Ile Ile Gly Asp Ala Met Pro Trp Ile Ala			
	1110	1115	1120
GGG CAG GAC GTG CAG CTG GTG ATG CTG GGC ACC GGC CCA CCT GAC CTG			1584
Gly Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Pro Pro Asp Leu			
	1125	1130	1135
GAA CGA ATG CTG CAG CAC TTG GAG CGG GAG CAT CCC AAC AAG GTG CGC			1632
Glu Arg Met Leu Gln His Leu Glu Arg Glu His Pro Asn Lys Val Arg			
	1140	1145	1150

GCC AGC GTG CTG GTG ATG CCC TCC CGC TTC GCC GGC GGG CTG AAC CAG 1728
Ala Ser Val Leu Val Met Pro Ser Arg Phe Ala Gly Gly Leu Asn Gln
1175 1180 1185

GGG CTC AGG GAC ACC GTG GCG CCG TTC GAC CCG TTC GGC GAC GCC GGG 1824
Gly Leu Arg Asp Thr Val Ala Pro Phe Asp Pro Phe Gly Asp Ala Gly
1205 1210 1215

CTC AGC CAC TGC CTC GAC ACG TAC CGA AAC TAC GAG GAG AGC TGG AAG 1920
Leu Ser His Cys Leu Asp Thr Tyr Arg Asn Tyr Glu Glu Ser Trp Lys
1235 1240 1245 1250

GCT GAG CTC TAC GAG GAC GTC CTT GTC AAG TAC CAG TGG 2007
Ala Glu Leu Tyr Glu Asp Val Leu Val Lys Tyr Gln Trp
1270 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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

Ala Glu Ala Glu Ala Gly Gly Lys Asp Ala Pro Pro Glu Arg Ser Gly

88

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

245	250	255
Gly Val Asp Phe Val Phe Ile Asp Ala Ser Phe Arg His Arg Gln Asp 260	265	270
Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu 275	280	285
Phe Cys Lys Val Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly 290	295	300
Val Cys Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Met Asn Trp His 305	310	315 320
Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly 325	330	335
Leu Met Gln Tyr Thr Arg Ser Val Leu Val Ile His Asn Ile Gly His 340	345	350
Gln Gly Arg Gly Pro Val His Glu Phe Pro Tyr Met Asp Leu Leu Asn 355	360	365
Thr Asn Leu Gln His Phe Glu Leu Tyr Asp Pro Val Gly Gly Glu His 370	375	380
Ala Asn Ile Phe Ala Ala Cys Val Leu Lys Met Ala Asp Arg Val Val 385	390	395 400
Thr Val Ser Arg Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly 405	410	415
Trp Gly Leu His Asp Ile Ile Arg Ser Asn Asp Trp Lys Ile Asn Gly 420	425	430
Ile Arg Glu Arg Ile Asp His Gln Glu Trp Asn Pro Lys Val Asp Val 435	440	445
His Leu Arg Ser Asp Gly Tyr Thr Asn Tyr Ser Leu Glu Thr Leu Asp 450	455	460
Ala Gly Lys Arg Gln Cys Lys Ala Ala Leu Gln Arg Asp Val Gly Leu 465	470	475 480
Glu Val Arg Asp Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp		

90

485	490	495
Gly Gln Lys Gly Val Asp Ile Ile Gly Asp Ala Met Pro Trp Ile Ala		
500	505	510
Gly Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Pro Pro Asp Leu		
515	520	525
Glu Arg Met Leu Gln His Leu Glu Arg Glu His Pro Asn Lys Val Arg		
530	535	540
Gly Trp Val Gly Phe Ser Val Leu Met Val His Arg Ile Thr Pro Gly		
545	550	555
Ala Ser Val Leu Val Met Pro Ser Arg Phe Ala Gly Gly Leu Asn Gln		
565	570	575
Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly		
580	585	590
Gly Leu Arg Asp Thr Val Ala Pro Phe Asp Pro Phe Gly Asp Ala Gly		
595	600	605
Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala Asn Lys Leu Ile Glu Val		
610	615	620
Leu Ser His Cys Leu Asp Thr Tyr Arg Asn Tyr Glu Glu Ser Trp Lys		
625	630	635
Ser Leu Gln Ala Arg Gly Met Ser Gln Asn Leu Ser Trp Asp His Ala		
645	650	655
Ala Glu Leu Tyr Glu Asp Val Leu Val Lys Tyr Gln Trp		
660	665	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zea mays*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2097

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

ATG CCG GGG GCA ATC TCT TCC TCG TCG TCG GCT TTT CTC CTC CCC GTC	48
Met Pro Gly Ala Ile Ser Ser Ser Ser Ser Ala Phe Leu Leu Pro Val	
670 675 680 685	
GCG TCC TCC TCG CCG CGG CGC AGG CGG GGC AGT GTG GGT GCT GCT CTG	96
Ala Ser Ser Ser Pro Arg Arg Arg Arg Gly Ser Val Gly Ala Ala Leu	
690 695 700	
CGC TCG TAC GGC TAC AGC GGC GCG GAG CTG CGG TTG CAT TGG GCG CGG	144
Arg Ser Tyr Gly Tyr Ser Gly Ala Glu Leu Arg Leu His Trp Ala Arg	
705 710 715	
CGG GGC CCG CCT CAG GAT GGA GCG GCG TCG GTA CGC GCC GCA GCG GCA	192
Arg Gly Pro Pro Gln Asp Gly Ala Ala Ser Val Arg Ala Ala Ala Ala	
720 725 730	
CCG GCC GGG GGC GAA AGC GAG GAG GCA GCG AAG AGC TCC TCC TCG TCC	240
Pro Ala Gly Gly Glu Ser Glu Glu Ala Ala Lys Ser Ser Ser Ser Ser	
735 740 745	
CAG GCG GGC GCT GTT CAG GGC AGC ACG GCC AAG GCT GTG GAT TCT GCT	288
Gln Ala Gly Ala Val Gln Gly Ser Thr Ala Lys Ala Val Asp Ser Ala	
750 755 760 765	
TCA CCT CCC AAT CCT TTG ACA TCT GCT CCG AAG CAA AGT CAG AGC GCT	336
Ser Pro Pro Asn Pro Leu Thr Ser Ala Pro Lys Gln Ser Gln Ser Ala	
770 775 780	
GCA ATG CAA AAC GGA ACG AGT GGG GGC AGC AGC GCG AGC ACC GCC GCG	384
Ala Met Gln Asn Gly Thr Ser Gly Gly Ser Ser Ala Ser Thr Ala Ala	
785 790 795	
CCG GTG TCC GGA CCC AAA GCT GAT CAT CCA TCA GCT CCT GTC ACC AAG	432

Pro	Val	Ser	Gly	Pro	Lys	Ala	Asp	His	Pro	Ser	Ala	Pro	Val	Thr	Lys	
	800						805					810				
AGA	GAA	ATC	GAT	GCC	AGT	GCG	GTG	AAG	CCA	GAG	CCC	GCA	GGT	GAT	GAT	480
Arg	Glu	Ile	Asp	Ala	Ser	Ala	Val	Lys	Pro	Glu	Pro	Ala	Gly	Asp	Asp	
	815					820					825					
GCT	AGA	CCG	GTG	GAA	AGC	ATA	GGC	ATC	GCT	GAA	CCG	GTG	GAT	GCT	AAG	528
Ala	Arg	Pro	Val	Glu	Ser	Ile	Gly	Ile	Ala	Glu	Pro	Val	Asp	Ala	Lys	
830					835					840					845	
GCT	GAT	GCA	GCT	CCG	GCT	ACA	GAT	GCG	GCG	GCG	AGT	GCT	CCT	TAT	GAC	576
Ala	Asp	Ala	Ala	Pro	Ala	Thr	Asp	Ala	Ala	Ala	Ser	Ala	Pro	Tyr	Asp	
				850				855					860			
AGG	GAG	GAT	AAT	GAA	CCT	GGC	CCT	TTG	GCT	GGG	CCT	AAT	GTG	ATG	AAC	624
Arg	Glu	Asp	Asn	Glu	Pro	Gly	Pro	Leu	Ala	Gly	Pro	Asn	Val	Met	Asn	
		865					870					875				
GTC	GTC	GTG	GTG	GCT	TCT	GAA	TGT	GCT	CCT	TTC	TGC	AAG	ACA	GGT	GGC	672
Val	Val	Val	Val	Ala	Ser	Glu	Cys	Ala	Pro	Phe	Cys	Lys	Thr	Gly	Gly	
	880						885					890				
CTT	GGA	GAT	GTC	GTG	GGT	GCT	TTG	CCT	AAG	GCT	CTG	GCG	AGG	AGA	GGA	720
Leu	Gly	Asp	Val	Val	Gly	Ala	Leu	Pro	Lys	Ala	Leu	Ala	Arg	Arg	Gly	
	895					900					905					
CAC	CGT	GTT	ATG	GTC	GTG	ATA	CCA	AGA	TAT	GGA	GAG	TAT	GCC	GAA	GCC	768
His	Arg	Val	Met	Val	Val	Ile	Pro	Arg	Tyr	Gly	Glu	Tyr	Ala	Glu	Ala	
910					915					920				925		
CGG	GAT	TTA	GGT	GTA	AGG	AGA	CGT	TAC	AAG	GTA	GCT	GGA	CAG	GAT	TCA	816
Arg	Asp	Leu	Gly	Val	Arg	Arg	Arg	Tyr	Lys	Val	Ala	Gly	Gln	Asp	Ser	
				930				935					940			
GAA	GTT	ACT	TAT	TTT	CAC	TCT	TAC	ATT	GAT	GGA	GTT	GAT	TTT	GTA	TTC	864
Glu	Val	Thr	Tyr	Phe	His	Ser	Tyr	Ile	Asp	Gly	Val	Asp	Phe	Val	Phe	
		945					950					955				
GTA	GAA	GCC	CCT	CCC	TTC	CGG	CAC	CGG	CAC	AAT	AAT	ATT	TAT	GGG	GGA	912
Val	Glu	Ala	Pro	Pro	Phe	Arg	His	Arg	His	Asn	Asn	Ile	Tyr	Gly	Gly	
	960					965					970					
GAA	AGA	TTG	GAT	ATT	TTG	AAG	CGC	ATG	ATT	TTG	TTC	TGC	AAG	GCC	GCT	960
Glu	Arg	Leu	Asp	Ile	Leu	Lys	Arg	Met	Ile	Leu	Phe	Cys	Lys	Ala	Ala	

975	980	985	
GTT GAG GTT CCA TGG TAT GCT CCA TGT GGC GGT ACT GTC TAT GGT GAT			1008
Val Glu Val Pro Trp Tyr Ala Pro Cys Gly Gly Thr Val Tyr Gly Asp			
990	995	1000	1005
GGC AAC TTA GTT TTC ATT GCT AAT GAT TGG CAT ACC GCA CTT CTG CCT			1056
Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro			
	1010	1015	1020
GTC TAT CTA AAG GCC TAT TAC CGG GAC AAT GGT TTG ATG CAG TAT GCT			1104
Val Tyr Leu Lys Ala Tyr Tyr Arg Asp Asn Gly Leu Met Gln Tyr Ala			
	1025	1030	1035
CGC TCT GTG CTT GTG ATA CAC AAC ATT GCT CAT CAG GGT CGT GGC CCT			1152
Arg Ser Val Leu Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro			
	1040	1045	1050
GTA GAC GAC TTC GTC AAT TTT GAC TTG CCT GAA CAC TAC ATC GAC CAC			1200
Val Asp Asp Phe Val Asn Phe Asp Leu Pro Glu His Tyr Ile Asp His			
	1055	1060	1065
TTC AAA CTG TAT GAC AAC ATT GGT GGG GAT CAC AGC AAC GTT TTT GCT			1248
Phe Lys Leu Tyr Asp Asn Ile Gly Gly Asp His Ser Asn Val Phe Ala			
1070	1075	1080	1085
GCG GGG CTG AAG ACG GCA GAC CGG GTG GTG ACC GTT AGC AAT GGC TAC			1296
Ala Gly Leu Lys Thr Ala Asp Arg Val Val Thr Val Ser Asn Gly Tyr			
	1090	1095	1100
ATG TGG GAG CTG AAG ACT TCG GAA GGC GGG TGG GGC CTC CAC GAC ATC			1344
Met Trp Glu Leu Lys Thr Ser Glu Gly Gly Trp Gly Leu His Asp Ile			
	1105	1110	1115
ATA AAC CAG AAC GAC TGG AAG CTG CAG GGC ATC GTG AAC GGC ATC GAC			1392
Ile Asn Gln Asn Asp Trp Lys Leu Gln Gly Ile Val Asn Gly Ile Asp			
	1120	1125	1130
ATG AGC GAG TGG AAC CCC GCT GTG GAC GTG CAC CTC CAC TCC GAC GAC			1440
Met Ser Glu Trp Asn Pro Ala Val Asp Val His Leu His Ser Asp Asp			
	1135	1140	1145
TAC ACC AAC TAC ACG TTC GAG ACG CTG GAC ACC GGC AAG CGG CAG TGC			1488
Tyr Thr Asn Tyr Thr Phe Glu Thr Leu Asp Thr Gly Lys Arg Gln Cys			
1150	1155	1160	1165

AAG GCC GCC CTG CAG CGG CAG CTG GGC CTG CAG GTC CGC GAC GAC GTG	1536
Lys Ala Ala Leu Gln Arg Gln Leu Gly Leu Gln Val Arg Asp Asp Val	
1170 1175 1180	
CCA CTG ATC GGG TTC ATC GGG CGG CTG GAC CAC CAG AAG GGC GTG GAC	1584
Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp His Gln Lys Gly Val Asp	
1185 1190 1195	
ATC ATC GCC GAC GCG ATC CAC TGG ATC GCG GGG CAG GAC GTG CAG CTC	1632
Ile Ile Ala Asp Ala Ile His Trp Ile Ala Gly Gln Asp Val Gln Leu	
1200 1205 1210	
GTG ATG CTG GGC ACC GGG CGG GCC GAC CTG GAG GAC ATG CTG CGG CGG	1680
Val Met Leu Gly Thr Gly Arg Ala Asp Leu Glu Asp Met Leu Arg Arg	
1215 1220 1225	
TTC GAG TCG GAG CAC AGC GAC AAG GTG CGC GCG TGG GTG GGG TTC TCG	1728
Phe Glu Ser Glu His Ser Asp Lys Val Arg Ala Trp Val Gly Phe Ser	
1230 1235 1240 1245	
GTG CCC CTG GCG CAC CGC ATC ACG GCG GGC GCG GAC ATC CTG CTG ATG	1776
Val Pro Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ile Leu Leu Met	
1250 1255 1260	
CCG TCG CGG TTC GAG CCG TGC GGG CTG AAC CAG CTC TAC GCC ATG GCG	1824
Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala	
1265 1270 1275	
TAC GGG ACC GTG CCC GTG GTG CAC GCC GTG GGG GGG CTC CGG GAC ACG	1872
Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu Arg Asp Thr	
1280 1285 1290	
GTG GCG CCG TTC GAC CCG TTC AAC GAC ACC GGG CTC GGG TGG ACG TTC	1920
Val Ala Pro Phe Asp Pro Phe Asn Asp Thr Gly Leu Gly Trp Thr Phe	
1295 1300 1305	
GAC CGC GCG GAG GCG AAC CGG ATG ATC GAC GCG CTC TCG CAC TGC CTC	1968
Asp Arg Ala Glu Ala Asn Arg Met Ile Asp Ala Leu Ser His Cys Leu	
1310 1315 1320 1325	
ACC ACG TAC CGG AAC TAC AAG GAG AGC TGG CGC GCC TGC AGG GCG CGC	2016
Thr Thr Tyr Arg Asn Tyr Lys Glu Ser Trp Arg Ala Cys Arg Ala Arg	
1330 1335 1340	
GGC ATG GCC GAG GAC CTC AGC TGG GAC CAC GCC GCC GTG CTG TAT GAG	2064

Gly Met Ala Glu Asp Leu Ser Trp Asp His Ala Ala Val Leu Tyr Glu
 1345 1350 1355

GAC GTG CTC GTC AAG GCG AAG TAC CAG TGG TGA 2097
 Asp Val Leu Val Lys Ala Lys Tyr Gln Trp *
 1360 1365

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met Pro Gly Ala Ile Ser Ser Ser Ser Ser Ala Phe Leu Leu Pro Val
 1 5 10 15

Ala Ser Ser Ser Pro Arg Arg Arg Arg Gly Ser Val Gly Ala Ala Leu
 20 25 30

Arg Ser Tyr Gly Tyr Ser Gly Ala Glu Leu Arg Leu His Trp Ala Arg
 35 40 45

Arg Gly Pro Pro Gln Asp Gly Ala Ala Ser Val Arg Ala Ala Ala Ala
 50 55 60

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

Gln Ala Gly Ala Val Gln Gly Ser Thr Ala Lys Ala Val Asp Ser Ala
 85 90 95

Ser Pro Pro Asn Pro Leu Thr Ser Ala Pro Lys Gln Ser Gln Ser Ala
 100 105 110

Ala Met Gln Asn Gly Thr Ser Gly Gly Ser Ser Ala Ser Thr Ala Ala
 115 120 125

Pro Val Ser Gly Pro Lys Ala Asp His Pro Ser Ala Pro Val Thr Lys
 130 135 140

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

Ala Arg Pro Val Glu Ser Ile Gly Ile Ala Glu Pro Val Asp Ala Lys
165 170 175

Ala Asp Ala Ala Pro Ala Thr Asp Ala Ala Ala Ser Ala Pro Tyr Asp
180 185 190

Arg Glu Asp Asn Glu Pro Gly Pro Leu Ala Gly Pro Asn Val Met Asn
195 200 205

Val Val Val Val Ala Ser Glu Cys Ala Pro Phe Cys Lys Thr Gly Gly
210 215 220

Leu Gly Asp Val Val Gly Ala Leu Pro Lys Ala Leu Ala Arg Arg Gly
225 230 235 240

His Arg Val Met Val Val Ile Pro Arg Tyr Gly Glu Tyr Ala Glu Ala
245 250 255

Arg Asp Leu Gly Val Arg Arg Arg Tyr Lys Val Ala Gly Gln Asp Ser
260 265 270

Glu Val Thr Tyr Phe His Ser Tyr Ile Asp Gly Val Asp Phe Val Phe
275 280 285

Val Glu Ala Pro Pro Phe Arg His Arg His Asn Asn Ile Tyr Gly Gly
290 295 300

Glu Arg Leu Asp Ile Leu Lys Arg Met Ile Leu Phe Cys Lys Ala Ala
305 310 315 320

Val Glu Val Pro Trp Tyr Ala Pro Cys Gly Gly Thr Val Tyr Gly Asp
325 330 335

Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro
340 345 350

Val Tyr Leu Lys Ala Tyr Tyr Arg Asp Asn Gly Leu Met Gln Tyr Ala
355 360 365

Arg Ser Val Leu Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro
370 375 380

Val Asp Asp Phe Val Asn Phe Asp Leu Pro Glu His Tyr Ile Asp His
 385 390 395 400
 Phe Lys Leu Tyr Asp Asn Ile Gly Gly Asp His Ser Asn Val Phe Ala
 405 410 415
 Ala Gly Leu Lys Thr Ala Asp Arg Val Val Thr Val Ser Asn Gly Tyr
 420 425 430
 Met Trp Glu Leu Lys Thr Ser Glu Gly Gly Trp Gly Leu His Asp Ile
 435 440 445
 Ile Asn Gln Asn Asp Trp Lys Leu Gln Gly Ile Val Asn Gly Ile Asp
 450 455 460
 Met Ser Glu Trp Asn Pro Ala Val Asp Val His Leu His Ser Asp Asp
 465 470 475 480
 Tyr Thr Asn Tyr Thr Phe Glu Thr Leu Asp Thr Gly Lys Arg Gln Cys
 485 490 495
 Lys Ala Ala Leu Gln Arg Gln Leu Gly Leu Gln Val Arg Asp Asp Val
 500 505 510
 Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp His Gln Lys Gly Val Asp
 515 520 525
 Ile Ile Ala Asp Ala Ile His Trp Ile Ala Gly Gln Asp Val Gln Leu
 530 535 540
 Val Met Leu Gly Thr Gly Arg Ala Asp Leu Glu Asp Met Leu Arg Arg
 545 550 555 560
 Phe Glu Ser Glu His Ser Asp Lys Val Arg Ala Trp Val Gly Phe Ser
 565 570 575
 Val Pro Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ile Leu Leu Met
 580 585 590
 Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala
 595 600 605
 Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu Arg Asp Thr
 610 615 620

98

Val Ala Pro Phe Asp Pro Phe Asn Asp Thr Gly Leu Gly Trp Thr Phe
625 630 635 640

Asp Arg Ala Glu Ala Asn Arg Met Ile Asp Ala Leu Ser His Cys Leu
645 650 655

Thr Thr Tyr Arg Asn Tyr Lys Glu Ser Trp Arg Ala Cys Arg Ala Arg
660 665 670

Gly Met Ala Glu Asp Leu Ser Trp Asp His Ala Ala Val Leu Tyr Glu
675 680 685

Asp Val Leu Val Lys Ala Lys Tyr Gln Trp *
690 695

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1752

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

TGC GTC GCG GAG CTG AGC AGG GAG GGG CCC GCG CCG CGC CCG CTG CCA 48
Cys Val Ala Glu Leu Ser Arg Glu Gly Pro Ala Pro Arg Pro Leu Pro
700 705 710 715

CCC GCG CTG CTG GCG CCC CCG CTC GTG CCC GGC TTC CTC GCG CCG CCG 96
Pro Ala Leu Leu Ala Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro
720 725 730

GCC GAG CCC ACG GGT GAG CCG GCA TCG ACG CCG CCG CCC GTG CCC GAC	144
Ala Glu Pro Thr Gly Glu Pro Ala Ser Thr Pro Pro Pro Val Pro Asp	
735 740 745	
GCC GGC CTG GGG GAC CTC GGT CTC GAA CCT GAA GGG ATT GCT GAA GGT	192
Ala Gly Leu Gly Asp Leu Gly Leu Glu Pro Glu Gly Ile Ala Glu Gly	
750 755 760	
TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA GAT TCT GAG ATT	240
Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln Asp Ser Glu Ile	
765 770 775	
GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA CAA AGC ATT GTC	288
Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr Gln Ser Ile Val	
780 785 790 795	
TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA AAG TCT GGG GGT CTA GGA	336
Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser Gly Gly Leu Gly	
800 805 810	
GAT GTT TGT GGT TCA TTG CCA GTT GCT CTT GCT GCT CGT GGT CAC CGT	384
Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala Arg Gly His Arg	
815 820 825	
GTG ATG GTT GTA ATG CCC AGA TAT TTA AAT GGT ACC TCC GAT AAG AAT	432
Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr Ser Asp Lys Asn	
830 835 840	
TAT GCA AAT GCA TTT TAC ACA GAA AAA CAC ATT CGG ATT CCA TGC TTT	480
Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg Ile Pro Cys Phe	
845 850 855	
GGC GGT GAA CAT GAA GTT ACC TTC TTC CAT GAG TAT AGA GAT TCA GTT	528
Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Ser Val	
860 865 870 875	
GAC TGG GTG TTT GTT GAT CAT CCC TCA TAT CAC AGA CCT GGA AAT TTA	576
Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Asn Leu	
880 885 890	
TAT GGA GAT AAG TTT GGT GCT TTT GGT GAT AAT CAG TTC AGA TAC ACA	624
Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr	
895 900 905	
CTC CTT TGC TAT GCT GCA TGT GAG GCT CCT TTG ATC CTT GAA TTG GGA	672

Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly	
910 915 920	
GGA TAT ATT TAT GGA CAG AAT TGC ATG TTT GTT GTC AAT GAT TGG CAT	720
Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His	
925 930 935	
GCC AGT CTA GTG CCA GTC CTT CTT GCT GCA AAA TAT AGA CCA TAT GGT	768
Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly	
940 945 950 955	
GTT TAT AAA GAC TCC CGC AGC ATT CTT GTA ATA CAT AAT TTA GCA CAT	816
Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His Asn Leu Ala His	
960 965 970	
CAG GGT GTA GAG CCT GCA AGC ACA TAT CCT GAC CTT GGG TTG CCA CCT	864
Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro	
975 980 985	
GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA TGG GCG AGG AGG	912
Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg	
990 995 1000	
CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG AAA GGT GCA GTT	960
His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val	
1005 1010 1015	
GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT TAT TCG TGG GAG	1008
Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly Tyr Ser Trp Glu	
1020 1025 1030 1035	
GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG CTC TTA AGC TCC	1056
Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser	
1040 1045 1050	
AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT GAC ATT AAT GAT	1104
Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp	
1055 1060 1065	
TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT TAT TCT GTT GAT	1152
Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His Tyr Ser Val Asp	
1070 1075 1080	
GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG CAG AAG GAG CTG	1200
Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu Gln Lys Glu Leu	

1085	1090	1095	
GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC TTT ATT GGA AGG			1248
Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg			
1100	1105	1110	1115
TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT ATC ATA CCA GAT			1296
Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp			
	1120	1125	1130
CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA TCT GGT GAC CCA			1344
Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro			
	1135	1140	1145
GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC TTC AAG GAT AAA			1392
Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys			
	1150	1155	1160
TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC CAC CGA ATA ACT			1440
Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr			
	1165	1170	1175
GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC GAA CCT TGT GGT			1488
Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly			
1180	1185	1190	1195
CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT CCT GTT GTC CAT			1536
Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His			
	1200	1205	1210
GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC AAC CCT TTC GGT			1584
Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly			
	1215	1220	1225
GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA CCC CTA ACC ACA			1632
Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr			
	1230	1235	1240
GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC TAC ATA CAG GGA			1680
Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly			
	1245	1250	1255
ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG CAT GTC AAA AGA			1728
Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg			
1260	1265	1270	1275

CTT CAC GTG GGA CCA TGC CGC TGA
 Leu His Val Gly Pro Cys Arg *
 1280

1752

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Cys Val Ala Glu Leu Ser Arg Glu Gly Pro Ala Pro Arg Pro Leu Pro
 1 5 10 15

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

Ala Glu Pro Thr Gly Glu Pro Ala Ser Thr Pro Pro Pro Val Pro Asp
 35 40 45

Ala Gly Leu Gly Asp Leu Gly Leu Glu Pro Glu Gly Ile Ala Glu Gly
 50 55 60

Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln Asp Ser Glu Ile
 65 70 75 80

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

Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser Gly Gly Leu Gly
 100 105 110

Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala Arg Gly His Arg
 115 120 125

Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr Ser Asp Lys Asn
 130 135 140

Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg Ile Pro Cys Phe
 145 150 155 160

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

104

Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg
 405 410 415

Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp
 420 425 430

Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro
 435 440 445

Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys
 450 455 460

Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr
 465 470 475 480

Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly
 485 490 495

Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His
 500 505 510

Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly
 515 520 525

Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr
 530 535 540

Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly
 545 550 555 560

Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg
 565 570 575

Leu His Val Gly Pro Cys Arg *
 580

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zea mays*

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 91..264

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 265..2487

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 91..2490

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

GGCCCAGAGC AGACCCGGAT TTCGCTCTTG CGGTCGCTGG GGTTTTAGCA TTGGCTGATC	60
AGTTCGATCC GATCCGGCTG CGAAGGCGAG ATG GCG TTC CGG GTT TCT GGG GCG	114
Met Ala Phe Arg Val Ser Gly Ala	
-58 -55	
GTG CTC GGT GGG GCC GTA AGG GCT CCC CGA CTC ACC GGC GGC GGG GAG	162
Val Leu Gly Gly Ala Val Arg Ala Pro Arg Leu Thr Gly Gly Gly Glu	
-50 -45 -40 -35	
GGT AGT CTA GTC TTC CGG CAC ACC GGC CTC TTC TTA ACT CGG GGT GCT	210
Gly Ser Leu Val Phe Arg His Thr Gly Leu Phe Leu Thr Arg Gly Ala	
-30 -25 -20	
CGA GTT GGA TGT TCG GGG ACG CAC GGG GCC ATG CGC GCG GCG GCC GCG	258
Arg Val Gly Cys Ser Gly Thr His Gly Ala Met Arg Ala Ala Ala Ala	
-15 -10 -5	
GCC AGG AAG GCG GTC ATG GTT CCT GAG GGC GAG AAT GAT GGC CTC GCA	306
Ala Arg Lys Ala Val Met Val Pro Glu Gly Glu Asn Asp Gly Leu Ala	
1 5 10	
TCA AGG GCT GAC TCG GCT CAA TTC CAG TCG GAT GAA CTG GAG GTA CCA	354
Ser Arg Ala Asp Ser Ala Gln Phe Gln Ser Asp Glu Leu Glu Val Pro	
15 20 25 30	

106

GAC ATT TCT GAA GAG ACA ACG TGC GGT GCT GGT GTG GCT GAT GCT CAA	402
Asp Ile Ser Glu Glu Thr Thr Cys Gly Ala Gly Val Ala Asp Ala Gln	
35 40 45	
GCC TTG AAC AGA GTT CGA GTG GTC CCC CCA CCA AGC GAT GGA CAA AAA	450
Ala Leu Asn Arg Val Arg Val Val Pro Pro Pro Ser Asp Gly Gln Lys	
50 55 60	
ATA TTC CAG ATT GAC CCC ATG TTG CAA GGC TAT AAG TAC CAT CTT GAG	498
Ile Phe Gln Ile Asp Pro Met Leu Gln Gly Tyr Lys Tyr His Leu Glu	
65 70 75	
TAT CGG TAC AGC CTC TAT AGA AGA ATC CGT TCA GAC ATT GAT GAA CAT	546
Tyr Arg Tyr Ser Leu Tyr Arg Arg Ile Arg Ser Asp Ile Asp Glu His	
80 85 90	
GAA GGA GGC TTG GAA GCC TTC TCC CGT AGT TAT GAG AAG TTT GGA TTT	594
Glu Gly Gly Leu Glu Ala Phe Ser Arg Ser Tyr Glu Lys Phe Gly Phe	
95 100 105 110	
AAT GCC AGC GCG GAA GGT ATC ACA TAT CGA GAA TGG GCT CCT GGA GCA	642
Asn Ala Ser Ala Glu Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly Ala	
115 120 125	
TTT TCT GCA GCA TTG GTG GGT GAC GTC AAC AAC TGG GAT CCA AAT GCA	690
Phe Ser Ala Ala Leu Val Gly Asp Val Asn Asn Trp Asp Pro Asn Ala	
130 135 140	
GAT CGT ATG AGC AAA AAT GAG TTT GGT GTT TGG GAA ATT TTT CTG CCT	738
Asp Arg Met Ser Lys Asn Glu Phe Gly Val Trp Glu Ile Phe Leu Pro	
145 150 155	
AAC AAT GCA GAT GGT ACA TCA CCT ATT CCT CAT GGA TCT CGT GTA AAG	786
Asn Asn Ala Asp Gly Thr Ser Pro Ile Pro His Gly Ser Arg Val Lys	
160 165 170	
GTG AGA ATG GAT ACT CCA TCA GGG ATA AAG GAT TCA ATT CCA GCC TGG	834
Val Arg Met Asp Thr Pro Ser Gly Ile Lys Asp Ser Ile Pro Ala Trp	
175 180 185 190	
ATC AAG TAC TCA GTG CAG GCC CCA GGA GAA ATA CCA TAT GAT GGG ATT	882
Ile Lys Tyr Ser Val Gln Ala Pro Gly Glu Ile Pro Tyr Asp Gly Ile	
195 200 205	
TAT TAT GAT CCT CCT GAA GAG GTA AAG TAT GTG TTC AGG CAT GCG CAA	930

Tyr	Tyr	Asp	Pro	Pro	Glu	Glu	Val	Lys	Tyr	Val	Phe	Arg	His	Ala	Gln	
			210					215					220			
CCT	AAA	CGA	CCA	AAA	TCA	TTG	CGG	ATA	TAT	GAA	ACA	CAT	GTC	GGA	ATG	978
Pro	Lys	Arg	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	Thr	His	Val	Gly	Met	
			225				230					235				
AGT	AGC	CCG	GAA	CCG	AAG	ATA	AAC	ACA	TAT	GTA	AAC	TTT	AGG	GAT	GAA	1026
Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Thr	Tyr	Val	Asn	Phe	Arg	Asp	Glu	
			240				245				250					
GTC	CTC	CCA	AGA	ATA	AAA	AAA	CTT	GGA	TAC	AAT	GCA	GTG	CAA	ATA	ATG	1074
Val	Leu	Pro	Arg	Ile	Lys	Lys	Leu	Gly	Tyr	Asn	Ala	Val	Gln	Ile	Met	
255					260				265					270		
GCA	ATC	CAA	GAG	CAC	TCA	TAT	TAT	GGA	AGC	TTT	GGA	TAC	CAT	GTA	ACT	1122
Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Gly	Ser	Phe	Gly	Tyr	His	Val	Thr	
				275				280					285			
AAT	TTT	TTT	GCG	CCA	AGT	AGT	CGT	TTT	GGT	ACC	CCA	GAA	GAT	TTG	AAG	1170
Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	Thr	Pro	Glu	Asp	Leu	Lys	
			290				295					300				
TCT	TTG	ATT	GAT	AGA	GCA	CAT	GAG	CTT	GGT	TTG	CTA	GTT	CTC	ATG	GAT	1218
Ser	Leu	Ile	Asp	Arg	Ala	His	Glu	Leu	Gly	Leu	Leu	Val	Leu	Met	Asp	
			305				310					315				
GTG	GTT	CAT	AGT	CAT	GCG	TCA	AGT	AAT	ACT	CTG	GAT	GGG	TTG	AAT	GGT	1266
Val	Val	His	Ser	His	Ala	Ser	Ser	Asn	Thr	Leu	Asp	Gly	Leu	Asn	Gly	
			320				325				330					
TTT	GAT	GGT	ACA	GAT	ACA	CAT	TAC	TTT	CAC	AGT	GGT	CCA	CGT	GGC	CAT	1314
Phe	Asp	Gly	Thr	Asp	Thr	His	Tyr	Phe	His	Ser	Gly	Pro	Arg	Gly	His	
335					340				345					350		
CAC	TGG	ATG	TGG	GAT	TCT	CGC	CTA	TTT	AAC	TAT	GGG	AAC	TGG	GAA	GTT	1362
His	Trp	Met	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	Gly	Asn	Trp	Glu	Val	
				355					360				365			
TTA	AGA	TTT	CTT	CTC	TCC	AAT	GCT	AGA	TGG	TGG	CTC	GAG	GAA	TAT	AAG	1410
Leu	Arg	Phe	Leu	Leu	Ser	Asn	Ala	Arg	Trp	Trp	Leu	Glu	Glu	Tyr	Lys	
			370					375				380				
TTT	GAT	GGT	TTC	CGT	TTT	GAT	GGT	GTG	ACC	TCC	ATG	ATG	TAC	ACT	CAC	1458
Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	Ser	Met	Met	Tyr	Thr	His	

385	390	395	
CAC GGA TTA CAA GTA ACA TTT ACG GGG AAC TTC AAT GAG TAT TTT GGC			1506
His Gly Leu Gln Val Thr Phe Thr Gly Asn Phe Asn Glu Tyr Phe Gly			
400	405	410	
TTT GCC ACC GAT GTA GAT GCA GTG GTT TAC TTG ATG CTG GTA AAT GAT			1554
Phe Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Val Asn Asp			
415	420	425	430
CTA ATT CAT GGA CTT TAT CCT GAG GCT GTA ACC ATT GGT GAA GAT GTT			1602
Leu Ile His Gly Leu Tyr Pro Glu Ala Val Thr Ile Gly Glu Asp Val			
	435	440	445
AGT GGA ATG CCT ACA TTT GCC CTT CCT GTT CAC GAT GGT GGG GTA GGT			1650
Ser Gly Met Pro Thr Phe Ala Leu Pro Val His Asp Gly Gly Val Gly			
	450	455	460
TTT GAC TAT CGG ATG CAT ATG GCT GTG GCT GAC AAA TGG ATT GAC CTT			1698
Phe Asp Tyr Arg Met His Met Ala Val Ala Asp Lys Trp Ile Asp Leu			
	465	470	475
CTC AAG CAA AGT GAT GAA ACT TGG AAG ATG GGT GAT ATT GTG CAC ACA			1746
Leu Lys Gln Ser Asp Glu Thr Trp Lys Met Gly Asp Ile Val His Thr			
	480	485	490
CTG ACA AAT AGG AGG TGG TTA GAG AAG TGT GTA ACT TAT GCT GAA AGT			1794
Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Thr Tyr Ala Glu Ser			
495	500	505	510
CAT GAT CAA GCA TTA GTC GGC GAC AAG ACT ATT GCG TTT TGG TTG ATG			1842
His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met			
	515	520	525
GAC AAG GAT ATG TAT GAT TTC ATG GCC CTC GAT AGA CCT TCA ACT CCT			1890
Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro			
	530	535	540
ACC ATT GAT CGT GGG ATA GCA TTA CAT AAG ATG ATT AGA CTT ATC ACA			1938
Thr Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Ile Thr			
	545	550	555
ATG GGT TTA GGA GGA GAG GGC TAT CTT AAT TTC ATG GGA AAT GAG TTT			1986
Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe			
	560	565	570

GGA CAT CCT GAA TGG ATA GAT TTT CCA AGA GGT CCG CAA AGA CTT CCA	2034
Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Arg Leu Pro	
575 580 585 590	
AGT GGT AAG TTT ATT CCA GGG AAT AAC AAC AGT TAT GAC AAA TGT CGT	2082
Ser Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg	
595 600 605	
CGA AGA TTT GAC CTG GGT GAT GCA GAC TAT CTT AGG TAT CAT GGT ATG	2130
Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr His Gly Met	
610 615 620	
CAA GAG TTT GAT CAG GCA ATG CAA CAT CTT GAG CAA AAA TAT GAA TTC	2178
Gln Glu Phe Asp Gln Ala Met Gln His Leu Glu Gln Lys Tyr Glu Phe	
625 630 635	
ATG ACA TCT GAT CAC CAG TAT ATT TCC CGG AAA CAT GAG GAG GAT AAG	2226
Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys His Glu Glu Asp Lys	
640 645 650	
GTG ATT GTG TTC GAA AAG GGA GAT TTG GTA TTT GTG TTC AAC TTC CAC	2274
Val Ile Val Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe His	
655 660 665 670	
TGC AAC AAC AGC TAT TTT GAC TAC CGT ATT GGT TGT CGA AAG CCT GGG	2322
Cys Asn Asn Ser Tyr Phe Asp Tyr Arg Ile Gly Cys Arg Lys Pro Gly	
675 680 685	
GTG TAT AAG GTG GTC TTG GAC TCC GAC GCT GGA CTA TTT GGT GGA TTT	2370
Val Tyr Lys Val Val Leu Asp Ser Asp Ala Gly Leu Phe Gly Gly Phe	
690 695 700	
AGC AGG ATC CAT CAC GCA GCC GAG CAC TTC ACC GCC GAC TGT TCG CAT	2418
Ser Arg Ile His His Ala Ala Glu His Phe Thr Ala Asp Cys Ser His	
705 710 715	
GAT AAT AGG CCA TAT TCA TTC TCG GTT TAT ACA CCA AGC AGA ACA TGT	2466
Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Thr Pro Ser Arg Thr Cys	
720 725 730	
GTC GTC TAT GCT CCA GTG GAG TGA TAGCGGGGTA CTCGTTGCTG CGCGGCATGT	2520
Val Val Tyr Ala Pro Val Glu *	
735 740	
GTGGGGCTGT CGATGTGAGG AAAAACCTTC TTCCAAAACC GGCAGATGCA TGCATGCATG	2580

CTACAATAAG	GTTCTGATAC	TTTAATCGAT	GCTGGAAAGC	CCATGCATCT	CGCTGCGTTG	2640
TCCTCTCTAT	ATATATAAGA	CCTTCAAGGT	GTCAATTAAA	CATAGAGTTT	TCGTTTTTTCG	2700
CTTTCCTAAA	AAAAAAAAAA	AAAAA				2725

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 800 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met Ala Phe Arg Val Ser Gly Ala Val Leu Gly Gly Ala Val Arg Ala
-58 -55 -50 -45

Pro Arg Leu Thr Gly Gly Gly Glu Gly Ser Leu Val Phe Arg His Thr
-40 -35 -30

Gly Leu Phe Leu Thr Arg Gly Ala Arg Val Gly Cys Ser Gly Thr His
-25 -20 -15

Gly Ala Met Arg Ala Ala Ala Ala Ala Arg Lys Ala Val Met Val Pro
-10 -5 1 5

Glu Gly Glu Asn Asp Gly Leu Ala Ser Arg Ala Asp Ser Ala Gln Phe
10 15 20

Gln Ser Asp Glu Leu Glu Val Pro Asp Ile Ser Glu Glu Thr Thr Cys
25 30 35

Gly Ala Gly Val Ala Asp Ala Gln Ala Leu Asn Arg Val Arg Val Val
40 45 50

Pro Pro Pro Ser Asp Gly Gln Lys Ile Phe Gln Ile Asp Pro Met Leu
55 60 65 70

Gln Gly Tyr Lys Tyr His Leu Glu Tyr Arg Tyr Ser Leu Tyr Arg Arg
75 80 85

111

Ile Arg Ser Asp Ile Asp Glu His Glu Gly Gly Leu Glu Ala Phe Ser
90 95 100

Arg Ser Tyr Glu Lys Phe Gly Phe Asn Ala Ser Ala Glu Gly Ile Thr
105 110 115

Tyr Arg Glu Trp Ala Pro Gly Ala Phe Ser Ala Ala Leu Val Gly Asp
120 125 130

Val Asn Asn Trp Asp Pro Asn Ala Asp Arg Met Ser Lys Asn Glu Phe
135 140 145 150

Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Thr Ser Pro
155 160 165

Ile Pro His Gly Ser Arg Val Lys Val Arg Met Asp Thr Pro Ser Gly
170 175 180

Ile Lys Asp Ser Ile Pro Ala Trp Ile Lys Tyr Ser Val Gln Ala Pro
185 190 195

Gly Glu Ile Pro Tyr Asp Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Val
200 205 210

Lys Tyr Val Phe Arg His Ala Gln Pro Lys Arg Pro Lys Ser Leu Arg
215 220 225 230

Ile Tyr Glu Thr His Val Gly Met Ser Ser Pro Glu Pro Lys Ile Asn
235 240 245

Thr Tyr Val Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Lys Leu
250 255 260

Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr
265 270 275

Gly Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg
280 285 290

Phe Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His Glu
295 300 305 310

Leu Gly Leu Leu Val Leu Met Asp Val Val His Ser His Ala Ser Ser
315 320 325

Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His Tyr		
330	335	340
Phe His Ser Gly Pro Arg Gly His His Trp Met Trp Asp Ser Arg Leu		
345	350	355
Phe Asn Tyr Gly Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala		
360	365	370
Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly		
375	380	385 390
Val Thr Ser Met Met Tyr Thr His His Gly Leu Gln Val Thr Phe Thr		
395	400	405
Gly Asn Phe Asn Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala Val		
410	415	420
Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu Tyr Pro Glu		
425	430	435
Ala Val Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala Leu		
440	445	450
Pro Val His Asp Gly Gly Val Gly Phe Asp Tyr Arg Met His Met Ala		
455	460	465 470
Val Ala Asp Lys Trp Ile Asp Leu Leu Lys Gln Ser Asp Glu Thr Trp		
475	480	485
Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu		
490	495	500
Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp		
505	510	515
Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met		
520	525	530
Ala Leu Asp Arg Pro Ser Thr Pro Thr Ile Asp Arg Gly Ile Ala Leu		
535	540	545 550
His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr		
555	560	565

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Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe
      570                      575                      580

Pro Arg Gly Pro Gln Arg Leu Pro Ser Gly Lys Phe Ile Pro Gly Asn
      585                      590                      595

Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala
      600                      605                      610

Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln
615                      620                      625                      630

His Leu Glu Gln Lys Tyr Glu Phe Met Thr Ser Asp His Gln Tyr Ile
      635                      640                      645

Ser Arg Lys His Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly Asp
      650                      655                      660

Leu Val Phe Val Phe Asn Phe His Cys Asn Asn Ser Tyr Phe Asp Tyr
      665                      670                      675

Arg Ile Gly Cys Arg Lys Pro Gly Val Tyr Lys Val Val Leu Asp Ser
      680                      685                      690

Asp Ala Gly Leu Phe Gly Gly Phe Ser Arg Ile His His Ala Ala Glu
695                      700                      705                      710

His Phe Thr Ala Asp Cys Ser His Asp Asn Arg Pro Tyr Ser Phe Ser
      715                      720                      725

Val Tyr Thr Pro Ser Arg Thr Cys Val Val Tyr Ala Pro Val Glu  *
      730                      735                      740

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: transit peptide

(B) LOCATION: 2..190

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 191..2467

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..2470

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

G	CTG	TGC	CTC	GTG	TCG	CCC	TCT	TCC	TCG	CCG	ACT	CCG	CTT	CCG	CCG	46
Leu	Cys	Leu	Val	Ser	Pro	Ser	Ser	Ser	Pro	Thr	Pro	Leu	Pro	Pro		
-63			-60					-55				-50				
CCG	CGG	CGC	TCT	CGC	TCG	CAT	GCT	GAT	CGG	GCG	GCA	CCG	CCG	GGG	ATC	94
Pro	Arg	Arg	Ser	Arg	Ser	His	Ala	Asp	Arg	Ala	Ala	Pro	Pro	Gly	Ile	
			-45					-40					-35			
GCG	GGT	GGC	GGC	AAT	GTG	CGC	CTG	AGT	GTG	TTG	TCT	GTC	CAG	TGC	AAG	142
Ala	Gly	Gly	Gly	Asn	Val	Arg	Leu	Ser	Val	Leu	Ser	Val	Gln	Cys	Lys	
		-30					-25					-20				
GCT	CGC	CGG	TCA	GGG	GTG	CGG	AAG	GTC	AAG	AGC	AAA	TTC	GCC	ACT	GCA	190
Ala	Arg	Arg	Ser	Gly	Val	Arg	Lys	Val	Lys	Ser	Lys	Phe	Ala	Thr	Ala	
	-15					-10				-5						
GCT	ACT	GTG	CAA	GAA	GAT	AAA	ACT	ATG	GCA	ACT	GCC	AAA	GGC	GAT	GTC	238
Ala	Thr	Val	Gln	Glu	Asp	Lys	Thr	Met	Ala	Thr	Ala	Lys	Gly	Asp	Val	
1				5				10					15			
GAC	CAT	CTC	CCC	ATA	TAC	GAC	CTG	GAC	CCC	AAG	CTG	GAG	ATA	TTC	AAG	286
Asp	His	Leu	Pro	Ile	Tyr	Asp	Leu	Asp	Pro	Lys	Leu	Glu	Ile	Phe	Lys	
			20					25					30			
GAC	CAT	TTC	AGG	TAC	CGG	ATG	AAA	AGA	TTC	CTA	GAG	CAG	AAA	GGA	TCA	334
Asp	His	Phe	Arg	Tyr	Arg	Met	Lys	Arg	Phe	Leu	Glu	Gln	Lys	Gly	Ser	
		35					40					45				

ATT GAA GAA AAT GAG GGA AGT CTT GAA TCT TTT TCT AAA GGC TAT TTG	382
Ile Glu Glu Asn Glu Gly Ser Leu Glu Ser Phe Ser Lys Gly Tyr Leu	
50 55 60	
AAA TTT GGG ATT AAT ACA AAT GAG GAT GGA ACT GTA TAT CGT GAA TGG	430
Lys Phe Gly Ile Asn Thr Asn Glu Asp Gly Thr Val Tyr Arg Glu Trp	
65 70 75 80	
GCA CCT GCT GCG CAG GAG GCA GAG CTT ATT GGT GAC TTC AAT GAC TGG	478
Ala Pro Ala Ala Gln Glu Ala Glu Leu Ile Gly Asp Phe Asn Asp Trp	
85 90 95	
AAT GGT GCA AAC CAT AAG ATG GAG AAG GAT AAA TTT GGT GTT TGG TCG	526
Asn Gly Ala Asn His Lys Met Glu Lys Asp Lys Phe Gly Val Trp Ser	
100 105 110	
ATC AAA ATT GAC CAT GTC AAA GGG AAA CCT GCC ATC CCT CAC AAT TCC	574
Ile Lys Ile Asp His Val Lys Gly Lys Pro Ala Ile Pro His Asn Ser	
115 120 125	
AAG GTT AAA TTT CGC TTT CTA CAT GGT GGA GTA TGG GTT GAT CGT ATT	622
Lys Val Lys Phe Arg Phe Leu His Gly Gly Val Trp Val Asp Arg Ile	
130 135 140	
CCA GCA TTG ATT CGT TAT GCG ACT GTT GAT GCC TCT AAA TTT GGA GCT	670
Pro Ala Leu Ile Arg Tyr Ala Thr Val Asp Ala Ser Lys Phe Gly Ala	
145 150 155 160	
CCC TAT GAT GGT GTT CAT TGG GAT CCT CCT GCT TCT GAA AGG TAC ACA	718
Pro Tyr Asp Gly Val His Trp Asp Pro Pro Ala Ser Glu Arg Tyr Thr	
165 170 175	
TTT AAG CAT CCT CGG CCT TCA AAG CCT GCT GCT CCA CGT ATC TAT GAA	766
Phe Lys His Pro Arg Pro Ser Lys Pro Ala Ala Pro Arg Ile Tyr Glu	
180 185 190	
GCC CAT GTA GGT ATG AGT GGT GAA AAG CCA GCA GTA AGC ACA TAT AGG	814
Ala His Val Gly Met Ser Gly Glu Lys Pro Ala Val Ser Thr Tyr Arg	
195 200 205	
GAA TTT GCA GAC AAT GTG TTG CCA CGC ATA CGA GCA AAT AAC TAC AAC	862
Glu Phe Ala Asp Asn Val Leu Pro Arg Ile Arg Ala Asn Asn Tyr Asn	
210 215 220	
ACA GTT CAG TTG ATG GCA GTT ATG GAG CAT TCG TAC TAT GCT TCT TTC	910

Thr	Val	Gln	Leu	Met	Ala	Val	Met	Glu	His	Ser	Tyr	Tyr	Ala	Ser	Phe	
225					230					235					240	
GGG	TAC	CAT	GTG	ACA	AAT	TTC	TTT	GCG	GTT	AGC	AGC	AGA	TCA	GGC	ACA	958
Gly	Tyr	His	Val	Thr	Asn	Phe	Phe	Ala	Val	Ser	Ser	Arg	Ser	Gly	Thr	
				245					250					255		
CCA	GAG	GAC	CTC	AAA	TAT	CTT	GTT	GAT	AAG	GCA	CAC	AGT	TTG	GGT	TTG	1006
Pro	Glu	Asp	Leu	Lys	Tyr	Leu	Val	Asp	Lys	Ala	His	Ser	Leu	Gly	Leu	
				260					265					270		
CGA	GTT	CTG	ATG	GAT	GTT	GTC	CAT	AGC	CAT	GCA	AGT	AAT	AAT	GTC	ACA	1054
Arg	Val	Leu	Met	Asp	Val	Val	His	Ser	His	Ala	Ser	Asn	Asn	Val	Thr	
				275					280					285		
GAT	GGT	TTA	AAT	GGC	TAT	GAT	GTT	GGA	CAA	AGC	ACC	CAA	GAG	TCC	TAT	1102
Asp	Gly	Leu	Asn	Gly	Tyr	Asp	Val	Gly	Gln	Ser	Thr	Gln	Glu	Ser	Tyr	
	290						295					300				
TTT	CAT	GCG	GGA	GAT	AGA	GGT	TAT	CAT	AAA	CTT	TGG	GAT	AGT	CGG	CTG	1150
Phe	His	Ala	Gly	Asp	Arg	Gly	Tyr	His	Lys	Leu	Trp	Asp	Ser	Arg	Leu	
305					310					315					320	
TTC	AAC	TAT	GCT	AAC	TGG	GAG	GTA	TTA	AGG	TTT	CTT	CTT	TCT	AAC	CTG	1198
Phe	Asn	Tyr	Ala	Asn	Trp	Glu	Val	Leu	Arg	Phe	Leu	Leu	Ser	Asn	Leu	
				325					330					335		
AGA	TAT	TGG	TTG	GAT	GAA	TTC	ATG	TTT	GAT	GGC	TTC	CGA	TTT	GAT	GGA	1246
Arg	Tyr	Trp	Leu	Asp	Glu	Phe	Met	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	
				340					345					350		
GTT	ACA	TCA	ATG	CTG	TAT	CAT	CAC	CAT	GGT	ATC	AAT	GTG	GGG	TTT	ACT	1294
Val	Thr	Ser	Met	Leu	Tyr	His	His	His	Gly	Ile	Asn	Val	Gly	Phe	Thr	
				355					360					365		
GGA	AAC	TAC	CAG	GAA	TAT	TTC	AGT	TTG	GAC	ACA	GCT	GTG	GAT	GCA	GTT	1342
Gly	Asn	Tyr	Gln	Glu	Tyr	Phe	Ser	Leu	Asp	Thr	Ala	Val	Asp	Ala	Val	
	370						375					380				
GTT	TAC	ATG	ATG	CTT	GCA	AAC	CAT	TTA	ATG	CAC	AAA	CTC	TTG	CCA	GAA	1390
Val	Tyr	Met	Met	Leu	Ala	Asn	His	Leu	Met	His	Lys	Leu	Leu	Pro	Glu	
385					390					395					400	
GCA	ACT	GTT	GTT	GCT	GAA	GAT	GTT	TCA	GGC	ATG	CCG	GTC	CTT	TGC	CGG	1438
Ala	Thr	Val	Val	Ala	Glu	Asp	Val	Ser	Gly	Met	Pro	Val	Leu	Cys	Arg	

405	410	415	
CCA GTT GAT GAA GGT GGG GTT GGG TTT GAC TAT CGC CTG GCA ATG GCT			1486
Pro Val Asp Glu Gly Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala			
420	425	430	
ATC CCT GAT AGA TGG ATT GAC TAC CTG AAG AAT AAA GAT GAC TCT GAG			1534
Ile Pro Asp Arg Trp Ile Asp Tyr Leu Lys Asn Lys Asp Asp Ser Glu			
435	440	445	
TGG TCG ATG GGT GAA ATA GCG CAT ACT TTG ACT AAC AGG AGA TAT ACT			1582
Trp Ser Met Gly Glu Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr			
450	455	460	
GAA AAA TGC ATC GCA TAT GCT GAG AGC CAT GAT CAG TCT ATT GTT GGC			1630
Glu Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly			
465	470	475	480
GAC AAA ACT ATT GCA TTT CTC CTG ATG GAC AAG GAA ATG TAC ACT GGC			1678
Asp Lys Thr Ile Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly			
485	490	495	
ATG TCA GAC TTG CAG CCT GCT TCA CCT ACA ATT GAT CGA GGG ATT GCA			1726
Met Ser Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala			
500	505	510	
CTC CAA AAG ATG ATT CAC TTC ATC ACA ATG GCC CTT GGA GGT GAT GGC			1774
Leu Gln Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly			
515	520	525	
TAC TTG AAT TTT ATG GGA AAT GAG TTT GGT CAC CCA GAA TGG ATT GAC			1822
Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp			
530	535	540	
TTT CCA AGA GAA GGG AAC AAC TGG AGC TAT GAT AAA TGC AGA CGA CAG			1870
Phe Pro Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln			
545	550	555	560
TGG AGC CTT GTG GAC ACT GAT CAC TTG CGG TAC AAG TAC ATG AAT GCG			1918
Trp Ser Leu Val Asp Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala			
565	570	575	
TTT GAC CAA GCG ATG AAT GCG CTC GAT GAG AGA TTT TCC TTC CTT TCG			1966
Phe Asp Gln Ala Met Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser			
580	585	590	

TCG TCA AAG CAG ATC GTC AGC GAC ATG AAC GAT GAG GAA AAG GTT ATT	2014
Ser Ser Lys Gln Ile Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile	
595 600 605	
GTC TTT GAA CGT GGA GAT TTA GTT TTT GTT TTC AAT TTC CAT CCC AAG	2062
Val Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys	
610 615 620	
AAA ACT TAC GAG GGC TAC AAA GTG GGA TGC GAT TTG CCT GGG AAA TAC	2110
Lys Thr Tyr Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr	
625 630 635 640	
AGA GTA GCC CTG GAC TCT GAT GCT CTG GTC TTC GGT GGA CAT GGA AGA	2158
Arg Val Ala Leu Asp Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg	
645 650 655	
GTT GGC CAC GAC GTG GAT CAC TTC ACG TCG CCT GAA GGG GTG CCA GGG	2206
Val Gly His Asp Val Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly	
660 665 670	
GTG CCC GAA ACG AAC TTC AAC AAC CGG CCG AAC TCG TTC AAA GTC CTT	2254
Val Pro Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu	
675 680 685	
TCT CCG CCC CGC ACC TGT GTG GCT TAT TAC CGT GTA GAC GAA GCA GGG	2302
Ser Pro Pro Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly	
690 695 700	
GCT GGA CGA CGT CTT CAC GCG AAA GCA GAG ACA GGA AAG ACG TCT CCA	2350
Ala Gly Arg Arg Leu His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro	
705 710 715 720	
GCA GAG AGC ATC GAC GTC AAA GCT TCC AGA GCT AGT AGC AAA GAA GAC	2398
Ala Glu Ser Ile Asp Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp	
725 730 735	
AAG GAG GCA ACG GCT GGT GGC AAG AAG GGA TGG AAG TTT GCG CGG CAG	2446
Lys Glu Ala Thr Ala Gly Gly Lys Lys Gly Trp Lys Phe Ala Arg Gln	
740 745 750	
CCA TCC GAT CAA GAT ACC AAA TGA AGCCACGAGT CCTTGGTGAG GACTGGACTG	2500
Pro Ser Asp Gln Asp Thr Lys *	
755 760	
GCTGCCGGCG CCCTGTTAGT AGTCCTGCTC TACTGGACTA GCCGCCGCTG GCGCCCTTGG	2560

AACGGTCCTT TCCTGTAGCT TGCAGGCGAC TGGTGTCTCA TCACCGAGCA GGCAGGCACT 2620
 GCTTGTATAG CTTTCTAGA ATAATAATCA GGGATGGATG GATGGTGTGT ATTGGCTATC 2680
 TGGCTAGACG TGCATGTGCC CAGTTTGTAT GTACAGGAGC AGTTCCCGTC CAGAATAAAA 2740
 AAAAAGTTGT TGGGGGGTTT TTC 2763

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Leu Cys Leu Val Ser Pro Ser Ser Ser Pro Thr Pro Leu Pro Pro Pro
 -63 -60 -55 -50

Arg Arg Ser Arg Ser His Ala Asp Arg Ala Ala Pro Pro Gly Ile Ala
 -45 -40 -35

Gly Gly Gly Asn Val Arg Leu Ser Val Leu Ser Val Gln Cys Lys Ala
 -30 -25 -20

Arg Arg Ser Gly Val Arg Lys Val Lys Ser Lys Phe Ala Thr Ala Ala
 -15 -10 -5 1

Thr Val Gln Glu Asp Lys Thr Met Ala Thr Ala Lys Gly Asp Val Asp
 5 10 15

His Leu Pro Ile Tyr Asp Leu Asp Pro Lys Leu Glu Ile Phe Lys Asp
 20 25 30

His Phe Arg Tyr Arg Met Lys Arg Phe Leu Glu Gln Lys Gly Ser Ile
 35 40 45

Glu Glu Asn Glu Gly Ser Leu Glu Ser Phe Ser Lys Gly Tyr Leu Lys
 50 55 60 65

Phe Gly Ile Asn Thr Asn Glu Asp Gly Thr Val Tyr Arg Glu Trp Ala

120

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

310

320

Tyr Trp Leu Asp Glu Phe Met Phe Asp Gly Phe Arg Phe Asp Gly Val
340 345 350

Thr Ser Met Leu Tyr His His His Gly Ile Asn Val Gly Phe Thr Gly
355 360 365

Asn Tyr Gln Glu Tyr Phe Ser Leu Asp Thr Ala Val Asp Ala Val Val
370 375 380 385

Tyr Met Met Leu Ala Asn His Leu Met His Lys Leu Leu Pro Glu Ala
390 395 400

Thr Val Val Ala Glu Asp Val Ser Gly Met Pro Val Leu Cys Arg Pro
405 410 415

Val	Asp	Glu	Gly	Gly	Val	Gly	Phe	Asp	Tyr	Arg	Leu	Ala	Met	Ala	Ile
		420					425					430			

Pro	Asp	Arg	Trp	Ile	Asp	Tyr	Leu	Lys	Asn	Lys	Asp	Asp	Ser	Glu	Trp
435						440					445				

Ser Met Gly Glu Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr Glu
450 455 460 465

Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp
470 475 480

Lys Thr Ile Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly Met
485 490 495

Ser Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu
500 505 510

Gln Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr
515 520 525

Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe
530 535 540 545

Pro Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp

122

550	555	560
Ser Leu Val Asp Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe		
565	570	575
Asp Gln Ala Met Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser Ser		
580	585	590
Ser Lys Gln Ile Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile Val		
595	600	605
Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys Lys		
610	615	620
Thr Tyr Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg		
630	635	640
Val Ala Leu Asp Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg Val		
645	650	655
Gly His Asp Val Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly Val		
660	665	670
Pro Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu Ser		
675	680	685
Pro Pro Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly Ala		
690	695	700
Gly Arg Arg Leu His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro Ala		
710	715	720
Glu Ser Ile Asp Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp Lys		
725	730	735
Glu Ala Thr Ala Gly Gly Lys Lys Gly Trp Lys Phe Ala Arg Gln Pro		
740	745	750
Ser Asp Gln Asp Thr Lys *		
755	760	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

123

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zea mays*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..153

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

ATG GCG ACG CCC TCG GCC GTG GGC GCC GCG TGC CTC CTC CTC GCG CGG	48
Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg	
765 770 775	
GCC GCC TGG CCG GCC GCC GTC GGC GAC CGG GCG CGC CCG CGG AGG CTC	96
Ala Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu	
780 785 790	
CAG CGC GTG CTG CGC CGC CGG TGC GTC GCG GAG CTG AGC AGG GAG GGG	144
Gln Arg Val Leu Arg Arg Arg Cys Val Ala Glu Leu Ser Arg Glu Gly	
795 800 805	
CCC CAT ATG	153
Pro His Met	
810	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

124

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

Ala Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu
 20 25 30

Gln Arg Val Leu Arg Arg Arg Cys Val Ala Glu Leu Ser Arg Glu Gly
 35 40 45

Pro His Met
 50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1620

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

TGC GTC GCG GAG CTG AGC AGG GAG GAC CTC GGT CTC GAA CCT GAA GGG	48
Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly	
55 60 65	
ATT GCT GAA GGT TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA	96
Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln	
70 75 80	
GAT TCT GAG ATT GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA	144
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr	
85 90 95	
CAA AGC ATT GTC TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA AAG TCT	192

Gln	Ser	Ile	Val	Phe	Val	Thr	Gly	Glu	Ala	Ser	Pro	Tyr	Ala	Lys	Ser	
100					105					110					115	
GGG	GGT	CTA	GGA	GAT	GTT	TGT	GGT	TCA	TTG	CCA	GTT	GCT	CTT	GCT	GCT	240
Gly	Gly	Leu	Gly	Asp	Val	Cys	Gly	Ser	Leu	Pro	Val	Ala	Leu	Ala	Ala	
				120					125					130		
CGT	GGT	CAC	CGT	GTG	ATG	GTT	GTA	ATG	CCC	AGA	TAT	TTA	AAT	GGT	ACC	288
Arg	Gly	His	Arg	Val	Met	Val	Val	Met	Pro	Arg	Tyr	Leu	Asn	Gly	Thr	
			135					140					145			
TCC	GAT	AAG	AAT	TAT	GCA	AAT	GCA	TTT	TAC	ACA	GAA	AAA	CAC	ATT	CGG	336
Ser	Asp	Lys	Asn	Tyr	Ala	Asn	Ala	Phe	Tyr	Thr	Glu	Lys	His	Ile	Arg	
		150					155					160				
ATT	CCA	TGC	TTT	GGC	GGT	GAA	CAT	GAA	GTT	ACC	TTC	TTC	CAT	GAG	TAT	384
Ile	Pro	Cys	Phe	Gly	Gly	Glu	His	Glu	Val	Thr	Phe	Phe	His	Glu	Tyr	
	165					170				175						
AGA	GAT	TCA	GTT	GAC	TGG	GTG	TTT	GTT	GAT	CAT	CCC	TCA	TAT	CAC	AGA	432
Arg	Asp	Ser	Val	Asp	Trp	Val	Phe	Val	Asp	His	Pro	Ser	Tyr	His	Arg	
180					185					190					195	
CCT	GGA	AAT	TTA	TAT	GGA	GAT	AAG	TTT	GGT	GCT	TTT	GGT	GAT	AAT	CAG	480
Pro	Gly	Asn	Leu	Tyr	Gly	Asp	Lys	Phe	Gly	Ala	Phe	Gly	Asp	Asn	Gln	
				200					205					210		
TTC	AGA	TAC	ACA	CTC	CTT	TGC	TAT	GCT	GCA	TGT	GAG	GCT	CCT	TTG	ATC	528
Phe	Arg	Tyr	Thr	Leu	Leu	Cys	Tyr	Ala	Ala	Cys	Glu	Ala	Pro	Leu	Ile	
			215					220					225			
CTT	GAA	TTG	GGA	GGA	TAT	ATT	TAT	GGA	CAG	AAT	TGC	ATG	TTT	GTT	GTC	576
Leu	Glu	Leu	Gly	Gly	Tyr	Ile	Tyr	Gly	Gln	Asn	Cys	Met	Phe	Val	Val	
		230					235					240				
AAT	GAT	TGG	CAT	GCC	AGT	CTA	GTG	CCA	GTC	CTT	CTT	GCT	GCA	AAA	TAT	624
Asn	Asp	Trp	His	Ala	Ser	Leu	Val	Pro	Val	Leu	Leu	Ala	Ala	Lys	Tyr	
	245					250					255					
AGA	CCA	TAT	GGT	GTT	TAT	AAA	GAC	TCC	CGC	AGC	ATT	CTT	GTA	ATA	CAT	672
Arg	Pro	Tyr	Gly	Val	Tyr	Lys	Asp	Ser	Arg	Ser	Ile	Leu	Val	Ile	His	
260					265				270						275	
AAT	TTA	GCA	CAT	CAG	GGT	GTA	GAG	CCT	GCA	AGC	ACA	TAT	CCT	GAC	CTT	720
Asn	Leu	Ala	His	Gln	Gly	Val	Glu	Pro	Ala	Ser	Thr	Tyr	Pro	Asp	Leu	

	280	285	290	
GGG TTG CCA CCT GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA				768
Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu				
	295	300	305	
TGG GCG AGG AGG CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG				816
Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu				
	310	315	320	
AAA GGT GCA GTT GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT				864
Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly				
	325	330	335	
TAT TCG TGG GAG GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG				912
Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu				
	340	345	350	355
CTC TTA AGC TCC AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT				960
Leu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile				
	360	365	370	
GAC ATT AAT GAT TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT				1008
Asp Ile Asn Asp Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His				
	375	380	385	
TAT TCT GTT GAT GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG				1056
Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu				
	390	395	400	
CAG AAG GAG CTG GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC				1104
Gln Lys Glu Leu Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly				
	405	410	415	
TTT ATT GGA AGG TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT				1152
Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu				
	420	425	430	435
ATC ATA CCA GAT CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA				1200
Ile Ile Pro Asp Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly				
	440	445	450	
TCT GGT GAC CCA GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC				1248
Ser Gly Asp Pro Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile				
	455	460	465	

127

TTC AAG GAT AAA TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC	1296
Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser	
470 475 480	
CAC CGA ATA ACT GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC	1344
His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe	
485 490 495	
GAA CCT TGT GGT CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT	1392
Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val	
500 505 510 515	
CCT GTT GTC CAT GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC	1440
Pro Val Val His Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe	
520 525 530	
AAC CCT TTC GGT GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA	1488
Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala	
535 540 545	
CCC CTA ACC ACA GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC	1536
Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile	
550 555 560	
TAC ATA CAG GGA ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG	1584
Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg	
565 570 575	
CAT GTC AAA AGA CTT CAC GTG GGA CCA TGC CGC TGA	1620
His Val Lys Arg Leu His Val Gly Pro Cys Arg *	
580 585 590	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly

128

1	5	10	15
Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln	20	25	30
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr	35	40	45
Gln Ser Ile Val Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser	50	55	60
Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala	65	70	75
Arg Gly His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr	85	90	95
Ser Asp Lys Asn Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg	100	105	110
Ile Pro Cys Phe Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr	115	120	125
Arg Asp Ser Val Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg	130	135	140
Pro Gly Asn Leu Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln	145	150	155
Phe Arg Tyr Thr Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile	165	170	175
Leu Glu Leu Gly Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val	180	185	190
Asn Asp Trp His Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr	195	200	205
Arg Pro Tyr Gly Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His	210	215	220
Asn Leu Ala His Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu	225	230	235
Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu			

	245		250		255										
Trp	Ala	Arg	Arg	His	Ala	Leu	Asp	Lys	Gly	Glu	Ala	Val	Asn	Phe	Leu
	260							265					270		
Lys	Gly	Ala	Val	Val	Thr	Ala	Asp	Arg	Ile	Val	Thr	Val	Ser	Lys	Gly
	275						280					285			
Tyr	Ser	Trp	Glu	Val	Thr	Thr	Ala	Glu	Gly	Gly	Gln	Gly	Leu	Asn	Glu
	290						295				300				
Leu	Leu	Ser	Ser	Arg	Lys	Ser	Val	Leu	Asn	Gly	Ile	Val	Asn	Gly	Ile
305					310					315				320	
Asp	Ile	Asn	Asp	Trp	Asn	Pro	Ala	Thr	Asp	Lys	Cys	Ile	Pro	Cys	His
			325						330					335	
Tyr	Ser	Val	Asp	Asp	Leu	Ser	Gly	Lys	Ala	Lys	Cys	Lys	Gly	Ala	Leu
		340						345					350		
Gln	Lys	Glu	Leu	Gly	Leu	Pro	Ile	Arg	Pro	Asp	Val	Pro	Leu	Ile	Gly
	355						360					365			
Phe	Ile	Gly	Arg	Leu	Asp	Tyr	Gln	Lys	Gly	Ile	Asp	Leu	Ile	Gln	Leu
	370					375					380				
Ile	Ile	Pro	Asp	Leu	Met	Arg	Glu	Asp	Val	Gln	Phe	Val	Met	Leu	Gly
385					390					395				400	
Ser	Gly	Asp	Pro	Glu	Leu	Glu	Asp	Trp	Met	Arg	Ser	Thr	Glu	Ser	Ile
			405						410				415		
Phe	Lys	Asp	Lys	Phe	Arg	Gly	Trp	Val	Gly	Phe	Ser	Val	Pro	Val	Ser
		420						425					430		
His	Arg	Ile	Thr	Ala	Gly	Cys	Asp	Ile	Leu	Leu	Met	Pro	Ser	Arg	Phe
	435						440					445			
Glu	Pro	Cys	Gly	Leu	Asn	Gln	Leu	Tyr	Ala	Met	Gln	Tyr	Gly	Thr	Val
	450					455					460				
Pro	Val	Val	His	Ala	Thr	Gly	Gly	Leu	Arg	Asp	Thr	Val	Glu	Asn	Phe
465					470					475			480		
Asn	Pro	Phe	Gly	Glu	Asn	Gly	Glu	Gln	Gly	Thr	Gly	Trp	Ala	Phe	Ala

130

485

490

495

Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile
500 505 510

Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg
515 520 525

His Val Lys Arg Leu His Val Gly Pro Cys Arg *
530 535 540

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGGATCCAT GGCGACGCCC TCGGCCGTGG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGAATTCCA TATGGGGCCC CTCCTGCTC AGCTC

35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTGAGCTC AAGCTTGCTA CTTTCTTTCC TTAATG

36

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTCTCCGCGG TGGTGCCTT GCTTCCTAG

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCGTCGCGG AGCTGAGCAG GGAGGTCTCC GCGGTGGTGT CCTTGCTTCC TAG

53

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Val Ala Glu Leu Ser Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGAGAGAGAG AGAGAG

16

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAAGAAGA AGAAGAAGAA GAAGAAGAAG AAGAAG

36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAAAAAAA AAAAAAAAAA

18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

134

- (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATAATGCA G

11

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AACAATGGCT

10

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

135

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ala	Ser	Ser	Met	Leu	Ser	Ser	Ala	Ala	Val	Ala	Thr	Arg	Thr	Asn
1				5				10						15	
Pro	Ala	Gln	Ala	Ser	Met	Val	Ala	Pro	Phe	Thr	Gly	Leu	Lys	Ser	Ala
			20					25					30		
Ala	Phe	Pro	Val	Ser	Arg	Lys	Gln	Asn	Leu	Asp	Ile	Thr	Ser	Ile	Ala
			35				40					45			
Ser	Asn	Gly	Gly	Arg	Val	Gln	Cys								
		50				55									

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Ala	Pro	Thr	Val	Met	Met	Ala	Ser	Ser	Ala	Thr	Ala	Thr	Arg	Thr
1				5				10						15	
Asn	Pro	Ala	Gln	Ala	Ser	Ala	Val	Ala	Pro	Phe	Gln	Gly	Leu	Lys	Ser
			20					25					30		
Thr	Ala	Ser	Leu	Pro	Val	Ala	Arg	Arg	Ser	Ser	Arg	Ser	Leu	Gly	Asn

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35

40

45

Val Ala Ser Asn Gly Gly Arg Ile Arg Cys
50 55

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ala Gln Ile Leu Ala Pro Ser Thr Gln Trp Gln Met Arg Ile Thr
1 5 10 15

Lys Thr Ser Pro Cys Ala Thr Pro Ile Thr Ser Lys Met Trp Ser Ser
20 25 30

Leu Val Met Lys Gln Thr Lys Lys Val Ala His Ser Ala Lys Phe Arg
35 40 45

Val Met Ala Val Asn Ser Glu Asn Gly Thr
50 55

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly His
1 5 10 15
Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly Leu
 20 25 30
Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg Thr
 35 40 45
Ser Ala Arg Ala Ala Pro Arg His Gln Gln Gln Ala Arg Arg Gly Gly
 50 55 60
Arg Phe Pro Phe Pro Ser Leu Val Val Cys
65 70

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg
1 5 10 15
Xaa Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu
 20 25 30
Gln Arg Val Leu Arg Arg Arg
 35

CLAIMS

1. A hybrid polypeptide comprising:
 - (a) a starch-encapsulating region;
 - (b) a payload polypeptide fused to said starch-encapsulating region.
- 5 2. The hybrid polypeptide of claim 1 wherein said payload polypeptide consists of not more than three different types of amino acids selected from the group consisting of: Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, and Val.
3. The hybrid polypeptide of claim 1 wherein said payload polypeptide is a biologically
10 active polypeptide.
4. The hybrid polypeptide of claim 3 wherein said payload polypeptide is selected from the group consisting of hormones, growth factors, antibodies, peptides, polypeptides, enzyme immunoglobulins, dyes and biologically active fragments thereof.
5. The hybrid polypeptide of claim 1 wherein said starch-encapsulating region is the
15 starch-encapsulating region of an enzyme selected from the group consisting of soluble starch synthase I, soluble starch synthase II, soluble starch synthase III, granule-bound starch synthase, branching enzyme I, branching enzyme IIa, branching enzyme IIBb and glucoamylase polypeptides.
6. The hybrid polypeptide of claim 1 comprising a cleavage site between said starch-
20 encapsulating region and said payload polypeptide.
7. A recombinant nucleic acid molecule encoding the hybrid polypeptide of claim 1.

8. The recombinant molecule of claim 7 which is a DNA molecule comprising control sequences adapted for expression of said starch-encapsulating region and said payload polypeptide in a bacterial host.
9. The recombinant molecule of claim 7 which is a DNA molecule comprising control sequences adapted for expression of said starch-encapsulating region and said payload polypeptide in a plant host.
10. The recombinant molecule of claim 9 wherein said control sequences are adapted for expression of said starch-encapsulating region and said payload polypeptide in a monocot.
11. The recombinant molecule of claim 9 wherein said control sequences are adapted for expression of said starch-encapsulating region and said payload polypeptide in a dicot.
12. The recombinant molecule of claim 9 wherein said control sequences are adapted for expression of said starch-encapsulating region and said payload polypeptide in an animal host.
13. An expression vector comprising the recombinant molecule of claim 7.
14. A cell transformed to comprise the recombinant molecule of claim 7, capable of expressing said DNA molecule.
15. The cell of claim 14 which is a plant cell.
16. A plant regenerated from the cell of claim 15.
17. A seed from the plant of claim 16 capable of expressing said recombinant molecule.
18. A modified starch derived from cells of claim 14 comprising said payload polypeptide.

19. A method of targeting digestion of a payload polypeptide to a selected site in the digestive system of an animal comprising feeding said animal a modified starch of claim 18 comprising said payload polypeptide in a matrix of a starch selected to be digested in the selected site in the digestive tract.

5 20. A method of producing a pure payload polypeptide from a hybrid polypeptide of claim 1 comprising:

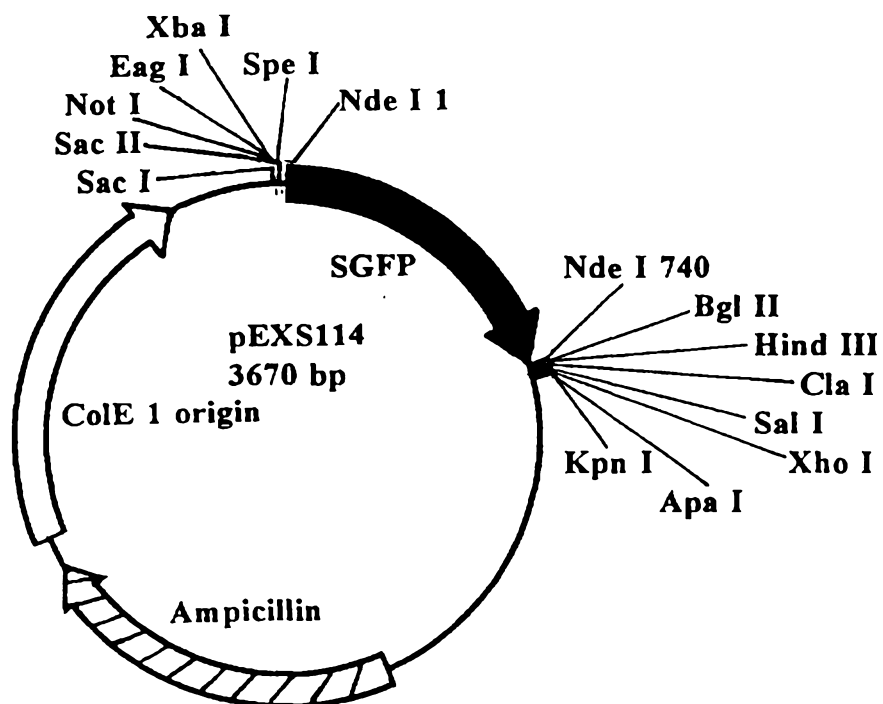
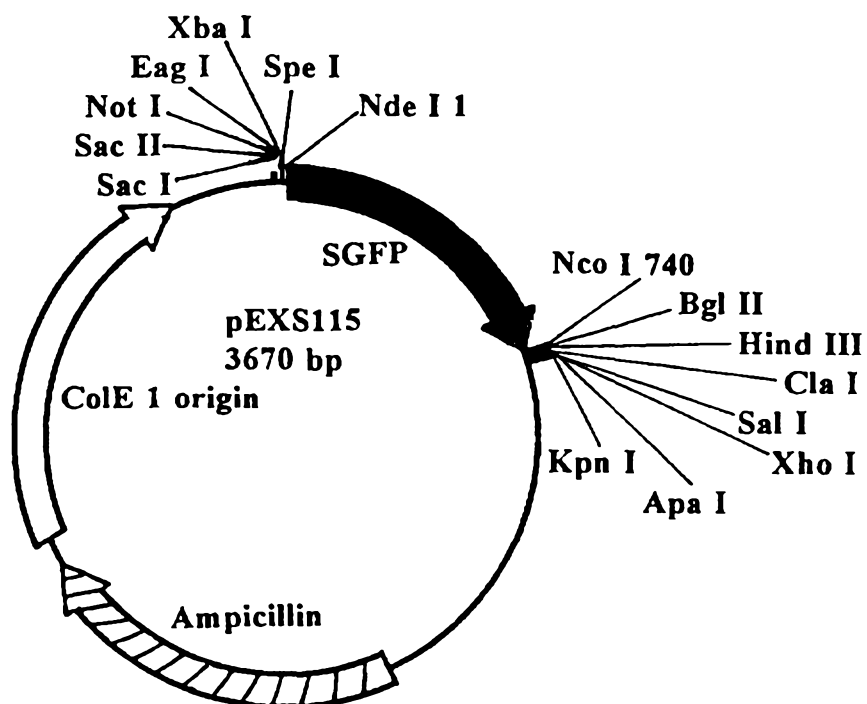
(a) transforming a host organism with DNA encoding said hybrid polypeptide;

(b) allowing said hybrid polypeptide to be expressed in said host;

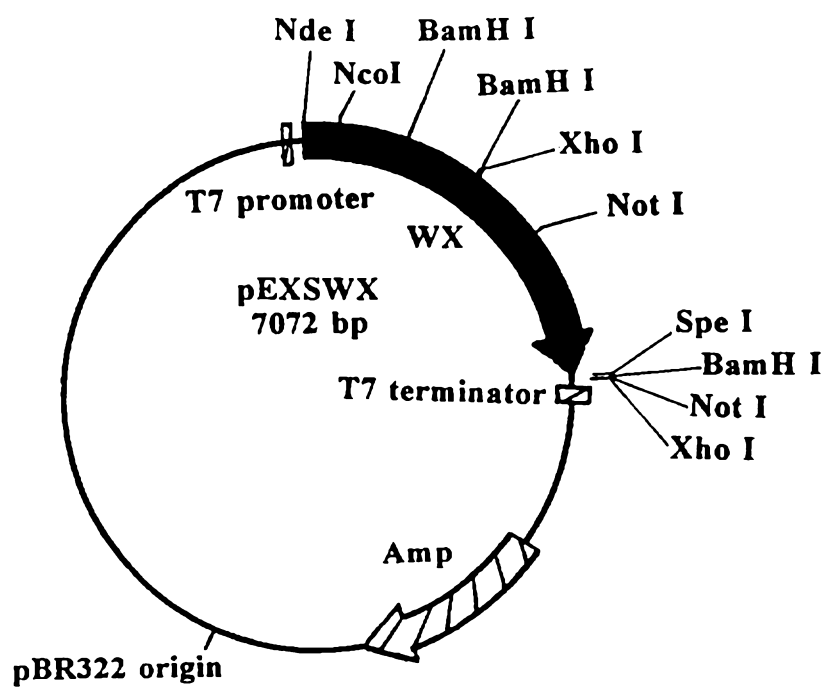
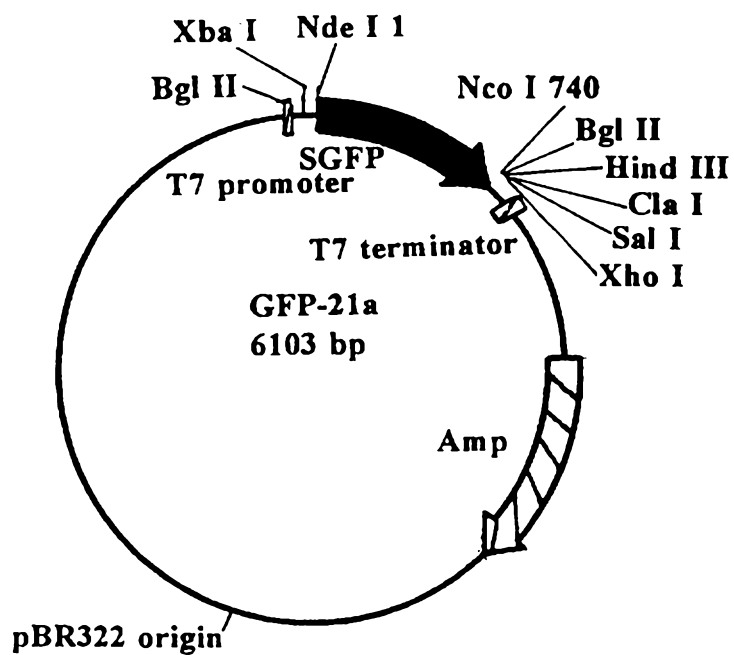
(c) isolating said hybrid polypeptide from said host;

10 (d) purifying said payload polypeptide from said hybrid polypeptide.

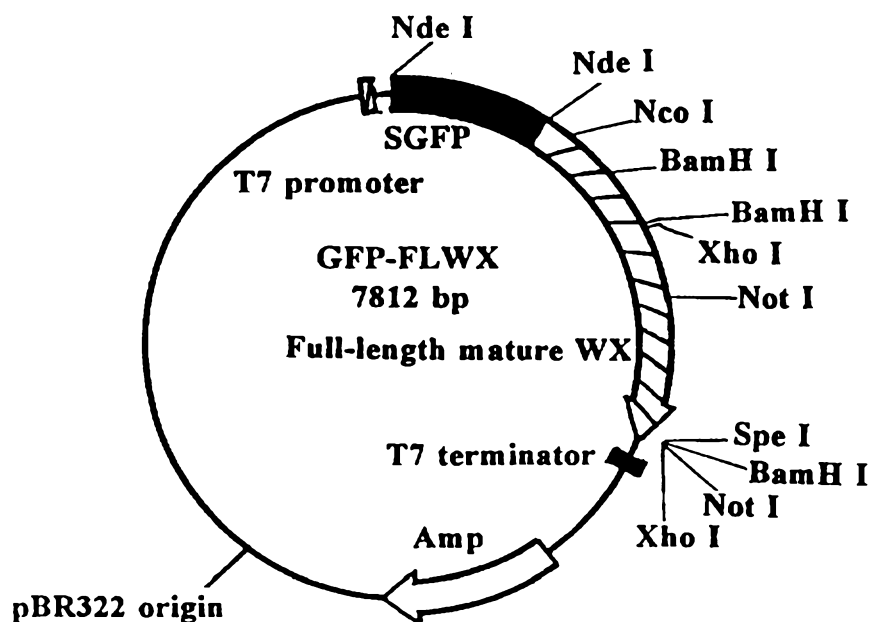
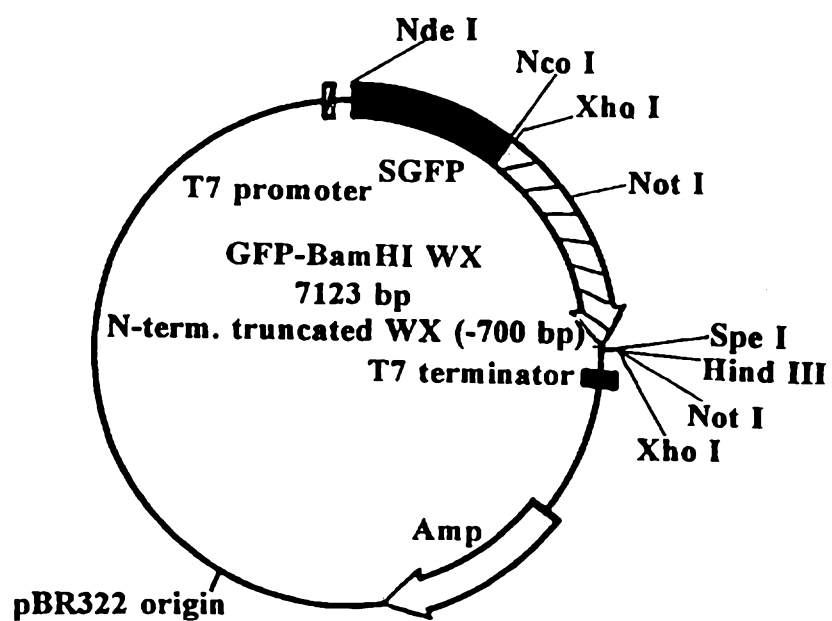
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**FIG. 1A****FIG. 1B**

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**FIG. 2A****FIG. 2B**

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**FIG. 3A****FIG. 3B**

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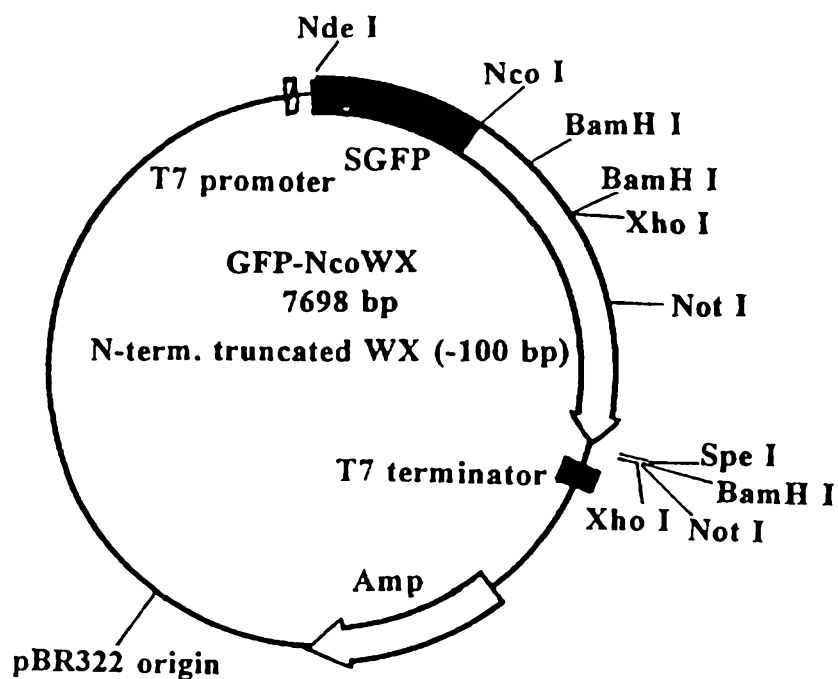


FIG. 4

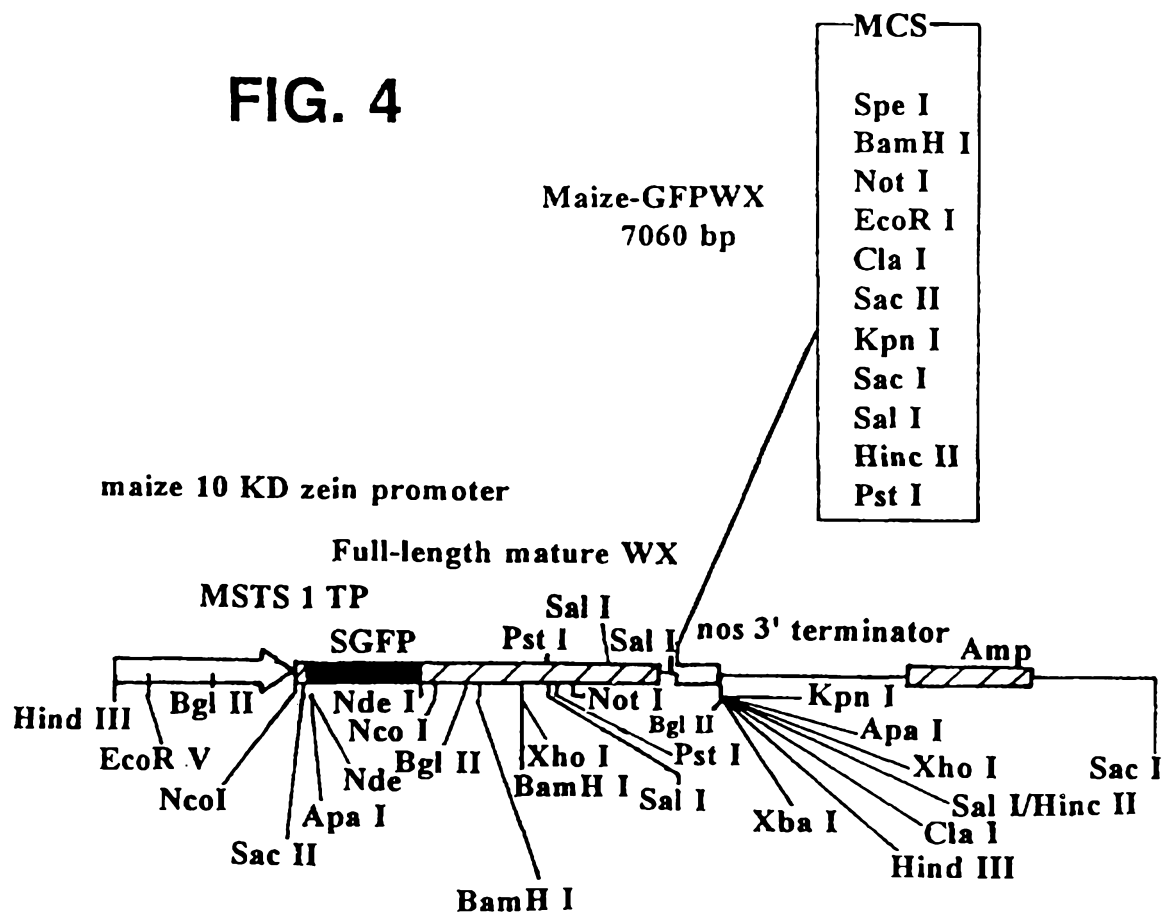
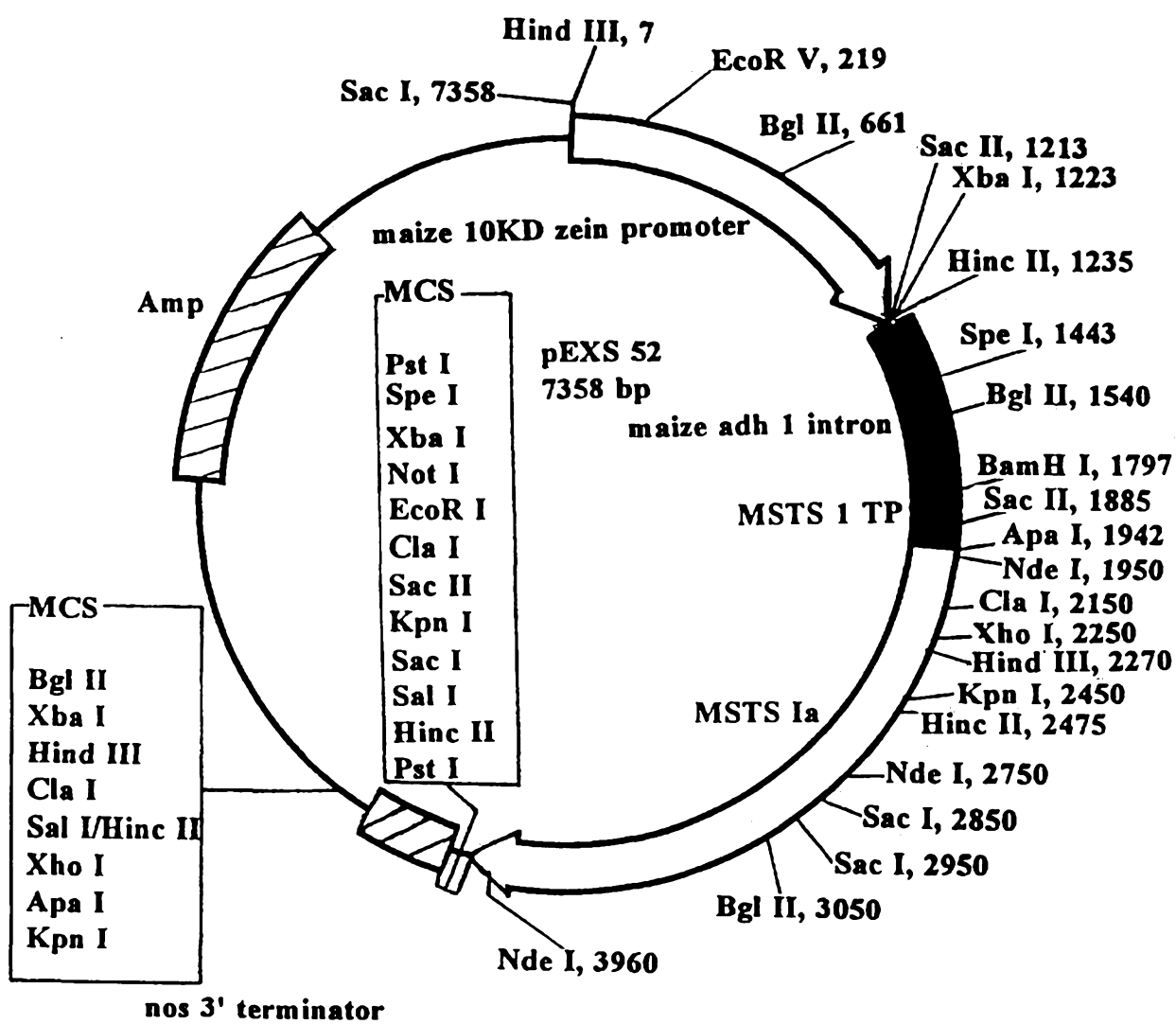


FIG. 5

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**FIG. 6**

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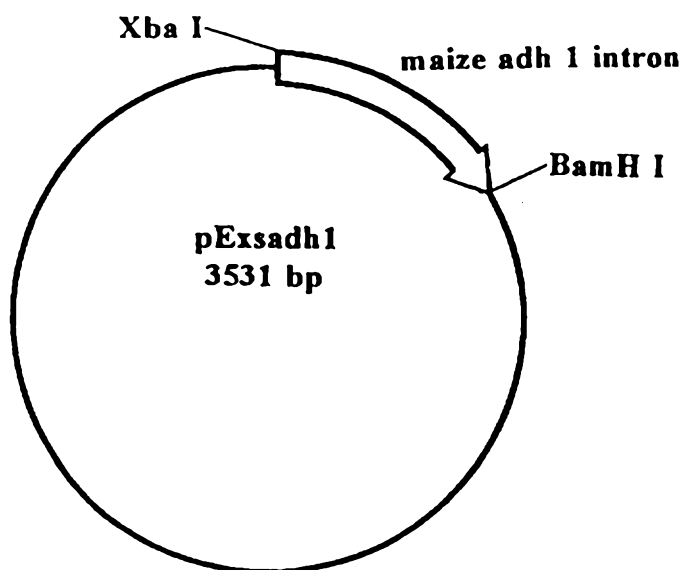


FIG. 7A

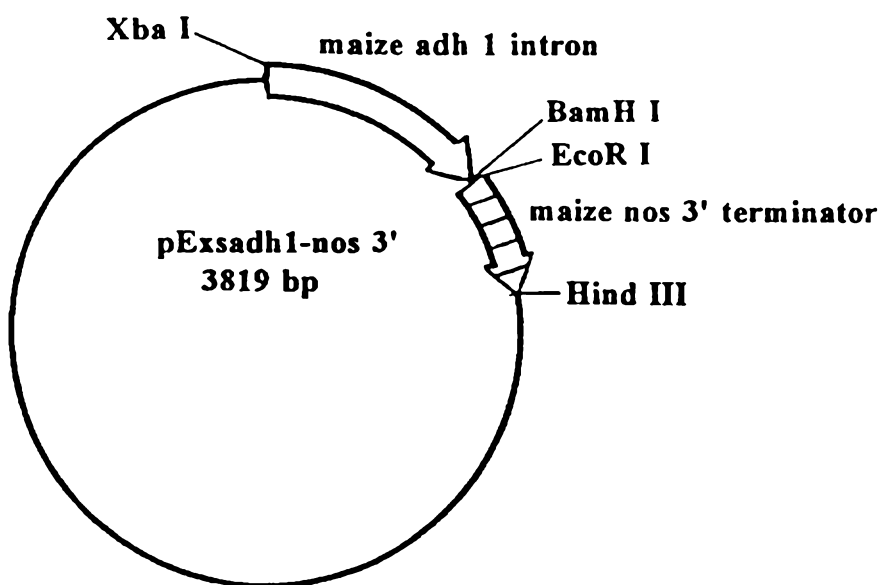
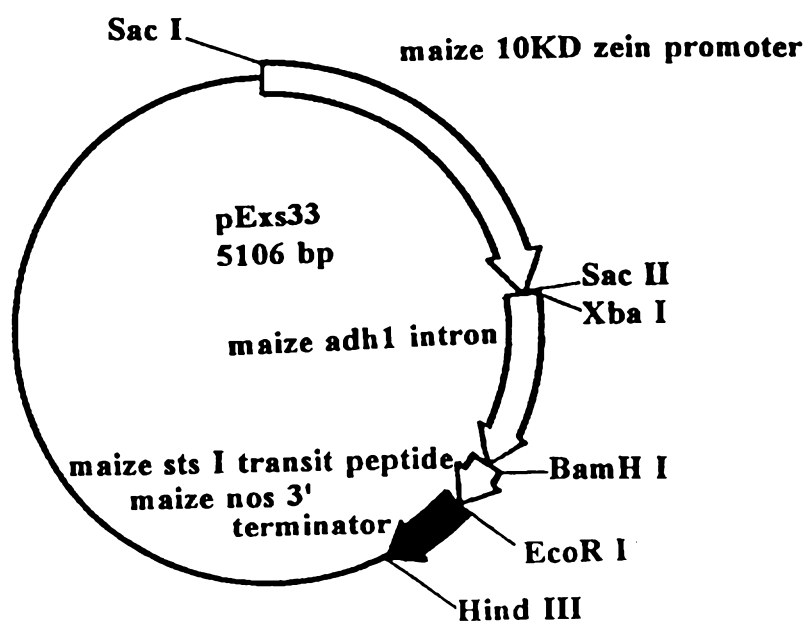
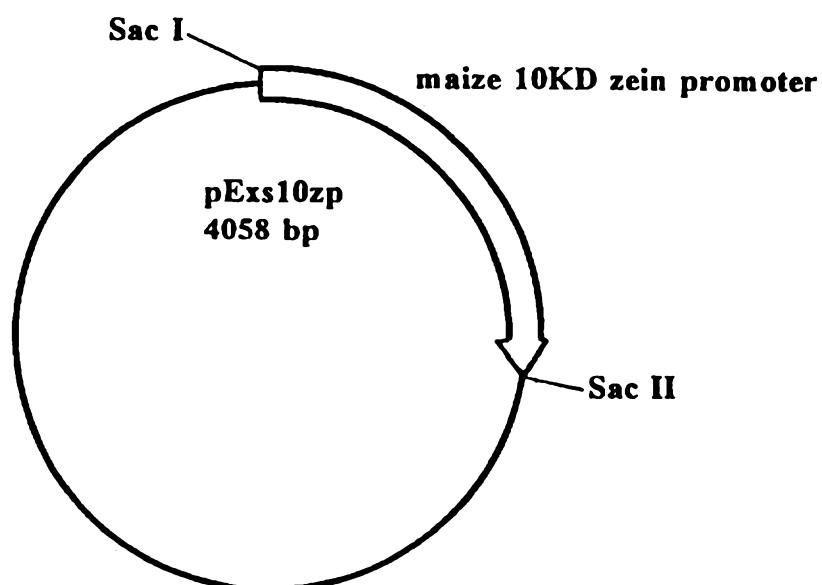
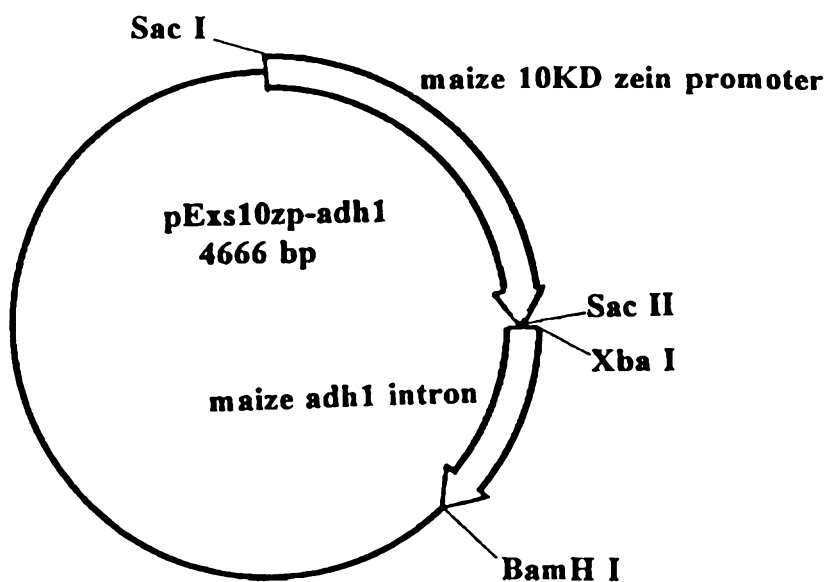
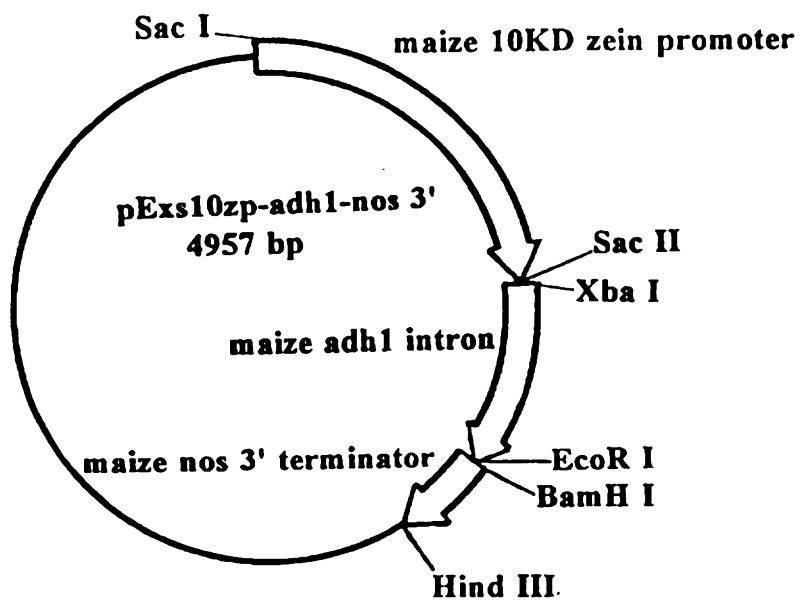


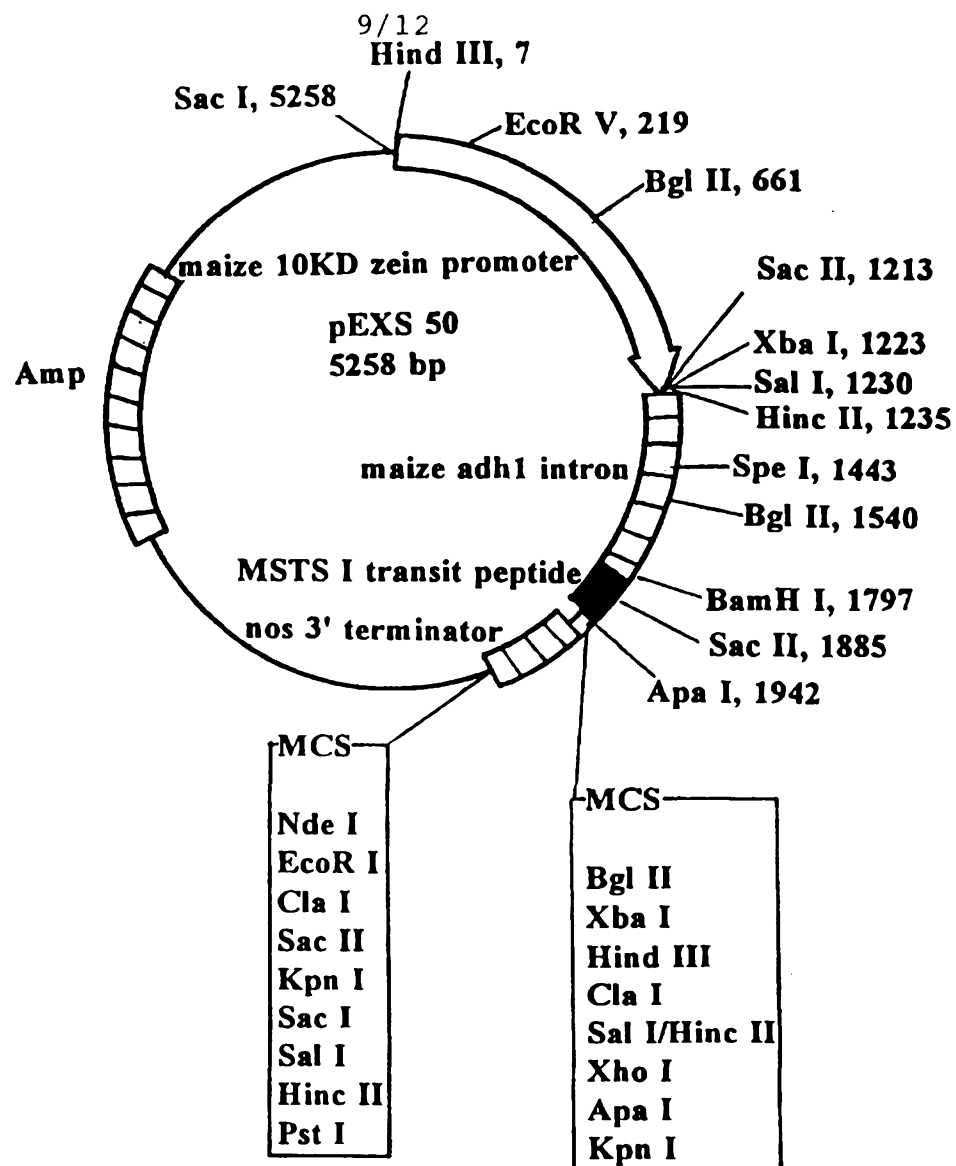
FIG. 7B

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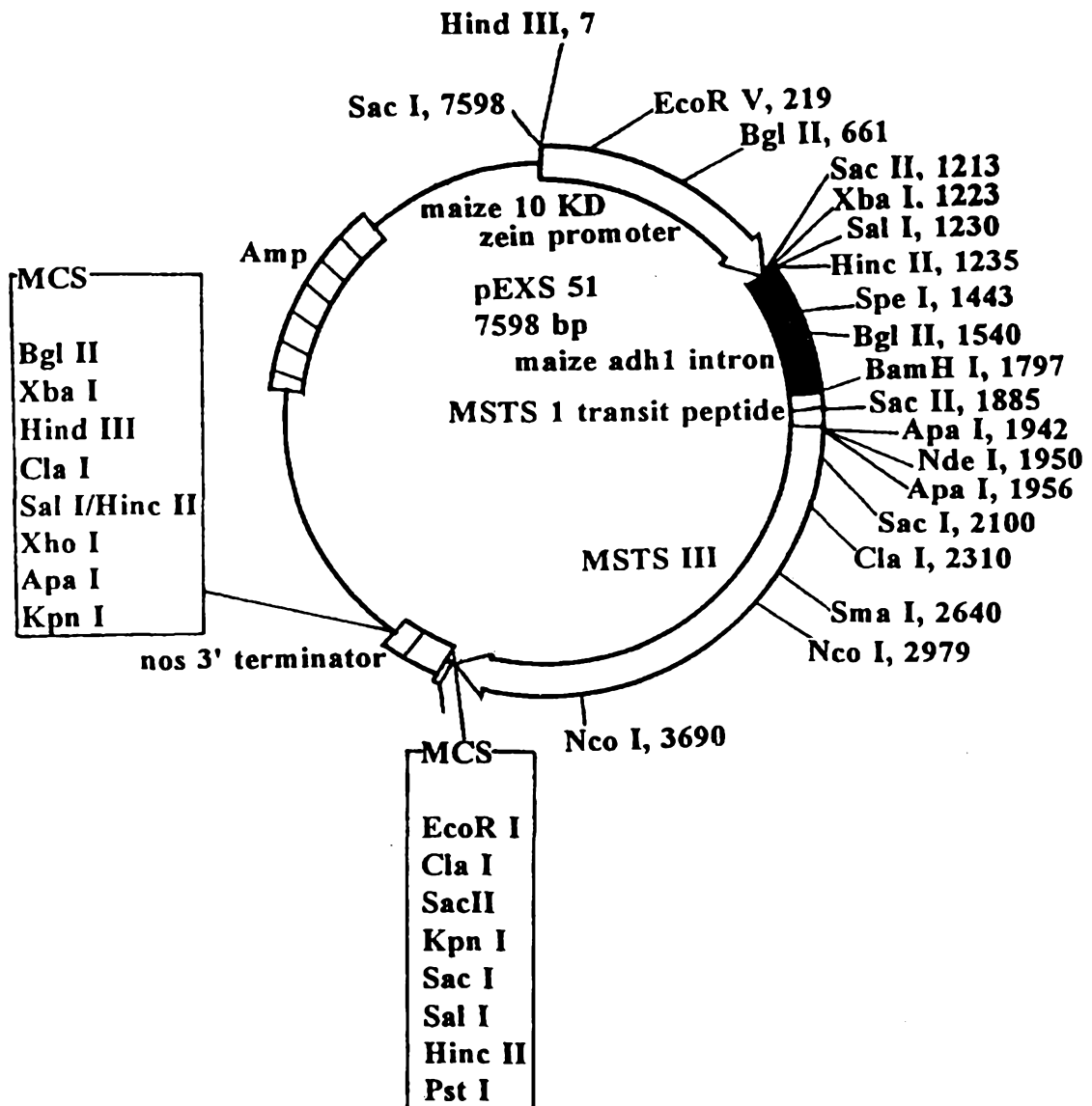
**FIG. 7C****FIG. 7D**

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**FIG. 7E****FIG. 7F**

**FIG. 8A**

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**FIG. 8B**

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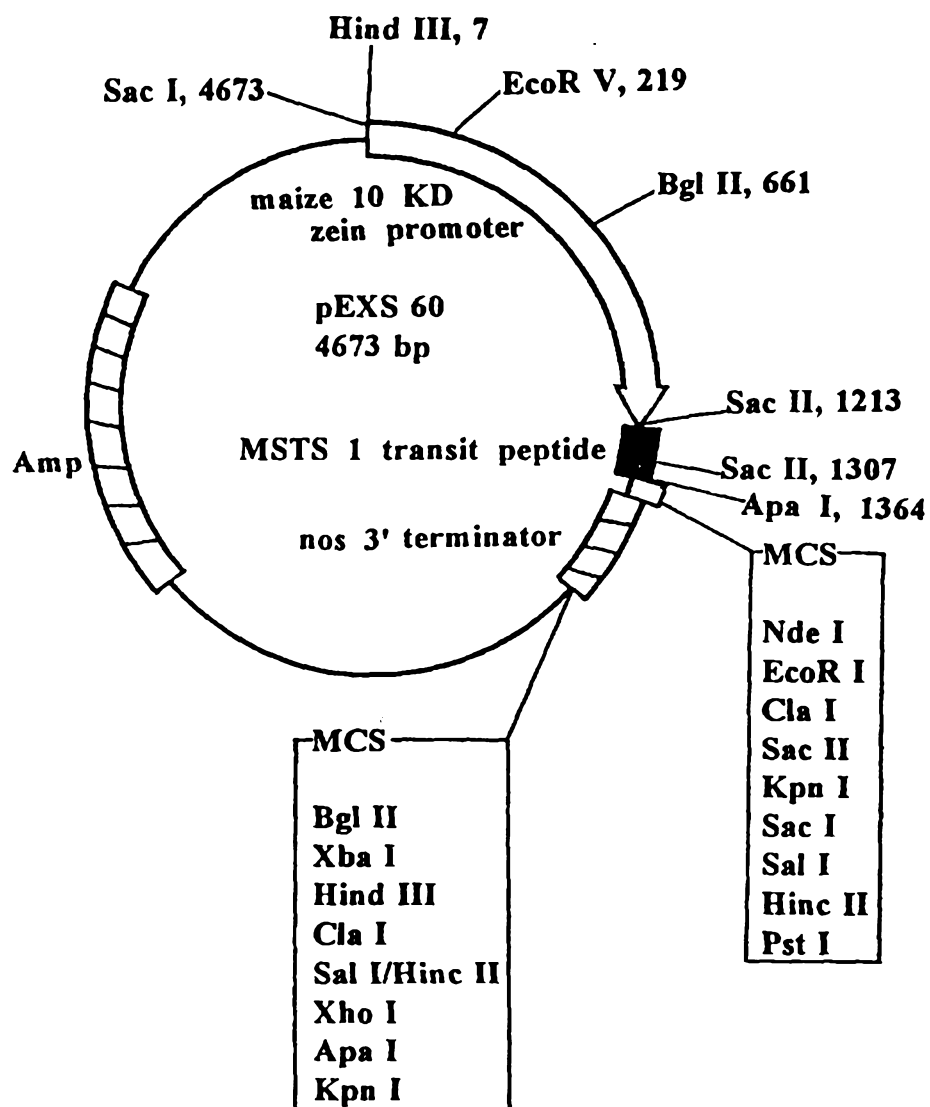
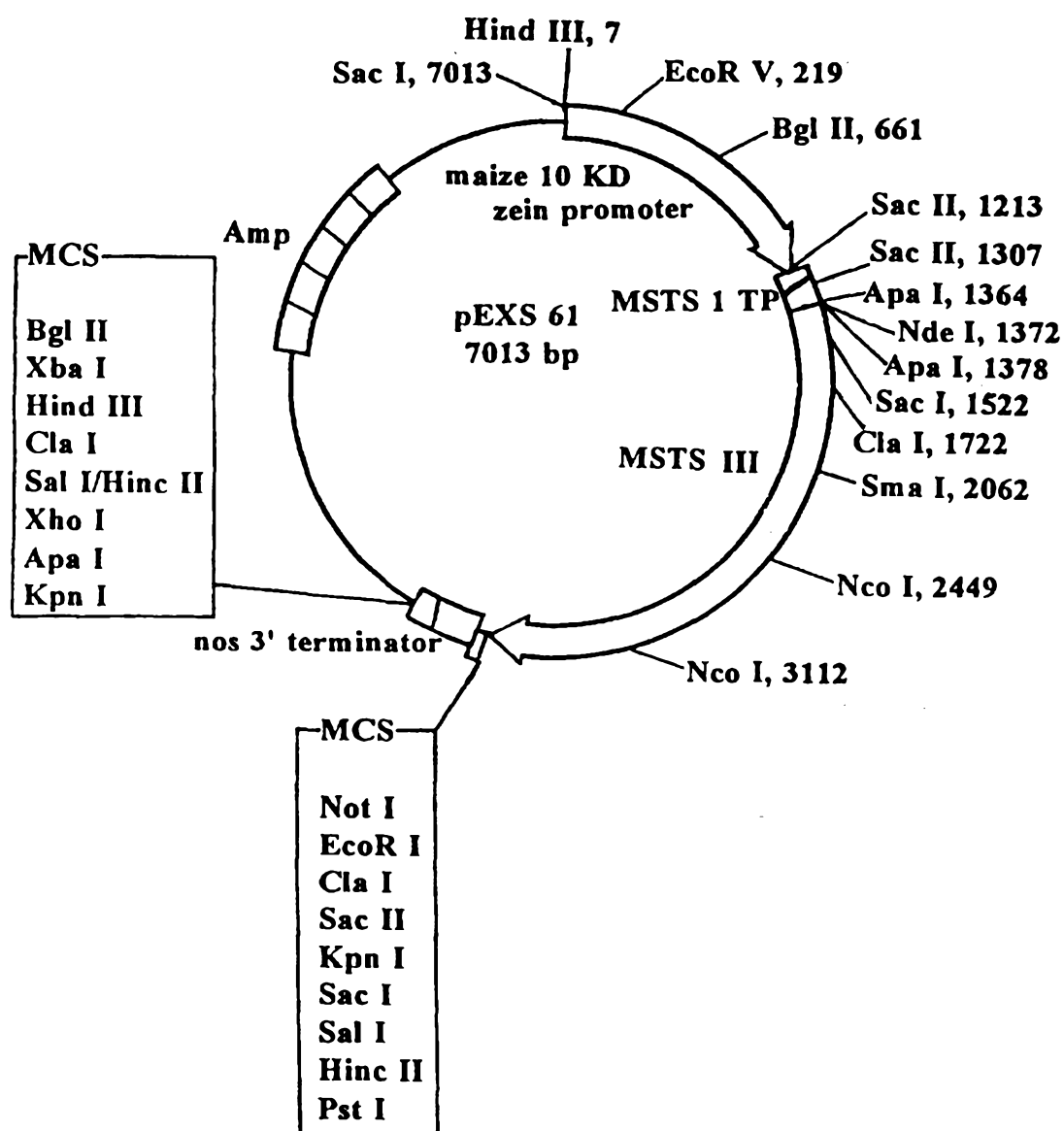


FIG. 9A

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**FIG. 9B**

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/17555

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/82 C12N9/10 C12N15/54 C12N15/62 C12Q1/68
C12N1/21 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12Q A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CHEN, L., ET AL.: "IMPROVED ADSORPTION TO STARCH OF A BETA-GALACTOSIDASE FUSION PROTEIN CONTAINING THE STARCH-BINDING DOMAIN FROM ASPERGILLUS GLUCOAMYLASE" BIOTECHNOLOGY PROGRESS, vol. 7, 1991, pages 225-229, XP002056940	1,3-5,7, 8,13,14, 20
Y	see the whole document	6
X	KUSNADI, A.R., ET AL.: "FUNCTIONAL STARCH-BINDING DOMAIN OF ASPERGILLUS GLUCOAMYLASE I IN ESCHERICHIA COLI" GENE, vol. 127, 1993, pages 193-197, XP002056413	1,3-5,7, 8,13,14, 20
Y	see the whole document	6
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☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

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- "O" document referring to an oral disclosure, use, exhibition or other means
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- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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- "&" document member of the same patent family

Date of the actual completion of the international search

25 February 1998

Date of mailing of the international search report

10/03/1998

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Authorized officer

Holtorf, S

INTERNATIONAL SEARCH REPORT

Inter: nal Application No
PCT/US 97/17555

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BROEKHUIJSEN M P ET AL: "SECRETION OF HETEROLOGOUS PROTEINS BY ASPERGILLUS NIGER: PRODUCTION OF ACTIVE HUMAN INTERLEUKIN-6 IN A PROTEASE-DEFICIENT MUTANT BY KEX2-LIKE PROCESSING OF A GLUCOAMYLASE-HI66 FUSION PROTEIN" JOURNAL OF BIOTECHNOLOGY, vol. 31, 1993, pages 135-145, XP002048588	1,3-7, 13,14,20
Y	see the whole document ----	6
A	MU-FORSTER, C., ET AL . : "PHYSICAL ASSOCIATION OF STARCH BIOSYNTHETIC ENZYMES WITH STARCH GRANULES OF MAIZE ENDOSPERM" PLANT PHYSIOLOGY, vol. 111, 1996, pages 821-829, XP002056414 see the whole document ----	1-20
A	GODDIJN O J M ET AL: "PLANTS AS BIOREACTORS" TRENDS IN BIOTECHNOLOGY, vol. 13, no. 9, 1 September 1995, pages 379-387, XP002005043 see page 384, right-hand column; figure 3 -----	1-20