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(54) Title: METHODS AND COMPOSITIONS FOR THE INTRODUCTION AND REGULATED EXPRESSION OF GENES IN PLANTS

(57) Abstract: Compositions and methods are provided for the introduction and the regulated expression of genes in plants. Compositions include promoter constructs that provide a level of activity useful for the regulated expression of site-specific recombinases, while avoiding premature excision. Further provided are isolated polynucleotides encoding novel babyboom polypeptides, expression cassettes, and plants comprising the same. Methods for the introduction of genes into plants are provided, including methods for plastid transformation and methods for the transformation of tissues from mature seeds and leaves.

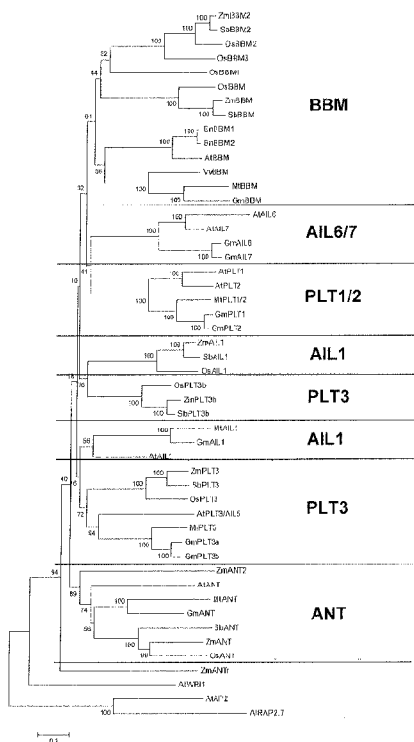


FIG. 1

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5 on December 29, 2010, and having a size of 534 kilobytes and is filed concurrently with the specification. The sequence listing contained in this ASCII formatted document is part of the specification and is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

10 The present invention is drawn to the field of plant genetics and molecular biology. More particularly, the compositions and methods are directed to the introduction and regulated expression of genes in plants.

BACKGROUND OF THE INVENTION

15 Current transformation technology provides an opportunity to engineer plants with desired traits. Major advances in plant transformation have occurred over the last few years. However, most transformation methods rely on the introduction of polynucleotides into embryonic tissues that are rapidly proliferating. Methods that allow for the transformation of more mature tissues would save considerable time and money.
20 Accordingly, methods are needed in the art to increase transformation efficiencies of plants and allow for the transformation of more mature tissues.

Further, it is often necessary to reduce the activity of a transgene because the transgene may negatively affect the growth or fertility of the plant. Recombination systems can be used to excise the transgene, wherein the expression of a site-specific
25 recombinase is regulated by an inducible promoter. Often, these systems are associated with premature excision. Accordingly, methods are needed in the art to efficiently excise transgenes with limited premature excision.

BRIEF SUMMARY OF THE INVENTION

Compositions and methods are provided for the introduction and regulated expression of genes in plants. Compositions include promoter constructs useful for regulated induction of expression of an operably linked coding sequence. In particular
 5 embodiments, the promoter construct comprises a maize *rab17* promoter or an active variant or fragment thereof and an attachment B (attB) site. The modified *rab17* promoter constructs find use in methods for regulating the expression of various coding sequences, including site-specific recombinases, which can minimize the premature excision of polynucleotides of interest in plants.

10 Further provided are methods for the transformation of plastids, such as chloroplasts, that involve the introduction of a heterologous polynucleotide encoding a cell proliferation factor, such as a babyboom (BBM) polypeptide. Novel BBM sequences are provided, along with methods of introducing the sequences into plants and plants comprising the novel BBM sequences. Methods for preparing and transforming mature
 15 embryo explants and leaf tissues are also provided.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 provides a depiction of a phylogenetic analysis of 50 sequences with homology to maize babyboom (BBM).

20 Figures 2A-2M show the consensus motif sequences 1-10, 14, 15, and 19, respectively, discovered in the analysis described herein, along with the alignments of the regions of various polypeptides used to generate the consensus motifs.

Figure 3 depicts the motifs found within 50 sequences with homology to maize BBM (ZmBBM).

25 Figure 4 shows an alignment of the amino acid sequence of various BBM polypeptides: maize babyboom 2 (ZmBBM2; SEQ ID NO: 12), sorghum babyboom 2 (SbBBM2; SEQ ID NO: 28), rice babyboom 2 (OsBBM2; SEQ ID NO: 18), rice babyboom 3 (OsBBM3; SEQ ID NO: 20), rice babyboom 1 (OsBBM1; SEQ ID NO: 16), maize babyboom (ZmBBM; SEQ ID NO: 10), sorghum babyboom (SbBBM; SEQ ID NO:
 30 4), rice babyboom (OsBBM; SEQ ID NO: 14), *Brassica* babyboom 1 (BnBBM1; SEQ ID NO: 24), *Brassica* babyboom 2 (BnBBM2; SEQ ID NO: 26), *Arabidopsis* babyboom (AtBBM; SEQ ID NO: 22), medicago babyboom (MtBBM; SEQ ID NO: 8), soybean babyboom (GmBBM; SEQ ID NO: 2), and grape babyboom (VvBBM; SEQ ID NO: 6).

Figure 5 provides a depiction of the motifs found in babyboom polypeptides.

DETAILED DESCRIPTION OF THE INVENTION

The presently disclosed compositions and methods are useful for the introduction and the regulated expression of genes in plants. Compositions comprise promoter
5 constructs that provide a level of activity useful for the regulated expression of various coding sequences, including site-specific recombinases. Further provided are compositions comprising novel babyboom (BBM) polynucleotide and polypeptide sequences and plants comprising the same. Methods for the introduction of genes into plants are provided, including methods for introducing novel BBM polynucleotides and
10 polypeptides into plants, methods for the enhancement of plastid transformation, and methods for the transformation of tissues from mature seeds.

The expression cassette having the sequence set forth in SEQ ID NO: 45, which is comprised of the maize *rab17* promoter, an attB site, and the coding sequence for the site-specific recombinase FLP, is capable of expressing FLP upon induction in such a manner
15 as to reduce premature excision. Without being bound by any theory or mechanism of action, it is believed that the presence of the attB site modifies the activity of the promoter, allowing for a tightly regulated induction of expression of an operably linked coding sequence. Therefore, compositions include promoter constructs comprising a modified maize *rab17* promoter or an active variant or fragment thereof. In some of these
20 embodiments, the promoter construct comprises the maize *rab17* promoter or an active variant or fragment thereof and an attB site or a variant or fragment thereof. In some of these embodiments, the maize *rab17* promoter has the sequence set forth in SEQ ID NO: 29 or an active variant or fragment thereof.

As used herein, the term "promoter" includes reference to a region of DNA
25 involved in the recognition and binding of RNA polymerase and other proteins to initiate transcription of a coding sequence. Promoters may be naturally occurring promoters, a variant or fragment thereof, or synthetically derived. A "promoter construct" is a polynucleotide comprising a promoter and optionally, sequences that are not necessary for transcription initiation or part of the coding sequence and are located in between the
30 promoter and the coding sequence in an expression cassette. These intervening sequences can include modulators, restriction sites, sequences of the 5'-untranslated region (5'-UTR), which is the region of a transcript that is transcribed, but is not translated into a polypeptide, and recombination sites.

The promoter in the promoter constructs is the maize *rab17* promoter or an active variant or fragment thereof. The maize *rab17* (responsive to abscisic acid) gene (GenBank Accession No. X15994; Vilardell *et al.* (1990) *Plant Mol Biol* 14:423-432; Vilardell *et al.* (1991) *Plant Mol Biol* 17:985-993; each of which is herein incorporated in its entirety) is expressed in late embryos, but its expression can be induced by exposure to abscisic acid or water stress. The sequence of the maize *rab17* promoter corresponds to nucleotides 1-558 of GenBank Accession No. X15994, which was disclosed in Vilardell *et al.* (1990) *Plant Mol Biol* 14:423-432 and is set forth in SEQ ID NO: 126. An alternative maize *rab17* promoter was disclosed in U.S. Patent Nos. 7,253,000 and 7,491,813, each of which is herein incorporated by reference in its entirety, and is set forth in SEQ ID NO: 29. The *rab17* promoter contains 5 putative abscisic acid responsive elements (ABRE) (Busk *et al.* (1997) *Plant J* 11:1285-1295, which is herein incorporated by reference in its entirety). The putative ABRE elements can be found at about -208 to -203 (nucleotides 304 to 309 of SEQ ID NO: 29), -162 to -157 (nucleotides 348 to 353 of SEQ ID NO: 29), -147 to -142 (nucleotides 363 to 368 of SEQ ID NO: 29), -141 to -136 (nucleotides 369 to 374 of SEQ ID NO: 29), and -96 to -91 (nucleotides 414 to 419 of SEQ ID NO: 29) in the maize *rab17* promoter. The *rab17* promoter also contains drought-responsive elements (DRE), of which the core sequence is identical to the DRE (drought-responsive) and CRT (cold-response elements) elements in *Arabidopsis*. The drought-responsive elements are found at -213 to -206 (nucleotides 299 to 306 of SEQ ID NO: 29) and -190 to -185 (nucleotides 322 to 327 of SEQ ID NO: 29) of the maize *rab17* promoter. The CAAT and TATAA box can be found from nucleotides 395 to 398 and 479 to 484 of SEQ ID NO: 29, respectively.

In some embodiments, the maize *rab17* promoter that is part of the presently disclosed promoter constructs has the sequence set forth in SEQ ID NO: 29 or an active variant or fragment thereof. In other embodiments, the maize *rab17* promoter that is part of the presently disclosed promoter constructs has the sequence set forth in SEQ ID NO: 125 or 126 or an active variant or fragment thereof.

In some embodiments of the methods and compositions, the promoter constructs comprise active variants or fragments of the maize *rab17* promoter. An active variant or fragment of a maize *rab17* promoter (*e.g.*, SEQ ID NO: 29, 125, 126) is a polynucleotide variant or fragment that retains the ability to initiate transcription. In some embodiments, an active fragment of a maize *rab17* promoter may comprise at least about 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 contiguous nucleotides of SEQ ID NO: 29, 125, or

126, or may have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 29, 125, or 126. In particular embodiments, an active variant or fragment of the maize *rab17* promoter is one that is capable of initiating transcription in response to abscisic acid (ABA). In some of these embodiments, the promoter comprises at least one ABRE element. In particular embodiments, the promoter of the compositions and methods comprises from about -219 to about -102 of the maize *rab17* promoter (corresponding to nucleotides 291 to 408 of SEQ ID NO: 29), which was shown to be sufficient to confer ABA responsiveness (Vilardell *et al.* (1991) *Plant Mol Biol* 17:985-993, which is herein incorporated by reference in its entirety).

In other embodiments, an active variant or fragment of the maize *rab17* promoter is one that is capable of initiating transcription in response to dessication. In some of these embodiments, the promoter comprises at least one DRE element.

In particular embodiments, the active maize *rab17* promoter fragment comprises from about -219 to about -80 of the maize *rab17* promoter (nucleotides 291 to 430 of SEQ ID NO: 29), which comprises all of the putative DRE and ABRE elements.

Without being bound by any theory or mechanism of action, it is believed that a promoter construct (the sequence of which is set forth in SEQ ID NO: 30) comprising a maize *rab17* promoter and a site-specific attachment B (attB) site has a modified level of activity in comparison to the promoter in the absence of the attB site due to the presence and/or the location of the attB site relative to the promoter. Therefore, it is believed the attB site functions as a modulator of the maize *rab17* promoter. Accordingly, promoter constructs comprising a maize *rab17* promoter or a fragment or variant thereof, and an attB site are provided, and in some of these embodiments, the attB site modifies the activity of the promoter. In other embodiments, the promoter construct comprises a maize *rab17* promoter or a fragment or variant thereof and a modulator that modifies the activity of the *rab17* promoter.

As used herein, a "modulator" refers to a polynucleotide that when present between a promoter and a coding sequence, serves to increase or decrease the activity of the promoter. Non-limiting examples of modulators include recombination sites, operators, and insulators.

Attachment sites are site-specific recombination sites found in viral and bacterial genomes that facilitate the integration or excision of the viral genome into and out of its host genome. Non-limiting examples of a viral and bacterial host system that utilize

attachment sites is the lambda bacteriophage and *E. coli* system (Weisberg and Landy (1983) In Lambda II, eds. Hendrix *et al.* (Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) pp.211-250). The modulator of the promoter constructs can be an *E. coli* attachment site B (attB) site. The attB site can be naturally occurring *E. coli* attB sites or an active variants or fragments thereof or a synthetically derived sequence. Synthetically derived attB sites and active variants and fragments of naturally occurring attB sites are those that are capable of recombining with a bacteriophage lambda attachment P site, a process that is catalyzed by the bacteriophage lambda Integrase (Int) and the *E. coli* Integration Host Factor (IHF) proteins (Landy (1989) *Ann Rev Biochem* 58: 913-949, which is herein incorporated by reference in its entirety). AttB sites typically have a length of about 25 nucleotides, with a core 15-base pair sequence that is involved in the actual crossover event. Alternatively, active variants and fragments of naturally occurring attB sites are those that are capable of modulating the activity of a promoter when present within a promoter construct. Non-limiting examples of attB sites that can be used include attB1 (SEQ ID NO: 31), attB2 (SEQ ID NO: 32), attB3 (SEQ ID NO: 33), and attB4 (SEQ ID NO: 34), and variants or fragments thereof. In some embodiments, the modulator is an active variant or fragment of an attB site that is capable of modulating (i.e., increasing, decreasing) the activity of a promoter, but is not capable of recombination with an attachment P site. Non-limiting examples of such active variants of an attB site include those having the sequence set forth in SEQ ID NO: 107, 108, or 109.

In some embodiments, the distance of the modulator from the promoter impacts the ability of the modulator to modify the activity of the promoter. The modulator may be contiguous with the promoter and/or the polynucleotide of interest. In other embodiments, a linker sequence separates the promoter sequence and the modulator. As used herein, a "linker sequence" is a nucleotide sequence that functions to link one functional sequence with another without otherwise contributing to the expression or translation of a polynucleotide of interest when present in a promoter construct. Accordingly, the actual sequence of the linker sequence can vary. The linker sequence can comprise plasmid sequences, restriction sites, and/or regions of the 5'-untranslated region (5'-UTR) of the gene from which the promoter is derived. The linker sequence separating the promoter and the modulator can have a length of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 400, 500, 1000 nucleotides or greater. In certain embodiments, a linker sequence of about 133 nucleotides separates the promoter and the modulator. In some embodiments, the linker

sequence comprises a fragment of the *rab17* 5'-UTR. The fragment of the 5'-UTR can be about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 nucleotides, or greater, in length. In certain embodiments, the promoter construct comprises a linker sequence separating the promoter and the modulator
 5 that comprises 95 nucleotides of the maize *rab17* 5'-UTR. In some of these embodiments, the 95 nucleotide sequence has the sequence set forth in SEQ ID NO: 35. In certain embodiments, the linker sequence between the promoter and modulator has the sequence set forth in SEQ ID NO: 36 or a variant or fragment thereof.

In some embodiments, the promoter construct comprises a linker sequence
 10 separating the modulator and the polynucleotide of interest. The length and sequence of this linker may also vary and can be about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 400, 500, 1000 nucleotides or greater in length. In certain embodiments, a linker sequence of about 61 nucleotides separates the modulator and the polynucleotide of interest. In certain
 15 embodiments, the linker sequence between the modulator and the polynucleotide of interest has the sequence set forth in SEQ ID NO: 37 or a variant or fragment thereof. In other embodiments, a linker sequence of about 25 nucleotides separates the modulator and the polynucleotide of interest. In certain embodiments, the linker sequence between the modulator and the polynucleotide of interest has the sequence set forth in SEQ ID NO:
 20 123.

In certain embodiments, the promoter construct has the sequence set forth in SEQ ID NO: 30 or a variant or fragment thereof.

The promoter constructs can be operably linked to a polynucleotide of interest that encodes a polynucleotide or polypeptide within an expression cassette. "Operably linked"
 25 denotes a functional linkage between two or more elements. For example, an operable linkage between a polynucleotide of interest and a promoter is a functional link that allows for expression of the polynucleotide of interest. Operably linked elements may be contiguous or non-contiguous. The expression cassette can comprise other 5' or 3' regulatory elements necessary for expression.

30 Regulatory elements that can be included in the expression cassette 5' to the polynucleotide of interest include 5' leader sequences. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:6126-6130); potyvirus leaders, for

example, TEV leader (Tobacco Etch Virus) (Gallie *et al.* (1995) *Gene* 165(2):233-238), MDMV leader (Maize Dwarf Mosaic Virus) (*Virology* 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP) (Macejak *et al.* (1991) *Nature* 353:90-94); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.* (1987) *Nature* 325:622-625); tobacco mosaic virus leader (TMV) (Gallie *et al.* (1989) in *Molecular Biology of RNA*, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel *et al.* (1991) *Virology* 81:382-385). See also, Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968. Other methods or sequences known to enhance translation can also be utilized, for example, introns, and the like.

The expression cassette may also comprise a transcriptional and/or translational termination region functional in plants. The termination region may be native with the transcriptional initiation region (*i.e.*, promoter), may be native with the operably linked polynucleotide of interest, may be native with the plant host, or may be derived from another source (*i.e.*, foreign to the promoter, the polynucleotide of interest, the plant host, or any combination thereof). Convenient termination regions are available from the potato proteinase inhibitor (PinII) gene or the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi *et al.* (1987) *Nucleic Acid Res.* 15:9627-9639. In some embodiments, the pinII termination sequence has the sequence set forth in SEQ ID NO: 38 or an active variant or fragment thereof that is capable of terminating transcription and/or translation in a plant cell.

In certain embodiments, the expression cassette can comprise a recombination site, such as an attachment site 3' to the polynucleotide of interest. In some of these embodiments, the recombination site is a second attB site. In some of those embodiments wherein the promoter comprises a first attB site, the second attB site following the polynucleotide of interest and the modulator attB are non-identical. In some of those embodiments wherein the modulator attB site is attB1 (SEQ ID NO: 31), the second attB site 3' of the polynucleotide of interest can have the sequence set forth in SEQ ID NO: 31 (attB1), SEQ ID NO: 32 (attB2), SEQ ID NO: 33 (attB3), or SEQ ID NO: 34 (attB4), or an active variant or fragment thereof.

The recombination site 3' to the polynucleotide of interest can be 5' or 3' to the termination region when present. The recombination site can be contiguous with the polynucleotide of interest and/or the termination sequence, if present. In some embodiments, however, a linker sequence separates the polynucleotide of interest and the recombination site. The length of this linker sequence can vary, but in some
5 embodiments, is about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 nucleotides in length. In particular embodiments, the linker sequence separating the recombination site and the polynucleotide of interest is about 16 nucleotides. In certain embodiments, the recombination site and the
10 polynucleotide of interest are separated by a linker sequence having the nucleotide sequence set forth in SEQ ID NO: 39, or a variant or fragment thereof. In other embodiments, the linker sequence separating the recombination site and the polynucleotide of interest is about 8 nucleotides. In certain embodiments, the recombination site and the polynucleotide of interest are separated by a linker sequence
15 having the nucleotide sequence set forth in SEQ ID NO: 124, or a variant or fragment thereof.

In some of those embodiments wherein a termination region is present on the expression cassette and the expression cassette further comprises a recombination site 3' to the polynucleotide of interest, the termination region is 3' to the recombination site and a
20 linker sequence separates the recombination site and the termination region. The length of this linker sequence can vary, but in some embodiments, is about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, or 90 nucleotides in length. In particular embodiments, the linker sequence separating the recombination site and the termination region is about 14 nucleotides. In certain
25 embodiments, the recombination site and the termination region are separated by a linker sequence having the nucleotide sequence set forth in SEQ ID NO: 40 or a variant or fragment thereof.

The expression cassettes comprise a presently disclosed promoter construct regulating the expression of a polynucleotide of interest. The polynucleotide of interest
30 may be any polynucleotide that encodes a polynucleotide (*e.g.*, antisense, siRNA) or encodes a polypeptide. Where appropriate, the polynucleotide(s) of interest may be optimized for increased expression in the transformed plant. That is, the polynucleotides can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-

preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 5,380,831, and 5,436,391, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

In some embodiments, the polynucleotide of interest comprises a polynucleotide that encodes a site-specific recombinase. A site-specific recombinase, also referred to herein as a recombinase, is a polypeptide that catalyzes conservative site-specific recombination between its compatible recombination sites, and includes native polypeptides as well as derivatives, variants and/or fragments that retain activity, and native polynucleotides, derivatives, variants, and/or fragments that encode a recombinase that retains activity. The recombinase used in the methods and compositions can be a native recombinase or a biologically active fragment or variant of the recombinase. For reviews of site-specific recombinases and their recognition sites, see Sauer (1994) *Curr Op Biotechnol* 5:521-527; and Sadowski (1993) *FASEB* 7:760-767, each of which is herein incorporated by reference in its entirety.

Any recombinase system can be used in the methods and compositions. Non-limiting examples of site-specific recombinases include FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, U153, and other site-specific recombinases known in the art, including those described in Thomson and Ow (2006) *Genesis* 44:465-476, which is herein incorporated by reference in its entirety. Examples of site-specific recombination systems used in plants can be found in U.S. Patent Nos. 5,929,301, 6,175,056, 6,331,661; and International Application Publication Nos. WO 99/25821, WO 99/25855, WO 99/25841, and WO 99/25840, the contents of each are herein incorporated by reference.

In some embodiments, the polynucleotide of interest encodes a recombinase from the Integrase or Resolvase families, including biologically active variants and fragments thereof. The Integrase family of recombinases has over one hundred members and includes, for example, FLP, Cre, lambda integrase, and R. For other members of the

Integrase family, see, for example, Esposito *et al.* (1997) *Nucleic Acids Res* 25:3605-3614; and Abremski *et al.* (1992) *Protein Eng* 5:87-91; each of which are herein incorporated by reference in its entirety. Other recombination systems include, for example, the *Streptomyces* bacteriophage phi C31 (Kuhstoss *et al.* (1991) *J Mol Biol* 20:897-908); the SSV1 site-specific recombination system from *Sulfolobus shibatae* (Maskhelishvili *et al.* (1993) *Mol Gen Genet* 237:334-342); and a retroviral integrase-based integration system (Tanaka *et al.* (1998) *Gene* 17:67-76). In some embodiments, the recombinase does not require cofactors or a supercoiled substrate. Such recombinases include Cre, FLP, or active variants or fragments thereof.

10 The FLP recombinase is a protein that catalyzes a site-specific reaction that is involved in amplifying the copy number of the two-micron plasmid of *S. cerevisiae* during DNA replication. FLP recombinase catalyzes site-specific recombination between two FRT sites. The FLP protein has been cloned and expressed (Cox (1993) *Proc Natl Acad Sci USA* 80:4223-4227, which is herein incorporated by reference in its entirety). The FLP recombinase for use in the methods and compositions may be derived from the genus *Saccharomyces*. In some embodiments, a recombinase polynucleotide modified to comprise more plant-preferred codons is used. A recombinant FLP enzyme encoded by a nucleotide sequence comprising maize preferred codons (FLPm) that catalyzes site-specific recombination events is known (the polynucleotide and polypeptide sequence of which is set forth in SEQ ID NO: 41 and 42, respectively; see, *e.g.*, US Patent 5,929,301, which is herein incorporated by reference in its entirety). Additional functional variants and fragments of FLP are known (Buchholz *et al.* (1998) *Nat Biotechnol* 16:657-662; Hartung *et al.* (1998) *J Biol Chem* 273:22884-22891; Saxena *et al.* (1997) *Biochim Biophys Acta* 1340:187-204; Hartley *et al.* (1980) *Nature* 286:860-864; Voznyanov *et al.* (2002) *Nucleic Acids Res* 30:1656-1663; Zhu & Sadowski (1995) *J Biol Chem* 270:23044-23054; and U.S. Patent No. 7,238,854, each of which is herein incorporated by reference in its entirety).

25 The bacteriophage recombinase Cre catalyzes site-specific recombination between two *lox* sites. The Cre recombinase is known (Guo *et al.* (1997) *Nature* 389:40-46; Abremski *et al.* (1984) *J Biol Chem* 259:1509-1514; Chen *et al.* (1996) *Somat Cell Mol Genet* 22:477-488; Shaikh *et al.* (1977) *J Biol Chem* 272:5695-5702; and, Buchholz *et al.* (1998) *Nat Biotechnol* 16:657-662, each of which is herein incorporated by reference in its entirety). Cre polynucleotide sequences may also be synthesized using plant-preferred codons, for example such sequences (moCre; the polynucleotide and polypeptide sequence

of which is set forth in SEQ ID NO: 43 and 44, respectively) are described, for example, in International Application Publication No. WO 99/25840, which is herein incorporated by reference in its entirety. Variants of the Cre recombinase are known (see, for example U.S. Patent No. 6,890,726; Rufer & Sauer (2002) *Nucleic Acids Res* 30:2764-2772;

5 Wierzbicki *et al.* (1987) *J Mol Biol* 195:785-794; Petyuk *et al.* (2004) *J Biol Chem* 279:37040-37048; Hartung & Kisters-Woike (1998) *J Biol Chem* 273:22884-22891; Santoro & Schultz (2002) *Proc Natl Acad Sci USA* 99:4185-4190; Korcsawa *et al.* (2000) *J Biochem* (Tokyo) 127:367-372; and Vergunst *et al.* (2000) *Science* 290:979-982, each of which are herein incorporated by reference in its entirety).

10 In some embodiments, the polynucleotide of interest encodes a chimeric recombinase. A chimeric recombinase is a recombinant fusion protein which is capable of catalyzing site-specific recombination between recombination sites that originate from different recombination systems. For example, if the set of recombination sites comprises a FRT site and a LoxP site, a chimeric FLP/Cre recombinase or active variant or fragment
15 thereof can be used, or both recombinases may be separately provided. Methods for the production and use of such chimeric recombinases or active variants or fragments thereof are described, for example, in International Application Publication No. WO 99/25840; and Shaikh & Sadowski (2000) *J Mol Biol* 302:27-48, each of which are herein incorporated by reference in its entirety.

20 In other embodiments, a variant recombinase is used. Methods for modifying the kinetics, cofactor interaction and requirements, expression, optimal conditions, and/or recognition site specificity, and screening for activity of recombinases and variants are known, see for example Miller *et al.* (1980) *Cell* 20:721-9; Lange-Gustafson and Nash (1984) *J Biol Chem* 259:12724-32; Christ *et al.* (1998) *J Mol Biol* 288:825-36; Lorbach *et al.* (2000) *J Mol Biol* 296:1175-81; Vergunst *et al.* (2000) *Science* 290:979-82; Dorgai *et al.* (1995) *J Mol Biol* 252:178-88; Dorgai *et al.* (1998) *J Mol Biol* 277:1059-70; Yagu *et al.* (1995) *J Mol Biol* 252:163-7; Scimiente *et al.* (2001) *Nucleic Acids Res* 29:5044-51; Santoro and Schultze (2002) *Proc Natl Acad Sci USA* 99:4185-90; Buchholz and Stewart (2001) *Nat Biotechnol* 19:1047-52; Voziyanov *et al.* (2002) *Nucleic Acids Res* 30:1656-
25 63; Voziyanov *et al.* (2003) *J Mol Biol* 326:65-76; Klippel *et al.* (1988) *EMBO J* 7:3983-9; Arnold *et al.* (1999) *EMBO J* 18:1407-14; and International Application Publication Nos. WO 03/08045, WO 99/25840, and WO 99/25841; each of which is herein incorporated by reference in its entirety.

In particular embodiments, the expression cassette has the sequence set forth in SEQ ID NO: 45 or a variant or fragment thereof.

The expression cassette can be part of a vector that comprises multiple expression cassettes or multiple genes, such as a selectable marker gene. Selectable marker genes may
 5 be used to identify transformed cells or tissues. Marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D). See generally, Yarranton (1992) *Curr. Opin. Biotech.*
 10 3:506-511; Christopherson *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:6314-6318; Yao *et al.* (1992) *Cell* 71:63-72; Reznikoff (1992) *Mol. Microbiol.* 6:2419-2422; Barkley *et al.* (1980) in *The Operon*, pp. 177-220; Hu *et al.* (1987) *Cell* 48:555-566; Brown *et al.* (1987) *Cell* 49:603-612; Figge *et al.* (1988) *Cell* 52:713-722; Deuschle *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:5400-5404; Fuerst *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:2549-2553;
 15 Deuschle *et al.* (1990) *Science* 248:480-483; Gossen (1993) Ph.D. Thesis, University of Heidelberg; Reines *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:1917-1921; Labow *et al.* (1990) *Mol. Cell. Biol.* 10:3343-3356; Zambretti *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:3952-3956; Baim *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88:5072-5076; Wyborski *et al.* (1991) *Nucleic Acids Res.* 19:4647-4653; Hillenand-Wissman (1989) *Topics Mol. Struc. Biol.*
 20 10:143-162; Degenkolb *et al.* (1991) *Antimicrob. Agents Chemother.* 35:1591-1595; Kleinschmidt *et al.* (1988) *Biochemistry* 27:1094-1104; Bonin (1993) Ph.D. Thesis, University of Heidelberg; Gossen *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Oliva *et al.* (1992) *Antimicrob. Agents Chemother.* 36:913-919; Hlavka *et al.* (1985) *Handbook of Experimental Pharmacology*, Vol. 78 (Springer-Verlag, Berlin); Gill *et al.*
 25 (1988) *Nature* 334:721-724. Such disclosures are herein incorporated by reference. The above list of selectable marker genes is not meant to be limiting. Any selectable marker gene can be used.

In some embodiments, an expression cassette comprising a presently disclosed promoter construct can further comprise a polynucleotide encoding a cell proliferation
 30 factor. As used herein, a "cell proliferation factor" is a polypeptide or a polynucleotide capable of stimulating growth of a cell or tissue, including but not limited to promoting progression through the cell cycle, inhibiting cell death, such as apoptosis, stimulating cell division, and/or stimulating embryogenesis. The polynucleotides can fall into several categories, including but not limited to, cell cycle stimulatory polynucleotides,

developmental polynucleotides, anti-apoptosis polynucleotides, hormone polynucleotides, or silencing constructs targeted against cell cycle repressors or pro-apoptotic factors. The following are provided as non-limiting examples of each category and are not considered a complete list of useful polynucleotides for each category: 1) cell cycle stimulatory

5 polynucleotides including plant viral replicase genes such as RepA, cyclins, E2F, proliferin, cdc2 and cdc25; 2) developmental polynucleotides such as Lec1, Kn1 family, WUSCHEL, Zwillig, BBM, Aintegumenta (ANT), FUS3, and members of the Knotted family, such as Kn1, STM, OSH1, and SbH1; 3) anti-apoptosis polynucleotides such as CED9, Bcl2, Bcl-X(L), Bcl-W, A1, Mcl-1, Mac1, Bcl-2, and Bax-inhibitors; 4) hormone

10 polynucleotides such as IPT, TZS, and CKI-1; and 5) silencing constructs targeted against cell cycle repressors, such as Rb, CKI, prohibitin, and weel, or stimulators of apoptosis such as APAF-1, bad, bax, CED-4, and caspase-3, and repressors of plant developmental transitions, such as Pickle and WD polycomb genes including FIE and Medea. The polynucleotides can be silenced by any known method such as antisense, RNA

15 interference, cosuppression, chimera, or transposon insertion.

The cell proliferation factors can be introduced into cells through the introduction of a polynucleotide that encodes the proliferation factor. The use of the term "polynucleotide" is not intended to limit compositions to polynucleotides comprising DNA. Polynucleotides can comprise ribonucleotides and combinations of ribonucleotides

20 and deoxyribonucleotides. Such deoxyribonucleotides and ribonucleotides include both naturally occurring molecules and synthetic analogues. The polynucleotides also encompass all forms of sequences including, but not limited to, single-, double-, or multi-stranded forms, hairpins, stem-and-loop structures, circular plasmids, and the like. The polynucleotide encoding the cell proliferation factor may be native to the cell or

25 heterologous. A native polypeptide or polynucleotide comprises a naturally occurring amino acid sequence or nucleotide sequence. "Heterologous" in reference to a polypeptide or a nucleotide sequence is a polypeptide or a sequence that originates from a different species, or if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention.

30 An "isolated" or "purified" polynucleotide or protein, or biologically active portion thereof, is substantially or essentially free from components that normally accompany or interact with the polynucleotide or protein as found in its naturally occurring environment. Thus, an isolated or purified polynucleotide or protein is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially

free of chemical precursors or other chemicals when chemically synthesized. Optimally, an "isolated" polynucleotide is free of sequences (optimally protein encoding sequences) that naturally flank the polynucleotide (*i.e.*, sequences located at the 5' and 3' ends of the polynucleotide) in the genomic DNA of the organism from which the polynucleotide is derived. For example, in various embodiments, the isolated polynucleotide can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequence that naturally flank the polynucleotide in genomic DNA of the cell from which the polynucleotide is derived. A protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of contaminating protein. When the protein or biologically active portion thereof is recombinantly produced, optimally culture medium represents less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of chemical precursors or non-protein-of-interest chemicals.

Any of a number of cell proliferation factors can be used. In certain embodiments, those cell proliferation factors that are capable of stimulating embryogenesis are used to enhance targeted polynucleotide modification. Such cell proliferation factors are referred to herein as embryogenesis-stimulating polypeptides and they include, but are not limited to, babyboom polypeptides.

In some embodiments, the cell proliferation factor is a member of the AP2/ERF family of proteins. The AP2/ERF family of proteins is a plant-specific class of putative transcription factors that regulate a wide variety of developmental processes and are characterized by the presence of an AP2 DNA binding domain that is predicted to form an amphipathic alpha helix that binds DNA (PFAM Accession PF00847). The AP2 domain was first identified in APETALA2, an *Arabidopsis* protein that regulates meristem identity, floral organ specification, seed coat development, and floral homeotic gene expression. The AP2/ERF proteins have been subdivided into distinct subfamilies based on the presence of conserved domains. Initially, the family was divided into two subfamilies based on the number of DNA binding domains, with the ERF subfamily having one DNA binding domain, and the AP2 subfamily having 2 DNA binding domains. As more sequences were identified, the family was subsequently subdivided into five subfamilies: AP2, DREB, ERF, RAV, and others. (Sakuma *et al.* (2002) *Biochem Biophys Res Comm* 290:998-1009).

Members of the APETALA2 (AP2) family of proteins function in a variety of biological events, including but not limited to, development, plant regeneration, cell

division, embryogenesis, and cell proliferation (see, *e.g.*, Riechmann and Meyerowitz (1998) *Biol Chem* 379:633-646; Saleh and Pagés (2003) *Genetika* 35:37-50 and Database of Arabidopsis Transcription Factors at daft.cbi.pku.edu.cn). The AP2 family includes, but is not limited to, AP2, ANT, Glossy15, AtBBM, BnBBM, and maize ODP2/BBM.

5 Provided herein is an analysis of fifty sequences with homology to a maize BBM sequence (also referred to as maize ODP2 or ZmODP2, the polynucleotide and amino acid sequence of the maize BBM is set forth in SEQ ID NO: 9 and 10, respectively; the polynucleotide and amino acid sequence of another ZmBBM is set forth in SEQ ID NO: 121 and 122, respectively). The analysis identified three motifs (motifs 4-6; set forth in
10 SEQ ID NOs: 51-53), along with the AP2 domains (motifs 2 and 3; SEQ ID NOs: 49 and 50) and linker sequence that bridges the AP2 domains (motif 1; SEQ ID NO: 48), that are found in all of the BBM homologues. Thus, motifs 1-6 distinguish these BBM homologues from other AP2-domain containing proteins (*e.g.*, WRI, AP2, and RAP2.7) and these BBM homologues comprise a subgroup of AP2 family of proteins referred to
15 herein as the BBM/PLT subgroup. In some embodiments, the cell proliferation factor that is used in the methods and compositions is a member of the BBM/PLT group of AP2 domain-containing polypeptides. In these embodiments, the cell proliferation factor comprises two AP2 domains and motifs 4-6 (SEQ ID NOs: 51-53) or a fragment or variant thereof. In some of these embodiments, the AP2 domains have the sequence set forth in
20 SEQ ID NOs: 49 and 50 or a fragment or variant thereof, and in particular embodiments, further comprises the linker sequence of SEQ ID NO: 48 or a fragment or variant thereof. In other embodiments, the cell proliferation factor comprises at least one of motifs 4-6 or a fragment or variant thereof, along with two AP2 domains, which in some embodiments have the sequence set forth in SEQ ID NO: 49 and/or 50 or a fragment or variant thereof,
25 and in particular embodiments have the linker sequence of SEQ ID NO: 48 or a fragment or variant thereof. Based on the phylogenetic analysis provided herein, the subgroup of BBM/PLT polypeptides can be subdivided into the BBM, AIL6/7, PLT1/2, AIL1, PLT3, and ANT groups of polypeptides.

30 In some embodiments, the cell proliferation factor is a babyboom (BBM) polypeptide, which is a member of the AP2 family of transcription factors. The BBM protein from *Arabidopsis* (AtBBM) is preferentially expressed in the developing embryo and seeds and has been shown to play a central role in regulating embryo-specific pathways. Overexpression of AtBBM has been shown to induce spontaneous formation of somatic embryos and cotyledon-like structures on seedlings. See, Boutilier *et al.* (2002)

The Plant Cell 14:1737-1749. The maize BBM protein also induces embryogenesis and promotes transformation (See, U.S. Patent No. 7,579,529, which is herein incorporated by reference in its entirety). Thus, BBM polypeptides stimulate proliferation, induce embryogenesis, enhance the regenerative capacity of a plant, enhance transformation, and as demonstrated herein, enhance rates of targeted polynucleotide modification. As used herein "regeneration" refers to a morphogenic response that results in the production of new tissues, organs, embryos, whole plants or parts of whole plants that are derived from a single cell or a group of cells. Regeneration may proceed indirectly via a callus phase or directly, without an intervening callus phase. "Regenerative capacity" refers to the ability of a plant cell to undergo regeneration.

In some embodiments, the babyboom polypeptide comprises two AP2 domains and at least one of motifs 7 and 10 (set forth in SEQ ID NO: 54 and 57, respectively) or a variant or fragment thereof. In certain embodiments, the AP2 domains are motifs 3 and 2 (SEQ ID NOs: 50 and 49, respectively) or a fragment or variant thereof, and in particular embodiments, the babyboom polypeptide further comprises a linker sequence between AP2 domain 1 and 2 having motif 1 (SEQ ID NO: 48) or a fragment or variant thereof. In particular embodiments, the BBM polypeptide further comprises motifs 4-6 (SEQ ID NOs 51-53) or a fragment or variant thereof. The BBM polypeptide can further comprise motifs 8 and 9 (SEQ ID NOs: 55 and 56, respectively) or a fragment or variant thereof, and in some embodiments, motif 10 (SEQ ID NO: 57) or a variant or fragment thereof. In some of these embodiments, the BBM polypeptide also comprises at least one of motif 14 (set forth in SEQ ID NO: 58), motif 15 (set forth in SEQ ID NO: 59), and motif 19 (set forth in SEQ ID NO: 60), or variants or fragments thereof. The variant of a particular amino acid motif can be an amino acid sequence having at least about 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity with the motif disclosed herein. Alternatively, variants of a particular amino acid motif can be an amino acid sequence that differs from the amino acid motif by 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids.

Non-limiting examples of babyboom polynucleotides and polypeptides that can be used in the methods and compositions include the *Arabidopsis thaliana* AtBBM (SEQ ID NOs: 21 and 22), *Brassica napus* BnBBM1 (SEQ ID NOs: 23 and 24), *Brassica napus* BnBBM2 (SEQ ID NOs: 25 and 26), *Medicago truncatula* MtBBM (SEQ ID NOs: 7 and 8), *Glycine max* GmBBM (SEQ ID NOs: 1 and 2), *Vitis vinifera* VvBBM (SEQ ID NOs: 5 and 6), *Zea mays* ZmBBM (SEQ ID NOs: 9 and 10 and genomic sequence set forth in

SEQ ID NO: 68; or SEQ ID NOs: 121 and 122 and genomic sequence set forth in SEQ ID NO: 116) and ZmBBM2 (SEQ ID NOs: 11 and 12), *Oryza sativa* OsBBM (polynucleotide sequences set forth in SEQ ID NOs: 13 and 120; amino acid sequence set forth in SEQ ID NO: 14; and genomic sequence set forth in SEQ ID NO: 117), OsBBM1 (SEQ ID NOs: 15 and 16), OsBBM2 (SEQ ID NOs: 17 and 18), and OsBBM3 (SEQ ID NOs: 19 and 20), *Sorghum bicolor* SbBBM (SEQ ID NOs: 3 and 4 and genomic sequence set forth in SEQ ID NO: 69) and SbBBM2 (SEQ ID NOs: 27 and 28) or active fragments or variants thereof. In particular embodiments, the cell proliferation factor is a maize BBM polypeptide (SEQ ID NO: 10, 122, or 12) or a variant or fragment thereof, or is encoded by a maize BBM polynucleotide (SEQ ID NO: 9, 68, 121, 116, or 11) or a variant or fragment thereof.

Thus, in some embodiments, a polynucleotide encoding a cell proliferation factor has a nucleotide sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69 or the cell proliferation factor has an amino acid sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28. In some of these embodiments, the cell proliferation factor has at least one of motifs 7 and 10 (SEQ ID NO: 54 and 57, respectively) or a variant or fragment thereof at the corresponding amino acid residue positions in the babyboom polypeptide. In other embodiments, the cell proliferation factor further comprises at least one of motif 14 (set forth in SEQ ID NO: 58), motif 15 (set forth in SEQ ID NO: 59), and motif 19 (set forth in SEQ ID NO: 60) or a variant or fragment thereof at the corresponding amino acid residue positions in the babyboom polypeptide.

In other embodiments, other cell proliferation factors, such as, Lec1, Kn1 family, WUSCHEL (*e.g.*, WUS1, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 61 and 62; WUS2, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 63 and 64; WUS2 alt, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 114 and 115; WUS3, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 105 and 106), Zwille, and Aintegumeta (ANT), may be used alone, or in combination with a babyboom polypeptide or other cell proliferation factor. See, for example, U.S. Application Publication No.

2003/0135889, International Application Publication No. WO 03/001902, and U.S. Patent No. 6,512,165, each of which is herein incorporated by reference. When multiple cell proliferation factors are used, or when a babyboom polypeptide is used along with any of the abovementioned polypeptides, the polynucleotides encoding each of the factors can be present on the same expression cassette or on separate expression cassettes. When two or more factors are coded for by separate expression cassettes, the expression cassettes can be provided to the plant simultaneously or sequentially.

In some embodiments, polynucleotides or polypeptides having homology to a known babyboom polynucleotide or polypeptide and/or sharing conserved functional domains can be identified by screening sequence databases using programs such as BLAST. The databases can be queried using full length sequences, or with fragments including, but not limited to, conserved domains or motifs. In some embodiments, the sequences retrieved from the search can be further characterized by alignment programs to quickly identify and compare conserved functional domains, regions of highest homology, and nucleotide and/or amino differences between sequences, including insertions, deletions, or substitutions, including those programs described in more detail elsewhere herein. The retrieved sequences can also be evaluated using a computer program to analyze and output the phylogenetic relationship between the sequences.

In other embodiments, polynucleotides or polypeptides having homology to a known babyboom polynucleotide or polypeptide or one that has been disclosed herein and/or sharing conserved functional domains can be identified using standard nucleic acid hybridization techniques, such as those described in more detail elsewhere herein. Extensive guides on nucleic acid hybridization include Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes, Part I, Chapter 2 (Elsevier, NY); Ausubel *et al.*, eds. (1995) Current Protocols in Molecular Biology, Chapter 2 (Greene Publishing and Wiley-Interscience, NY); and, Sambrook *et al.* (1989) Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Plainview, NY).

Compositions further comprise isolated BBM polynucleotides and isolated BBM polypeptides and variants and fragments thereof, expression cassettes comprising the same, and plants comprising the same. Compositions can comprise isolated polynucleotides encoding GmBBM (SEQ ID NO: 1), SbBBM (SEQ ID NO: 3), MtBBM (SEQ ID NO: 7), or OsBBM2 (SEQ ID NO: 17) or an active variant or fragment thereof. Isolated polypeptides include those having SEQ ID NO: 2, 4, 8, or 18 (GmBBM, SbBBM,

MtBBM, or OsBBM2, respectively) or an active variant or fragment thereof. The percent identity of the novel BBM polypeptide sequences with those known in the art is presented in Table 1.

Table 1. The percent sequence identity between each of 14 babyboom polypeptides.

	Zm BBM2	Sb BBM2	Os BBM2	Os BBM3	Os BBM1	Zm BBM	Sb BBM	Os BBM	Bn BBM1	Bn BBM2	At BBM	Mt BBM	Gm BBM	Vv BBM
ZmBBM2	100													
SbBBM2	92	100												
OsBBM2	79	77	100											
OsBBM3	64	66	67	100										
OsBBM1	50	46	46	46	100									
ZmBBM	43	44	44	47	47	100								
SbBBM	43	44	42	45	44	90	100							
OsBBM	44	44	45	46	49	69	70	100						
BnBBM1	42	41	42	41	40	45	42	43	100					
BnBBM2	43	41	42	41	39	46	44	44	97	100				
AtBBM	43	41	39	42	41	43	43	42	81	82	100			
MtBBM	41	40	40	41	43	42	43	41	47	47	47	100		
GmBBM	45	44	42	45	44	41	42	44	46	46	43	68	100	
VvBBM	51	48	50	48	50	48	47	48	49	49	48	58	62	100

By "fragment" is intended a portion of the polynucleotide or a portion of an amino acid sequence and hence protein encoded thereby. Fragments of a polynucleotide may retain the biological activity of the native polynucleotide and, for example, have promoter activity (*i.e.*, capable of initiating transcription), or are capable of stimulating proliferation, inducing embryogenesis, or modifying the regenerative capacity of a plant. In those
5 embodiments wherein the polynucleotide encodes a polypeptide, fragments of the polynucleotide may encode protein fragments that retain the biological activity of the native protein. Alternatively, fragments of a polynucleotide that are useful as hybridization probes generally do not retain biological activity or encode fragment
10 proteins that retain biological activity. Thus, fragments of a nucleotide sequence may range from at least about 20, 50, 100, 150, 200, 250, 300, 400, 500 nucleotides, or greater.

A fragment of a polynucleotide that encodes a biologically active portion of a cell proliferation factor, for example, will encode at least 15, 25, 30, 50, 100, 150, 200, 250, 300, 400, 500 contiguous amino acids, or up to the total number of amino acids present in
15 the full-length cell proliferation factor. Fragments of a cell proliferation factor polynucleotide that are useful as hybridization probes or PCR primers generally need not encode a biologically active portion of a cell proliferation factor.

"Variants" is intended to mean substantially similar sequences. For polynucleotides, a variant comprises a polynucleotide having deletions at the 5' and/or 3'
20 end; deletion and/or addition of one or more nucleotides at one or more internal sites in the native polynucleotide; and/or substitution of one or more nucleotides at one or more sites in the native polynucleotide. As used herein, a "native" polynucleotide or polypeptide comprises a naturally occurring nucleotide sequence or amino acid sequence, respectively. For polynucleotides encoding polypeptides conservative variants include those sequences
25 that, because of the degeneracy of the genetic code, encode the amino acid sequence the polypeptide (*e.g.*, cell proliferation factor). Naturally occurring variants such as these can be identified with the use of well-known molecular biology techniques, such as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant polynucleotides also include synthetically derived polynucleotides, such as those
30 generated, for example, by using site-directed mutagenesis. Generally, variants of a particular will have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular polynucleotide as determined by sequence alignment programs and parameters.

Variants of a particular polynucleotide that encodes a polypeptide can also be evaluated by comparison of the percent sequence identity between the polypeptide encoded by a variant polynucleotide and the polypeptide encoded by the particular polynucleotide. Percent sequence identity between any two polypeptides can be

5 calculated using sequence alignment programs and parameters. Where any given pair of polynucleotides is evaluated by comparison of the percent sequence identity shared by the two polypeptides they encode, the percent sequence identity between the two encoded polypeptides is at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity.

10 "Variant" protein is intended to mean a protein derived from the native protein by deletion of one or more amino acids at the N-terminal and/or C-terminal end of the native protein; deletion and/or addition of one or more amino acids at one or more internal sites in the native protein; and/or substitution of one or more amino acids at one or more sites in the native protein. Variant proteins retain the desired biological activity of the native

15 protein. For example, variant cell proliferation factors stimulate proliferation and variant babyboom polypeptides are capable of stimulating proliferation, inducing embryogenesis, modifying the regenerative capacity of a plant, increasing the transformation efficiency in a plant, increasing or maintaining the yield in a plant under abiotic stress, producing asexually derived embryos in a plant, and/or enhancing rates of targeted polynucleotide

20 modification. Such variants may result from, for example, genetic polymorphism or from human manipulation. Biologically active variants of a native cell proliferation factor will have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence for the native protein as determined by sequence alignment programs and

25 parameters. A biologically active variant of a cell proliferation factor protein may differ from that protein by as few as 1-15 amino acid residues, as few as 1-10, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

In some embodiments, variants or fragments of the BBM polypeptide have amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 311,

30 312, and 313, respectively, of SEQ ID NO: 4 or variants or fragments of the BBM polynucleotide encodes a polypeptide having amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 311, 312, and 313, respectively, of SEQ ID NO: 4. In certain embodiments, variants or fragments of the BBM polypeptide have

amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 337, 338, and 339, respectively, of SEQ ID NO: 18 or variants or fragments of the BBM polynucleotide encodes a polypeptide having amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 337, 338, and 339, respectively, of SEQ ID NO: 18. In other embodiments, variants or fragments of the BBM polypeptide have amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8 or variants or fragments of the BBM polynucleotide encodes a polypeptide having amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively of SEQ ID NO: 8.

The babyboom polynucleotides and polypeptides can be introduced into a plant or plant cell in order to stimulate embryogenesis, modify the regenerative capacity of the plant, increase the transformation efficiency of the plant, increase or maintain the yield in the plant under abiotic stress, and/or to enhance targeted polynucleotide modification. The babyboom polynucleotide or polypeptide can be provided to a plant simultaneously with or prior to the introduction of a polynucleotide of interest in order to facilitate transformation of the plant with the polynucleotide of interest. Further, a haploid plant cell can be provided a novel babyboom polynucleotide or polypeptide to produce a haploid plant embryo (see U.S. Patent No. 7,579,529, which is herein incorporated by reference in its entirety).

The cell proliferation factor polynucleotide can be operably linked to a promoter active in a plant. Various promoters can be used for the regulation of the expression of the cell proliferation factor. The promoter may be selected based on the desired outcome or expression pattern (for a review of plant promoters, see Potenza *et al.* (2004) *In Vitro Cell Dev Biol* 40:1-22).

Constitutive promoters include, for example, the core promoter of the Rsyn7 promoter and other constitutive promoters disclosed in WO 99/43838 and U.S. Patent No. 6,072,050; the core CaMV 35S promoter (Odell *et al.* (1985) *Nature* 313:810-812); rice actin (McElroy *et al.* (1990) *Plant Cell* 2:163-171); ubiquitin (Christensen *et al.* (1989) *Plant Mol. Biol.* 12:619-632 and Christensen *et al.* (1992) *Plant Mol. Biol.* 18:675-689); pEMU (Last *et al.* (1991) *Theor. Appl. Genet.* 81:581-588); MAS (Velten *et al.* (1984) *EMBO J.* 3:2723-2730); ALS promoter (U.S. Patent No. 5,659,026), the *Agrobacterium* nopaline synthase (NOS) promoter (Bevan *et al.* (1983) *Nucl. Acids Res.* 11:369-385), and

the like. Other constitutive promoters are described in, for example, U.S. Patent Nos. 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,611.

In some embodiments, an inducible promoter can be used, such as from a
 5 pathogen-inducible promoter. Such promoters include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; *e.g.*, PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, etc. See, for example, Redolfi *et al.* (1983) *Neth. J. Plant Pathol.* 89:245-254; Uknes *et al.* (1992) *Plant Cell* 4:645-656; and Van Loon (1985) *Plant Mol. Virol.* 4:111-116. See also WO 99/43819, herein
 10 incorporated by reference. Promoters that are expressed locally at or near the site of pathogen infection include, for example, Marineau *et al.* (1987) *Plant Mol. Biol.* 9:335-342; Matton *et al.* (1989) *Mol Plant-Microbe Interact* 2:325-331; Somsisch *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:2427-2430; Somsisch *et al.* (1988) *Mol. Gen. Genet.* 2:93-98; and Yang (1996) *Proc. Natl. Acad. Sci. USA* 93:14972-14977. See also, Chen *et al.*
 15 (1996) *Plant J.* 10:955-966; Zhang *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:2507-2511; Warner *et al.* (1993) *Plant J.* 3:191-201; Siebertz *et al.* (1989) *Plant Cell* 1:961-968; U.S. Patent No. 5,750,386 (nematode-inducible); and the references cited therein. Additional promoters include the inducible promoter for the maize PRms gene, whose expression is induced by the pathogen *Fusarium moniliforme* (see, for example, Cordero *et al.* (1992)
 20 *Physiol. Mol. Plant Pathol.* 41:189-200). Wound-inducible promoters include potato proteinase inhibitor (pin II) gene (Ryan (1990) *Ann. Rev. Phytopath.* 28:425-449; Duan *et al.* (1996) *Nat Biotechnol* 14:494-498); *wun1* and *wun2*, U.S. Patent No. 5,428,148; *win1* and *win2* (Stanford *et al.* (1989) *Mol. Gen. Genet.* 215:200-208); *systemin* (McGurl *et al.* (1992) *Science* 225:1570-1573); *WIP1* (Rohmeier *et al.* (1993) *Plant Mol. Biol.* 22:783-
 25 792; Eckelkamp *et al.* (1993) *FEBS Lett* 323:73-76); *MPI* gene (Corderok *et al.* (1994) *Plant J.* 6:141-150); and the like, herein incorporated by reference. Another inducible promoter is the maize *In2-2* promoter (deVeylder *et al.* (2007) *Plant Cell Physiol* 38:568-577, herein incorporated by reference).

Chemical-regulated promoters can be used to modulate the expression of a gene in
 30 a plant through the application of an exogenous chemical regulator. The promoter may be a chemical-inducible promoter, where application of the chemical induces gene expression, or a chemical-repressible promoter, where application of the chemical represses gene expression. Chemical-inducible promoters are known in the art and include, but are not limited to, the maize *In2-2* promoter, which is activated by

benzenesulfonamide herbicide safeners (De Veylder *et al.* (1997) *Plant Cell Physiol.* 38:568-77), the maize GST promoter (GST-II-27, WO 93/01294), which is activated by hydrophobic electrophilic compounds that are used as pre-emergent herbicides, the PR-1 promoter (Cao *et al.* (2006) *Plant Cell Reports* 6:554-60), which is activated by BTH or
 5 benzo(1,2,3)thiadiazole-7-carbothioic acid s-methyl ester, the tobacco PR-1a promoter (Ono *et al.* (2004) *Biosci. Biotechnol. Biochem.* 68:803-7), which is activated by salicylic acid, the copper inducible ACE1 promoter (Mett *et al.* (1993) *PNAS* 90:4567-4571), the ethanol-inducible promoter AlcA (Caddick *et al.* (1988) *Nature Biotechnol* 16:177-80), an estradiol-inducible promoter (Bruce *et al.* (2000) *Plant Cell* 12:65-79), the XVE estradiol-
 10 inducible promoter (Zao *et al.* (2000) *Plant J* 24:265-273), the VGE methoxyfenozide inducible promoter (Padidam *et al.* (2003) *Transgenic Res* 12:101-109), and the TGV dexamethasone-inducible promoter (Bohner *et al.* (1999) *Plant J* 19:87-95). Other chemical-regulated promoters of interest include steroid-responsive promoters (see, for example, the glucocorticoid-inducible promoter in Schena *et al.* (1991) *Proc. Natl. Acad.*
 15 *Sci. USA* 88:10421-10425 and McNellis *et al.* (1998) *Plant J.* 14(2):247-257) and tetracycline-inducible and tetracycline-repressible promoters (see, for example, Gatz *et al.* (1991) *Mol. Gen. Genet.* 227:229-237; Gatz *et al.* (1992) *Plant J* 2:397-404; and U.S. Patent Nos. 5,814,618 and 5,789,156), herein incorporated by reference.

Tissue-preferred promoters can be utilized to target enhanced expression of a
 20 sequence of interest within a particular plant tissue. Tissue-preferred promoters include Kawamata *et al.* (1997) *Plant Cell Physiol.* 38(7):792-803; Hansen *et al.* (1997) *Mol. Gen Genet.* 254(3):337-343; Russell *et al.* (1997) *Transgenic Res.* 6(2):157-168; Rinehart *et al.* (1996) *Plant Physiol.* 112(3):1331-1341; Van Camp *et al.* (1996) *Plant Physiol.* 112(2):525-535; Canevascini *et al.* (1996) *Plant Physiol.* 112(2):513-524; Lam (1994)
 25 *Results Probl. Cell Differ.* 20:181-196; and Guevara-Garcia *et al.* (1993) *Plant J.* 4(3):495-505.

Leaf-preferred promoters are known in the art. See, for example, Yamamoto *et al.* (1997) *Plant J.* 12:255-265; Kwon *et al.* (1994) *Plant Physiol.* 105:357-67; Yamamoto *et al.* (1994) *Plant Cell Physiol.* 35:773-778; Gotor *et al.* (1993) *Plant J.* 3:509-18; Orozco *et al.* (1993) *Plant Mol. Biol.* 23:1129-1138; and Matsuoka *et al.* (1993) *Proc. Natl. Acad.*
 30 *Sci. USA* 90:9586-9590. In addition, promoter of cab and rubisco can also be used. See, for example, Simpson *et al.* (1958) *EMBO J* 4:2723-2729 and Timko *et al.* (1988) *Nature* 318:57-58.

Root-preferred promoters are known and can be selected from the many available. See, for example, Hire *et al.* (1992) *Plant Mol. Biol.* 20:207-218 (soybean root-specific glutamine synthase gene); Keller and Baumgartner (1991) *Plant Cell* 3:1051-1061 (root-specific control element in the GRP 1.8 gene of French bean); Sanger *et al.* (1990) *Plant Mol. Biol.* 14:433-443 (root-specific promoter of the mannopine synthase (MAS) gene of *Agrobacterium tumefaciens*); and Miao *et al.* (1991) *Plant Cell* 3:11-22 (full-length cDNA clone encoding cytosolic glutamine synthase (GS), which is expressed in roots and root nodules of soybean). See also Bogusz *et al.* (1990) *Plant Cell* 2:633-641, where two root-specific promoters isolated from hemoglobin genes from the nitrogen-fixing nonlegume *Parasponia andersonii* and the related non-nitrogen-fixing nonlegume *Trema tomentosa* are described. Leach and Aoyagi (1991) describe their analysis of the promoters of the highly expressed rolC and rolD root-inducing genes of *Agrobacterium rhizogenes* (see *Plant Sci* (Limerick) 79:69-76). Teeri *et al.* (1989) used gene fusion to lacZ to show that the *Agrobacterium* T-DNA gene encoding octopine synthase is especially active in the epidermis of the root tip and that the TR2' gene is root specific in the intact plant and stimulated by wounding in leaf tissue (see *EMBO J.* 8:343-350). The TR1' gene, fused to *nptII* (neomycin phosphotransferase II) showed similar characteristics. Additional root-preferred promoters include the VfENOD-GRP3 gene promoter (Kuster *et al.* (1995) *Plant Mol. Biol.* 29:759-772); and rolB promoter (Capana *et al.* (1994) *Plant Mol. Biol.* 25:681-691. See also U.S. Patent Nos. 5,837,876; 5,750,386; 5,633,363; 5,459,252; 5,401,836; 5,110,732; and 5,023,179. Another root-preferred promoter includes the promoter of the phaseolin gene (Murai *et al.* (1983) *Science* 23:476-482 and Sengopta-Gopalen *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 82:3320-3324.

Seed-preferred promoters include both those promoters active during seed development as well as promoters active during seed germination. See Thompson *et al.* (1989) *BioEssays* 10:108, herein incorporated by reference. Such seed-preferred promoters include, but are not limited to, Cim1 (cytokinin-induced message); cZ19B1 (maize 19 kDa zein); and milps (myo-inositol-1-phosphate synthase); (see WO 00/11177 and U.S. Patent No. 6,225,529; herein incorporated by reference). For dicots, seed-preferred promoters include, but are not limited to, bean β -phaseolin, napin, β -conglycinin, soybean lectin, cruciferin, and the like. For monocots, seed-preferred promoters include, but are not limited to, maize 15 kDa zein, 22 kDa zein, 27 kDa gamma zein, waxy,

shrunk1, shrunk2, globulin 1, oleosin, nuc1, etc. See also WO 00/12733, where seed-preferred promoters from *end1* and *end2* genes are disclosed; herein incorporated by reference.

Where low-level expression is desired, weak promoters will be used. Generally, by "weak promoter" is intended a promoter that drives expression of a coding sequence at a low level. By low level is intended at levels of about 1/1000 transcripts to about 1/100,000 transcripts to about 1/500,000 transcripts. Alternatively, it is recognized that weak promoters also encompasses promoters that are expressed in only a few cells and not in others to give a total low level of expression. Where a promoter is expressed at unacceptably high levels, portions of the promoter sequence can be deleted or modified to decrease expression levels. Such weak constitutive promoters include, for example, the core promoter of the Rsyn7 promoter (WO 99/43838 and U.S. Patent No. 6,072,050), the core 35S CaMV promoter, and the like.

Other promoters of interest include the Rab16 promoter (Mundy *et al.* (1990) *PNAS* 87: 1406-1410), the *Brassica* LEA3-1 promoter (U.S. Application Publication No. US 2008/0244793), the HVA1s, Dhn8s, and Dhn4s from barley and the wsi18j, rab16Bj from rice (Xiao and Xue (2001) *Plant Cell Rep* 20:667-73), and D113 from cotton (Luo *et al.* (2008) *Plant Cell Rep* 27:707-717).

In some embodiments, the polynucleotide encoding a cell proliferation factor (*e.g.*, babyboom polypeptide) is operably linked to a maize ubiquitin promoter or a maize oleosin promoter (*e.g.*, SEQ ID NO: 65 or a variant or fragment thereof).

In some of those embodiments wherein the vector comprises a presently disclosed promoter construct operably linked to a polynucleotide encoding a site-specific recombinase and in some embodiments, a polynucleotide encoding a babyboom polypeptide, the vector can further comprise a polynucleotide encoding a Wuschel polypeptide (see International Application Publication No. WO 01/23575 and U.S. Patent No. 7,256,322, each of which are herein incorporated by reference in its entirety). In certain embodiments, the polynucleotide encoding the Wuschel polypeptide has the sequence set forth in SEQ ID NO: 61, 63, 114, or 105 (WUS1, WUS2, WUS2 alt, or WUS3, respectively) or an active variant or fragment thereof. In particular embodiments, the Wuschel polypeptide has the sequence set forth in SEQ ID NO: 62, 64, 115, or 106 (WUS1, WUS2, WUS2 alt, or WUS3, respectively) or an active variant or fragment thereof. In some of these embodiments, the polynucleotide encoding a Wuschel polypeptide is operably linked to a promoter active in the plant, including but not limited

to the maize In2-2 promoter or a nopaline synthase promoter. In some of these embodiments, the expression cassettes for the site-specific recombinase, the babyboom polypeptide, and the Wuschel polypeptide are all flanked by site-specific recombination sites that are directly repeated and are recognized by the site-specific recombinase whose expression is regulated by a presently disclosed promoter construct, such that expression of the site-specific recombinase results in the excision of the three expression cassettes.

In some embodiments, the vector comprises a promoter disclosed herein (maize Rab17 promoter with an attB1 site) operably linked to a site-specific recombinase (e.g., Cre, FLP); a second promoter operably linked to a cell proliferation factor (e.g., a babyboom polypeptide); and a third promoter operably linked to a polynucleotide of interest, such as those disclosed elsewhere herein (e.g., trait gene), or multiple polynucleotides of interest operably linked to one or more promoters; and in some embodiments, a fourth promoter operably linked to a WUS gene. In some of these embodiments, the expression cassettes for the site-specific recombinase, the cell proliferation factor, and the Wuschel polypeptide are all flanked by site-specific recombination sites that are directly repeated and are recognized by the site-specific recombinase, such that expression of the site-specific recombinase results in the excision of the three expression cassettes, leaving the polynucleotides of interest (e.g., trait genes) behind. In other embodiments, the polynucleotide of interest (e.g., trait gene) is introduced along with or following the vector comprising a presently disclosed promoter operably linked to a site-specific recombinase, and at least one cell proliferation factor (e.g., babyboom polypeptide, Wuschel polypeptide) operably linked to one or more promoters, wherein the polynucleotide of interest is present on a separate vector from the expression cassettes for the site-specific recombinase and cell proliferation factor(s). In some of these embodiments, the expression cassettes for the site-specific recombinase and cell proliferation factor(s) are flanked by recombination sites that are recognized by the site-specific recombinase. Expression of the cell proliferation factors facilitates the transformation of the polynucleotide of interest (e.g., trait gene) and expression of the site-specific recombinase results in the excision of the expression cassettes for the site-specific recombinase and cell proliferation factor(s).

The presently disclosed promoter constructs, expression cassettes, and vectors can be introduced into a host cell. By "host cell" is meant a cell, which comprises a heterologous nucleic acid sequence. Host cells may be prokaryotic cells such as *E. coli*, or

eukaryotic cells such as yeast, insect, amphibian, or mammalian cells. In some examples, host cells are monocotyledonous or dicotyledonous plant cells. In particular embodiments, the monocotyledonous host cell is a maize host cell.

5 An intermediate host cell may be used, for example, to increase the copy number of the cloning vector and/or to mediate transformation of a different host cell. With an increased copy number, the vector containing the nucleic acid of interest can be isolated in significant quantities for introduction into the desired plant cells. In one embodiment, plant promoters that do not cause expression of the polypeptide in bacteria are employed.

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

20 The vector is selected to allow introduction into the appropriate host cell. Bacterial vectors are typically of plasmid or phage origin. Appropriate bacterial cells are infected with phage vector particles or transfected with naked phage vector DNA. If a plasmid vector is used, the bacterial cells are transfected with the plasmid vector DNA. Expression systems for expressing a protein are available using *Bacillus sp.* and *Salmonella* (Palva *et al.* (1983) *Gene* 22:229-235); Mosbach *et al.* (1983) *Nature* 302:543-545).

Methods for expressing a polynucleotide of interest in a plant comprise introducing an expression cassette or vector. Alternatively, the method can comprise introducing a promoter construct, wherein the promoter construct is stably integrated into the genome of the plant and operably linked to a polynucleotide of interest.

30 "Introducing" is intended to mean presenting to the organism, such as a plant, or the cell the polynucleotide or polypeptide in such a manner that the sequence gains access to the interior of a cell of the organism or to the cell itself. The methods and compositions do not depend on a particular method for introducing a sequence into an organism or cell, only that the polynucleotide or polypeptide gains access to the interior of at least one cell

of the organism. Methods for introducing polynucleotides or polypeptides into plants are known in the art including, but not limited to, stable transformation methods, transient transformation methods, virus-mediated methods, and sexual breeding.

"Stable transformation" is intended to mean that the nucleotide construct
 5 introduced into a plant integrates into a genome of the plant and is capable of being inherited by the progeny thereof. "Transient transformation" is intended to mean that a polynucleotide is introduced into the plant and does not integrate into a genome of the plant or a polypeptide is introduced into a plant.

Protocols for introducing polypeptides or polynucleotide sequences into plants may
 10 vary depending on the type of plant or plant cell, *i.e.*, monocot or dicot, targeted for transformation. Suitable methods of introducing polypeptides and polynucleotides into plant cells include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (U.S. Patent No. 5,563,055 and U.S. Patent No.
 15 5,981,840), direct gene transfer (Paszowski *et al.* (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Patent Nos. 4,945,050; U.S. Patent No. 5,879,918; U.S. Patent No. 5,886,244; and, 5,932,782; Tomes *et al.* (1995) in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); McCabe *et al.* (1988) *Biotechnology* 6:923-926); and Lect
 20 transformation (WO 00/28058). Also see Weissinger *et al.* (1988) *Ann. Rev. Genet.* 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou *et al.* (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe *et al.* (1988) *Bio/Technology* 6:923-926 (soybean); Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182 (soybean); Singh *et al.* (1998) *Theor. Appl. Genet.* 96:319-324 (soybean);
 25 Datta *et al.* (1990) *Biotechnology* 8:736-740 (rice); Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein *et al.* (1988) *Biotechnology* 6:559-563 (maize); U.S. Patent Nos. 5,240,855; 5,322,783; and, 5,324,646; Klein *et al.* (1988) *Plant Physiol.* 91:440-444 (maize); Fromm *et al.* (1990) *Biotechnology* 8:833-839 (maize); Hooykaas-Van Slogteren *et al.* (1984) *Nature* 311:763-764; U.S. Patent No. 5,736,369 (cereals);
 30 Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman *et al.* (Longman, New York), pp. 197-209 (pollen); Kaeppler *et al.* (1990) *Plant Cell Rep* 9:415-418 and Kaeppler *et al.* (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin *et al.* (1992) *Plant Cell* 4:1495-1505 (electroporation); Li *et al.* (1993) *Plant*

Cell Rep 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413 (rice); Osjoda *et al.* (1996) *Nat Biotechnol* 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

In specific embodiments, the sequences can be provided to a plant using a variety of transient transformation methods. Such transient transformation methods include, but are not limited to, the introduction of the polypeptide of interest directly into the plant or the introduction of a polynucleotide encoding the polypeptide of interest into the plant. Such methods include, for example, microinjection or particle bombardment. See, for example, Crossway *et al.* (1986) *Mol Gen. Genet.* 202:179-185; Nomura *et al.* (1986) *Plant Sci.* 44:53-58; Hepler *et al.* (1994) *Proc. Natl. Acad. Sci.* 91:2176-2180 and Hush *et al.* (1994) *J Cell Sci* 107:775-784, all of which are herein incorporated by reference. Alternatively, the polynucleotide can be transiently transformed into the plant using techniques known in the art. Such techniques include viral vector system and the precipitation of the polynucleotide in a manner that precludes subsequent release of the DNA. Thus, the transcription from the particle-bound DNA can occur, but the frequency with which its released to become integrated into the genome is greatly reduced. Such methods include the use particles coated with polyethylimine (PEI; Sigma #P3143).

In other embodiments, the polynucleotide may be introduced into plants by contacting plants with a virus or viral nucleic acids. Generally, such methods involve incorporating a nucleotide construct within a viral DNA or RNA molecule. It is recognized that the cell proliferation factor may be initially synthesized as part of a viral polyprotein, which later may be processed by proteolysis *in vivo* or *in vitro* to produce the desired recombinant protein. Further, it is recognized that promoters also encompass promoters utilized for transcription by viral RNA polymerases. Methods for introducing polynucleotides into plants and expressing a protein encoded therein, involving viral DNA or RNA molecules, are known in the art. See, for example, U.S. Patent Nos. 5,889,191, 5,889,190, 5,866,785, 5,589,367, 5,316,931, and Porta *et al.* (1996) *Molecular Biotechnology* 5:209-221; herein incorporated by reference.

Other methods of introducing polynucleotides into a plant can be used, including plastid transformation methods, and the methods for introducing polynucleotides into tissues from seedlings or mature seeds.

Methods are known in the art for the targeted insertion of a polynucleotide at a specific location in the plant genome. In one embodiment, the insertion of the polynucleotide at a desired genomic location is achieved using a site-specific

recombination system. See, for example, WO99/25821, WO99/25854, WO99/25840, WO99/25855, and WO99/25853, all of which are herein incorporated by reference.

Briefly, the polynucleotide can be contained in a transfer cassette flanked by two non-recombinogenic recombination sites. The transfer cassette is introduced into a plant
5 having stably incorporated into its genome a target site which is flanked by two non-recombinogenic recombination sites that correspond to the sites of the transfer cassette. An appropriate recombinase is provided and the transfer cassette is integrated at the target site. The polynucleotide of interest is thereby integrated at a specific chromosomal position in the plant genome.

10 In specific embodiments, methods are provided for the excision of a polynucleotide of interest from a target site in a plant, wherein the polynucleotide of interest is flanked by a first and a second recombination site that are recombinogenic with respect to one another and that are directly repeated. The method comprises introducing into the plant an expression cassette comprising a presently disclosed promoter construct
15 (*e.g.*, SEQ ID NO: 30 or a variant or fragment thereof) operably linked to a site-specific recombinase, expressing the recombinase, so that the recombinase recognizes and implements recombination at the recombination sites flanking the polynucleotide of interest, thereby excising the polynucleotide of interest. The expression cassette can comprise any of the linker sequences, attB sites, termination regions, etc., such as those
20 described herein.

The terms "target site," and "target sequence," as used interchangeably herein, refer to a polynucleotide sequence present in a cell of an organism, such as a plant, that comprises at least one site-specific recombination site. The target site may be part of the organism's native genome or integrated therein or may be present on an episomal
25 polynucleotide. The genomic target sequence may be on any region of any chromosome, and may or may not be in a region encoding a protein or RNA. The target site may be native to the cell or heterologous. In some embodiments, the heterologous target sequence may have been transgenically inserted into the organism's genome, and may be on any region of any chromosome, including an artificial or satellite chromosome, and may or
30 may not be in a region encoding a protein or RNA. It is recognized that the cell or the organism may comprise multiple target sites, which may be located at one or multiple loci within or across chromosomes.

Alternative methods for excising a polynucleotide of interest from a target site in a plant include providing a plant comprising a target site comprising in operable linkage: a first site-specific recombination site, a first promoter, the polynucleotide of interest, a second promoter, a polynucleotide encoding a site-specific recombinase, and a second site-specific recombination site. The first and the second site-specific recombination sites are recombinogenic with respect to one another and directly repeated. The polynucleotide of interest and its operably linked promoter may precede or follow the polynucleotide encoding the site-specific recombinase and its operably linked promoter. The second promoter is one of the presently disclosed promoter constructs (*e.g.*, SEQ ID NO: 30 or a variant or fragment thereof). The method comprises expressing the site-specific recombinase, whereby the site-specific recombinase recognizes and implements recombination at the first and the second site-specific recombination sites, thereby excising the polynucleotide of interest and the polynucleotide encoding the site-specific recombinase.

In some embodiments, the target site further comprises a third promoter operably linked to a polynucleotide encoding a Wuschel polypeptide. The three expression cassettes may be in any order, but in some embodiments, the target site comprises in operable linkage: the first site-specific recombination site, the third promoter, the polynucleotide encoding a Wuschel polypeptide, the first promoter, the polynucleotide of interest, the second promoter, the polynucleotide encoding the site-specific recombinase, and the second site-specific recombination site, wherein expression of the recombinase results in the excision of all three expression cassettes. The expression cassette can comprise any of the linker sequences, attB sites, termination regions, etc., such as those described herein.

Methods are provided to enhance the efficiency of plastid transformation, which include introducing into a plant cell a heterologous polynucleotide encoding a cell proliferation factor and expressing the heterologous polynucleotide before, during, or immediately following the transformation of the plastid of the plant cell with a polynucleotide of interest. The heterologous polynucleotide encoding a cell proliferation factor can be co-delivered with the polynucleotide of interest or the cell proliferation polynucleotide can first be introduced into the plant, followed by the introduction of the polynucleotide of interest.

As used herein, a “plastid” refers to an organelle present in plant cells that stores and manufactures chemical compounds used by the cell, such as starch, fatty acids, terpenes, and that has been derived from a proplastid. Thus, plastids of plants typically have the same genetic content. Plastids include chloroplasts, which are responsible for photosynthesis, amyloplasts, chromoplasts, statoliths, leucoplasts, elaioplasts, and proteinoplasts.

The plastid genome is circular and varies in size among plant species from about 120 to about 217 kilobase pairs (kb). The genome typically includes a large inverted repeat, which can contain up to about 76 kilobase pairs, but which is more typically in the range of about 20 to about 30 kilobase pairs. The inverted repeat present in the plastid genome of various organisms has been described (Palmer (1990) *Trends Genet* 6:115-120).

Transformation of plastids can result in a homoplasmic state, wherein essentially all of the plastids in a plant cell have the introduced DNA integrated into the plastid genome. This occurs through a selection process, whereby those cells that comprise a sufficient number of transformed plastids having an introduced selectable marker gene survive on the selection medium, and through the reproduction of the transformed plastid genomes. Plastids can be present in a plant cell at a very high copy number, with up to 50,000 copies per cell present for the chloroplast genome (Bendich (1987) *BioEssays* 6:279-282). Thus, through plastid transformation, plant cells can be engineered to maintain an introduced gene of interest at a very high copy number.

While plastid transformation is routine and relatively efficient in tobacco by bombardment of leaves, the application of plastid transformation technology in important crop species is not routine. For example, plastid transformation in maize and wheat has not been reported. Plastid transformation is possible in soybean, but the frequency of transformation with vectors carrying trait genes is low. Plastid transformation is possible in rice, but homoplasmic events have not been recovered.

The introduction and expression of polynucleotides encoding cell proliferation factors may be used to enhance the efficiency of plastid transformation. Any cell proliferation factor known in the art or described elsewhere herein may be used to enhance plastid transformation, including babyboom polypeptides. In certain embodiments, embryogenesis-stimulating polypeptides are used to enhance plastid transformation.

Methods are known in the art for introducing genes into the plastid genome. See, for example, Svab *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87: 8526-8530; Svab and

Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90: 913-917; Svab and Maliga (1993) *EMBO J.* 12: 601-606; and U.S. Patent Nos. 5,451,513 and 5,545,818; each of which is herein incorporated by reference in its entirety.

One method involves the integration of a polynucleotide of interest into the plastid
5 genome through homologous recombination. Such methods involve the introduction of a
polynucleotide of interest flanked by regions of homology with regions of the plastid
genome into a plant cell. Delivery of the polynucleotide of interest into the plant cell can
be via any method of transformation known in the art, including those described elsewhere
herein. These include, but are not limited to, particle gun delivery (Svab, Z. *et al.* (1990)
10 *Proc Natl Acad Sci USA* 87:8526-8530; Svab and Maliga (1993) *Proc Natl Acad Sci USA*
90:913-917; and Staub and Maliga (1993) *EMBO J* 12:601-606; and U.S. Pat. Nos.
5,451,513 and 5,545,818; each of which is herein incorporated by reference in its entirety)
and *Agrobacterium*-mediated transformation (U.S. Patent No. 5,563,055 and U.S. Patent
No. 5,981,840). In some species, protoplasts can also be used for chloroplast
15 transformation (O'Neill *et al.* (1993) *Plant J* 3:729-38; and Spocrlcin *et al.* (1991) *Theor*
Appl Gen 82:717-722; each of which is herein incorporated by reference in its entirety).
Once the polynucleotide of interest flanked by the homologous regions enters the cell, the
polynucleotide of interest will be integrated within the plastid genome.

The homologous regions flanking the polynucleotide of interest, and in some
20 embodiments, its operably linked promoter, and in particular embodiments, the selectable
marker gene as well, may vary in length. In some embodiments, the region of homology
with the plastid genome is about 50, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000
base pairs or greater in length. In most instances, the frequency of recombination and thus
the frequency of obtaining plants having transformed plastids decreases with the
25 decreasing size of the homologous regions. In those embodiments wherein the regions of
homology are present in the inverted repeat regions of the plastid genome, two copies of
the polynucleotide of interest are expected per transformed plastid.

In some embodiments, the polynucleotide of interest can be co-delivered with a
selectable marker gene that is active in the plastid. The selectable marker gene and the
30 polynucleotide of interest can be present on a single DNA construct or on separate
constructs. A number of markers have been developed for use with plant cells, such as
resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. Genes
conferring resistance to kanamycin (NPTII or AphA6) have been used as a selectable
marker for plastid transformation (Carrer *et al.* (1993) *Mol Gen Genetics* 241:49-56; and

Huang *et al.* (2002) *Mol Gen Genomics* 268:19-27; each of which is herein incorporated by reference in its entirety). Other genes which encode a product involved in chloroplast metabolism may also be used as selectable markers.

Another example of a selectable marker gene for plastid transformation is a
 5 selectable marker gene that confers resistance to a substance which inhibits protein synthesis by the plastids, such that cells which have acquired the phenotype are selected for by contacting the cells with a substance which inhibits protein synthesis by the plastids. The plastid DNA encoding the nonlethal selectable phenotype may comprise 16S ribosomal DNA mutated to confer resistance to the effects of streptomycin, or to
 10 spectinomycin, or to both antibiotics simultaneously. Expression of heterologous genes that modify non-lethal antibiotics such as streptomycin or spectinomycin by phosphorylation, adenylation or acetylation also are suitable for the selection of plastid transformation events. Another non-limiting example of a gene that confers resistance to streptomycin and spectinomycin is the bacterial *aadA* gene that codes for
 15 streptomycin/spectinomycin adenylyltransferase (Svab *et al.* (1993) *Proc Natl Acad Sci USA* 90:913-917). The *aadA* gene product allows for continued growth and greening of cells in the presence of streptomycin or spectinomycin whose chloroplasts comprise the selectable marker gene product. Cells which do not contain the selectable marker gene product are bleached. Selection for the *aadA* gene marker is thus based on identification of plant cells
 20 which are not bleached by the presence of streptomycin or spectinomycin, in the plant growth medium.

Other examples of selectable marker genes are those that confer resistance to an herbicide, including a photosystem II herbicide, such as a triazine herbicide, specifically
 25 the triazine herbicide atrazine. This phenotype not only provides nonlethal selection, but also provides herbicide resistance. Genes that provide resistance to plant herbicides such as glyphosate, bromoxynil, or imidazolinone may find use as a selectable marker gene. Such genes have been reported (Stalker *et al.* (1985) *J Biol Chem* 260:4724-4728 (glyphosate resistant EPSP); Stalker *et al.* (1985) *J Biol Chem* 263:6310-6314 (bromoxynil resistant nitrilase gene); and Sathasivan *et al.* (1990) *Nucl Acids Res* 18:2188
 30 (AHAS imidazolinone resistance gene); each of which is herein incorporated by reference in its entirety).

The selectable marker gene and/or the polynucleotide of interest can be placed under the regulatory control of a chloroplast 5' promoter and 3' transcription termination regions, such as the tobacco 16S rRNA promoter *rrn* region and *rps16* 3' termination

region. Numerous additional promoter regions may also be used to drive expression of the selectable marker gene and/or the polynucleotide of interest, including various plastid promoters and bacterial promoters which have been shown to function in plant plastids. Further, if nuclear expression of the selectable marker gene and/or the polynucleotide of interest is not desired, plastid introns can be incorporated into the selectable marker gene and/or the polynucleotide of interest. Certain classes of plastid introns can not be correctly spliced out in the nucleus, thereby preventing expression of the selectable marker gene and/or the polynucleotide of interest within the nucleus. The polynucleotide of interest and/or the heterologous polynucleotide encoding the cell proliferation factor may be optimized for expression in the chloroplast to account for differences in codon usage between the plant nucleus and this organelle. In this manner, the polynucleotide may be synthesized using chloroplast-preferred codons. See, for example, U.S. Patent No. 5,380,831, herein incorporated by reference.

An additional method of plastid transformation occurs through the transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91: 7301-7305, which is herein incorporated by reference in its entirety. In these methods, the heterologous polynucleotide encoding the cell proliferation factor is introduced into the cell and expressed prior to, during, or immediately after the expression of the plastid-directed RNA polymerase.

In order to select those cells having transformed plastids, following introduction of the chloroplast transformation vectors, the treated tissue is placed on tissue culture medium containing the appropriate selection agent. After a suitable period of incubation on selection medium, transformed cells can be identified and grown to a stage that allows regeneration of the whole plants. The regeneration processes are basically identical to those used for standard nuclear transformation events. Special care must be taken to ensure that selection and regeneration conditions promote the elimination of most wild-type chloroplast genomes. The status of the proportion of wild-type to transformed chloroplast genomes can be monitored by standard molecular techniques including Southern and PCR analysis.

For tobacco and a number of other species, leaves are a preferred target for plastid transformation. In some embodiments, one or more cell proliferation factors (*e.g.*, babyboom polypeptides) can be used to trigger a tissue culture response from leaves of maize and other species. For boosting chloroplast transformation, polynucleotides

encoding cell proliferation factors under the control of inducible promoters can be introduced into the species of interest by standard nuclear transformation protocols. Events that contain the transgene can be characterized for expression of the inducible embryogenesis-stimulating polypeptides. Then, the expression of the polynucleotide
5 encoding the cell proliferation factor is induced, thereby stimulating an embryogenic tissue culture response. For example, leaves from plants transformed with the polynucleotide(s) encoding a cell proliferation factor under the control of the tetracycline-repressor system can be placed on medium containing appropriate concentrations of doxycycline for induction of expression. The leaves can be maintained on the induction
10 medium to allow for cell division and the initiation of embryogenic callus to take place. The plastids of the leaves can be transformed with the polynucleotide of interest, and in certain embodiments, a selectable marker gene just prior to the induction of the polynucleotide(s) encoding cell proliferation factor, during induction, or immediately after induction. Alternatively, leaf tissue can be transformed using the methods disclosed
15 elsewhere herein. After plastid transformation, the plastid transformation events can be selected by incubating the leaves on selection medium. Following selection, the leaves or plant cells are grown on medium that stimulates callus formation.

Methods are provided for the preparation and transformation of dried mature seeds, mature embryos, and mature embryo explants. A mature embryo explant is a tissue
20 dissected from a mature embryo, which is an embryo that has an age of at least about 18 days after pollination. Methods for preparing a mature embryo comprise dissecting a mature embryo from a mature seed and methods for preparing a mature embryo explant further comprise preparing slices (*e.g.*, longitudinal slices) of the mature embryo. The mature embryo explant comprises at least one of the following tissues: leaf primordia,
25 mesocotyl, shoot apical meristem, and root primordia. In some embodiments, the mature embryo explant comprises leaf primordia, mesocotyl, and root primordia. In some of these embodiments, the mature embryo explant further comprises a shoot apical meristem. The slices may be prepared using any method or suitable apparatus known in the art, including slices prepared by hand with a scalpel. In certain embodiments, each mature
30 embryo is sliced into about 3 to 4 thin sections using a scalpel. The use of a dissecting microscope can aid in slicing of the mature embryo.

The mature seed from which the mature embryo or mature embryo explant is derived can be a seed of any plant. In some embodiments, the mature seed is from a monocot. In particular embodiments, the mature seed is from maize, rice, sorghum,

barley, wheat, oats, or millet. In certain embodiments, the mature seed is from a recalcitrant plant, such as an elite maize inbred. As used herein, a “recalcitrant tissue” or “recalcitrant plant” is a tissue or a plant that has a low rate of transformation using traditional methods of transformation, such as those disclosed elsewhere herein. In some
5 embodiments, the recalcitrant tissue or plant is unable to be transformed in the absence of the cell proliferation factor. In other embodiments, the recalcitrant tissue or plant has a rate of successful transformation of less than about 20%, less than about 15%, less than about 10%, less than about 5%, less than about 1%, less than about 0.1%, less than about 0.01%, less than about 0.001%, or less.

10 The mature embryo or mature embryo explant can be prepared from a dried mature seed. The dried mature seed can comprise about 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, 1%, 0.1% or less water than a mature seed that has not been dried. The dried mature seed can be imbibed with an aqueous solution for a sufficient period of time to allow the dried mature seed to soften so
15 that the mature embryo may be dissected from the seed and in some embodiments, mature embryo explant slices prepared from the mature embryo. In some embodiments, the dried mature seed is imbibed in an aqueous solution for about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 hours or greater. In certain embodiments, the
20 aqueous solution is water. In certain embodiments, the dried mature seed is imbibed for a sufficient period of time to induce germination of the seed. A germinated seed is one in which the radical has emerged.

 Mature embryos and mature embryo explants can be transformed with a polynucleotide of interest through the provision of a cell proliferation factor (*e.g.*,
25 babyboom polypeptide). A heterologous polynucleotide encoding the cell proliferation factor is introduced into the mature embryo explant prior to or at the same time as the introduction of the polynucleotide of interest. The heterologous polynucleotide encoding the cell proliferation factor and the polynucleotide of interest can be provided on the same expression cassette or on separate expression cassettes.

30 The polynucleotides can be introduced into the mature embryo explant using any method known in the art, including but not limited to, *Agrobacterium*-mediated transformation.

In some embodiments, transformed mature embryo explants can be identified. Any method can be used to identify a plant cell or tissue comprising the polynucleotide of interest. In some examples, plant cells or tissues comprising the polynucleotide of interest are identified using one or more of the following techniques, including but not limited to

5 PCR methods, hybridization methods such as Southern or Northern blots, restriction digest analyses, or DNA sequencing. In some embodiments, the transformed mature embryo explants can be identified by incubating the leaf mature embryo explants under conditions to allow for growth of a callus. In some embodiments, those mature embryo explants that are able to grow into a callus with significant proliferation indicate those mature embryo

10 explants that have been transformed. In other embodiments, the transformed mature embryo explants can be identified and selected for through the introduction and expression of a selectable marker gene into the mature embryo explant.

Methods are also provided herein for the transformation of leaf tissues, which can be a leaf base. A leaf base is the tissue of a leaf above the first leaf base node. The leaf

15 tissue can be derived from any plant. In some embodiments, the leaf tissue is derived from a monocot. In particular embodiments, the leaf tissue is derived from maize, rice, sorghum, barley, wheat, oats, or millet. In certain embodiments, the leaf tissue is derived from a recalcitrant plant, such as an elite maize inbred.

The leaf base can be from a mature leaf or a leaf from a seedling. As used herein,

20 a "seedling" refers to a germinated seed or germinated embryo, or a plantlet generated in an *in vitro* system (*e.g.*, from callus). The seedlings can be prepared by germinating seeds or dissecting mature embryos from mature seeds for germination. In some embodiments, the mature embryos are dissected from dried mature seeds that have been imbibed with an aqueous solution, as described herein.

25 In some embodiments, the coleoptile is removed from the leaf tissue and the leaf fragment is split longitudinally, and then horizontal slices are made to cross-dissect the leaf fragment into leaf tissue pieces. In particular embodiments, the pieces of leaf tissue are about 1 to 2 mm in length.

The leaf tissue can be transformed with a polynucleotide of interest through the

30 provision of a cell proliferation factor (*e.g.*, babyboom polypeptide). The polynucleotides can be introduced into the leaf tissue using any method known in the art, including but not limited to, *Agrobacterium*-mediated transformation. A heterologous polynucleotide of interest encoding the cell proliferation factor is introduced into the leaf tissue prior to or at the same time as the introduction of the polynucleotide of interest. The heterologous

polynucleotide encoding the cell proliferation factor is expressed. The heterologous polynucleotide encoding the cell proliferation factor and the polynucleotide of interest can be provided on the same expression cassette or on separate expression cassettes.

In some embodiments, transformed leaf tissues can be identified. Any method can be used to identify a plant cell or tissue comprising the polynucleotide of interest. In some examples, plant cells or tissues comprising the polynucleotide of interest are identified using one or more of the following techniques, including but not limited to PCR methods, hybridization methods such as Southern or Northern blots, restriction digest analyses, or DNA sequencing. In some embodiments, the transformed leaf tissues can be identified by incubating the leaf tissues under conditions to allow for growth of a callus. In some embodiments, those leaf tissues that are able to grow a callus with significant proliferation indicate those leaf tissues that have been transformed. In other embodiments, the transformed leaf tissue can be identified and selected for through the introduction and expression of a selectable marker gene into the leaf tissue.

The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell Rep* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, transformed seed (also referred to as "transgenic seed") having a nucleotide construct, for example, an expression cassette, stably incorporated into their genome is provided. Thus, compositions of the invention include plant cells, plant tissues, plant parts, and plants comprising the presently disclosed polynucleotides, polypeptides, promoter constructs, expression cassettes, or vectors. Likewise, the methods of the invention can be performed in plant cells, plant tissues, plant parts, and plants.

In some embodiments, the activity and/or level of the cell proliferation factor (*e.g.*, babyboom polypeptide, Wuschel) is reduced prior to regenerating a plant from a cell or tissue having the polynucleotide of interest. In some of these embodiments, the polynucleotide encoding the cell proliferation factor is excised prior to the regeneration of a plant. In certain embodiments, the promoter and other regulatory elements that are operably linked to the heterologous polynucleotide encoding the cell proliferation factor are excised along with the cell proliferation factor coding sequence. In certain

embodiments, the polynucleotide encoding the cell proliferation factor is flanked by recombination sites and an appropriate site-specific recombinase is introduced into the mature embryo explant or callus grown therefrom to excise the polynucleotide encoding the cell proliferation factor prior to regeneration of the mature embryo explant or callus into a plant. In some of those embodiments wherein both a babyboom polypeptide and a Wuschel polypeptide are provided to the plant cell, both the polynucleotide encoding the babyboom polypeptide and the polynucleotide encoding the Wuschel polypeptide are excised. The two polynucleotides can be present on the same or different expression cassettes and, therefore, can be excised in one or two different excision reactions. In some of these embodiments, the polynucleotide encoding the site-specific recombinase for excising the babyboom and Wuschel polynucleotides can be located on the same expression cassette as the babyboom and Wuschel polynucleotides and all three polynucleotides can be excised through the activity of the site-specific recombinase.

In order to control the excision of the cell proliferation factor, the expression of the site-specific recombinase that is responsible for the excision can be controlled by a late embryo promoter or an inducible promoter. In some embodiments, the late embryo promoter is GZ (Uead *et al.* (1994) *Mol Cell Biol* 14:4350-4359), gamma-kafarin promoter (Mishra *et al.* (2008) *Mol Biol Rep* 35:81-88), Glb1 promoter (Liu *et al.* (1998) *Plant Cell Reports* 17:650-655), ZM-LEG1 (U.S. Patent No. 7,211,712), EEP1 (U.S. Patent Application No. US 2007/0169226), B22E (Klemsdal *et al.* (1991) *Mol Gen Genet* 228:9-16), or EAP1 (U.S. Patent No. 7,321,031). In some embodiments, the inducible promoter that regulates the expression of the site-specific recombinase is a heat-shock, light-induced promoter, a drought-inducible promoter, including but not limited to Hva1 (Straub *et al.* (1994) *Plant Mol Biol* 26:617-630), Dhn, and WSI18 (Xiao & Xue (2001) *Plant Cell Rep* 20:667-673). In other embodiments, expression of the site-specific recombinase is regulated by the maize *rab17* promoter, or one of the presently disclosed promoter constructs (*e.g.*, maize *rab17* promoter and an attB site). In some embodiments, the site-specific recombinase that excises the polynucleotide encoding the cell proliferation factor is FLP or Cre.

Any plant species can be transformed, including, but not limited to, monocots and dicots. Examples of plant species of interest include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (*e.g.*, *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (*e.g.*, pearl millet (*Pennisetum*

glaucum), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*,
5 *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*),
10 macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats (*Avena*), barley (*Hordeum*), *Arabidopsis*, switchgrass, vegetables, ornamentals, grasses, and conifers.

Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum.

20 Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*)
25 and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). In specific embodiments, plants of the present invention are crop plants (for example, corn, alfalfa, sunflower, *Brassica*, soybean, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.). In other embodiments, corn and soybean and sugarcane plants are optimal, and in yet other embodiments corn plants are
30 optimal.

Other plants of interest include grain plants that provide seeds of interest, oil-seed plants, and leguminous plants. Seeds of interest include grain seeds, such as corn, wheat, barley, rice, sorghum, rye, etc. Oil-seed plants include cotton, soybean, safflower,

sunflower, *Brassica*, maize, alfalfa, palm, coconut, etc. Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc.

As used herein, the term plant also includes plant cells, plant protoplasts, plant cell
5 tissue cultures from which plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants such as embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears, cobs, husks, stalks, roots, root tips, anthers, and the like. Grain is intended to mean the mature seed produced by commercial growers for purposes other than growing or reproducing the species. Progeny, variants, and
10 mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced polynucleotides.

If the polynucleotide of interest is introduced into an organism, it may impart various changes in the organism, particularly plants, including, but not limited to, modification of the fatty acid composition in the plant, altering the amino acid content of
15 the plant, altering pathogen resistance, and the like. These results can be achieved by providing expression of heterologous products, increased expression of endogenous products in plants, or suppressed expression of endogenous produces in plants.

General categories of polynucleotides of interest include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as
20 kinases, those involved in biosynthetic pathways, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include sequences encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, oil, starch, carbohydrate, phytate, protein, nutrient, metabolism, digestability, kernel size, sucrose loading, and commercial
25 products.

Traits such as oil, starch, and protein content can be genetically altered in addition to using traditional breeding methods. Modifications include increasing content of oleic acid, saturated and unsaturated oils, increasing levels of lysine and sulfur, providing essential amino acids, and also modification of starch. Protein modifications to alter
30 amino acid levels are described in U.S. Patent Nos. 5,703,049, 5,885,801, 5,885,802, and 5,990,389 and WO 98/20122, herein incorporated by reference.

Insect resistance genes may encode resistance to pests such as rootworm, cutworm, European Corn Borer, and the like. Such genes include, for example, *Bacillus*

thuringiensis toxic protein genes (U.S. Patent Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; and Geiser *et al.* (1986) *Gene* 48:109); lectins (Van Damme *et al.* (1994) *Plant Mol. Biol.* 24:825); and the like.

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

Herbicide resistance traits may include genes coding for resistance to herbicides that act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-
10 type herbicides (*e.g.*, the S4 and/or Hra mutations in ALS), genes coding for resistance to herbicides that act to inhibit action of glutamine synthase, such as phosphinothricin or basta (*e.g.*, the bar gene), genes providing resistance to glyphosate, such as GAT (glyphosate *N*-acetyltransferase; U.S. Patent 6,395,485), EPSPS (enolpyruvylshikimate-3-phosphate synthase; U.S. Patents 6,867,293, 5,188,642, 5,627,061), or GOX (glyphosate
15 oxidoreductase; U.S. Patent No. 5,463,175), or other such genes known in the art. The *nptII* gene encodes resistance to the antibiotics kanamycin and geneticin.

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

Commercial traits can also be encoded on a gene or genes that could, for example increase starch for ethanol production, or provide expression of proteins.

Reduction of the activity of specific genes (also known as gene silencing, or gene
25 suppression) is desirable for several aspects of genetic engineering in plants. Many techniques for gene silencing are well known to one of skill in the art, including but not limited to antisense technology (see, *e.g.*, Sheehy *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:8805-8809; and U.S. Patent Nos. 5,107,065; 5,453,566; and 5,759,829); cosuppression (*e.g.*, Taylor (1997) *Plant Cell* 9:1245; Jorgensen (1990) *Trends Biotech.* 8(12):340-344; Flavell (1994) *Proc. Natl. Acad. Sci. USA* 91:3490-3496; Finnegan *et al.* (1994) *Bio/Technology* 12: 883-888; and Neuhuber *et al.* (1994) *Mol. Gen. Genet.* 244:230-241); RNA interference (Napoli *et al.* (1990) *Plant Cell* 2:279-289; U.S. Patent No. 5,034,323; Sharp (1999) *Genes Dev.* 13:139-141; Zamore *et al.* (2000) *Cell* 101:25-33; Javier (2003)

Nature 425:257-263; and, Montgomery *et al.* (1998) *Proc. Natl. Acad. Sci. USA*
 95:15502-15507), virus-induced gene silencing (Burton, *et al.* (2000) *Plant Cell* 12:691-
 705; and Baulcombe (1999) *Curr. Op. Plant Bio.* 2:109-113); target-RNA-specific
 ribozymes (Haseloff *et al.* (1988) *Nature* 334: 585-591); hairpin structures (Smith *et al.*
 5 (2000) *Nature* 407:319-320; WO 99/53050; WO 02/00904; and WO 98/53083);
 ribozymes (Steinecke *et al.* (1992) *EMBO J.* 11:1525; U.S. Patent No. 4,987,071; and,
 Perriman *et al.* (1993) *Antisense Res. Dev.* 3:253); oligonucleotide mediated targeted
 modification (*e.g.*, WO 03/076574 and WO 99/25853); Zn-finger targeted molecules (*e.g.*,
 WO 01/52620; WO 03/048345; and WO 00/42219); and other methods or combinations of
 10 the above methods known to those of skill in the art.

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

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

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

Methods of alignment of sequences for comparison are well known in the art.
 Thus, the determination of percent sequence identity between any two sequences can be
 accomplished using a mathematical algorithm. Non-limiting examples of such
 30 mathematical algorithms are the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17;
 the local alignment algorithm of Smith *et al.* (1981) *Adv. Appl. Math.* 2:482; the global
 alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453; the
 search-for-local alignment method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.*

85:2444-2448; the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the GCG Wisconsin Genetics Software Package, Version 10 (available from Accelrys Inc., 9685 Scranton Road, San Diego, California, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (1988) *Gene* 73:237-244 (1988); Higgins *et al.* (1989) *CABIOS* 5:151-153; Corpet *et al.* (1988) *Nucleic Acids Res.* 16:10881-90; Huang *et al.* (1992) *CABIOS* 8:155-65; and Pearson *et al.* (1994) *Meth. Mol. Biol.* 24:307-331. The ALIGN program is based on the algorithm of Myers and Miller (1988) *supra*. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (*e.g.*, BLASTN for nucleotide sequences, BLASTX for proteins) can be used. See www.ncbi.nlm.nih.gov. Alignment may also be performed manually by inspection.

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using GAP Version 10 using the following parameters: % identity and % similarity for a nucleotide sequence using GAP Weight of 50 and Length Weight of 3, and the nwsgapdna.cmp scoring matrix; % identity and % similarity for an amino acid

sequence using GAP Weight of 8 and Length Weight of 2, and the BLOSUM62 scoring matrix; or any equivalent program thereof. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical
5 percent sequence identity when compared to the corresponding alignment generated by GAP Version 10.

GAP uses the algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and
10 gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap
15 times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the GCG Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers
20 consisting of from 0 to 200. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or greater.

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

(c) As used herein, "sequence identity" or "identity" in the context of two polynucleotides or polypeptide sequences makes reference to the residues in the two

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

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

In hybridization techniques, all or part of a known polynucleotide is used as a probe that selectively hybridizes to other corresponding polynucleotides present in a population of cloned genomic DNA fragments or cDNA fragments (*i.e.*, genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ³²P, or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the babyboom polynucleotide. Methods for preparation of probes for

hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

For example, the entire babyboom polynucleotide, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding babyboom polynucleotide and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among babyboom polynucleotide sequences and are optimally at least about 10 nucleotides in length, and most optimally at least about 20 nucleotides in length. Such probes may be used to amplify corresponding babyboom polynucleotide from a chosen plant by PCR. This technique may be used to isolate additional coding sequences from a desired plant or as a diagnostic assay to determine the presence of coding sequences in a plant. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (*e.g.*, at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, optimally less than 500 nucleotides in length.

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

40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours. The duration of the wash time will be at least a length of time sufficient to reach equilibrium.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is optimal to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene

Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

It is to be noted that the term “a” or “an” entity refers to one or more of that entity; for example, “a polypeptide” is understood to represent one or more polypeptides. As such, the terms “a” (or “an”), “one or more,” and “at least one” can be used interchangeably herein.

Throughout this specification and the claims, the words “comprise,” “comprises,” and “comprising” are used in a non-exclusive sense, except where the context requires otherwise.

As used herein, the term “about,” when referring to a value is meant to encompass variations of, in some embodiments $\pm 50\%$, in some embodiments $\pm 20\%$, in some embodiments $\pm 10\%$, in some embodiments $\pm 5\%$, in some embodiments $\pm 1\%$, in some embodiments $\pm 0.5\%$, and in some embodiments $\pm 0.1\%$ from the specified amount, as such variations are appropriate to perform the disclosed methods or employ the disclosed compositions.

Further, when an amount, concentration, or other value or parameter is given as either a range, preferred range, or a list of upper preferable values and lower preferable values, this is to be understood as specifically disclosing all ranges formed from any pair of any upper range limit or preferred value and any lower range limit or preferred value, regardless of whether ranges are separately disclosed. Where a range of numerical values is recited herein, unless otherwise stated, the range is intended to include the endpoints thereof, and all integers and fractions within the range. It is not intended that the scope of the presently disclosed subject matter be limited to the specific values recited when defining a range.

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1. A modified Rab17 promoter for the regulated expression of genes

Gateway™ technology (Invitrogen, Carlsbad, CA) was used to place Gateway™ recombination sites between a promoter and a coding sequence, and between the coding sequence and a terminator. The product of a Gateway™ reaction set up in this manner leaves attB sites in those locations.

The *rab17* promoter was identified as a candidate for regulating the expression of FLP recombinase for excision of polynucleotides encoding cell proliferation factors in tissue culture. It was tested for FLP/FRT excision of cell proliferation factor genes in culture. The PHP31004 plasmid was constructed, which has the following operably linked components: Rab17 Pro-attB1::FLPm-attB2::PinII+Ubi Pro-FRT1::CFP::PinII+Ubi Pro::ZmBBM::PinII-FRT1::YFP::PinII+Ubi Pro::moPAT::PinII. The sequence of the expression cassette for the FLPm gene in the PHP31004 plasmid is provided in SEQ ID NO: 46.

After excision by the FLP recombinase, the PHP31004 plasmid has the following operably linked components: Rab17 Pro-attB1::FLPm-attB2::PinII+Ubi Pro-FRT1::YFP::PinII+Ubi Pro::moPAT::PinII.

A plasmid (PHP30642) lacking the attB sites, but comprising the FLPm gene was constructed. The PHP30642 has the following operably linked components: Rab17 pro::FLPm::Gz-W64A term+Ubi pro-FRT1::CFP::PinII+Ubi Pro::ZmBBM::PinII-FRT1::YFP::PinII+Ubi Pro::moPAT::PinII. The sequence of the expression cassette for the FLPm gene in the PHP30642 plasmid is provided in SEQ ID NO: 47.

After excision by the FLP recombinase, the PHP30642 plasmid has the following operably linked components: Rab17 pro::FLPm::Gz-W64A term+Ubi pro-FRT1::YFP::PinII+Ubi pro::moPAT::PinII. The construct lacking the attB sites resulted in frequent premature excision of the cell proliferation factor genes.

Example 2. Transformation of maize immature embryos

Transformation can be accomplished by various methods known to be effective in plants, including particle-mediated delivery, *Agrobacterium*-mediated transformation, PEG-mediated delivery, and electroporation.

a. Particle-mediated delivery

Transformation of maize immature embryos using particle delivery is performed as follows. Media recipes follow below.

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

A plasmid comprising the Zm-BBM (also referred to as Zm-ODP2) coding sequence (set forth in SEQ ID NO: 9) operably linked to a promoter is constructed. This could be a weak promoter such as nos, a tissue-specific promoter, such as globulin-1 or oleosin, an inducible promoter such as In2, or a strong promoter such as ubiquitin plus a
5 plasmid containing the selectable marker gene phosphinothricin N-acetyltransferase (PAT; Wohlleben *et al.* (1988) *Gene* 70:25-37) that confers resistance to the herbicide bialaphos. The plasmid DNA containing the selectable marker gene PAT and the BBM plasmid are precipitated onto 1.1 μm (average diameter) tungsten pellets using a calcium chloride (CaCl_2) precipitation procedure by mixing 100 μl prepared tungsten particles in water,
10 10 μl (1 μg) DNA in Tris EDTA buffer (1 μg total DNA), 100 μl 2.5 M CaCl_2 , and 10 μl 0.1 M spermidine. Each reagent is added sequentially to the tungsten particle suspension, with mixing. The final mixture is sonicated briefly and allowed to incubate under constant vortexing for 10 minutes. After the precipitation period, the tubes are centrifuged briefly, liquid is removed, and the particles are washed with 500 ml 100% ethanol, followed by a
15 30 second centrifugation. Again, the liquid is removed, and 105 μl 100% ethanol is added to the final tungsten particle pellet. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated. 10 μl of the tungsten/DNA particles is spotted onto the center of each macrocarrier, after which the spotted particles are allowed to dry about 2 minutes before bombardment.

20 The sample plates are bombarded at level #4 with a Biorad Helium Gun. All samples receive a single shot at 450 PSI, with a total of ten aliquots taken from each tube of prepared particles/DNA.

Following bombardment, the embryos are incubated on 560Y medium for 2 days, then transferred to 560R selection medium containing 3 mg/liter Bialaphos, and
25 subcultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to medium for germination and transferred to a lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V hormone-free medium in tubes for
30 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to a 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to Classic 600 pots (1.6 gallon) and grown to maturity. Plants are monitored and scored for transformation efficiency, and/or modification of regenerative capabilities.

Bombardment medium (560Y) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000X SIGMA-1511), 0.5 mg/l thiamine HCl, 120.0 g/l sucrose, 1.0 mg/l 2,4-D, and 2.88 g/l L-proline (brought to volume with D-I H₂O following adjustment to pH 5.8 with KOH); 2.0 g/l Gelrite (added after bringing to volume with D-I H₂O); and 8.5 mg/l silver nitrate (added after sterilizing the medium and cooling to room temperature).

Selection medium (560R) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000X SIGMA-1511), 0.5 mg/l thiamine HCl, 30.0 g/l sucrose, and 2.0 mg/l 2,4-D (brought to volume with D-I H₂O following adjustment to pH 5.8 with KOH); 3.0 g/l Gelrite (added after bringing to volume with D-I H₂O); and 0.85 mg/l silver nitrate and 3.0 mg/l bialaphos (both added after sterilizing the medium and cooling to room temperature).

Plant regeneration medium (288J) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g nicotinic acid, 0.02 g/l thiamine HCL, 0.10 g/l pyridoxine HCL, and 0.40 g/l glycine brought to volume with polished D-I H₂O) (Murashige and Skoog (1962) *Physiol. Plant.* 15:473), 100 mg/l myo-inositol, 0.5 mg/l zeatin, 60 g/l sucrose, and 1.0 ml/l of 0.1 mM abscisic acid (brought to volume with polished D-I H₂O after adjusting to pH 5.6); 3.0 g/l Gelrite (added after bringing to volume with D-I H₂O); and 1.0 mg/l indoleacetic acid and 3.0 mg/l bialaphos (added after sterilizing the medium and cooling to 60°C).

Hormone-free medium (272V) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g/l nicotinic acid, 0.02 g/l thiamine HCL, 0.10 g/l pyridoxine HCL, and 0.40 g/l glycine brought to volume with polished D-I H₂O), 0.1 g/l myo-inositol, and 40.0 g/l sucrose (brought to volume with polished D-I H₂O after adjusting pH to 5.6); and 6 g/l bacto-agar (added after bringing to volume with polished D-I H₂O), sterilized and cooled to 60°C.

b. Agrobacterium-mediated transformation

Agrobacterium-mediated transformation was performed essentially as described in Djukanovic *et al.* (2006) *Plant Biotech J* 4:345-57. Briefly, 10-12 day old immature embryos (0.8 -2.5 mm in size) were dissected from sterilized kernels and placed into liquid medium (4.0 g/L N6 Basal Salts (Sigma C-1416), 1.0 ml/L Eriksson's Vitamin Mix (Sigma E-1511), 1.0 mg/L thiamine HCl, 1.5 mg/L 2, 4-D, 0.690 g/L L-proline, 68.5 g/L sucrose, 36.0 g/L glucose, pH 5.2). After embryo collection, the medium was replaced

with 1 ml *Agrobacterium* at a concentration of 0.35-0.45 OD₅₅₀. Maize embryos were incubated with *Agrobacterium* for 5 min at room temperature, then the mixture was poured onto a media plate containing 4.0 g/L N6 Basal Salts (Sigma C-1416), 1.0 ml/L Eriksson's Vitamin Mix (Sigma E-1511), 1.0 mg/L thiamine HCl, 1.5 mg/L 2, 4-D, 0.690 g/L L-proline, 30.0 g/L sucrose, 0.85 mg/L silver nitrate, 0.1 nM acetosyringone, and 3.0 g/L Gelrite, pH 5.8. Embryos were incubated axis down, in the dark for 3 days at 20°C, then incubated 4 days in the dark at 28°C, then transferred onto new media plates containing 4.0 g/L N6 Basal Salts (Sigma C-1416), 1.0 ml/L Eriksson's Vitamin Mix (Sigma E-1511), 1.0 mg/L thiamine HCl, 1.5 mg/L 2, 4-D, 0.69 g/L L-proline, 30.0 g/L sucrose, 0.5 g/L MES buffer, 0.85 mg/L silver nitrate, 3.0 mg/L Bialaphos, 100 mg/L carbenicillin, and 6.0 g/L agar, pH 5.8. Embryos were subcultured every three weeks until transgenic events were identified. Somatic embryogenesis was induced by transferring a small amount of tissue onto regeneration medium (4.3 g/L MS salts (Gibco 11117), 5.0 ml/L MS Vitamins Stock Solution, 100 mg/L myo-inositol, 0.1 µM ABA, 1 mg/L IAA, 0.5 mg/L zeatin, 60.0 g/L sucrose, 1.5 mg/L Bialaphos, 100 mg/L carbenicillin, 3.0 g/L Gelrite, pH 5.6) and incubation in the dark for two weeks at 28°C. All material with visible shoots and roots were transferred onto media containing 4.3 g/L MS salts (Gibco 11117), 5.0 ml/L MS Vitamins Stock Solution, 100 mg/L myo-inositol, 40.0 g/L sucrose, 1.5 g/L Gelrite, pH 5.6, and incubated under artificial light at 28°C. One week later, plantlets were moved into glass tubes containing the same medium and grown until they were sampled and/or transplanted into soil.

Example 3. Transient Expression of BBM Enhances Transformation

Parameters of the transformation protocol can be modified to ensure that the BBM activity is transient. One such method involves precipitating the BBM-containing plasmid in a manner that allows for transcription and expression, but precludes subsequent release of the DNA, for example, by using the chemical PEI.

In one example, the BBM plasmid is precipitated onto gold particles with PEI, while the transgenic expression cassette (UBI::moPAT~GFPm::PinII; moPAT is the maize optimized PAT gene) to be integrated is precipitated onto gold particles using the standard calcium chloride method.

Briefly, gold particles were coated with PEI as follows. First, the gold particles were washed. Thirty-five mg of gold particles, 1.0 in average diameter (A.S.I. #162-0010), were weighed out in a microcentrifuge tube, and 1.2 ml absolute EtOH was added

and vortexed for one minute. The tube was incubated for 15 minutes at room temperature and then centrifuged at high speed using a microfuge for 15 minutes at 4°C. The supernatant was discarded and a fresh 1.2 ml aliquot of ethanol (EtOH) was added, vortexed for one minute, centrifuged for one minute, and the supernatant again discarded (this is repeated twice). A fresh 1.2 ml aliquot of EtOH was added, and this suspension (gold particles in EtOH) was stored at -20°C for weeks. To coat particles with polyethylimine (PEI; Sigma #P3143), 250 µl of the washed gold particle/EtOH mix was centrifuged and the EtOH discarded. The particles were washed once in 100 µl ddH₂O to remove residual ethanol, 250 µl of 0.25 mM PEI was added, followed by a pulse-sonication to suspend the particles and then the tube was plunged into a dry ice/EtOH bath to flash-freeze the suspension, which was then lyophilized overnight. At this point, dry, coated particles could be stored at -80°C for at least 3 weeks. Before use, the particles were rinsed 3 times with 250 µl aliquots of 2.5 mM HEPES buffer, pH 7.1, with 1x pulse-sonication, and then a quick vortex before each centrifugation. The particles were then suspended in a final volume of 250 µl HEPES buffer. A 25 µl aliquot of the particles was added to fresh tubes before attaching DNA. To attach uncoated DNA, the particles were pulse-sonicated, then 1 µg of DNA (in 5 µl water) was added, followed by mixing by pipetting up and down a few times with a Pipetteman and incubated for 10 minutes. The particles were spun briefly (*i.e.* 10 seconds), the supernatant removed, and 60 µl EtOH added. The particles with PEI-precipitated DNA-1 were washed twice in 60 µl of EtOH. The particles were centrifuged, the supernatant discarded, and the particles were resuspended in 45 µl water. To attach the second DNA (DNA-2), precipitation using TFX-50 was used. The 45 µl of particles/DNA-1 suspension was briefly sonicated, and then 5 µl of 100 ng/µl of DNA-2 and 2.5 µl of TFX-50 were added. The solution was placed on a rotary shaker for 10 minutes, centrifuged at 10,000g for 1 minute. The supernatant was removed, and the particles resuspended in 60 µl of EtOH. The solution was spotted onto macrocarriers and the gold particles onto which DNA-1 and DNA-2 had been sequentially attached were delivered into scutellar cells of 10 DAP Hi-II immature embryos using a standard protocol for the PDS-1000. For this experiment, the DNA-1 plasmid contained a UBI::RFP::pinII expression cassette, and DNA-2 contained a UBI::CFP::pinII expression cassette. Two days after bombardment, transient expression of both the CFP and RFP fluorescent markers was observed as numerous red & blue cells on the surface of the immature embryo. The embryos were then placed on non-selective culture medium and allowed to grow for 3 weeks before scoring for stable colonies. After

this 3-week period, 10 multicellular, stably-expressing blue colonies were observed, in comparison to only one red colony. This demonstrated that PEI-precipitation could be used to effectively introduce DNA for transient expression while dramatically reducing integration of the PEI-introduced DNA and thus reducing the recovery of RFP-expressing transgenic events. In this manner, PEI-precipitation can be used to deliver transient expression of BBM and/or WUS2.

For example, the particles are first coated with UBI::BBM::pinII using PEI, then coated with UBI::moPAT~YFP using TFX-50, and then bombarded into scutellar cells on the surface of immature embryos. PEI-mediated precipitation results in a high frequency of transiently expressing cells on the surface of the immature embryo and extremely low frequencies of recovery of stable transformants (relative to the TFX-50 method). Thus, it is expected that the PEI-precipitated BBM cassette expresses transiently and stimulates a burst of embryogenic growth on the bombarded surface of the tissue (*i.e.* the scutellar surface), but this plasmid will not integrate. The PAT~GFP plasmid released from the Ca^{++} /gold particles is expected to integrate and express the selectable marker at a frequency that results in substantially improved recovery of transgenic events. As a control treatment, PEI-precipitated particles containing a UBI::GUS::pinII (instead of BBM) are mixed with the PAT~GFP/ Ca^{++} particles. Immature embryos from both treatments are moved onto culture medium containing 3mg/l bialaphos. After 6-8 weeks, it is expected that GFP+, bialaphos-resistant calli will be observed in the PEI/BBM treatment at a much higher frequency relative to the control treatment (PEI/GUS).

As an alternative method, the BBM plasmid is precipitated onto gold particles with PEI, and then introduced into scutellar cells on the surface of immature embryos, and subsequent transient expression of the BBM gene elicits a rapid proliferation of embryogenic growth. During this period of induced growth, the explants are treated with *Agrobacterium* using standard methods for maize (see Example 1), with T-DNA delivery into the cell introducing a transgenic expression cassette such as UBI::moPAT~GFPm::pinII. After co-cultivation, explants are allowed to recover on normal culture medium, and then are moved onto culture medium containing 3 mg/l bialaphos. After 6-8 weeks, it is expected that GFP+, bialaphos-resistant calli will be observed in the PEI/BBM treatment at a much higher frequency relative to the control treatment (PEI/GUS).

It may be desirable to “kick start” callus growth by transiently expressing the BBM and/or WUS2 polynucleotide products. This can be done by delivering BBM and WUS2

5'-capped polyadenylated RNA, expression cassettes containing BBM and WUS2 DNA, or BBM and/or WUS2 proteins. All of these molecules can be delivered using a biolistics particle gun. For example 5'-capped polyadenylated BBM and/or WUS2 RNA can easily be made *in vitro* using Ambion's mMessage mMachine kit. RNA is co-delivered along with DNA containing a polynucleotide of interest and a marker used for selection/screening such as Ubi::moPAT~GFPm::PinII. It is expected that the cells receiving the RNA will immediately begin dividing more rapidly and a large portion of these will have integrated the agronomic gene. These events can further be validated as being transgenic clonal colonies because they will also express the PAT~GFP fusion protein (and thus will display green fluorescence under appropriate illumination). Plants regenerated from these embryos can then be screened for the presence of the polynucleotide of interest.

Example 4. Excision of genes encoding cell proliferation factors

15 *a. Rab17::CRE*

The following T-DNA was constructed: RB-Ubi pro-loxP::Rab17 pro-attB1::Cre-attB2::PinII+NOS::ZmWUS2::PinII+Ubi pro::ZmBBM::PinII-loxP::YFP::PinII + Ubi pro::moPAT::PinII-LB. As a control, a T-DNA containing Ubi pro::moPAT::PinII was constructed. These T-DNA are introduced into immature embryos (approximately 0.8 – 2.5 mm in length) of the maize inbred PHH5G using standard *Agrobacterium*-mediated transformation methods. Non-transformed immature embryos of this inbred swell and initiate a small volume of callus cells, but proliferation does not occur on media compositions typically used for maize tissue culture (for example, 605J media, which comprises 4.3 g/l MS salts, 0.6 g/l Shenk & Hildebrand vitamins, 100 mg/l calcium chloride, 275 mg/l ammonium sulfate, 275 mg/l ammonium sulfate, 240 mg/l potassium phosphate, 100 mg/l magnesium sulfate, 3.4 g/l potassium nitrate, 1.8 mg/l boric acid, 6 mg/l manganese sulfate, 0.15 mg/l sodium molybdate, 0.5 mg/l potassium iodide, 22 mg/l disodium EDTA, 17 mg/l ferrous sulfate, 3.4 mg/l silver nitrate, 1 g/l L-proline, 0.2 mg/l nicotinic acid, 0.4 mg/l thiamine, 0.2 mg/l pyridoxine, 0.8 mg/l glycine, 100 mg/l carbenicillin, 0.8 mg/l 2-4D, 1.2 mg/l dicamba, 0.3 g/l casein hydrosylate, 20 g/l sucrose, 0.6 g/l glucose, and 6 g/l TC agar, pH 5.8). Likewise, PHH5G immature embryos transformed with Ubi pro::moPAT::PinII alone do not produce healthy, growing callus, irrespective of whether bialaphos selection is provided. Thus, no transformed events were produced after introducing Ubi pro::moPAT::PinII alone (or with Ubi pro::moPAT::PinII

+ Ubi pro::YFP::PinII). In contrast, when the genes encoding cell proliferation factors (BBM and WUS2) + Ubi pro::moPAT::PinII were introduced into PHH5G immature embryos, vigorously-growing callus transformants were recovered from 45% of the treated embryos. To remove the genes encoding cell proliferation factors, the Rab17 promoter
 5 can be induced through exposure to either 20 mM abscisic acid (ABA), 20-30% sucrose, or desiccation. In this experiment, callus was placed on dry filter papers for three days to induce excision, and then transferred to regeneration medium. If callus was not treated to induce the expression of Cre recombinase, excision of the genes encoding cell
 10 proliferation factors did not occur and viable plantlets were not regenerated. However, for events that were taken through the desiccation treatment, Cre excision occurred in over 90% of single copy events (activating YFP) and subsequent regeneration was not inhibited. Transgenic plants were screened using combinations of PCR primers designed to detect the presence of the Ubi pro-loxP::YFP junction formed as a result of excision, and moPAT (not effected by excision), and the absence of Cre, WUS2 and BBM. Plants
 15 in which excision was complete were grown to maturity and were either selfed or out-crossed to wild-type plants. Transgenic progeny seed were readily identified through the yellow fluorescence phenotype and plants were easily tracked through either BASTA resistance or yellow fluorescence. PCR analysis in both the T1 and T2 generations indicated that only the excised locus was present in a single genomic copy and that no
 20 *Agrobacterium* plasmid backbone was present.

Both FLP and Cre recombinase have been successfully used to excise genes encoding cell proliferation factors before regeneration. The following two constructs represent examples of how the recombinases can be used for controlled excision:

25 PHP32371 – FLP / FRT

RB-Ubi-FRT1::CFP::PinII-attB4+Rab17 Pro-attB1::FLP-
 attB2::PinII+Nos::ZmWUS2::PinII+Ubi::ZmBBM::PinII-FRT1::YFP::PinII +
 Ubi::moPAT::PinII-LB

The T-DNA sequence of PHP32371 is set forth in SEQ ID NO: 110.

30

PHP35648 – Cre / LoxP

RB-Ubi-LoxP::CFP::PinII-attB4+Rab17 Pro-attb1::Cre-
 attB2::PinII+Nos::ZmWUS2::PinII+Ubi::ZmBBM::PinII-
 LoxP::YFP::PinII+Ubi::MOPAT::PinII-LB

The T-DNA sequence of PHP35648 is set forth in SEQ ID NO: 111.

For both recombinases, expression was controlled by the Rab17 promoter (Vilardell *et al.* (1991) *Plant Mol. Biol* 17:985-993) with the attb1 site.

- 5 For both constructs, transgenic callus events were readily recovered, and both constructs worked well for excision of the expression cassettes comprising genes encoding cell proliferation factors (see Table 2). Of the total number of calli exposed to the 3-day desiccation treatment, 61% (Cre) and 29% (FLP) of the resultant plants exhibited a normal wild-type phenotype. As confirmation of excision, PCR analysis in both the T1 and T2
10 generations indicated that only the excised locus was present in a single genomic copy and that no *Agrobacterium* plasmid backbone was present.

Table 2. Desiccation-induced excision of the recombinase, BBM & WUS expression cassettes prior to regeneration.

	# of Callus events exposed to desiccation	# of events with normal T0 plant phenotype	# of T0 plantlets analyzed using PCR	# of single copy plants	# with a totally-excised DevGene package
PHP35648	180	110 (61%)	168	94 (56%)	81 (86%)
PHP32371	118	34 (29%)	75	51 (68%)	31 (61%)

15

Additional constructs that utilize Cre/LoxP were generated.

PHP46446: RB-LoxP-Rab17 Pro-attB1::Cre-attB2::PinII + Nos::Zm-WUS2::PinII::GZ-W64A Term-attB2 + Ubi::ZmBBM::PinII-LoxP-LB

- 20 PHP48733: RB-LoxP-Rab17 Pro-attB1::Cre-attB2::PinII + Nos:ZmWUS2::PinII + Ubi::ZmBBM::PinII-LoxP-LB

The T-DNA sequences of PHP46446 and PHP48733 is set forth in SEQ ID NO: 112 and 113, respectively.

Introduction of PHP35648, PHP48733, or PHP46446 into PHH5G immature maize embryos via *Agrobacterium* resulted in a transformation frequency of 46%, 67%, or 37%, respectively (see Table 3).

- 5 Table 3. Transformation of PHH5G immature maize embryos with maize BBM and WUS2 cell proliferation factors.

Construct	No. of ears	No. of embryos	No. of callus events	Transformation frequency at callus level
PHP35648	14	589	268	45.5
PHP48733	14	584	389	66.6
PHP46446	14	547	203	37.1

- 10 The use of the PHP35648, PHP48733, PHP46446, and PHP32371 constructs (all of which comprised the Rab17 promoter (Vilardell *et al.* (1991) *Plant Mol. Biol* 17:985-993) with the attb1 site regulating the expression of the recombinase), did not result in frequent premature excision of the cell proliferation factor genes, similar to the results presented in Example 1 with the PHP31004 construct.

b. Tetracycline-inducible CRE

- 15 A 35S promoter in which three tetracycline operator sequences (Top3) have been introduced in proximity to the TATA box (Gatz *et al.* (1992) *Plant J* 2:397-404) was operably linked to the CRE structural gene in the following T-DNA which also includes an expression cassette for the tetracycline repressor (TETR), BBM, WUS2, and moPAT, as follows:

20

RB-loxP-35S::Top3::CRE::PinII + Ubi pro::TETR::PinII + NOS::ZmWUS2::PinII + UBI::ZmBBM::PinII-loxP + UBI::moPAT::PinII-LB

- 25 After *Agrobacterium*-mediated transformation of 12 DAP PH581 immature embryos, followed by 6 weeks of selection on 3 mg/l bialaphos, embryos into which the control T-DNA was introduced (RB-UBI::moPAT::PinII-LB) produced transformed events at a 1% frequency. In contrast, when the above T-DNA containing ZmBBM & ZmWUS2 was transformed into immature embryos harvested from the same PH581 ears, transgenic calli were recovered at a 15% frequency. Before regenerating plantlets, callus

is moved onto medium containing 0.5 mg/l tetracycline for 1 week to induce CRE-mediated excision of CRE, WUS and BBM expression cassettes. Glufosinate ammonium-resistant plants are then readily regenerated.

5 Example 5. Control of BBM and WUS expression with regulated promoters to increase transformation frequencies

a. OLE PRO::BBM

In the inbred PH581 maize line, the introduction of UBI::ZmBBM + NOS::ZmWUS2 increased transformation frequencies from < 1% in the control treatment (UBI PRO::moPAT::PinII alone) to 15%. However, such strong over-expression of BBM negatively affects the regeneration of plantlets. Therefore, an oleosin promoter having high levels of expression in callus, with little to no activity during vegetative growth was used to express BBM. When OLE::ZmBBM::PinII + NOS::ZmWUS2::PinII was introduced into PH581 on a first T-DNA and UBI PRO::moPAT::PinII was introduced into the same cells on a second T-DNA, callus transformants were recovered at a 25% frequency. Normal, fertile plants were regenerated and crossed to wild-type PH581. T1 progeny in which the cell proliferation gene locus had segregated away from the UBI PRO::moPAT::PinII locus were readily recovered.

20 *b. Tetracycline-inducible BBM and WUS2*

A 35S promoter in which three tetracycline operator sequences have been introduced in proximity to the TATA box (Gatz *et al.* (1992) *Plant J* 2:397-404) is operably linked to both the BBM and WUS2 genes, and these expression cassettes are put into a T-DNA along with an expression cassette for the tetracycline repressor (TETR) as follows.

RB-35S-Top3::ZmBBM::PinII + 35S-Top3::ZmWUS2::PinII +
UBI::moPAT::PinII-LB

30 Following *Agrobacterium*-mediated transformation of Hi-II immature maize embryos, the embryos are transferred to selection medium 560R with 3 mg/l bialaphos +/- 0.5 mg/l tetracycline. In the control treatment in which only the UBI::moPAT::PinII expression cassette is introduced, the transformation frequency is typically around 5-10%.

For embryos in which the inducible BBM and WUS2 genes are introduced, transformation frequency is expected to be greatly increased upon the addition of tetracycline to the medium.

5 Example 6. Regulated expression of BBM and WUS2 for re-transformation

Stable transgenic events in PHH5G are produced that express ZmBBM and ZmWUS2 in a regulated fashion, for example, having BBM and WUS2 under the control of the OLE and NOS promoters, respectively, or having them being driven by a tetracycline-inducible promoter. Immature embryos are then harvested and re-transformed using *Agrobacterium* to deliver UBI::moPAT::PinII. PHH5G embryos not expressing BBM and WUS2 (*i.e.* wild-type control embryos) produce no transformation events. However, embryos expressing OLE PRO::ZmBBM::PinII and NOS PRO::ZmWUS2::PinII are expected to produce a much higher frequency of bialaphos-resistant events. Regulated expression of the genes encoding cell proliferation factors is expected to enhance the regeneration frequency of normal fertile plants, and the cell proliferation gene locus should readily segregate away from the newly-generated “trait” locus (represented here by the UBI::moPAT::PinII locus). Likewise, when the expression of tetracycline-inducible genes encoding cell proliferation factors are stimulated by the addition of 0.5 mg/l tetracycline, *Agrobacterium*-mediated transformation to deliver the RB-UBI::moPAT::PinII-LB T-DNA is expected to result in enhanced transformation frequencies.

Example 7. Two T-DNA co-transformation to deliver genes encoding cell proliferation factors and trait genes separately

25 An *Agrobacterium* was modified to contain two engineered plasmids, each containing a separate T-DNA. T-DNA-1 was PHP35648 (see Example 4 for description), and T-DNA-2 (PHP41877) contained RB-attB4-UBI::moPAT::PinII + UBI-FRT1::RFP::PinII-attB1 + UBI::GAT::PinII-attB2-FRT87-attB3-LB (GAT=glyphosate-N-acetyltransferase) representing the T-DNA that will contain the desired stack of trait genes). *Agrobacterium*-mediated transformation of PHH5G immature maize embryos was followed by glyphosate selection. Only embryos that have integrated T-DNA-1 grew since growth in culture for PHH5G only occurred when the ZmWUS2 and ZmBBM genes

were present. Only embryos containing T-DNA-2 were glyphosate-resistant and exhibited red fluorescence. Thus, only embryos that were co-transformed with both T-DNAs grew on glyphosate.

5 Example 8. Identification of BBM motifs

Fifty genes from different plant species were identified through a homology search using the maize BBM amino acid sequence (SEQ ID NO: 10) queried against annotated protein sequences (see Figure 1). The gene structure and sequences of these BBM homologs were manually inspected and compared with EST/cDNA alignments whenever possible. The fifty polypeptides are set forth in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 67, and 70-104. To systematically identify possible motifs within the BBM homologs, protein sequences of these fifty homologs were submitted to the MEME web server, available on the world wide web at meme.nber.net/meme4_1/cgi-bin/meme.cgi, with the following specific parameters:

- 15 Number of different motifs: 20
- Minimum motif width: 5
- Maximum motif width: 300
- Minimum number of sites: 5

20 Default values were applied for all other parameters. The raw results from MEME were manually compared with multiple sequence alignments generated by clustalw. Only those candidates showing good consensus with the sequence alignments were considered as motifs for further analysis.

The fifty genes were subjected to a phylogenetic analysis and a total of six subgroups were identified, including BBM, PLT3, PLT1/2, AIL6/7, AIL1, and ANT (see Figure 1). Figure 3 depicts all 50 sequences with each of the motifs that were identified using the MEME web server. Figure 2 provides the motif consensus sequences along with alignments of the various polypeptides used by the MEME web server to generate the consensus motif. With a few exceptions, motifs 1-6, as defined immediately hereinbelow, are present in all 50 genes. This includes motifs 1-3 (SEQ ID NOs 48-50, respectively), which represent the two AP2 domains and a sequence linking the two domains (linker sequence). Motif 4, with the consensus sequence of PK[L/V][E/A][D/N]FLG (SEQ ID NO: 51) is amino-terminal to the two AP2 domains. Motif 5 (SEQ ID NO: 52) flanks the

two AP2 domains on the carboxy terminal end of the polypeptides. Near the amino terminus of the polypeptides is motif 6, with the consensus sequence of NWL[G/S]FSLSP (SEQ ID NO: 53).

There were motifs that were relatively specific for the BBM subgroup of the homologous sequences (referred to herein as BBM polypeptides). An alignment of the BBM polypeptides can be found in Figure 4. Motif 7 is found in all BBM polypeptides at the amino terminus of the polypeptide and has the consensus sequence of [G/E]LSMIK[T/N]WLR (SEQ ID NO: 54). Another motif that is present in all of the BBM polypeptides except for the polypeptides from *Brassica* and from *Arabidopsis*, is Motif 10. Motif 10 has the consensus sequence of WCK[Q/P]EQD (SEQ ID NO: 57) and is located downstream of the AP2 domains.

There are three more motifs specific to the BBM group of polypeptides, including Motif 15 (SEQ ID NO: 59) which appears only in BBM orthologs, but not in the monocot BBM2 polypeptides; a monocot specific motif (Motif 19; SEQ ID NO: 60); and a general BBM specific motif (Motif 14; SEQ ID NO: 58), which appears in BBM homologs except for the *Brassica* and legume branch.

Figure 5 provides a summary of the motif structure of the BBM homologs. The amino terminal motifs 4 and 6 and the AP2 flanking motif 5 distinguish the BBM homologous sequences from other two AP2 domain-containing homologs, such as WRI, AP2, and RAP2.7. Therefore, motifs 1-6 can be considered as core BBM/PLT family motifs. Many subgroups of the BBM/PLT family (BBM, PLT1/2, AIL1, and ANT) also have a carboxy-terminal motif (motif 8; SEQ ID NO: 55) and the third amino terminal motif (motif 9; SEQ ID NO: 56).

The BBM polypeptides all have one additional motif (motif 7; SEQ ID NO: 54) in the amino terminus, and all but the *Brassica* and *Arabidopsis* BBM homologs have an AP2 downstream motif (motif 10; SEQ ID NO: 57). Some other BBM/PLT family members (*e.g.*, monocot AIL1) may have a similar motif as motif 7, but none of them also have motif 9. Motif 10 appears only in BBM polypeptides. In summary, the MEME predicted motifs 1-10 can be regarded as BBM polypeptide motifs. All monocot BBM polypeptides (corn, sorghum, and rice) also have motif 14, 15, and 19 (see Figure 3). Some dicot BBM polypeptides and the second monocot BBM group (BBM2) have one or two of these motifs, but none have all three motifs.

Example 9. Use of maize BBM and WUS2 to increase transformation in ricea. *Oryza sativa* L. ssp. *Indica*

Mature and immature Indica embryos were transformed using *Agrobacterium* with a T-DNA comprising the PHP46911 plasmid (control for immature embryos; see immediately hereinbelow for a description), the PHP32269 plasmid (control for mature embryos; see immediately hereinbelow for a description), or PHP35648.

PHP46911: RB-CaMV35S::Hyg::Nos term + Ubi-FRT1::Zs-yellow1::PinII-FRT87-LB

10 PHP32269: RB-Ubi::PMI::PinII + Ubi::mo-PAT~Zs-yellow1::PinII-LB
(PMI= phosphomannose isomerase)

i. Immature embryo transformation

15 Immature embryos of proprietary Indica strain 851G were transformed using the methods disclosed in International Application Publication No. WO/1995/06722 and Hici and Komari (2006) *Plant Cell, Tissue and Organ Culture* 85:271-283, each of which is herein incorporated by reference in its entirety. Results are shown hereinbelow in Table 4.

Table 4. Transformation events in *Oryza sativa* L. ssp. *Indica* 851G immature embryos infected with *Agrobacterium* containing PHP35648.

Embryo No.	No. of Pieces/Embryo	Total No. of Events/Embryo
1	2	1 (100%)
2	3	1 (100%)
3	6	3 (300%)
4	2	2 (200%)
5	3	3 (300%)
6	3	2 (200%)
7	6	2 (200%)
8	7	2 (200%)
9	11	6 (600%)
10	3	3 (300%)
11	5	3 (300%)
12	3	3 (300%)
TOTAL	54	31 (258%)

In total, infection of 12 immature Indica embryos with *Agrobacterium* containing the PHP35648 plasmid resulted in 31 transformation events, a transformation frequency of 258% events/embryo. The 31 events were derived from 54 pieces of embryo, for a transformation frequency of 57% events/embryo pieces. On the other hand, the infection of nine embryos with *Agrobacterium* containing PHP46911 resulted in only one single transformation event and an overall transformation frequency of 11%.

10

ii. Mature embryo transformation

Mature embryos of Indica strains IRV95 and 851G were transformed using the following protocol. Healthy rice seeds were dehusked and soaked in 50 ml of sterile water with a drop of Tween 20 for 5 minutes. The seeds were sterilized with 75% ethanol for 2-3 minutes, followed by a soak in 50 ml sodium hypochlorite and a drop of Tween 20 for 15-20 minutes. The seeds were rinsed and then callus was initiated in callus induction medium (4.3 g/l MS salts, 10 ml/l B5 vitamins (100X), 2 mg/l 2,4-D, 500 mg/l L-proline, 30 g/l sucrose, 0.3 g/ casein hydrolysate, 3 g/l Gelrite (added after bringing to volume with D-I H₂O and adjusting pH to 5.8) under continuous light at 32°C for 12 days.

Established callus was transformed using *Agrobacterium* by incubating the callus with the *Agrobacterium* for 10-15 minutes. The *Agrobacterium* solution was then decanted and 12-15 seeds were placed onto a filter paper disk that had been pre-moistened with 0.5 ml of AAM medium (50 ml/l AA macro elements (20X), 10 ml/l AA

5 microelements (B5 microelements; 100X), 10 ml/l AA vitamins (B5 vitamins; 100X), 5 ml/l Fe-EDTA-B5 (200X), 1 mg/L 2,4-D, 100 ml/l amino acids, 68.5 g/l sucrose, 36 g/l glucose, 500 mg/l cas amino acid at pH 5.2) containing 50 μ M acetosyringone. The seeds and pre-moistened filter papers were cultured in the dark at 21°C for 72 hours in ACCM

10 medium (4.3 g/l MS salts, 10 ml/l B5 vitamins (100X), 2 mg/l 2,4-D, 20 g/l sucrose, 10 g/l glucose, 0.5 g/l casein hydrolysate, 3g/l Gelrite (added after bringing to volume with D-I H₂O and adjusting pH to 5.2) containing 200 μ M acetosyringone. The calli were washed and then transferred to resting ASM medium (100 ml/l 580S major salts (10X), 10 ml/l 580S minor salts (100X), 5 ml/l 580S FeEDTA-L (200X), 5 ml/l 580S vitamins (200X), 100 mg/l myo-inositol, 300 mg/l casein hydrolysate, 30 g/l maltose, 2 mg/l 2,4-D, 500

15 mg/l L-proline, 0.5 g/l MES buffer, 8 g/l agar (added after bringing to volume with D-I H₂O and adjusting pH to 5.8) containing 250 mg/l carbenicillin for 15 days. Following the 15 day incubation, the calli were transferred to selection medium (100 ml/l 580S major salts (10X), 10 ml/l 580S minor salts (100X), 5 ml/l 580S FeEDTA-L (200X), 5 ml/l 580S vitamins (200X), 100 mg/l myo-inositol, 300 mg/l casein hydrolysate, 30 g/l sucrose, 2

20 mg/l 2,4-D, 500 mg/l L-proline, 0.5 g/l MES buffer, 8 g/l agar (added after bringing to volume with D-I H₂O and adjusting pH to 5.8) with 200 mg/l carbenicillin and 2 mg/l bialaphos and subcultured every 15 days until transformation events arose.

The event was then dessicated on filter paper at 28°C for 48 hours to excise the developmental genes. Dessicated events were identified based on the expression of Zs-

25 yellow visualized under the microscope. The dessicated event was transferred to regeneration medium (100 ml/l N6 major salts (10X), 10 ml/l FeEDTA (100X), 10 ml/l B5 minor salts (100X), 10 ml/l B5 vitamins (100X), 1 mg/l 1-naphthalene acetic acid, 3 mg/l 6- benzyl amino purine, 30g/L maltose, 0.3g/l proline, 0.3g/l vitamin assay casamino acids, 4 g/l agarose type 1, 30 mg/l glutamine (added after adjusting pH to 5.8 and

30 sterilization) and grown at 32°C under light. After 1-1.5 months, green shoots emerged from the callus and it was transferred to rooting medium (100 ml/l MS major salts (10X), 10 ml/l FeEDTA (100X), 10 ml/l MS minor salts (100X), 10 ml/l MS vitamins (100X), 2 mg/l indole-3-butyric acid, 15 g/l sucrose, 1 g/l vitamin assay casamino acids, 10X AA amino acid at pH 5.8). After another 15-20 days, the rooted plants are hardened in Y-

- medium (1.25 ml/l Stock A (9.14 g/100 ml ammonium nitrate (HIMEDIA RM5657)), 1.25 ml/l Stock B (4.03 g/100 ml sodium hydrogen phosphate (HIMEDIA 58282)), 1.25 ml/l Stock C (7.14 g/100 ml potassium sulfate (HIMEDIA 29658-4B)), 1.25 ml/l Stock D (8.86 g/100 ml calcium chloride (HIMEDIA C5080)), 1.25 ml/l Stock E (3.234 g/100 ml magnesium sulfate (HIMEDIA RM683)), 1.25 ml/l Stock F (15 mg/100 ml magnesium chloride tetra hydrate (HIMEDIA 10149), 6.74 mg/100 ml ammonium molybdate (HIMEDIA 271974), 9.34 mg/100 ml boric acid (SIGMA 136768), 0.35 mg/100 ml zinc sulfate hepta hydrate (HIMEDIA RM695), 0.31 mg/100 ml copper sulfate hepta hydrate (HIMEDIA C8027), 0.77 mg/100 ml ferric chloride hexa hydrate (SIGMA 236489), 119 mg/100 ml citric acid monohydrate (HIMEDIA C4540)) at pH 5.2.

Results are shown hereinbelow in Table 5.

Table 5. Transformation events in *Oryza sativa* L. ssp. *Indica* 851G and IRV95 mature embryo-derived callus.

Seed No	Variety	Construct	No. of infected calli	No. of events	% of events	No. of events regenerated	% of regenerated events/infected calli
1	851G	PHP35648	100	8	8.00%	5	5.00%
		PHP32269	50	1	2.00%	0	0.00%
2	851G	PHP35648	130	18	13.85%	N/A ^a	N/A
		PHP32269	50	1	2.00%	N/A	N/A
3	IRV95	PHP35648	128	20	15.63%	N/A	N/A
		PHP32269	50	1	2.00%	N/A	N/A

- ^a N/A: data not available; calli are currently being desiccated, so no data on number or percentage of regenerated events are available

b. *Nipponbare* rice (cv. *Kitake*)

Callus was initiated from mature embryos of *Oryza sativa*, var. *Nipponbare*, cv. *Kitake*, and established callus was transformed using *Agrobacterium* strain LBA4404 containing UBI::ZmBBM::PinII and NOS PRO::ZmWUS2::PinII between the T-DNA borders. Callus culture medium for rice consisted of N6 salts, Eriksson's vitamins, 0.5 mg/l thiamine, 2 mg/l 2,4-D, 2.1 g/l proline, 30 g/l sucrose, 300 mg/l casein hydrolysate, 100 mg/l myo-inositol, and 3 g/l gelrite at pH 5.8. Five days after *Agro*-infection, callus was observed under an epifluorescent dissecting microscope. For calli that were transformed with UBI::ZS-GREEN::PinII alone, all the visible fluorescent foci were single cells, with a few possible 2-4 cell foci. When callus was transformed with NOS::ZmWUS2::PinII + UBI::ZmBBM::PinII + UBI::ZS-GREEN::PinII and observed 5 days later, numerous rapidly-growing, green-fluorescent, multicellular colonies were present.

Example 10. The rice, sorghum and grape BBM genes increase transformation frequency in maize.

Growth assays were performed to test whether BBM genes from various species would stimulate growth in maize. For these experiments, 10-13 DAP embryos of the genotype PH581 were bombarded with a first plasmid containing a UBI PRO::moPAT~GFP::pinII expression cassette plus either a plasmid containing 35S::GUS::pinII (control treatment) or a BBM gene driven by the ubiquitin promoter. To attach the DNAs to gold particles, a 25 µl aliquot of 0.6 µm particles (0.01 mg/µl) was added to fresh tubes before attaching DNA. To attach uncoated DNA, the particles were pulse-sonicated, then 500 ng of each DNA (in 5 µl water) was added, followed by mixing (pipetting up and down a few times with a Pipettman). Then 2.5 µl of TFX-50 was added, and the solution was placed on a rotary shaker for 10 minutes. After centrifugation at 10,000g for 1 minute, the supernatant was removed, and the particles were resuspended in 60 µl of EtOH, followed by a 10 minute incubation. The particles were spun briefly (*i.e.*, 10 seconds), the supernatant removed, and 60 µl EtOH added. The solution was spotted onto macrocarriers and the gold particles onto which DNA had been attached were delivered into scutellar cells of 10-13 DAP immature embryos using a standard protocol for the DuPont PDS-1000 Helium Gun. After 4-5 weeks on culture medium, the embryos were examined and the number of GFP-expressing multicellular colonies were counted.

a. OsBBM

Based on the rice BBM genomic sequence (SEQ ID NO: 117), TIGR software was used to predict intron splicing and the resultant cDNA sequence (OsBBM (MOD1) is set forth in SEQ ID NO: 118). A plasmid containing an expression cassette for the rice BBM (MOD1) gene (UBI PRO::OsBBM (MOD1)::PinII) was co-delivered with UBI::moPAT~GFP::PinII into 13 DAP PH581 immature embryos using the particle gun. When the UBI PRO::moPAT~GFP::pinII cassette was introduced with 35S::GUS, few multicellular growing sectors were observed (see Tables 6-10). When UBI::ZmBBM::PinII was introduced along with UBI::moPAT~GFP::PinII, a stimulation of growth was observed as indicated by the total number of growing multicellular colonies observed as well as the number of embryos with multiple growing colonies. Despite many conserved amino acid motifs between the encoded maize protein and the protein encoded by the predicted OsBBM (MOD1) cDNA, when the rice expression cassette UBI::OsBBM (MOD1)::PinII, was introduced along with the moPAT~GFP cassette, no stimulation of growth was observed relative to the control treatment (35S::GUS) (see Tables 6 and 7). Based on a comparison of the maize and rice MOD1 amino acid sequences, and a more careful analysis of the rice genomic sequence, it was determined that the TIGR software failed to predict the splicing around a 9-bp exon that encodes the amino acids VYL in the first AP2 domain. Upon including this 9bp exon in a re-synthesized rice cDNA (OsBBM (MOD2); set forth in SEQ ID NO: 120), and introducing this in the expression cassette UBI::OsBBM (MOD2)::PinII, a growth stimulation similar to that observed for the maize BBM gene was observed (Table 7, 8, 9 and 10).

Table 6. Number of green-fluorescent multicellular colonies six weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

TRT	GFP+ Colonies/Bombarded Embryo											Total Number of Multicellular Colonies
	0	1	2	3	4	5	6	7	8	9	10	
35S::GUS	44											0
UBI::ZmBBM	15	10	5	4	3	1	1			1		25
UBI::OsBBM (MOD1)	42											0
OLE::ZmBBM	14	16	6	1								14
OLE::ZmANT	44											0

Table 7. Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

TRT	GFP+ Colonies/Bombarded Embryo									Total Number of Multicellular Colonies
	0	1	2	3	4	5	6	7	8	
35S::GUS	70	5	0	3						8
UBI::ZmBBM	19	24	17	7	3	1				52
UBI::OsBBM (MOD1)	70	4	2							6
UBI::OsBBM (MOD2)	28	29	11	3	1	1				45
OLE::ZmBBM	28	24	11	9	2	1	2			49
OLE::ZmANT	55	16	1	1	1					19

- 5 Table 8. Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

Treatment	Number of GFP+ Colonies per Scored Embryo							Total Number of Multicellular Colonies
	0	1	2	3	4	5	6	
35S::GUS	70	5	0	3	0	0	0	8
UBI::ZmBBM	19	24	17	7	3	1	0	52
UBI::OsBBM (MOD2)	28	29	11	3	1	1	0	73
OLE::ZmBBM	28	24	11	9	2	1	2	49
OLE::ZmANT	55	16	1	1	1	0	0	19

10

Table 9. Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

Treatment	Number of GFP+ Colonies per Scored Embryo							Total Number of Multicellular Colonies
	0	1	2	3	4	5	6	
35S::GUS	61	6	1	0	0	0	0	7
UBI::ZmBBM	21	29	12	3	2	0	0	46
UBI::OsBBM (MOD2)	27	29	5	2	0	1	0	37
UBI::VvBBM	32	21	6	0	1	0	0	28
UBI::ZmBBM (genomic)	9	36	13	6	3	0	0	58

Table 10. Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

GFP+ Colonies/Scored Embryo												Total Number of Multicellular Colonies
TRT	0	1	2	3	4	5	6	7	8	9	10	
35S::GUS	80	11										11
UBI::ZmBBM	43	28	13	5	2							48
UBI::OsBBM (MOD2)	45	32	11	3								46
UBI::SbBBM (MOD1)	81	10										10

b. SbBBM

- 5 Based on the sorghum genomic BBM sequence (SEQ ID NO: 69), TIGR software was used to predict intron splicing and the resultant cDNA sequence (SbBBM (MOD1) is set forth in SEQ ID NO: 3). A plasmid containing an expression cassette for the sorghum BBM (MOD1) gene (UBI PRO::SbBBM (MOD1)::PinII) was co-delivered with UBI::moPAT~GFP::PinII into 13 DAP PH581 immature embryos using the particle gun.
- 10 When the UBI PRO::moPAT~GFP::PinII cassette was introduced with 35S::GUS, few multicellular growing sectors were observed (see Table 10). Unlike UBI::ZmBBM and UBI::OsBBM (MOD2), which in this experiment produced a similar positive growth stimulation, UBI::SbBBM (MOD1)::PinII failed to simulate growth. Assuming there was some unknown defect in the SbBBM (MOD1) synthetic cDNA, the sorghum genomic
- 15 BBM was cloned using PCR and sequenced to verify fidelity. In an earlier experiment, the maize genomic BBM (SEQ ID NO: 116) was placed behind the UBI promoter and when compared to the UBI::ZmBBM cDNA construct it produced a similar degree of growth stimulation (Table 9). Using the genomic sorghum clone [UBI::SbBBM (GEN)], a similar level of growth stimulation was also observed (Tables 11 and 12).

20

Table 11. Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

Treatment	GFP+ Colonies/Scored Embryo									Total Number of Multicellular Colonies *
	0	1	2	3	4	5	6	7	8	
35S::GUS	57	3								3
UBI::VvBBM-NoVYL	57	3								3
UBI::VvBBM	36	15	4	1	1	1				22
UBI::SbBBM (Genomic)	10	19	11	11	4	3	2			50
UBI::ZmBBM	12	18	8	10	4	3	1		1	45

5 Table 12. Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

TRT	GFP+ Colonies/Scored Embryo						Total Number of Multicellular Colonies
	0	1	2	3	4	5	
35S::GUS	60						0
UBI::ZmBBM	19	18	11	7	4	1	41
UBI::SbBBM (Genomic)	20	15	14	6	5		60
UBI::VvBBM	46	11	3				14
UBI::VvBBM - No VYL	60						0

c. VvBBM

A nucleotide sequence was derived that provided good codon usage for maize, but expressed the amino acid sequence of a grape BBM (VvBBM; SEQ ID NO: 5). A plasmid containing an expression cassette for a synthetic grape BBM gene (UBI PRO::VvBBM::PinII) was co-delivered with UBI::moPAT~GFP::PinII into 10 DAP PH581 immature maize embryos using the particle gun. When the UBI PRO::moPAT~GFP::PinII cassette was introduced alone, no (Table 12) or very few (Tables 9 and 11) multicellular growing sectors were observed. When UBI::VvBBM::PinII + UBI::moPAT~GFP::PinII were co-delivered, numerous RFP+ multicellular colonies were observed growing on the surface of bombarded embryo after 4 weeks. As with growth stimulation by the maize, rice and sorghum BBM genes, the growth stimulation imparted by the UBI::VvBBM::PinII cassette was manifested by an increase in the overall number of multicellular colonies, and also an increase in the number of multicellular colonies growing on single embryos (see Tables 9, 11 and 12).

When a construct comprising the VvBBM sequence, in which the 9-bp sequence encoding VYL in the AP2 domain was removed, was introduced into maize, there was no observed growth stimulation (Tables 11 and 12), similar to the observations made with the rice BBM gene lacking this same exon.

5

d. maize ANT gene

The following constructs were used for comparison: OLE PRO::ZmBBM::pinII, and OLE PRO::ZmANT::pinII. The nucleotide and amino acid sequences of ZmANT are set forth in SEQ ID NOs: 66 and 67. Each of these plasmids was co-delivered with

10 UBI::moPAT~GFP::pinII into 10 or 13 DAP PH581 immature embryos using the particle gun. When the UBI PRO::moPAT~GFP::pinII cassette was introduced alone, no (Table 6) or few multicellular growing sectors (Tables 7 and 8) were observed. When OLE::ZmBBM::pinII + UBI::moPAT~GFP::pinII were co-delivered, a substantial increase in the number of embryos with GFP+ multicellular colonies were observed

15 growing on the surface of each bombarded embryo after 5 weeks (*i.e.* relative to the control treatment). In addition, the number of embryos supporting multiple GFP+ colonies increased. Embryos co-bombarded with OLE::ZmANT::pinII + UBI::moPAT::pinII appeared identical (Table 6, with no multicellular colonies in either treatment) or similar to the control treatment (Figures 6 and 7, with only a 2-fold increase

20 in colony formation and numerous single GFP+ cells (indicating only transient expression but no division) and a reduced number of GFP+ colonies relative to the BBM treatment. In a second experiment with the same treatments (control with no BBM or ANT, Ole::BBM or Ole::ANT), out of 44 embryos shot per treatment, the control and ANT treatments produced no multicellular GFP+ colonies after 3 weeks while the BBM

25 treatment produced 14 colonies.

Example 11. Expression of the maize BBM and WUS genes improves transformation in sorghum.

Agrobacterium tumefaciens LBA4404 and a super-binary vector constructed with

30 pSB1 and pSB11 (Komari *et al.* (1996) *Plant J* 10:165-174; Thompson *et al.* (1987) *EMBO J* 6:2519-2523) can be used for sorghum transformation (Zhao (2006) In "Agrobacterium Protocols," vol. 1, Kan Wang, ed. Hamana Press, Totowa, NJ; U.S. Patent No. 6,369,298; and International Application Publication No. WO 98/49332). The super-binary vector contained a selectable marker gene, bar (Chalfie *et al.* (1994) *Science*

263:802-805) and a visible marker gene, such as red fluorescent protein (RFP), yellow fluorescent protein (YFP), or intron-GFP (Jefferson *et al.* (1986) *Proc Natl Acad Sci USA* 83:8447-8451).

Minimal AB media included 50 ml/l Stock A, 50 ml/l Stock B, 5 g/l glucose, 9 g/l
 5 Phytagar. For the *Agrobacterium* strain used in this protocol, 50 mg/l spectinomycin is added after autoclaving. Stock A included 60 g/l K₂HPO₄, and 20 g/l NaH₂PO₄, pH 7.0. Stock B is 20 g/l NH₄Cl, 6 g/l MgSO₄ 7H₂O, 3 g/l KCl, 0.2 g/l CaCl₂, and 0.5 g/l FeSO₄ H₂O. YP medium contained 5 g/l yeast extract, 10 g/l peptone, 5 g/l NaCl, and 15 g/l Bacto-agar. For the *Agrobacterium* stain used in this protocol, 50 mg/l spectinomycin was
 10 added after autoclaving.

PHI-I media included 4.3 g/l MS salts (GIBCO BRL catalog no. 11117-874), 0.5 mg/l nicotinic acid, 0.5 mg/l pyridoxine HCl, 1 mg/l thiamine HCl, 0.1 g/l myo-inositol, 1 g/l vitamin assay casamino acids, 1.5 mg/l 2,4-D, 68.5 g/l sucrose, 36 g/l glucose, pH 5.2. 100 µM acetosyringone is added before using.

15 PHI-T media included PHI-I with sucrose reduced to 20 g/l and glucose reduced to 10 g/l, 2, 4-D increased to 2 mg/l, and with 0.5 g/l MES buffer, 0.7 g/l L-proline, 10 mg/l ascorbic acid, 100 µM acetosyringone and 8 g/l agar, pH 5.8 added.

PHI-U media included PHI-T without glucose and acetosyringone, and with 1.5 mg/l 2,4-D, 100 mg/l carbenicillin, and 5 mg/l PPT (glufosinate-HN4) added.

20 PHI-RF media included 4.3 g/L MS salts (GIBCO BRL 11117-074), 0.5 mg/L nicotinic acid, 0.1 mg/L thiamine HCl, 0.5 mg/L pyridoxine HCl, 2.0 mg/L glycine, 0.1 g/L myo-inositol, 0.49 µM cupric sulfate, 0.5 mg/L zeatin (Sigma Z-0164), 1 mg/L IAA, 26.4 µg/L ABA, 0.1 mg/L thidiazuron, 60 g/L sucrose, 3 mg/L bialaphos, 100 mg/L carbenicillin, and 8 g/L agar, pH 5.6.

25 PHI-Z media included 2.15 g/L MS salts, 2.5 ml/L MS vitamin mix, 20 g/L sucrose, and 3 g/L gelrite, pH 5.6

Suspension for immature embryo infection consisted of 100 µM acetosyringone in PHI-I medium (pre-warmed to room temperature). Bacteria were scraped off a working plate with a sterile bacteria loop and placed in PHI-I with 100 µM acetosyringone. The
 30 suspension was vigorously vortexed to break clumps and form a uniform suspension as determined by visual inspection. 1 ml of *Agro*-suspension was taken to measure optical density at 550 nm. The suspension was diluted with PHI-I plus 100 µM acetosyringone to 10⁹ cfu/ml (OD at 0.7).

Sorghum plants were grown under greenhouse, growth chamber, or field conditions. Healthy sorghum plants were always important for a successful transformation. Immature panicles were harvested 9-13 days post-pollination depending on the growing conditions. The size of immature zygotic embryos used in transformation
5 ranged from 0.8 to 2.5 mm in length. Immature kernels were removed from the panicles and sterilized with 50% bleach and 0.1% Tween-20 for 30 min. with vacuum, then the kernels were rinsed three times with sterile water. The kernels were kept in sterile water before isolating embryos. Embryos were aseptically dissected from each sterilized sorghum kernel and placed in a 2-ml microtube containing 2 ml PHI-I with 100 μ M
10 acetosyringone. Usually, about 100 embryos were placed in each tube.

PHI-I liquid medium was removed from the tube comprising the embryos with a 1 ml micropipettor and replaced with 1 ml of the *Agrobacterium* suspension. The tube was gently inverted a few times to mix well and incubated 5 minutes at room temperature. The *Agrobacterium* suspension was removed from the tube with a 1 ml micropipettor. The
15 embryos were scraped from the tube using a sterile spatula. Immature embryos were transferred to a plate of PHI-T medium in a 100 x 15 mm Petri dish. The embryos were oriented with embryonic axis down on the surface of the medium. These embryos were incubated at 21 - 25°C in the dark for 3 days. The embryos were transferred to PHI-U minus PPT with the same orientation and incubated at 28°C in the dark for 4 days.

20 The embryos were transferred to PHI-U medium and incubated at 28°C in the dark for 2 - 3 weeks and were subcultured every two to three weeks for about 10 – 20 weeks to obtain enough callus for regeneration into plants.

These calli were transferred to PHI-RF medium and incubated at 28°C in the dark for approximately 2-3 weeks to develop shoots. When shoots formed, these cultures were
25 moved to a lighted culture room under conditions of 16 hours light (270 μ E m⁻² sec⁻¹) and 8 hours dark at 25°C. Shoots (about 3-5 cm tall) were transferred to plastic boxes (10x9x10 cm) containing PHI-Z medium. These shoots were cultured under the same light and temperature conditions for 3-5 days. Each box contained shoots derived from a single embryo. When the plantlets reached about 8-10 cm tall with healthy roots, these
30 plantlets were transferred to pots with Universal Mix (Strong-Lite, Seneca, IL61360) in the greenhouse.

Embryos were harvested from developing sorghum seed and transformed using *Agrobacterium*, delivering the PHP32371 T-DNA (see Example 4). As a control treatment, embryos were transformed with RB- Ubi::moPAT + Ubi:CFP-LB. Callus was selected on 3 mg/l bialaphos, and monitored for fluorescence to aid in identifying transgenic sectors. Sorghum transformation frequencies using Ubi:moPAT + Ubi:CFP averaged 0.5%. By comparison, in six experiments, a total of 393 embryos were transformed with PHP32371, producing an average transformation frequency of 18.3% (see Table 13). Callus from the first experiment (30 events from a starting total of 140 embryos) was used to test the desiccation-induced excision controlled by the Rab17 promoter, and subsequent plant regeneration. Twenty-one events were desiccated for three days on dry filter papers and then taken through the standard regeneration protocol. Fifteen of the 21 events produced a total of 81 plants, with multiple plants being regenerated for many of the individual events. Of these, 60% contained a single copy of the integrated DNA, and of the single copy events, 91% produced PCR results indicating complete excision of the genes encoding cell proliferation factors. From excised events, normal phenotype plants lacking FLP and WUS2 were readily regenerated.

Table 13. Transformation efficiencies after *Agrobacterium*-mediated transformation with PHP32371.

Experiment ID	Number of Embryos	Number of Transformation Events	Transformation Frequency (%)
1	140	30	21.4
2	40	3	7.5
3	60	8	13.3
4	40	7	17.5
5	61	12	19.7
6	52	12	23.1
Average			18.3

20

Example 12. Expression of the maize BBM and WUS genes improves transformation in sugarcane.

A developmental gene binary vector with the ZmBBM/ZmWUS2 gene cassette was compared with a standard vector containing moPAT plus either DsRED or YFP without the ZmBBM/ZmWUS2 gene cassette for transformation frequency using two *Agrobacterium* strains, AGL1 and LBA4404, in CP89-2376 and CP01-1372 sugarcane cultivars. The developmental gene binary vector contains Ubi::LoxP::CFP+Rab17Pro-attB1::Cre-attB2::PinII+Nos::ZmWUS2::PinII+Ubi::ZmBBM::PinII-LoxP::YFP+Ubi::MOPAT::PinII. The Lox cassette containing CFP::Cre::WUS::BBM can be excised by Cre recombinase controlled by the Rab17 promoter. Callus tissues of both CP89-2376 and CP01-1372 cultivars were induced and maintained on DBC3 medium. Tissues were infected with *Agrobacterium* containing the developmental gene binary vector in 10 mM MgSO₄ plus 100 µM acetosyringone and then cocultivated with liquid DBC3(M5G) medium plus 100 µM acetosyringone on the filter paper in Petri dishes at 21°C in the dark. Three days after cocultivation, the tissues were transferred to DBC3 containing 100 mg/L cefotaxime and 150 mg/L timentin for AGL1, and DBC3 containing 100 mg/L carbenicillin for LBA4404, and incubated at 26°C (±1°C) in the dark or dim light for 3-7 days. Afterwards, the tissues were transferred to the same media as the previous step plus 3 or 5 mg/L bialaphos. After two months from the initiation of the experiment, transformation frequency was calculated by the number of tissues showing CFP expression divided by the number of explants infected by *Agrobacterium*. Table 14 demonstrated that AGL1 was even more efficient in transformation than LBA4404 in both CP89-2376 and CP01-1372. There was also a genotype difference in transformation frequency; CP89-2376 had much higher transformation frequencies than CP01-1372 using either of the *Agrobacterium* strains.

AGL1 containing the developmental gene vector was also used to test sugarcane germplasm screening in another set of experiments using 5 different cultivars (CP96-1252, CP01-1372, CP89-2376, CPCL97-2730 and HoCP85-845). Callus tissues of all 5 cultivars tested were induced and maintained on DBC3 medium and tissues were infected with AGL1 containing the developmental gene binary vector. The use of developmental genes dramatically increased transformation frequency in all 5 cultivars tested. Transformation frequencies in the most amenable cultivar, CP89-2376, using a standard binary vector averaged 116.7% (56/48) (Table 14). In contrast, an average transformation frequency in this cultivar from 5 experiments was >2,512.5% (>1,005

events/40 tissues infected) using the developmental gene binary vector. Similar results were obtained from the remaining 4 cultivars, CP96-1252, CP01-1372, CPCL97-2730 and HoCP85-845; transformation frequencies ranged from 62.5% to 187.5% in these 4 cultivars while no transgenic events were obtained using the standard vector without the

5 BBM/WUS gene cassette from these cultivars.

Table 14. Transformation frequency in sugarcane using the developmental genes ZmBBM and ZmWUS2.

<i>Agrobacterium</i>		Sugarcane Cultivar				
Strain	Binary Vector	CP96-1252	CP01-1372	CP89-2376	CPCL97-2730	HoCP85-845
AGL1	DG ^a	n.t. ^c	37.5% (3/8)	n.t.	n.t.	n.t.
LBA4404	DG	n.t.	0% (0/8)	n.t.	n.t.	n.t.
AGL1	DG	n.t.	>1,250.0% (>100/8)	>6,250.0% (>500/8)	n.t.	n.t.
LBA4404	DG	n.t.	12.5% (1/8)	>1,500% (>120/8)	n.t.	n.t.
AGL1	DG	n.t.	n.t.	687.5% (>55/8)	n.t.	n.t.
AGL1	DG	n.t.	n.t.	>2,500% (>200/8)	175.0% (14/8)	n.t.
AGL1	DG	150.0% (12/8)	62.5% (5/8)	>625.0% (>50/8)	62.5% (6/8)	n.t.
AGL1	DG	n.t.	n.t.	>2,500% (>200/8)	n.t.	187.5% (15/8)
AGL1	Std ^b	0% (0/8)	0% (0/8)	116.7% (56/48)	0% (0/8)	0% (0/8)

Each transformation treatment had 8 pieces of callus tissues 0.4-0.5 cm in size.

DG^a: developmental gene vector with BBM/WUS gene cassette

Std^b: standard vector without BBM/WUS gene cassette

n.t.^c: not tested

10

Transgenic callus tissues were desiccated on dry filter papers for three days to induce excision of the Lox cassette containing CFP::Cre::WUS::BBM by Cre recombinase driven by the Rab17 promoter. Excision was monitored by observing YFP expression on desiccated transgenic callus events by the presence of the UBI:loxP:YFP junction formed as a result of excision. Cre excision occurred at 83 of 87 transgenic events (95.4%) (Table 15). Plants from some transgenic events after excision are being regenerated on MSB plus 1 mg/L bialaphos and antibiotics.

Table 15. Excision efficiency of the BBM/WUS gene cassette in transgenic sugarcane events by desiccation.

Sugarcane Cultivar	<i>Agrobacterium</i> Strain	Binary Vector	Excision Efficiency (%)
CP89-2376	AGL1	DG ^a	93% (40/43)
CP89-2376	LBA4404	DG	100% (25/25)
CP01-1372	AGL1	DG	100% (13/13)
CP01-1372	LBA4404	DG	0% (0/1)
CP89-2376	AGL1	DG	100% (5/5)
Average			95.4% (83/87)

DG^a: developmental gene vector with BBM/WUS gene cassette

Example 13. Complementation of separately transformed BBM and WUS2 genes.

Nos::ZmWUS2::PinII and Rab17-attB1::CRE::PinII are integrated into the genome of an inbred maize plant. LoxP-UBI::BBM::PinII-LoxP + a trait gene operably linked to a promoter are re-transformed into the inbred as a single T-DNA. The BBM and WUS2 genes will complement each other, stimulating rapid growth only in the cells where both are present. BBM is then excised and normal fertile plants are regenerated. Later, the WUS2/CRE locus is segregated away from the genome.

Example 14. Transformation of mature dried maize seed.

Cell proliferation factors can be used to increase transformation and/or recovery frequencies in recalcitrant plants and/or target tissues, such as mature seed.

A T-DNA containing an excisable construct comprising a maize BBM and a maize

WUS gene was constructed:

PHP38333: RB-Ubi-LoxP::CFP::PinII-attB4 + Rab17 Pro-attb1::Cre-attB2::PinII +
Nos::ZmWUS2::PinII + Ubi::ZmBBM::PinII-LoxP::YFP::PinII + Ubi::moPAT::PinII-LB

5

As a control treatment, embryos were transformed with PHP32269: RB-Ubi::moPAT-YFP::PinII-LB.

The glycerol stock of a thymidine-auxotrophic mutant *Agrobacterium* strain LBA4404 with vector PHP38333, or the control vector were stored at -80°C before use. A
10 master plate was made by dipping an inoculation loop into a glycerol stock and streaking onto 12V solid medium with 50mg/l thymidine in a 100x15 Petri dish (for PHP38333) or onto 12S solid medium with 50 mg/l spectinomycin (for the control plasmid). Plates were incubated (inverted) at 28°C in the dark for 2-3 days to produce single colonies. Master plates were stored at 4°C for up to 4 weeks and are used for initiating fresh culture for
15 transformation. Several colonies were picked from the master plates and streaked onto 810F solid medium with 50mg/l thymidine and incubated at 28°C, in the dark for 1 day and fresh *Agrobacterium* was used for transformation.

To make the *Agrobacterium* suspension, 20ml of 700 liquid medium with 50mg/l thymidine was added into a 50ml snap cap tube. A stock solution of acetosyringone (AS)
20 was added to achieve a final concentration of 200 uM and a stock solution of Silwet L-77 was added to achieve a final concentration of 0.04%. *Agrobacterium* was collected from a 1-day culture plate and suspended in the 700 liquid medium. The tube was vortexed until the *Agrobacterium* culture clumps were completely broken up and evenly dispersed throughout the solution. One ml of the suspension was transferred to a spectrophotometer
25 tube and the OD of the suspension was adjusted to 0.7 at 550nm by adding either more *Agrobacterium* or more of the same suspension medium.

Maize inbred line PHN46 was used as the initial genotype for transformation tests. Dry seeds were placed in a covered glass jar, in an 80% ethanol solution with stirring for 5 min. The ethanol was decanted and a 50% bleach solution with a few drops of the
30 surfactant Tween-20 were added and seeds in the bleach solution were stirred for 30 min and washed three times with sterile water in a sterile flow hood. Surface sterilized seed were soaked in the sterile water for approximately 24h at room temperature, which is

sufficient to trigger germination. After 24 hours, the softened seeds were sterilized once again with a 50% bleach solution for 5 min, and then washed three times with sterile water in a sterile flow hood.

Mature embryos were dissected out of the softened and sterilized kernels. Each
5 mature embryo was sliced into 3- 4 thin sections by hand using a No.10 surgical scalpel under the dissecting microscope. Each explant contained exposed leaf primordia, mesocotyl and root primordia regions. These regions on the embryo chips were the target area for T-DNA delivery during *Agrobacterium*-mediated transformation and contain cells that are culture responsive. Sliced explants were transferred into a 6-well culture plate
10 containing 4ml 700 liquid medium. About 45 explants were placed into each well for *Agrobacterium* infection.

Liquid medium in the 6-well plate was removed from the explants and replaced with 4ml of prepared *Agrobacterium* suspension. The 6-well plate was transferred into a transparent polycarbonate desiccator container. The desiccator was covered and placed on
15 a platform shaker rotating at a speed of 100RPM and connected to an in-house vacuum system for 30 min. After infection, the *Agrobacterium* suspension was drawn off from the wells and the explants were transferred onto solid 710I co-cultivation medium with 50mg/l thymidine. The infected embryo explants on the solid medium were incubated at 21°C in the dark for 3 days. The number of infected explants was recorded to later calculate
20 transformation efficiencies.

To evaluate T-DNA delivery efficiency, both the control vector without genes encoding cell proliferation factors and the vector with the genes encoding cell proliferation factors were used to infect embryo explants. After 3d co-cultivation, all of the chips were transferred onto 605J medium for continuous culture. T-DNA delivery was evaluated
25 around 5d after *Agrobacterium* infection. Transient expression of the color marker YFP (control vector) or CFP (test vector PHP38333) was a reliable indicator of the T-DNA delivery efficiency. In general, 30%-50% of the infected explants showed T-DNA delivery in the right target tissues or cells. Using an optimized infection medium and protocol, 70%-80% T-DNA delivery efficiency to the target area was achieved. Infected
30 explants were sub-cultured to fresh medium every 3 weeks. After 6 weeks of culture, healthy, vigorously growing, embryogenic type I callus could be identified from those explants that had been infected with vector PHP38333 containing the genes encoding cell proliferation factors. These growing calli represented transformed events confirmed by the color marker (CFP) expression. Non-transformed tissues showed either no growth or

very limited growth. Embryogenic type I callus were picked and transferred onto fresh culture medium to let the callus proliferate before plant regeneration (10-12 weeks). Transformation efficiency for PHP38333 at the callus level ranged from 12% to 20% calculated as the number events recovered per total number of infected explants (Table 16). Embryo explants that were infected with control vector PHP32269 also showed good T-DNA delivery based on transient YFP expression in the infected cells. However, these cells did not show significant proliferation and no healthy callus was formed during continuous culture.

Table 16. Transformation frequency of PHP38333 in PHN46 embryo chips.

Experiment No.	Number of Chips infected	Number of CFP(+) Events	Transformation Frequency (%)
1	137	23	16.8%
2	134	19	14.2%
3	149	20	13.4%
4	140	25	17.9%
5	148	18	12.2%
6	137	26	19.0%
7	129	27	20.9%
8	136	20	14.7%
9	137	21	15.3%
10	147	24	16.3%
Total	1393	223	16.0%

Transformed callus tissues were treated with either one of the following two desiccation methods to induce excision of the genes encoding cell proliferation factors before plant regeneration.

- 1) Desiccation by natural air exchange: Transformed callus tissues were transferred to an empty 60mm x 25mm Petri dish containing a piece of autoclaved glass filter paper and covered with a lid but not sealed. Petri dishes with callus tissues were placed into a culture box with a loose cover. The box was kept at 28°C in the dark for 3 days.

2) Desiccation in chambers containing a saturated salt solution: Transformed callus tissues were transferred to an empty 60mm x 25mm Petri dish containing a piece of autoclaved glass filter paper and covered with a lid. The Petri dishes with callus tissues were placed into a container with a tight sealing cover. A glass jar containing saturated (NH₄)₂SO₄ salt solution without a cover was placed in the container. The container was kept at 28°C in the dark for 3 days (as the moisture in the air inside the container was absorbed by the saturated salt solution, the callus tissue gradually lost water and experienced desiccation stress).

After 3 days of desiccation treatment, the callus tissues were transferred to 289L regeneration media for 2-3 weeks in the dark. When shoots formed with a length of about 1-2cm, callus tissues with shoots were transferred to hormone-free 272V medium for further development of shoots and roots in the light culture room. When plantlets had formed well-developed shoots and roots, plant regeneration efficiency was evaluated. The plant regeneration frequency (number of callus producing plants out of total number of callus events for plant regeneration) varied from 45% to 75% among 10 initial experiments. At this stage, leaf samples were collected from the plantlets derived from each callus event for molecular analysis. Detailed PCR analyses were performed to determine the copy number of transgenes as well as to confirm that the genes encoding proliferation factors were excised and were not present in the regenerated transgenic plants.

Based on the molecular analysis of 316 T0 plants from 162 events, about 60% of the transgenic plants contain a single copy of the transgenes. These single-copy transgenic plants showed very efficient excision of the genes encoding cell proliferation factors from the desiccation-treatment-induction (see results in Table 17). In general, plants with complete excision of genes encoding cell proliferation factors displayed normal phenotype in the tube and also in later developmental stages in the greenhouse. In contrast, T0 plants in which excision did not occur (or where it was incomplete) displayed an abnormal phenotype, such as thickened roots.

Based on PCR analysis results, chimeric or incomplete excision T0 plants can be eliminated and only complete-excision (free of genes encoding cell proliferation factors) events were sent to the greenhouse.

Table 17. Analysis of T0 plants for excision of genes encoding cell proliferation factors.

Number of Events/T0 Plants	Single Copy	Complete Excision
162 (Events)	103 (63.6%)	94 (91.3%)
316 (Plants)	189 (59.8%)	173 (91.5%)

Example 15. Transformation of leaf tissues*a. Preparation of Agrobacterium and maize leaf explants*

5 *Agrobacterium* suspensions were prepared as described in Example 14. Pioneer maize inbred lines PHN46, PHR03 and PHEJW were used as the initial genotypes for transformation tests. Dry seed was sterilized and imbibed overnight as described above.

Sterilized seeds were placed onto 272V solid medium for direct germination. Alternatively, mature embryos were dissected from softened and sterilized seeds and
 10 placed onto 272V solid medium for faster germination. Plates with seeds or isolated embryos were placed in a culture box and incubated at 28°C in the dark for 3-7 days. Shoot segments of about 2-3cm long above the first leaf base node of the seedling were excised under sterile conditions. The coleoptile was removed and the leaf fragment was split longitudinally first, then cross-dissected into smaller segments (0.5 to 2 mm).
 15 Alternatively, the 2-3 cm-long segment above the first leaf base node of the seedling was simply diced with the scalpel to produce small leaf segments. Small leaf segments were transferred into a 6-well culture plate containing 4ml of 700 liquid medium.

Liquid medium in the 6-well plate with leaf pieces were drawn off and replaced with 4ml prepared *Agrobacterium* suspension. The 6-well plate was transferred into a
 20 transparent polycarbonate desiccator container. The desiccator was covered and placed on a platform of the shaker with a speed of 100RPM and connected to an in-house vacuum system for 15 min. After infection, the *Agrobacterium* suspension was drawn off from the wells and the leaf tissues were transferred onto solid 710I co-cultivation medium with 50mg/l thymidine and were incubated at 21°C in the dark for 3 days.

25 After 3d co-cultivation, all of the leaf tissues were transferred to 13152C culture medium. T-DNA delivery was evaluated about 5d after *Agrobacterium* infection. Transient expression of the color marker YFP (control vector) or CFP (test vector PHP38333) was a reliable indicator of the T-DNA delivery efficiency. 10%-25% of infected leaf segments showed multiple fluorescent cells along the cut edges or surface of
 30 leaf segments in all three inbred lines tested. Infected leaf tissues were sub-cultured every

2 weeks. After 6-8 weeks of culture, stable transformed callus events could be identified. The transgenic nature of these stable callus events was indicated by the expression of the fluorescent gene. Callus events with significant proliferation were subjected to desiccation treatment, and transferred onto regeneration medium for 2-4 weeks. Stable transgenic plantlets were regenerated from two tested maize inbreds, PHN46 and PHR03. Results from numerous experiments clearly demonstrated that stable transgenic plants could be produced from transformation of seedling tissue by using the vector that expresses the genes encoding cell proliferation factors. Leaf tissues infected with the control vector also showed good T-DNA delivery based on transient YFP expression, but the infected cells did not exhibit any subsequent proliferation and no stable callus events were identified from this treatment.

Example 16. The utilization of cell proliferation factors for enhancing chloroplast transformation

For tobacco and a number of other species, leaves are a preferred target for chloroplast transformation. Cell proliferation factors are used to trigger a tissue culture response from leaves of maize and other species. For boosting chloroplast transformation, cell proliferation factor genes under the control of inducible promoters are introduced into the species of interest by standard nuclear transformation protocols. Events that contain the transgene are characterized for expression of the inducible cell proliferation factor genes. For example, leaves of maize from plants transformed with the cell proliferation factor genes under the control of the tetracycline-repressor system are placed on medium containing appropriate concentrations of doxycycline. The doxycycline then activates the cell proliferation factor genes and thereby induces an embryogenic tissue culture response. The leaves are maintained on this medium for about 7-21 days during which time cell division and the initiation of embryogenic callus will take place. The leaves are bombarded with chloroplast transformation vectors carrying the aadA selectable marker gene and trait gene just prior to induction of the cell proliferation genes, during induction or just after induction. One to seven days after bombardment with the chloroplast transformation vector, the tissue is placed in petri plates containing agarose-solidified media supplemented with spectinomycin. The plates are then incubated at 28°C in the light. The tissue is transferred to fresh medium every two weeks. After about 8 weeks of incubation, green callus is observed. This tissue can be further proliferated on 13152 medium (4.3 g/l MS salts, 0.25 g/l myo-inositol, 1.0 g/l casein hydrolysate, 1 mg/l

thiamine, 1 mg/l 2,4-D, 30 g/l maltose, 0.69 g/l proline, 1.2 mg/l cupric sulfate, and 3.5 g/l phytigel, pH 5.8) and the tissue analyzed for the presence of the transgene using appropriate methods including PCR and Southern analysis.

In an alternative approach, expression cassettes containing the tetracycline-inducible BBM and WUS genes are co-bombarded along with the chloroplast transformation vectors carrying the aadA gene for selection. Either leaf explants or established green tissue callus are used as the target tissue for bombardment. Tetracycline or doxycycline at a concentration of 0.5 to 2.0 mg/l is added to the culture medium (13152) after particle bombardment. Expression of BBM and WUS in cells that have received DNA stimulate callus growth rates during the period while tetracycline (or doxycycline) is present in the medium. The accelerated growth that is stimulated by BBM & WUS will result in improved recovery of homoplastic transgenic events, and the nuclear-integrated BBM/WUS genes can be removed by outcrossing T0 plants to wild-type plants and selecting BBM/WUS null plants in the T1 generation.

In another variation on the particle gun approach for delivery of BBM and WUS, a UBI::BBM::PinII and a nos::WUS2::pinII are co-delivered along with the chloroplast transformation vectors.

In another alternative approach, the cell proliferation factor genes are delivered into leaf tissue by vacuum infiltration of an *Agrobacterium* solution. The cell proliferation factor genes are under the control of strong constitutive promoters such as *ubi* or *act* or viral promoters such as 35S (Gardner *et al.* (1981) *Nucl Acids Res* 9:2871-2888), MMV (Dey and Maiti (1999) *Plant Mol Biol* 40:771-782), or BSV (Shenk *et al.* (2001) *Plant Mol Biol* 47:399-412). The cell proliferation factor genes are carried on binary vectors that facilitate transfer from the bacteria to plant cells. Following vacuum infiltration, the tissue is incubated for an appropriate period of time to allow expression of the cell proliferation factor genes in the leaf tissue. Transient expression from the cell proliferation factor genes delivered by *Agrobacterium* is expected to provide a strong boost in cell division and tissue culture response. After vacuum infiltration with *Agrobacterium*, the tissue is bombarded with a chloroplast transformation vector carrying the aadA selectable marker gene. The tissue is then transferred to media containing spectinomycin and transgenic events selected. It is expected that the *Agrobacterium*-delivered cell proliferation factor genes will not be integrated into the nuclear genome of most of the events that are recovered.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and
5 individually indicated to be incorporated by reference.

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

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A promoter construct comprising a promoter followed by a first attachment B (attB) site, wherein:
 - a) said promoter comprises the sequence set forth in SEQ ID NO:29 or in nucleotides 291-430 of SEQ ID NO:29;
 - b) said first attB site has the nucleotide sequence set forth in SEQ ID NO:31; and
 - c) said promoter construct further comprises a linker sequence that separates said promoter and said first attB site, wherein
 - i) said linker sequence is about 133 nucleotides in length, optionally wherein said linker is selected from nucleotides of a maize *rab17* 5' untranslated region (5'-UTR) and the nucleotide sequence set forth in SEQ ID NO:35; or
 - ii) said linker sequence has the sequence set forth in SEQ ID NO:36 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:36.
2. The promoter construct of claim 1, wherein:
 - i) said first attB site modulates the activity of said promoter; and/or
 - ii) said promoter drives expression in a plant.
3. An expression cassette comprising the promoter construct of claim 1 or 2 operably linked to a polynucleotide of interest.
4. The expression cassette of claim 3, wherein:
 - i) said expression cassette further comprises a linker sequence that separates said first attB site and said polynucleotide of interest; optionally wherein said linker sequence that separates said first attB site and said polynucleotide of interest is selected from the group consisting of: a polynucleotide having a length of about 25 or about 61 nucleotides; a polynucleotide having the sequence set forth in SEQ ID NO:37 or 123; and a polynucleotide having at least 70% sequence identity to the sequence set forth in SEQ ID NO:37 or 123; and/or

- 5 ii) said expression cassette further comprises a second site-specific attachment B (attB) site, wherein said first and said second attB sites flank the polynucleotide of interest; optionally wherein said first and said second attB sites are non-identical and/or said second attB site has a nucleotide sequence selected from the group consisting of SEQ ID NOs:32, 33, and 34; or
- 10 iii) said expression cassette according to ii) further comprises a linker sequence that separates said polynucleotide of interest and said second attB site; optionally wherein said linker sequence that separates said polynucleotide of interest and said second attB site: is about 8 or about 16 nucleotides in length; or has the sequence set forth in SEQ ID NO:39 or 124 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:39 or 124; or
- 15 iv) said expression cassette according to ii) and iii) further comprises a termination sequence following said second attB site; optionally wherein said termination sequence comprises the termination region from the potato proteinase inhibitor (PinII) gene or wherein said termination sequence has the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:38, wherein said nucleotide sequence terminates transcription in a plant cell; or
- 20 v) said expression cassette according to iv) further comprises a linker sequence that separates said second attB site and said termination sequence; optionally wherein said linker sequence that separates said second attB site and said termination sequence is about 14 nucleotides in length or wherein said linker sequence that separates said second attB site and said termination sequence has the sequence set forth in SEQ ID NO:40 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:40; or
- 25 vi) said polynucleotide of interest is a nucleotide sequence encoding a site-specific recombinase; optionally wherein said site-specific recombinase is selected from the group consisting of FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, and U153, or wherein said nucleotide sequence encoding said site-specific recombinase is selected from the group consisting of:
- 30 a) the nucleotide sequence set forth in SEQ ID NO:41 or 43;

- 5 b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:41 or 43;
- c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:42 or 44; and
- d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to SEQ ID NO:42 or 44.
- 10 5. An expression cassette having the nucleotide sequence set forth in SEQ ID NO:45 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:45.
6. A vector comprising the promoter construct of claim 1 or 2, or the expression cassette of any one of claims 3 to 5.
- 15 7. The vector of claim 6, further comprising a polynucleotide encoding a babyboom polypeptide; optionally wherein:
- i) said babyboom polypeptide comprises at least two AP2 domains and at least one of the following amino acid sequences:
- 20 a) the amino acid sequence set forth in SEQ ID NO:54 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:54 by one amino acid; and
- b) the amino acid sequence set forth in SEQ ID NO:57 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:57 by one amino acid; or
- 25 ii) said polynucleotide encoding said babyboom polypeptide has a nucleotide sequence selected from the group consisting of:
- a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- 30 c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and

- 5 d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; or
- 10 iii) said polynucleotide encoding said babyboom polypeptide is operably linked to a second promoter active in a plant; optionally wherein said second promoter is a maize ubiquitin promoter or a maize oleosin promoter, wherein said maize oleosin promoter has the nucleotide sequence set forth in SEQ ID NO:65 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:65; or
- 15 iv) said vector further comprises a polynucleotide encoding a Wuschel polypeptide; optionally wherein said polynucleotide encoding said Wuschel polypeptide has a nucleotide sequence selected from the group consisting of:
- a) the nucleotide sequence set forth in SEQ ID NO:61, 63, 114, or 105;
- b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:61, 63, 114, or 105;
- c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:62, 64, 115, or 106; and
- 20 d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to SEQ ID NO:62, 64, 115, or 106;
- and/or wherein said polynucleotide encoding said Wuschel polypeptide is operably linked to a maize In2-2 promoter or a nopaline synthase promoter.
- 25 8. A host cell or a plant cell comprising the promoter construct of claim 1 or 2, the expression cassette of any one of claims 3 to 5, or the vector of claim 6 or 7.
9. A transgenic seed of a plant comprising the plant cell of claim 8, wherein said seed comprises said promoter construct, said expression cassette, or said vector.
- 30 10. A plant cell comprising an expression cassette comprising a promoter construct according to claim 1 or 2 operably linked to a polynucleotide encoding a site-specific recombinase, wherein said plant cell further comprises a polynucleotide of interest flanked by a first and a second recombination site, wherein said first and

second recombination sites are recombinogenic with respect to one another and are directly repeated, and wherein said site-specific recombinase can recognize and implement recombination at said first and said second recombination sites, thereby excising said polynucleotide of interest, optionally wherein:

- 5 i) said expression cassette further comprises a linker sequence that separates said first attB site and said polynucleotide encoding said site-specific recombinase; optionally wherein: said linker sequence that separates said first attB site and said polynucleotide encoding said site-specific recombinase has a length of about 25 or about 61 nucleotides; or said linker sequence that
10 separates said first attB site and said polynucleotide encoding said site-specific recombinase has the sequence set forth in SEQ ID NO:37 or 123 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:37 or 123; and/or
- 15 ii) said expression cassette further comprises a second site-specific attachment B (attB) site, wherein said first and said second attB sites flank the polynucleotide encoding said site-specific recombinase; optionally wherein said first and said second attB sites are non-identical; optionally wherein said second attB site has a nucleotide sequence selected from the group consisting of SEQ ID NOs:32, 33, and 34; or
- 20 iii) said expression cassette of the plant cell according to ii) further comprises a linker sequence that separates said polynucleotide encoding said site-specific recombinase and said second attB site; optionally wherein said linker sequence that separates said polynucleotide encoding said site-specific
25 recombinase and said second attB site is about 8 or about 16 nucleotides in length or said linker sequence that separates said polynucleotide encoding said site-specific recombinase and said second attB site has the sequence set forth in SEQ ID NO:39 or 124 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:39 or 124; or
- 30 iv) said expression cassette of the plant cell according to ii) or iii), further comprises a termination sequence following said second attB site; optionally wherein said termination sequence comprises the termination region from the potato proteinase inhibitor (PinII) gene; or said termination sequence has the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:38, wherein said

nucleotide sequence terminates transcription in a plant cell; and/or said expression cassette further comprises a linker sequence that separates said second attB site and said termination sequence; and/or said linker sequence that separates said second attB site and said termination sequence is about 14 nucleotides in length or said linker sequence that separates said second attB site and said termination sequence has the sequence set forth in SEQ ID NO:40 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:40; and/or

- v) said site-specific recombinase is selected from the group consisting of FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, and U153, optionally wherein said nucleotide sequence encoding said site-specific recombinase is selected from the list consisting of:
- a) the nucleotide sequence set forth in SEQ ID NO:41 or 43;
 - b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:41 or 43;
 - c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:42 or 44; and
 - d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to SEQ ID NO:42 or 44; and/or
- vi) said first and said second recombination sites are FRT recombination sites or lox recombination sites; and/or
- vii) said polynucleotide of interest is a polynucleotide encoding a cell proliferation factor, optionally wherein said cell proliferation factor comprises a babyboom polypeptide, wherein said babyboom polypeptide optionally comprises at least two AP2 domains and at least one of the following amino acid sequences:
- a) the amino acid sequence set forth in SEQ ID NO:54 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:54 by one amino acid; and
 - b) the amino acid sequence set forth in SEQ ID NO:57 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:57 by one amino acid;

or wherein said polynucleotide encoding said babyboom polypeptide has a nucleotide sequence selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and
- d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; or

- viii) said polynucleotide according to vii) encoding said cell proliferation factor is operably linked to a promoter active in said plant cell, optionally wherein said promoter is a maize ubiquitin promoter or a maize oleosin promoter, wherein said maize oleosin promoter optionally has the nucleotide sequence set forth in SEQ ID NO:65 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:65; and/or
- ix) said polynucleotide of interest is stably integrated into the genome of said plant cell; and/or
- x) said plant is a dicot or a monocot, wherein said monocot is optionally selected from the group consisting of maize, rice, sorghum, barley, wheat, millet, oats, sugarcane, turfgrass, and switch grass.

11. A transgenic seed from a plant comprising said plant cell of claim 10, wherein said seed comprises said expression cassette and said polynucleotide of interest.

12. A method for expressing a polynucleotide of interest in a plant cell, said method comprising introducing into said plant cell an expression cassette or a vector, wherein said expression cassette is the expression cassette according to any one of claims 3 to 5, or wherein said vector is the vector of claim 6 or 7.

13. A method for excising a polynucleotide of interest from a target site in a plant cell, wherein said target site comprises a first site-specific recombination site, said polynucleotide of interest, and a second site-specific recombination site, wherein said first and said second site-specific recombination sites are recombinogenic with respect to one another and are directly repeated, said method comprising:
- 5
- a) introducing into said plant cell an expression cassette comprising a first promoter operably linked to a polynucleotide encoding a site-specific recombinase, wherein said first promoter comprises the promoter construct of claim 1 or 2; and
- 10
- b) expressing said polynucleotide encoding said site-specific recombinase, wherein said site-specific recombinase recognizes and implements recombination at said first and said second site-specific recombination sites, thereby excising said polynucleotide of interest; optionally wherein:
- 15
- i) said expression cassette further comprises a linker sequence that separates said first attB site and said polynucleotide encoding said site-specific recombinase, and optionally said linker sequence that separates said first attB site and said polynucleotide encoding said site-specific recombinase has a length of about 25 or about 61 nucleotides or has the sequence set forth in SEQ ID NO:37 or 123 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:37 or 123; and/or
- 20
- ii) said expression cassette further comprises a second site-specific attachment B (attB) site, wherein said first and said second attB sites flank the polynucleotide encoding said site-specific recombinase, optionally wherein:
- 25
- (a) said first and said second attB sites are non-identical, and/or said second attB site has a nucleotide sequence selected from the group consisting of SEQ ID NOs:32, 33, and 34; and/or
- 30
- (b) said expression cassette further comprises a linker sequence that separates said polynucleotide encoding said site-specific recombinase and said second attB site, optionally wherein said linker sequence that separates said polynucleotide encoding said site-specific recombinase and said second attB site is about 8 or about 16 nucleotides in length, and/or has the sequence set forth

- in SEQ ID NO:39 or 124 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:39 or 124; and/or
- (c) said expression cassette further comprises a termination sequence following said second attB site, optionally wherein said termination sequence comprises the termination region from the potato proteinase inhibitor (PinII) gene, or has the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:38, wherein said nucleotide sequence terminates transcription in a plant cell and optionally further comprising a linker sequence that separates said second attB site and said termination sequence, optionally wherein said linker sequence that separates said second attB site and said termination sequence is about 14 nucleotides in length, or has the sequence set forth in SEQ ID NO:40 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO:40; and/or
- iii) said polynucleotide of interest is operably linked to a second promoter active in said plant cell, wherein said polynucleotide of interest and said second promoter are flanked by said first and said second recombination sites, optionally wherein said second promoter is a maize ubiquitin promoter or a maize oleosin promoter, and optionally wherein said maize oleosin promoter has the nucleotide sequence set forth in SEQ ID NO:65 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:65; and/or
- iv) said target site comprises in operable linkage: said first recombination site, a second promoter, a polynucleotide sequence encoding a Wuschel polypeptide, a third promoter, a polynucleotide encoding a babyboom polypeptide, and said second recombination site, wherein said polynucleotide encoding said Wuschel polypeptide and its operably linked second promoter can follow or precede said polynucleotide encoding said babyboom polypeptide and its operably linked third promoter in the target site, optionally wherein:

- (a) said second promoter is a maize In2-2 promoter or a nopaline synthase promoter; and/or
- (b) said third promoter is a maize ubiquitin promoter or a maize oleosin promoter, and optionally wherein said maize oleosin promoter has the nucleotide sequence set forth in SEQ ID NO:65 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:65; and/or

v) said target site is stably integrated into the genome of said plant cell.

10 14. A method for excising a polynucleotide of interest from a target site in a plant cell, wherein said target site comprises in operable linkage: a first site-specific recombination site, a first promoter, said polynucleotide of interest, a second promoter, a polynucleotide encoding a site-specific recombinase, and a second site-specific recombination site; wherein said first and said second site-specific
15 recombination sites are recombinogenic with respect to one another and are directly repeated; wherein said second promoter comprises the promoter construct of claim 1 or 2, wherein the polynucleotide of interest and its operably linked first promoter can follow or precede the polynucleotide encoding the site-specific recombinase and its operably linked second promoter in the target site; said method
20 comprising expressing said polynucleotide encoding said site-specific recombinase; wherein said site-specific recombinase recognizes and implements recombination at said first and said second site-specific recombination sites, thereby excising said polynucleotide of interest and said polynucleotide encoding said site-specific recombinase; optionally wherein:

- 25 i) said first promoter is a maize ubiquitin promoter or a maize oleosin promoter, wherein said maize oleosin promoter optionally has the nucleotide sequence set forth in SEQ ID NO:65 or a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:65; and/or
- 30 ii) said target site further comprises a third promoter operably linked to a polynucleotide encoding a Wuschel polypeptide, wherein the target site comprises in operable linkage: said first site-specific recombination site, said third promoter, said polynucleotide encoding a Wuschel polypeptide, said first promoter, said polynucleotide of interest, said second promoter, said polynucleotide encoding said site-specific recombinase, and said second site-

specific recombination site, wherein the polynucleotide encoding the Wuschel polypeptide and its operably linked third promoter, the polynucleotide of interest and its operably linked first promoter, and the polynucleotide encoding the site-specific recombinase and its operably linked second promoter can be in any order at the target site; optionally wherein the target site comprises in the following order: said first site-specific recombination site, said third promoter, said polynucleotide encoding a Wuschel polypeptide, said first promoter, said polynucleotide of interest, said second promoter, said polynucleotide encoding said site-specific recombinase, and said second site-specific recombination site.

15. The method according to claim 14, wherein:

- i) said site-specific recombinase is selected from the group consisting of FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, and U153; or
- ii) said nucleotide sequence encoding said site-specific recombinase is selected from the list consisting of:
 - a) the nucleotide sequence set forth in SEQ ID NO:41 or 43;
 - b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:41 or 43;
 - c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:42 or 44; and
 - d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to SEQ ID NO:42 or 44; or
- iii) said first and said second recombination sites are FRT recombination sites or lox recombination sites; and/or
- iv) said polynucleotide of interest is a polynucleotide encoding a cell proliferation factor, optionally wherein said cell proliferation factor comprises a babyboom polypeptide, wherein said babyboom polypeptide optionally comprises at least two AP2 domains and at least one of the following amino acid sequences:

- a) the amino acid sequence set forth in SEQ ID NO:54 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:54 by one amino acid; and
- b) the amino acid sequence set forth in SEQ ID NO:57 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:57 by one amino acid;

or wherein said polynucleotide encoding said babyboom polypeptide has a nucleotide sequence selected from the group consisting of:

- c) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- d) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- e) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and
- f) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and/or
- g) said plant is a dicot or a monocot, wherein said monocot is optionally selected from the group consisting of maize, rice, sorghum, barley, wheat, millet, oats, sugarcane, turfgrass, and switch grass.

16. A method for introducing a polynucleotide of interest into a leaf tissue and regenerating a plant therefrom, said method comprising:

- a) excising a leaf segment from a leaf above the first leaf base node;
- b) dissecting said leaf fragment into leaf tissue;
- c) introducing into said leaf tissue:
 - i) a heterologous polynucleotide encoding a cell proliferation factor flanked by recombination sites;
 - ii) an expression cassette comprising the promoter construct according to claim 1 or 2 operably linked to a polynucleotide encoding a site-

specific recombinase that is capable of recognizing and implementing recombination at said recombination sites; and

- iii) a polynucleotide of interest;
 - d) expressing said heterologous polynucleotide encoding said cell proliferation factor;
 - e) incubating said leaf tissue under conditions to allow for growth of a callus;
 - f) expressing said polynucleotide encoding said site-specific recombinase, thereby excising said heterologous polynucleotide encoding said cell proliferation factor;
 - g) regenerating a plant from said callus;
- optionally wherein:

- i) said leaf tissue is about 1 to about 2 mm in length; and/or
- ii) said leaf segment is excised from a seedling; and/or
- iii) said polynucleotides are introduced into said leaf tissue with *Agrobacterium*-mediated transformation; and/or
- iv) said site-specific recombinase is selected from the group consisting of FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, and U153; and/or
- v) said nucleotide sequence encoding said site-specific recombinase is selected from the list consisting of:
 - (a) the nucleotide sequence set forth in SEQ ID NO:41 or 43;
 - (b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:41 or 43;
 - (c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:42 or 44; and
 - (d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to SEQ ID NO:42 or 44.

17. The method according to claim 16, wherein said cell proliferation factor comprises a babyboom polypeptide, optionally wherein:
- i) said babyboom polypeptide comprises at least two AP2 domains and at least one of the following amino acid sequences:

5

- a) the amino acid sequence set forth in SEQ ID NO:54 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:54 by one amino acid; and
- b) the amino acid sequence set forth in SEQ ID NO:57 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO:57 by one amino acid; or

10

ii) said polynucleotide encoding said babyboom polypeptide has a nucleotide sequence selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and
- d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and/or

15

20

iii) said leaf is from a dicot or a monocot, wherein said monocot is optionally selected from the group consisting of maize, rice, sorghum, barley, wheat, millet, oats, sugarcane, turfgrass, and switch grass.

25

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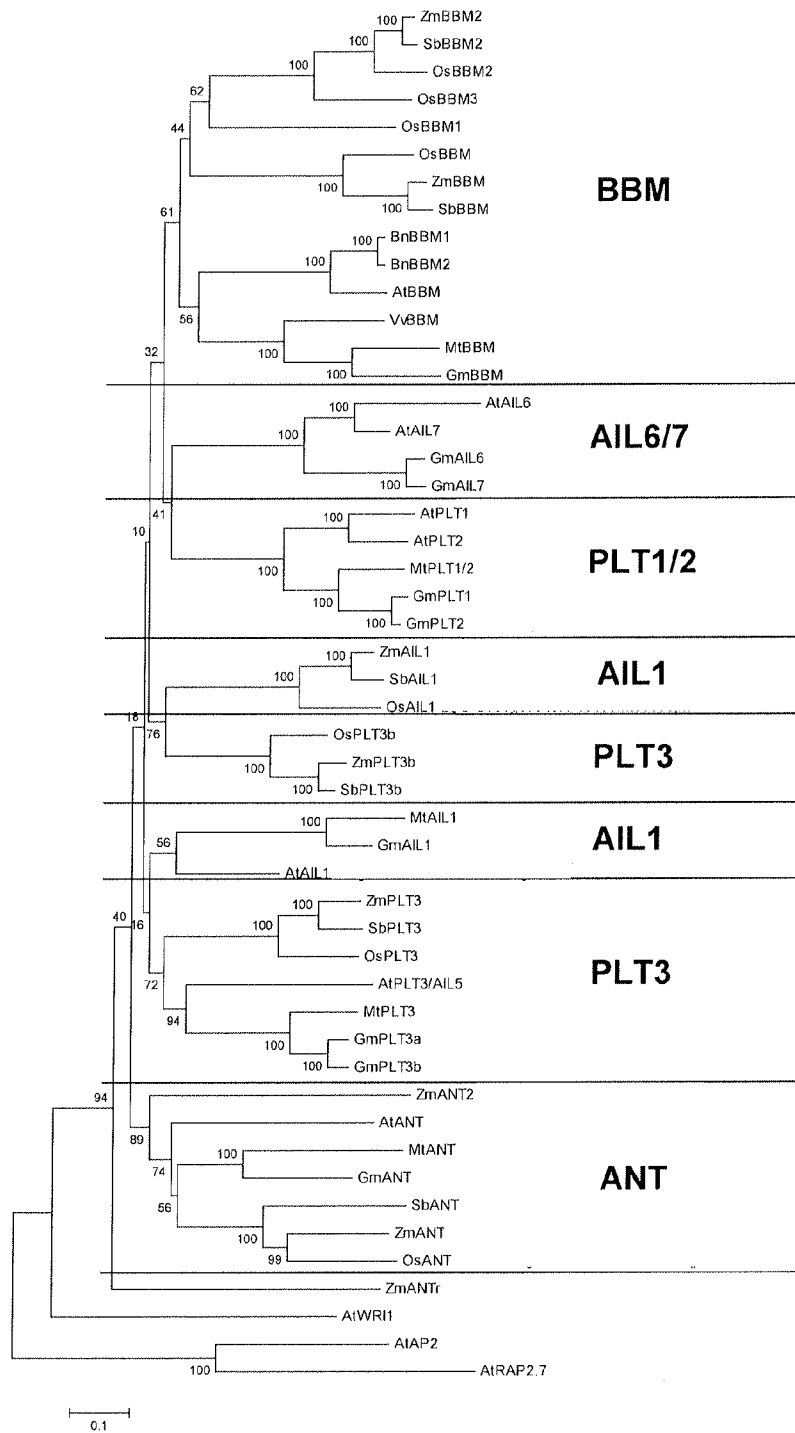


FIG. 1

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SEQ ID NO:			
GmPLT3b	70	(221)	YEKELEEMKNMTRQEFVASLRRKSSGFSRGA
GmPLT3a	71	(217)	YEKELEEMKNMTRQEFVASLRRKSSGFSRGA
OsBBM	14	(353)	YEKELEEMKHMTRQEFVASLRRKSSGFSRGA
VvBBM	6	(278)	YEKEIEEMKHMTRQEFVASLRRKSSGFSRGA
GmBBM	2	(339)	YEKELEEMKHMTRQEFVASLRRKSSGFSRGA
ZmPLT3b	72	(210)	YEKELEEMKSMTRQEFIASLRRKSSGFSRGA
AtBBM	22	(280)	YEKEVEEMKHMTRQEFVASLRRKSSGFSRGA
OsPLT3	73	(214)	YEKELEEMKHMTRQEFVASLRRKSSGFSRGA
ZmBBM	10	(343)	YEKELEDMKHMTRQEFVASLRRKSSGFSRGA
BnBBM2	26	(280)	YEKEIEEMKHMTRQEFVASLRRKSSGFSRGA
BnBBM1	24	(280)	YEKEVEEMKHMTRQEFVASLRRKSSGFSRGA
OsBBM1	16	(238)	YEKELEDMKHMNRQEFVASLRRKSSGFSRGA
AtPLT3/AIL5	74	(273)	YESELEEMKHMTRQEFVASLRRKSSGFSRGA
AtPLT2	75	(260)	YEKEVEEMKNMTRQEFVASIRRKSSGFSRGA
SbPLT3b	76	(205)	YEKELEEMKSMTRQEFIASLRRKSSGFSRGA
OsAIL1	77	(323)	YEKELEEMKHMTRQEFIAHLRRNSSGFSRGA
SbBBM	4	(347)	YEKELEDMKHMTRQEFVASLRRKSSGFSRGA
MtBBM	8	(329)	YEKEVEEMKHMTRQEFVASLRRKSSGFSRGA
SbBBM2	28	(356)	YEKELEEMKHMTRQEFYIAYLRRNSSGFSRGA
ZmBBM2	12	(349)	YEKELEEMKHMTRQEFYIAYLRRNSSGFSRGA
GmPLT2	78	(234)	YEKELEDMKHMTRQEFVAAIRRKSSGFSRGA
OsBBM3	20	(349)	YEKELEEMKHMTRQEFYIAHLRRNSSGFSRGA
MtPLT3	79	(229)	YEKEIDDMKNMTRQEFVASLRRKSSGFSRGA
ZmPLT3	80	(197)	YEKEVEEMKNMTRQEFVASLRRKSSGFSRGA
OsPLT3b	81	(200)	YETELEEMKSMTRQEFIASLRRKSSGFSRGA
GmPLT1	82	(239)	YEKELEDMKHMTRQEFVAAIRRKSSGFSRGA
AtPLT1	83	(251)	YEKEVEEMKHMTRQEFVAAIRRKSSGFSRGA
OsBBM2	18	(370)	YEKELEDMKHMTRQEFYIAYLRRNSSGFSRGA
MtPLT1/2	84	(233)	YEKEIDEMKHMTRQEFVASIRRKSSGFSRGA
ZmAIL1	85	(341)	YEKELEEMKHMSTRQEFIAHLRRNSSGFSRGA
GmAIL1	86	(272)	YEKELEEMKHMTRQEFVANLRRKSSGFSRGA
SbPLT3	87	(208)	YEKELEEMKTMTRQEFVASLRRKSSGFSRGA
GmAIL6	88	(291)	YSKEVEEMKHVTKQEFIASLRRKSSGFSRGA
AtAIL6	89	(323)	YSKEVEEMKHMTRQEFIASLRRKSSGFSRGA
MtAIL1	90	(318)	YDKELEEMKHMTRQEFVANLRRKSSGFSRGA
SbAIL1	91	(333)	YEKELEEMKHMSTRQEFIAHLRRNSSGFSRGA
AtANT	92	(353)	YQKEIEDMKNMTRQEFYVAHLRRKSSGFSRGA
SbANT	93	(353)	YQEELEEMKNMTRQEFYVAHLRRKSSGFSRGA
GmAIL7	94	(290)	YSKEVEEMKHVTKQEFIASLRRKSSGFSRGA
ZmANT	67	(372)	YREELEEMKNMTRQEFYVAHLRRKSSGFSRGA
OsANT	95	(372)	YQEELEEMKNMSTRQEFYVAHLRRKSSGFSRGA
AtAIL7	96	(243)	YSKELEEMNHMTKQEFIASLRRKSSGFSRGA
ZmANT2	97	(354)	YRDELEEMKGMTRQEFVAHLRRRSSGFSRGA
MtANT	98	(380)	YQNQLEEMKNMTRQEFYVAHLRRKSSGFSRGA
GmANT	99	(334)	YQVQLEEMKNMSTRQEFYVAHLRRKSSGFSRGA
AtAIL1	100	(293)	YEKEIEELNNMNRQEFVAMLRRNSSGFSRGA
ZmANTr	101	(218)	YIREIQDMQNMNRDVAHLRRKSSGFSRGA
AtWRI1	102	(135)	YTKELEEMQRTVTKEEYLAHLRRQSSGFSRGA
AtAP2	103	(191)	YDDDLKQMTNLTKEEFVHVLRRQSTGFPRGS
AtRAP2.7	104	(213)	YEEDMKQVQNLSKEEFVHILRRQSTGFPRGS
Consensus	48		YEKELEEMK1MTRQE23A4LRRKSSGFSRGA

1= H or N; 2= F or Y; 3= V or I; 4=S or H

FIG. 2A

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SEQ ID NO:			
SbBBM	4	(378)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsBBM	13	(384)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmBBM	10	(374)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmPLT3b	70	(252)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmPLT3a	71	(248)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtPLT3	79	(260)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtPLT3/AIL5	74	(304)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbBBM2	28	(387)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
OsBBM2	18	(401)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
ZmBBM2	12	(380)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
GmPLT2	78	(265)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
GmPLT1	82	(270)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
ZmPLT3b	72	(241)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtAIL1	100	(324)	SVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbPLT3b	76	(236)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsPLT3b	81	(231)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsBBM1	16	(269)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtPLT1/2	84	(264)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
SbAIL1	91	(364)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsAIL1	77	(354)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmAIL1	85	(372)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtPLT2	75	(291)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
AtPLT1	83	(282)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
OsBBM3	20	(380)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
VvBBM	6	(309)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmANT	99	(365)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmBBM	2	(370)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtBBM	8	(360)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbANT	93	(384)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmAIL1	86	(303)	SVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtAIL1	90	(349)	SVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbPLT3	87	(239)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
ZmPLT3	80	(228)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEBAA
AtBBM	22	(311)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsANT	95	(403)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
BnBBM2	26	(311)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
BnBBM1	24	(311)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtANT	98	(412)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtANT	92	(384)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtAIL6	89	(354)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmANT	67	(403)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsPLT3	73	(245)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmAIL7	94	(321)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmAIL6	88	(322)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtAIL7	96	(274)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmANT2	97	(385)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmANTr	101	(249)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtWRI1	102	(166)	SKYRGVARHHHNGRWEARIGRVAGNKDLYLGTFSTQEEAA
Consensus	49		SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFST2EEAA

FIG. 2B

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SEQ ID NO:			
SbBBM	4	(418)	EAYDIAAIKFRGLNAVTFNFDMSR
OsBBM	14	(424)	EAYDIAAIKFRGLNAVTFNFDMSR
ZmBBM	10	(414)	EAYDIAAIKFRGLNAVTFNFDMSR
GmPLT3b	70	(292)	EAYDIAAIKFRGLNAVTFNFDMSR
GmPLT3a	71	(288)	EAYDIAAIKFRGLNAVTFNFDMSR
MtPLT3	79	(300)	EAYDIAAIKFRGLNAVTFNFDMSR
AtPLT3/AIL5	74	(344)	EAYDIAAIKFRGLNAVTFNFDISR
SbBBM2	28	(427)	EAYDIAAIKFRGLNAVTFNFDMSR
OsBBM2	18	(441)	EAYDIAAIKFRGLNAVTFNFDMSR
ZmBBM2	12	(420)	EAYDIAAIKFRGLNAVTFNFDMSR
GmPLT2	78	(305)	EAYDIAAIKFRGLNAVTFNFDMSR
GmPLT1	82	(310)	EAYDIAAIKFRGLNAVTFNFDMSR
ZmPLT3b	72	(281)	EAYDIAAIKFRGLNAVTFNFDMSR
AtAIL1	100	(364)	EAYDIAAIKFRGLNAVTFNFDINR
SbPLT3b	76	(276)	EAYDIAAIKFRGLNAVTFNFDMSR
OsPLT3b	81	(271)	EAYDIAAIKFRGLNAVTFNFDMSR
OsBBM1	16	(309)	EAYDIAAIKFRGLNAVTFNFDMSR
MtPLT1/2	84	(304)	EAYDIAAIKFRGLNAVTFNFDMTNR
SbAIL1	91	(404)	EAYDIAAIKFRGLNAVTFNFDISK
OsAIL1	77	(394)	EAYDIAAIKFRGLNAVTFNFDISK
ZmAIL1	85	(412)	EAYDIAAIKFRGLNAVTFNFDISK
AtPLT2	75	(331)	EAYDIAAIKFRGLNAVTFNFEINR
AtPLT1	83	(322)	EAYDIAAIKFRGLNAVTFNFEINR
OsBBM3	20	(420)	EAYDIAAIKFRGLNAVTFNFDMSR
VvBBM	6	(349)	EAYDIAAIKFRGLNAVTFNFDMSR
GmANT	99	(405)	EAYDIAAIKFRGANAVTFNFDISR
GmBBM	2	(410)	EAYDVAAIKFRGLSAVTFNFDMSR
MtBBM	8	(400)	EAYDVAAIKFRGLSAVTFNFDMSR
SbANT	93	(424)	EAYDIAAIKFRGLNAVTFNFDITR
GmAIL1	86	(343)	EAYDIAAIKFRGTSAVTFNFDISR
MtAIL1	90	(389)	EAYDIAAIKFRGTSAVTFNFDISR
SbPLT3	87	(279)	EAYDIAAIKFRGLNAVTFNFEISR
ZmPLT3	80	(268)	EAYDIAAIKFRGLNAVTFNFEISR
AtBBM	22	(351)	EAYDIAAIKFRGLSAVTFNFDMNR
OsANT	95	(443)	EAYDVAAIKFRGLNAVTFNFDITR
BnBBM2	26	(351)	EAYDIAAIKFRGLTAVTFNFDMNR
BnBBM1	24	(351)	EAYDIAAIKFRGLTAVTFNFDMNR
MtANT	98	(452)	EAYDIAAIKFRGANAVTFNFDIIK
AtANT	92	(424)	EAYDVAAIKFRGTNAVTFNFDITR
AtAIL6	89	(394)	EAYDIAAIKFRGINAVTFNFEMNR
ZmANT	67	(443)	EAYDVAAIKFRGLSAVTFNFDITR
OsPLT3	73	(285)	EAYDIAAIKFRGLNAVTFNFEIGR
GmAIL7	94	(361)	EAYDIAAIKFRGANAVTFNFEMNR
GmAIL6	88	(362)	EAYDIAAIKFRGANAVTFNFEMNR
AtAIL7	96	(314)	EAYDIAAIKFRGINAVTFNFEMNR
ZmANT2	97	(425)	EAYDIAAIKFRGLNAVTFNFDIAR
ZmANTr	101	(289)	EAYDIAALKFRGENAVTFNFEPSR
AtWRI1	102	(206)	AAYDMAAIEYRGANAVTFNFDISN
Consensus	49		EAYD3AAIKFRGLNAVTFN456R

1= I or M; 2= Q or E; 3= I or V; 4= D or E; 5=M or I; 6=S or N

FIG. 2B (continued)

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SEQ ID NO:			
SbBBM	4	(276)	SIYRGVTRHRWTGRYEHLWDNSCRREGQTRK
ZmBBM	10	(272)	SIYRGVTRHRWTGRYEHLWDNSCRREGQTRK
VvBBM	6	(207)	SIYRGVTRHRWTGRYEHLWDNSCRREGQTRK
GmBBM	2	(268)	SIYRGVTRHRWTGRYEHLWDNSCRREGQTRK
OsBBM	14	(282)	SIYRGVTRHRWTGRYEHLWDNSCRREGQTRK
MtBBM	8	(261)	SIYRGVTRHRWTGRYEHLWDNSCRREGQTRK
SbBBM2	28	(285)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
OsBBM3	20	(278)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
OsBBM2	18	(302)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
ZmBBM2	12	(278)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
GmPLT3b	70	(150)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
GmPLT3a	71	(146)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
MtPLT3	79	(161)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
ZmANT	67	(301)	SQYRGVTRHRWTGRYEHLWDNSCRKEGQTRK
GmAIL1	86	(204)	SQYRGVTRHRWTGRYEHLWDNSCRKEGQTRK
MtAIL1	90	(250)	SQYRGVTRHRWTGRYEHLWDNSCRKEGQTRK
SbANT	93	(285)	SQYRGVTRHRWTGRYEHLWDNSCKKEGQTRK
OsANT	95	(304)	SQYRGVTRHRWTGRYEHLWDNSCKKEGQTRK
GmANT	99	(267)	SQYRGVTRHRWTGRYEHLWDNSCKKEGQTRK
GmAIL6	88	(223)	SIYRGVTRHRWTGRYEHLWDNSCRREGQARK
MtANT	98	(312)	SQYRGVTRHRWTGRYEHLWDNSCKKEGQSRK
BnBBM2	26	(209)	SIYRGVTRHRWTGRYEHLWDNSCKREGQTRK
BnBBM1	24	(209)	SIYRGVTRHRWTGRYEHLWDNSCKREGQTRK
AtBBM	22	(209)	SIYRGVTRHRWTGRYEHLWDNSCKREGQTRK
SbPLT3	87	(140)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
ZmPLT3	80	(126)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
GmPLT2	78	(163)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
GmPLT1	82	(168)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
OsPLT3	73	(143)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
GmAIL7	94	(223)	SIYRGVTRHRWTGRYEHLWDNSCRREGQARK
AtAIL6	89	(253)	SIYRGVTRHRWTGRYEHLWDNSCRREGQARK
AtPLT2	75	(189)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
OsPLT3b	81	(129)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
AtPLT1	83	(180)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
AtPLT3/AIL5	74	(202)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
SbPLT3b	76	(134)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
ZmPLT3b	72	(139)	SIYRGVTRHRWTGRYEHLWDNSCRREGQSRK
ZmANT2	97	(283)	SRYRGVTRHRWTGRYEHLWDNSCRKDGQTRK
AtAIL7	96	(172)	SIYRGVTRHRWTGRYEHLWDNSCRREGQARK
MtPLT1/2	84	(165)	SIYRGVTKHRWTGRYEHLWDNSCRREGQSRK
SbAIL1	91	(265)	SQFRGVTRHRWTGRYEHLWDNTCRKEGQTRK
OsAIL1	77	(252)	SQFRGVTRHRWTGRYEHLWDNTCRKEGQTRK
ZmAIL1	85	(270)	SQFRGVTRHRWTGRYEHLWDNTCRKEGQTRK
OsBBM1	16	(167)	SIYRGVTKHRWTGRYEHLWDNSCRREGQTRK
AtAIL1	100	(222)	SQYRGVTRHRWTGRYEHLWDNSCKKEGQTRR
AtANT	92	(282)	SQYRGVTRHRWTGRYEHLWDNSPKKEGHSRK
ZmANTr	101	(147)	SIYRGVTRHRWTGRYEHLWDNTCRKEGQKRR
AtWRI1	102	(64)	SIYRGVTRHRWTGRFEHLWDKSSWNSIQNKK
Consensus	50		S0YRGVTRHRWTGRYEHLWDNSCR1EGQ2RK

FIG. 2C

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SEQ ID NO:			
SbBBM	4	(308)	GRQGGYDKEEKAARAYDLAALKYWGPTTTTTFPVNN
ZmBBM	10	(307)	VYLGGYDKEEKAARAYDLAALKYWGATTTTTFPVSN
VvBBM	6	(242)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTTFPISN
GmBBM	2	(303)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTTFPISH
OsBBM	14	(317)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTTFPVNN
MtBBM	8	(293)	GRQGGYDKEEKAARAYDLAALKYWGTTTTTTFPISH
SbBBM2	28	(320)	VYLGGYDKEDKAARAYDLAALKYWGTTTTTTFPISN
OsBBM3	20	(313)	VYLGGYDKEDKAARAYDLAALKYWGTTTTTTFPMSN
OsBBM2	18	(334)	GRQGGYDKEDKAARAYDLAALKYWGTTTTTTFPISN
ZmBBM2	12	(313)	VYLGGYDKEDKAARAYDLAALKYWGTTTTTTFPISN
GmPLT3b	70	(185)	VYLGGYDKEDKAARAYDLAALKYWGPTTTTTFPISN
GmPLT3a	71	(181)	VYLGGYDKEDKAARAYDLAALKYWGPTTTTTFPISN
MtPLT3	79	(193)	GRQGGYDKEEKAARAYDLAALKYWGPTTTTTFPISN
ZmANT	67	(336)	VYLGGYDVEEKAARAYDLAALKYWGTSSTHVNFPVED
GmAIL1	86	(236)	GRQGGYDKEEKAARAYDLAALKYWGPTTTHINFPPLST
MtAIL1	90	(282)	GRQGGYDKEEKAARAYDLAALKYWGPTTTHINFPPLST
SbANT	93	(317)	GRQGGYDMEEKAARAYDLAALKYWGPTSTHINFPLED
OsANT	95	(336)	GRQGGYDMEEKAARAYDLAALKYWGPTSTHINFPLED
GmANT	99	(298)	GRQGGYDMEEKAARAYDLAALKYWGPTSTHINFPISIEN
GmAIL6	88	(255)	GRQGGYDKEEKAARAYDLAALKYWGPTATTNFPVSN
MtANT	98	(344)	GRQGGYDMEEKAARAYDLAALKYWGPTSTHINFPLEN
BnBBM2	26	(244)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTTFPMSE
BnBBM1	24	(244)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTTFPMSE
AtBBM	22	(244)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTTFPPLSE
SbPLT3	87	(172)	GRQGGYDKEEKAARAYDLAALKYWGSSSTTTTFPVAE
ZmPLT3	80	(161)	VYLGGYDKEEKAARAYDLAALKYWGSSSTTTTFPVAE
GmPLT2	78	(198)	VYLGGYDKEEKAARAYDLAALKYWGTSSTTTTFPISN
GmPLT1	82	(203)	VYLGGYDKEEKAARAYDLAALKYWGTSSTTTTFPISN
OsPLT3	73	(178)	VYLGGYDKEEKAARAYDLAALKYWGPTSTTTTFPVAE
GmAIL7	94	(254)	GRQGGYDKEEKAARAYDLAALKYWGPTATTNFPVSN
AtAIL6	89	(287)	VYLGGYDKEDKAARAYDLAALKYWNATATTNFPITN
AtPLT2	75	(224)	VYLGGYDKEEKAARAYDLAALKYWGPTSTTTNFPITN
OsPLT3b	81	(164)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTTFPVAN
AtPLT1	83	(215)	VYLGGYDKEDKAARAYDLAALKYWGPTSTTTNFPITN
AtPLT3/AIL5	74	(237)	VYLGGYDKEDKAARAYDLAALKYWGPTTTTTFPISN
SbPLT3b	76	(169)	VYLGGYDKEEKAARAYDLAALKYWGATTTTTFPVSN
ZmPLT3b	72	(174)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTTFPVSN
ZmANT2	97	(318)	VYLGGYDTEEKAARAYDLAALKYWGPATHVNFPVEN
AtAIL7	96	(207)	VYLGGYDKEDKAARAYDLAALKYWGSTATTNFPVSS
MtPLT1/2	84	(197)	GRQGGYDKEEKAARAYDLAALKYWGTSSTTTTFPVSN
SbAIL1	91	(297)	GRQGGYDREEKAARAYDLAALKYWGPTSTHINFPPLSH
OsAIL1	77	(287)	VYLGGYDKEEKAARAYDLAALKYWGPTTTHINFPPLST
ZmAIL1	85	(305)	VYLGGYDREEKAARAYDLAALKYWGPTSTHINFPPLSH
OsBBM1	16	(202)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTTFPVSN
AtAIL1	100	(257)	VYLGGYDEEKAARAYDLAALKYWGPTTHLNFPPLSN
AtANT	92	(317)	VYLGGYDMEEKAARAYDLAALKYWGPTSTHINFPISAEN
ZmANTr	101	(182)	VYLGGYDKEDKAARAYDLAALKYWGDNATTNFPREN
AtWRI1	102	(99)	VYLGAIDSEEAHAHTYDLAALKYWGPDITLNFPAET
Consensus	50		345GGYDKE6KAARAYDLAALKYWG72T89NFP*SN

0=I or Q; 1=R or K; 2= S or T; 3= V or G; 4= Y or R; 5=L or Q; 6=E or D; 7= P or T; 8=T or H; 9=T or I; *=I, V, or L

FIG. 2C (continued)

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SEQ ID NO:			
SbBBM2	28	(113)	AVEDSEPKLEDFLGNSFVSEH
OsBBM2	18	(108)	AVEETEPKLEDFLGNSFVSEQ
ZmBBM2	12	(110)	AVEDSEPKLEDFLGNSFVSDQ
SbBBM	4	(55)	SALVAEPKLEDFLGGISFSEQH
ZmBBM	10	(56)	SALVAEPKLEDFLGGISFSEQH
OsBBM	14	(61)	SALVAEPKLEDFLGGISFSEQQ
GmAIL6	88	(77)	HVPPPPPKLEDFLGDSSAVMRY
MtBBM	8	(106)	NNQQAQPKLENFLGGHSFTDHQ
GmAIL7	94	(75)	SVSHAPPKLEDFLGDSSAVMRY
MtAIL1	90	(85)	NSNEEGPKLEDFLGCSYNQNQN
GmANT	99	(97)	MVPTSSPKLEDFLGGATMGTHE
AtAIL6	89	(71)	HSQNHI PKLEDFLGDSSSIVRY
VvBBM	6	(103)	NLENQEPKLENFLGCRSFADHE
GmBBM	2	(107)	QQQQQQPKLENFLGGHSFGEHE
ZmANT2	97	(106)	MVPSSPPKLEDFLGGGNGGGQE
BrBBM2	26	(89)	NDEQDGPKENFLGRTTTIYNT
BrBBM1	24	(89)	NDEQDGPKENFLGRTTTIYNT
OsPLT3	73	(37)	AGAAPPKLEDFLGGGCGGSS
GmAIL1	86	(50)	NSNEEGPKLEDFLGCSYNPAK
AtBBM	22	(91)	NNEQNGPKLENFLGRTTTIYNT
GmPLT2	78	(54)	HSSNEIPKVADFLGVSKSENQS
MtPLT1/2	84	(54)	HNSNEVPKVADFLGVCKSENHS
GmPLT3b	70	(68)	SIFTGGPKFEDFLGSSAATATT
SbPLT3	87	(35)	AGAAPPKLEDFLGGGVINGES
ZmPLT3	80	(36)	AGAAPPKLEDFLGGGVATGGP
GmPLT3a	71	(64)	SIFTGAPKFEDFLGSSATATA
GmPLT1	82	(54)	HSSSEVPKVADFLGVSKSENES
AtPLT3/AIL5	74	(95)	SVYPGGPKLENFLGGGASTTTT
AtAIL7	96	(13)	HSQTQIPKLEDFLGDSFVRYSD
SbAIL1	91	(72)	AAEANGPKLEDFMSVTCSSNNK
OsBBM1	16	(47)	GEETAAPKLEDFLGMQVQETA
AtPLT2	75	(58)	GEGGEVPKVADFLGVSKSGDHH
ZmAIL1	85	(76)	AAEAKGPKLEDFMSITCSNKSS
ZmANT	67	(123)	VVSSSPKLEDFLGASASTAMA
OsAIL1	77	(66)	HAEAKDPKLEDFMSVSYSNKSS
AtPLT1	83	(52)	DEGGEVPKVADFLGVSKPDENQ
OsBBM3	20	(109)	DGVGEAPKLENFLDGNSFSDVH
MtANT	98	(110)	MSTTSAPKLENFLGNEAMGTPH
SbANT	93	(103)	QPDHHGPKLEDFLGAQAQSQA
AtANT	92	(108)	HHQDSSPKVEDFFGTHHNTSH
OsANT	95	(124)	VVVSASPKLEDFLGAGPAMALS
MtPLT3	79	(79)	SIFTGGHKFEDFLGSSVAPTRT
AtAIL1	100	(41)	HHDEDVPKVEDLLSNHQTEYP
OsPLT3b	81	(42)	GPAEGAPKMEDFLGGLGGGGGA
ZmPLT3b	72	(44)	AVEESPRTVEDFLGGVGGAGAP
SbPLT3b	76	(45)	TVEBSPKMVEDFLGGVGGAGAP
Consensus	51		PK123FLG

1= L or V; 2= E or A; 3= D or N

FIG. 2D

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SEQ ID NO:			
VvBBM	6	(377)	<u>ILESSTLPIGGAAKRL</u>
MtBBM	8	(428)	<u>ILESSTLPIGGAAKRL</u>
GmBBM	2	(438)	<u>ILESTTLPIGGAAKRL</u>
SbBBM2	28	(455)	<u>ILESSTLPVGGAAARRL</u>
OsBBM2	18	(469)	<u>ILESSTLPVGGAAARRL</u>
ZmBBM2	12	(448)	<u>ILESSTLPVGGAAARRL</u>
AtPLT1	83	(350)	<u>ILESSTLPIGGGAAKR</u>
OsBBM3	20	(448)	<u>ILDSSTLPVGGAAARRL</u>
GmPLT2	78	(333)	<u>ILESNTLPIGGGAAKR</u>
GmPLT1	82	(338)	<u>ILESNTLPIGGGAAKR</u>
MtPLT1/2	84	(332)	<u>ILESNTLPIGGGAAKR</u>
AtPLT2	75	(359)	<u>ILESNTLPIGGGAAKR</u>
BnBBM2	26	(379)	<u>ILESPSLPIGSAAKRL</u>
BnBBM1	24	(379)	<u>ILESPSLPIGSAAKRL</u>
SbBBM	4	(446)	<u>ILDSSALPIGSAAKRL</u>
ZmBBM	10	(442)	<u>ILDSSALPIGSAAKRL</u>
OsANT	95	(471)	<u>ILESSTLLPGE LARRK</u>
AtAIL6	89	(421)	<u>AIMKSALPIGGAAKRL</u>
AtBBM	22	(379)	<u>ILESPSLPIGSSAKRL</u>
GmAIL7	94	(388)	<u>AIMKSSLPVGGAAKRL</u>
GmAIL6	88	(389)	<u>AIMKSSLPVGGAAKRL</u>
SbANT	93	(452)	<u>IMASNTLLPGDLARRR</u>
ZmANT	67	(471)	<u>IMESSTLLPGEQVRRR</u>
SbAIL1	91	(432)	<u>ICASTHLIGGGDACRR</u>
ZmAIL1	85	(440)	<u>ICASTHLIGGGDACRR</u>
OsBBM1	16	(337)	<u>IIESSNLPIGTGTTTR</u>
GmAIL1	86	(371)	<u>ICSSSTLIAGDLAKRS</u>
OsBBM	14	(452)	<u>ILDSAALPVGTAAKRL</u>
OsAIL1	77	(422)	<u>ICSSTHLIGGDLACRR</u>
GmANT	99	(433)	<u>IMASSNLLAGELARRN</u>
MtAIL1	90	(417)	<u>ICSSSTLITGDLAKRS</u>
GmPLT3b	70	(319)	<u>SIANSTLPIGGLSGKN</u>
GmPLT3a	71	(315)	<u>SIANSTLPIGGLSGKN</u>
AtANT	92	(452)	<u>IMSSNTLLSGELARRN</u>
AtAIL7	96	(341)	<u>AVMNSSLPVGGAAAKR</u>
SbPLT3b	76	(303)	<u>SILNSDLPVGGGAAGR</u>
OsPLT3b	81	(298)	<u>SILNSDLPVGGGAATR</u>
ZmANT2	97	(453)	<u>IMESSTLLAVEEARKV</u>
MtPLT3	79	(327)	<u>SIANCSLPIGGLSNKN</u>
ZmPLT3b	72	(308)	<u>SILSSDLPVGGGASGR</u>
OsPLT3	73	(312)	<u>SIISSNLPIGSMAGNR</u>
MtANT	98	(480)	<u>IMASSNLLNIEQARRN</u>
AtPLT3/AIL5	74	(371)	<u>SIASCNLPVGGLMPKP</u>
Consensus	52		<u>SSTLP1GG2A334</u>

1=I or V; 2= A, L, or G; 3= K or R; 4= L or R

FIG. 2E

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SEQ ID NO:			
AtBBM	22	(4)	MNNWLGFSLSPHDQNH
GmANT	99	(15)	NHNWLGFSLSPHKME
BnBBM2	26	(2)	NNWLGFSLSPYEQNH
BnBBM1	24	(2)	NNWLGFSLSPYEQNH
VvBBM	6	(4)	MNNWLGFSLSPRELPP
OsBBM	14	(4)	MNNWLAFSLSPQDQLP
SbBBM	4	(4)	VNNWLAFSLSPQELPP
ZmBBM	10	(4)	VNNWLAFSLSPQELPP
MtANT	98	(16)	ENNWLGFSLSPQMNNI
OsBBM2	18	(4)	ANNWLGFSLSGQENPQ
ZmBBM2	12	(4)	ANNWLGFSLSGQDNPQ
SbBBM2	28	(5)	NNHWLGFSLSGQDNPQ
GmAIL1	86	(1)	MSNWLGFSLTPHLRID
MtAIL1	90	(1)	MSNWLGFSLTPHLRID
ZmANT2	97	(4)	GSNWLGFSLSPHTAME
GmAIL6	88	(4)	ATNWLGFSLSPMEMLR
GmPLT2	78	(2)	NNNWLGFSLSPTHSSL
GmPLT1	82	(2)	NNNWLGFSLSPTHSSL
MtPLT1/2	84	(2)	NNNWLGFSLSPSHSSL
GmAIL7	94	(5)	STNWLGFSLSPMDMLR
AtPLT1	83	(3)	SNNWLGFPLSPNSSL
MtBBM	8	(3)	SMNLLGFSLSPQEQHP
AtPLT2	75	(3)	SNNWLAFPLSPTHSSL
ZmAIL1	85	(4)	NNGWLGFSLSPSAASR
OsBBM3	20	(4)	ADNWLGFSLSGQGNPQ
SbANT	93	(13)	ASSWLGFSLSPHMASA
OsANT	95	(20)	VGGWLGFSLSPHMATY
SbPLT3b	76	(10)	PHHWLSFSLSNNYHHG
OsPLT3b	81	(10)	PHHWLSFSLSNNYHHG
ZmPLT3b	72	(10)	PHHWLSFSLSNNYHHG
SbAIL1	91	(4)	NNGWLGFSLSPSAGRG
GmBBM	2	(3)	SMNLLGFSLSPQEHPS
AtPLT3/AIL5	74	(27)	HQNWLGFSLSNNNNNF
GmPLT3b	70	(13)	NNNSLAFSLSNHFPNP
GmPLT3a	71	(9)	NNNSLAFSLSNHFPNP
AtAIL1	100	(1)	MKKWLGFSLTPPLRIC
ZmANT	67	(23)	GGSWLGFSLSPHMAAT
OsPLT3	73	(8)	HYPWLNFSLAHHCEME
ZmPLT3	80	(7)	YHPWLNFSLAHHCdle
SbPLT3	87	(6)	HYPWLNFSLAHHCdle
OsAIL1	77	(4)	NSGWLGFSLSSSSARG
AtANT	92	(15)	TTNLLGFSLSSNMMKM
OsBBM1	16	(4)	ITNWLGFSSSSFSGAG
Consensus	53		NWLXFSLSP

X=G or S

FIG. 2F

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SEQ ID NO:			
MtBBM	8	(159)	NNSIGLSMIKTWLRNQPPPPPE
BnBBM2	26	(130)	GGSLGLSMIKTWLRNQPVNDV
BnBBM1	24	(130)	GGSLGLSMIKTWLRNQPVNDV
SbBBM	4	(156)	SGSIGLSMIKNWLRSQPAPMQ
SbBBM2	28	(157)	SNTMELSMIKTWLRNNQVPQP
OsBBM	14	(156)	NGGIGLSMIKNWLRSQPAPQP
ZmBBM	10	(152)	GGGIGLSMIKNWLRSQPAPMQ
VvBBM	6	(131)	YISIGLSMIKTWLRNQPAPTH
ZmBBM2	12	(154)	SNTMELSMIKTWLRNNQVAQP
GmBBM	2	(164)	SSSIGLSMIKTWLRNQPPHSE
OsBBM3	20	(157)	GGTIELSMIKTWLRNQSQQQ
OsBBM2	18	(154)	SNTMELSMIKTWLRNNGQVPA
OsBBM1	16	(80)	SSVVGLSMIKNWLRSQPPPAV
AtBBM	22	(131)	GGSLGLSMIKTWLNSHVSANA
Consensus	54		1LSMIK2WLR

1= G or E; 2= T or N

FIG. 2G

SEQ ID NO:			
SbAIL1	91	(527)	AGVHQLPVFALWND
OsAIL1	77	(536)	TVHHQLPVFALWND
ZmAIL1	85	(529)	PGVHQLPMFALWND
ZmANT	67	(624)	VSLAHLPVFAAWTD
SbANT	93	(664)	VSLAHMPVFAAWTD
OsANT	95	(638)	VSLAHLPMFAAWTD
MtANT	98	(642)	LSLPQMPVFAAWTD
VvBBM	6	(629)	AVCHGTPTFTVWND
GmANT	99	(532)	ISLSHLPVFAAWTD
OsBBM	14	(681)	GVCHGAQLFSVWND
BnBBM2	26	(565)	GGGEVAPTFTVWND
BnBBM1	24	(565)	GGGEVAPTFTVWND
GmAIL1	86	(499)	GLVNQVPMFALWNE
MtAIL1	90	(561)	GLVNQVPMFALWNE
ZmANT2	97	(637)	VVVSHRPVFAAWAD
AtBBM	22	(570)	GGGEGAPTFSVWND
AtANT	92	(541)	LTLPQMPVFAAWAD
SbBBM	4	(689)	VGHGGAQLFSVWND
ZmBBM	10	(695)	VGHGGAQLFSVWND
GmPLT2	78	(540)	MQTSNGGVFTMWND
GmPLT1	82	(549)	MQTSNSGVFTMWND
GmPLT3b	70	(92)	CAPPQLPQFSTDNN
GmPLT3a	71	(88)	CAPPQLPQFSTDNN
MtPLT3	79	(105)	CAPTQLQQFSTDND
AtPLT2	75	(555)	QGSNPGGVFTMWNE
AtPLT1	83	(561)	QGSNPGGVFTMWNE
MtPLT1/2	84	(524)	ENMQTADLFTMWND
Consensus	55		PXFXXWND

X= any amino acid

FIG. 2H

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SEQ ID NO:

GmANT	99	(210)	LQSLSLSMSPGSGQSSC
AtANT	92	(194)	QQSLSLSMSPGSGQSSC
GmPLT2	78	(120)	LQSLTL ~~SL~~ SMGSGKDSTC
GmPLT1	82	(121)	LQSLTL ~~SL~~ SMGSGKDSTC
MtPLT1/2	84	(122)	LQSLTL ~~SL~~ SMGSGKDSTC
MtANT	98	(250)	LHSLSLSMSPSSQSSC
MtBBM	8	(192)	VQTL ~~SL~~ SLMSTGSGQSSS
GmBBM	2	(202)	QQTL ~~SL~~ SLMSTGSGQSSS
VvBBM	6	(174)	AQTL ~~SL~~ SLMSTGSHQTG
SbBBM2	28	(221)	SQSLAL ~~SL~~ SMSTGSHLPM
OsBBM2	18	(234)	SQSLAL ~~SL~~ SMSTGSHSHL
ZmBBM2	12	(214)	SQSLAL ~~SL~~ SMSTGSHLPM
SbANT	93	(217)	HHALAL ~~SL~~ SMSSGSLSSC
ZmBBM	10	(181)	AQGL ~~SL~~ SLSMNMAGTTQG
GmAIL1	86	(150)	FQSL ~~SL~~ SLTMSPSVQNGV
OsBBM	14	(177)	AQAL ~~SL~~ SLSMNMAGTTTA
BnBBM2	26	(159)	AKGL ~~SL~~ SLSMNSSTSCDN
BnBBM1	24	(159)	AKGL ~~SL~~ SLSMNSSTSCDN
SbBBM	4	(185)	VQGL ~~SL~~ SLSMNMAGATQG
OsANT	95	(241)	LHPLTL ~~SL~~ SMSSAGSQSS
MtAIL1	90	(191)	FQSLNLT ~~SL~~ MSPCVQNGV
ZmANT	67	(231)	PHPLAL ~~SL~~ SMSSGTGSGQS
AtPLT1	83	(126)	LQSLTL ~~SL~~ SMGTAGNNV
AtPLT2	75	(129)	LQSLTL ~~SL~~ SMGSTGAAAA
AtBBM	22	(160)	ARGL ~~SL~~ SLSMNSSTSDSN
OsBBM3	20	(220)	GQGLAL ~~SL~~ SMSTGSVAAA
ZmANT2	97	(202)	TRPL ~~SL~~ SLMMSPGTQLS
Consensus	56		LXL ~~SL~~ SM

X = S, T or A

FIG. 2I

SEQ ID NO:

SbBBM	4	(529)	GWCKQE ~~QD~~ HAVIAAAH
OsBBM	14	(534)	GWCKQE ~~QD~~ HAVIAAAH
ZmBBM	10	(531)	GWCKQE ~~QD~~ HAVIAAAH
SbBBM2	28	(536)	GWCKPE ~~QD~~ AAVAAAAH
OsBBM2	18	(560)	GWCKPE ~~QD~~ AAVAAAAH
ZmBBM2	12	(528)	GWCKPE ~~QD~~ AAAAAAHS
OsBBM3	20	(522)	GWCKPE ~~QD~~ AVIAAGHC
MtBBM	8	(522)	LWCKQE ~~QD~~ SDDHSTYT
VvBBM	6	(453)	VWCKQE ~~QD~~ PDGTHNFQ
OsBBM1	16	(416)	AWLKQE ~~QD~~ SSVVTTAAQ
GmBBM	2	(527)	NWCKQE ~~QD~~ NSDASHSL
Consensus	57		WCKXE ~~QD~~

X= Q or P

FIG. 2J

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SEQ ID NO:			
OsBBM2	18	(529)	HHHGWPTIAFQQPPPLAVHYPY
SbBBM2	28	(508)	GHHAWPTIAFQQPSPLSVHYPY
ZmBBM2	12	(501)	GHHGWPTIAFQQPSPLSVHYPY
VvBBM	6	(425)	HHHGWPTVAFQQAQPFMSHYPY
SbBBM	4	(502)	YHGAWPTIAFQPSAATGLYHPY
ZmBBM	10	(500)	HGAAWPTIAFQPGAATTGLYHP
OsBBM	14	(502)	AAAWPTIAFQAAAAPPPHAAG
Consensus 58			WPTIAFQ

FIG. 2K

SEQ ID NO:			
SbBBM	4	(572)	MHGLGSM DNASLEHSTGSNSV VYNG
ZmBBM	10	(577)	MHGLASID SASLEHSTGSNSV VYNG
OsBBM	14	(576)	QHGLGSIDNASLEHSTGSNSV VYNG
VvBBM	6	(487)	LHNLM SMDSSSMDHSSGSNSV IYSG
MtBBM	8	(560)	LQNIM SMDSASMDNSSGSNSV VYGG
GmBBM	2	(567)	LHPMLSMD SASIDNSSSSNSV VYDG
Consensus 59			SXGSNSV VYNG

X= S or T

FIG. 2L

SEQ ID NO:			
SbBBM2	28	(78)	ETQDWNMRGLDY
ZmBBM2	12	(75)	ETQDWNMRGLDY
OsBBM2	18	(76)	EAQDWNMRGLDY
OsBBM3	20	(74)	ETQDWAMRGLDY
SbBBM	4	(43)	IPQDWSMRGSEL
OsBBM	14	(49)	IPQDWSMRGSEL
ZmBBM	10	(44)	IPQDWSMRGSEL
Consensus 60			QDWXMRG

X= S or N

FIG. 2M

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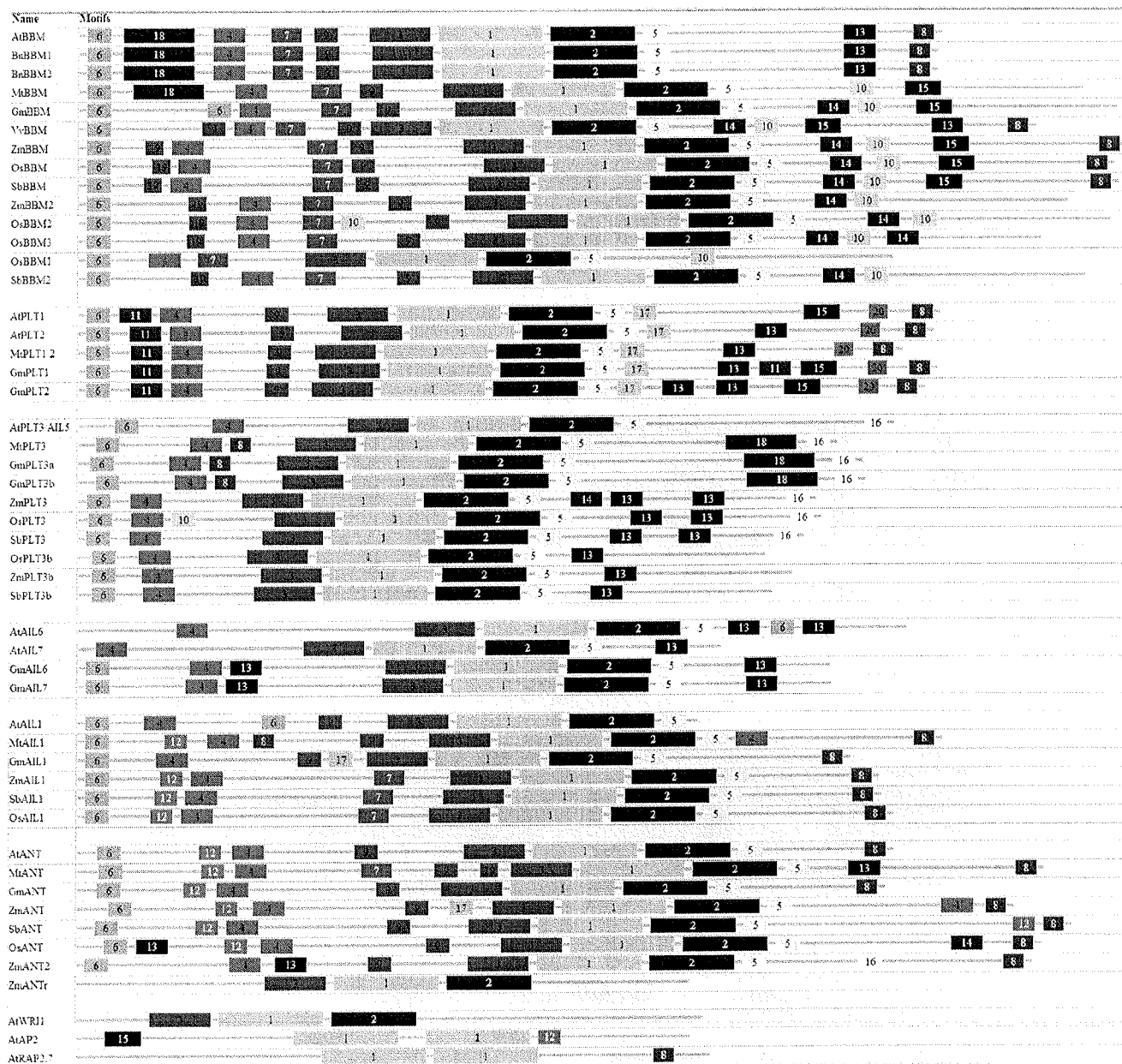


FIG. 3

[illegible]

FIG. 4-1

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	340	*	360	*	380	*	400	*	420	*	440	
ZmBBM2	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	380							
SbBBM2	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	387							
OsBBM2	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	404							
OsBBM3	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	380							
OsBBM1	:	DTFGQRTSIYRGVTKHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	269							
ZmBBM	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	374							
SbBBM	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	378							
OsBBM	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	384							
BnBBM1	:	ESFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	311							
BnBBM2	:	ESFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	311							
AtBBM	:	ESFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	311							
MtBBM	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	363							
GmBBM	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	370							
VvBBM	:	DTFGQRTSIYRGVTRHRWTGRYEHLWDNSCRREGQSRKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFPISNYEKELDKMKHMTROEYIAYLRN	SSGFSRGAS	:	309							
		d3FGQRTSIYRGVT4HRWTGRYEHLWDNSC4REGQ3RKGRQVYLGGYDKEKAARAYDLAALKYWGTTTTNFP6s	YEKE6eaMKHMTROE56A	LRR	SSGFSRGAS							
		*	460	*	480	*	500	*	520	*	540	*
ZmBBM2	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKDAVDHVEAG-AT IWR	ADMDGA	:	484							
SbBBM2	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKDAVDHVEAG-AT IWR	ADMDGG	:	491							
OsBBM2	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKEAADHAAAGAT I WRA	ADMDGA	:	510							
OsBBM3	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKEAEVAAAAA	GGG	:	476							
OsBBM1	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSNLP IGTGTTTRRLKSSDHTDNVDYINVN	TEPN	:	373							
ZmBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSALPIG-SAKRLKEAEAAASQAHHAGV	VSYDVG	:	479							
SbBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSALPIG-SAKRLKEAEAAASQAHHAGV	VSYDVG	:	482							
OsBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSALPIG-SAKRLKEAEAAASQAHHAGV	AYDVG	:	479							
BnBBM1	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSALPIG-SAKRLKEANRPVPSMMMI S		:	408							
BnBBM2	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSALPIG-SAKRLKEANRPVPSMMMI S		:	408							
AtBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSALPIG-SAKRLKDVNNPVP-AMMI S		:	407							
MtBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDVAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKDAVDHVEAG-AT IWR		:	472							
GmBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDVAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKDAVDHVEAG-AT IWR		:	477							
VvBBM	:	KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDIAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKDAVDHVEAG-AT IWR		:	412							
		KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFTSTEEAAEAYDVAAIFKFRGLNAVTFNFDMSRYDVKSILESSSTLPVG-GAARRLKDAVDHVEAG-AT IWR										
		*	560	*	580	*	600	*	620	*	640	*
ZmBBM2	:	VIISQAEAGMGGYAS-YGHH-GPTIAF-QQPSPLSVHP-YGQP-SRGVQPEQD-AAAAAAHSLODQQL-HL	SAATHFF	:	560							
SbBBM2	:	VIISQAEAGMGGYAS-YGHH-GPTIAF-QQPSPLSVHP-YGQP-SRGVQPEQD-AAAAAAHSLODQQL-HL	SAATHFF	:	569							
OsBBM2	:	GVISGADVGMAAYAAHYHHHHH-GPTIAF-QQPPPLAVHP-YGQAPAPSRGVQPEQD-AAAAAAHSLODQQL-HL	SAATHFF	:	597							
OsBBM3	:	VIVSHADCGVGGYGGY-CGPTAFGGGQAPLAVHP-PSYGGAS-GVQPEQD-AVIAAGHCATDQQL-HL	SG	:	558							
OsBBM1	:	NVVSHTFNGVGNVGSQH-YGYN-GSPISM-QPIPSQJA-NGQPR-AWLQEQDSSVVTAAQNLHMHFFSL	YTHFF	:	449							
ZmBBM	:	RIASQGDGGALAAAYGAHYHGA-APTIAFQPGAATT-GLHPYAGQPMRG-GVQPEQDHAIAAHSLODQQL-HL	NLA	:	565							
SbBBM	:	RIASQGDGGALAAAYGAHYHGA-APTIAFQPGAATT-GLHPYAGQPMRG-GVQPEQDHAIAAHSLODQQL-HL	NLA	:	564							
OsBBM	:	RIASQGDGGALAAAYGAHYHHHSAHA-APTIAFQPGAATT-GLHPYAGQPMRG-GVQPEQDHAIAAHSLODQQL-HL	NLA	:	569							
BnBBM1	:	NNSESENS-ASGWQNAAYQHGGVD-LSLLHQHQERYNGY-YYNGGNLSSESARACFKQEDQHH-FL	SNT	:	484							
BnBBM2	:	NNSESENS-ASGWQNAAYQHGGVD-LSLLHQHQERYNGY-YYNGGNLSSESARACFKQEDQHH-FL	SNT	:	484							
AtBBM	:	NNSESENS-ASGWQNAAYQHGGVD-LSLLHQHQERYNGY-YYNGGNLSSESARACFKQEDQHH-FL	SNT	:	482							
MtBBM	:	NNSHTEQAII-YAATNASNWHALSQHQQPHHHYANNMQLONPYGTQTQK-LWGQEQDSDHSTYTTATDQQL-HL	CLNN	:	573							
GmBBM	:	MN-SHTQGIINNYAAGGTTATHHHHNNALAFHQDP-CTTTHPYGQRIN-LWGQEQDSDHSTYTTATDQQL-HL	CLNN	:	577							
VvBBM	:	SQTDGINN-YGAHHHG-WPTVAQQAQPFSS-MHPYGHQGRA-VWGQEQDSDHSTYTTATDQQL-HL	CLNT	:	497							
		s	y	5 k eqd	Lg							

FIG. 4-2

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		*	680	*	700	*	720	*	740	*	760	*	
ZmBBM2	: QA-SS	-----	SSITVYN	GGAG	-----	ASGGY-QGLG	GSS-FLM	SS-TVVAADQGHSS-TANQGSTCSYGDDHQEGKLI	-----	: 626			
SbBBM2	: QA-SS	-----	SSAVYNSGGGG	-----	ASGGYHQGLG	GSSSFLM	SS-TVVAGADQGHSSSTANQGSTCSYGDDHQEGKLI	-----	: 639				
OsBBM2	: QA-SS	-----	SSITVYN	-G	-----	GGGGY-QGLG	GNAFLM	AS-TVVA-DQGHSSSTATNHCNTCSYGNEEQ-GKLI	-----	: 657			
OsBBM3	: QQPAS	-----	SSAVYG	-----	NGGG	GGNAFMM	MG-AVVAADHQGSSAYGGG	-----	DESGRLVVG	: 611			
OsBBM1	: QQ-SD	-----	VPDVTG	-----	FVDAPSRSSDSYSFRYNGTNGFHGLPGG	ISYAMPVATAVDQGGQIHGYGEDG	-----	: 511					
ZmBBM	: SAGQAAAAAAAMHGLAS	IDSASLEHSTGSNSVYNGG	-----	VGDSNGASAV	SGGGYMM	MSAAGATTTSAMVSHEQM HARAY	-----	DEAKQAAQMG	: 654				
SbBBM	: SAGQQ	-----	AAHMHGLGSMNDASLEHSTGSNSVYNG	-----	VGDSNGSTVVG	SGG-YMM	MSAATATATTAMVSHEQVHARAQGDHDEAKQAAQMG	-----	: 651				
OsBBM	: SQAMQ	-----	QQHGLGSIDNASLEHSTGSNSVYNG	-----	DNGG	GGGYIM	MSAVSATATAVASSHDHG	-----	GDGGKQVQMG	: 641			
BnBBM1	: HQSSV	-----	SDDVTVCN	VVG	-----	YGYQGF-AA	V	-----	NCDAYAASEFD	-----	: 524		
BnBBM2	: HQSSV	-----	SDDVTVCN	VVG	-----	YGYQGF-AA	V	-----	NCDAYAASEFD	-----	: 524		
AtBBM	: HHSST	-----	SDDVTVCN	VVS	-----	YGYQGF-AI	VG	-----	TSVNYDPFTA	AEIA	-----	: 526	
MtBBM	: MDNSS	-----	GNSVYGGGDHGG	-----	YGGNGY-MI	IM	-----	AIANDGNONPRSNNNFGESEIKGFGYENVF	TTTD	: 638			
GmBBM	: IDNSS	-----	SSNSVYDG	-----	YGGGYNVI	IMGTTTTTVVANDQDNPRSNHGF	GDNEIKALGYESVY	STTD	: 643				
VvBBM	: MDHSS	-----	GNSVITYSGGAADGSAATGSGSGSFQGVGYGNNIGF	VM	TS	-----	TVIAHEGGHG-QGNGGFGDSEVKA	IGYDNMF	STD	: 579			
			s		g	p		g					
			780	*	800	*	820	*					
ZmBBM2	: -DAAMVATAAGDPYA	-----	AARNGYQFS-QGSGSTVSIAR	-----	ANGYANNWSSP	NNGMG	-----	: 679					
SbBBM2	: -DAMVAATAAGDPYA	-----	AARSGYQFSSQSGSTVSIAR	-----	ANGYSNNWSSP	NGGMG	-----	: 693					
OsBBM2	: -DAMAMASGAAG	-----	GGYOLS-QGSASTVSIAR	-----	ANGYSANWSSP	NGAMG	-----	: 703					
OsBBM3	: -LDGVDPYAAMR	-----	SAYELSQGSSSSSVSVAKA	-----	ANGYPDNNWSSP	N-GMG	-----	: 658					
OsBBM1	: -VAGIDTTHDLYG	-----	SRNVYYLSEGSLLADVEKEG	-----	DYQGSVGGNSWVLP	TP	-----	: 559					
ZmBBM	: -TESYLVNAENNGGG	-----	RMSAWGTVVSAASNDN	IAADVGHGGAQL	SVWNDT	: 709							
SbBBM	: -TESYLVNAENYGGG	-----	RMSAAWATVSAPPAASNDN	-----	MADVGHGGAQL	SVWNDT	: 703						
OsBBM	: -DSYLVGADAYGGGGA	-----	GRMPSWAMTPASAPAA	TSSSD	MTGVCHG-AQL	SVWNDT	: 695						
BnBBM1	: -INAR	NHYFFAQ	-----	QQQTQSGPGGDFPAAMTNVGSNMYYHGE	GGGEVAPT	TVWNDN	: 579						
BnBBM2	: -INAR	NHYFFAQ	-----	QQQTQSGPGGDFPAAMTNVGSNMYYHGE	GGGEVAPT	TVWNDN	: 579						
AtBBM	: -INAR	NHYFFAQHQ	-----	QQQIQSGPGGDFPVAISNNHSSNMYYHGE	GGGEVAPT	SVWNDT	: 584						
MtBBM	: PTHAQAARNLYYQPGQ	-----	LSVDQG	-----	SNWVPTAIP	TLAPR-TTNVSLCP	-----	P-TLLHE	: 689				
GmBBM	: PTHAH	ARNLYLTQQQPSSVD	AVKASAYDQGSACNTWVPTAIP	THAPRSSTSMALCHGATP	-----	SLLHE	: 710						
VvBBM	: PTHAR	-----	SLYLSQQSSAG-MVKGSSAYDQSGGCNNWVPTAVPTLAPR-TNSLAVCHGTPT	-----	TVWNDT	: 643							
	y				f								

FIG. 4-3

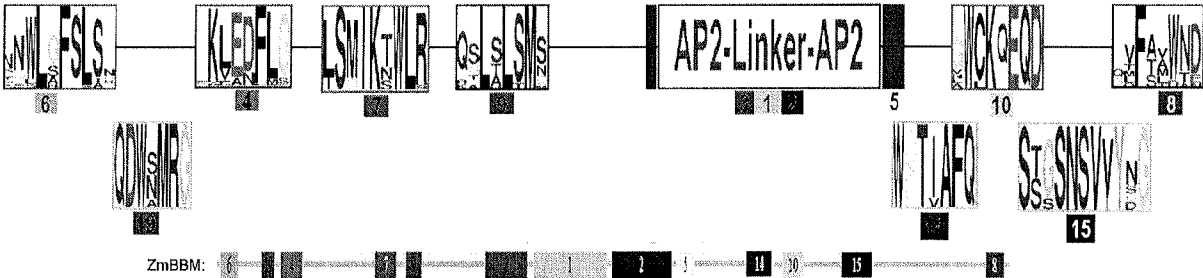


FIG. 5

Sequence Listing from Patent scope

SEQUENCE LISTING

<110> Gordon-Kamm, William J.
Klein, Theodore M
Lowe, Keith S.
McBride, Kevin E.
Scelonge, Christopher J.
Wang, Bing-Bing
Wang, Ning
Wu, Xinli E.

<120> Methods and Compositions for the
Introduction and Regulated Expression of Genes in Plants

<130> 35718/ 400069

<150> 61/ 291, 257

<151> 2009- 12- 30

<160> 126

<170> Fast SEQ for Windows Version 4.0

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1 5 10 15	
cct tct agt caa gat cac tct caa acg gca cct tct cgt ttt tgc ttc	96
Pro Ser Ser Gln Asp His Ser Gln Thr Ala Pro Ser Arg Phe Cys Phe	
20 25 30	
aac cct gat gga atc tca agc act gat gta gca gga gac tgc ttt gat	144
Asn Pro Asp Gly Ile Ser Ser Thr Asp Val Ala Gly Asp Cys Phe Asp	
35 40 45	
ctc act tct gac tca act cct cat tta ctg aac ctt ccc tct tac ggc	192
Leu Thr Ser Asp Ser Thr Pro His Leu Leu Asn Leu Pro Ser Tyr Gly	
50 55 60	
ata tac gaa gct ttt cat agg agc aac aat att cac acc act caa gat	240
Ile Tyr Glu Ala Phe His Arg Ser Asn Asn Ile His Thr Thr Gln Asp	
65 70 75 80	
tgg aag gag aac tac aac agc caa aac ttg cta ttg gga act tca tgc	288
Trp Lys Glu Asn Tyr Asn Ser Gln Asn Leu Leu Leu Gly Thr Ser Cys	
85 90 95	
agc aac caa aac atg aac cac aac cat cag caa caa caa caa caa cag	336
Ser Asn Gln Asn Met Asn His Asn His Gln Gln Gln Gln Gln Gln Gln	
100 105 110	

Sequence Listing from Patent scope																	
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Pro	Lys	Leu	Glu	Asn	Phe	Leu	Gly	Gly	His	Ser	Phe	Gly	Glu	His	Glu		
		115					120					125					
caa	ccc	tac	ggg	ggg	aac	tca	gcc	tct	aca	gaa	tac	atg	ttc	ccg	gct		432
Gln	Pro	Tyr	Gly	Gly	Asn	Ser	Ala	Ser	Thr	Glu	Tyr	Met	Phe	Pro	Ala		
		130				135					140						
cag	ccg	gta	ttg	gcc	ggg	ggc	ggc	ggc	ggg	ggg	agc	aat	agc	agc	aac		480
Gln	Pro	Val	Leu	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Asn	Ser	Ser	Asn		
		145			150					155					160		
aca	agc	aac	agt	agc	tcc	ata	ggg	tta	tcc	atg	ata	aag	aca	tgg	ttg		528
Thr	Ser	Asn	Ser	Ser	Ser	Ile	Gly	Leu	Ser	Met	Ile	Lys	Thr	Trp	Leu		
				165					170					175			
agg	aac	caa	cca	cca	cac	tca	gaa	aac	aac	aat	aac	aac	aac	aat	gaa		576
Arg	Asn	Gln	Pro	Pro	His	Ser	Glu	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Glu		
			180					185					190				
agt	ggg	ggc	aat	agt	aga	agc	agt	gtg	cag	cag	act	cta	tca	ctt	tcc		624
Ser	Gly	Gly	Asn	Ser	Arg	Ser	Ser	Val	Gln	Gln	Thr	Leu	Ser	Leu	Ser		
		195					200					205					
atg	agt	act	ggg	tca	caa	tca	agc	aca	tca	cta	ccc	ctt	ctc	act	gct		672
Met	Ser	Thr	Gly	Ser	Gln	Ser	Ser	Thr	Ser	Leu	Pro	Leu	Leu	Thr	Ala		
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agt	gtg	gat	aat	gga	gag	agt	tct	tct	gat	aac	aaa	caa	cca	cat	acc		720
Ser	Val	Asp	Asn	Gly	Glu	Ser	Ser	Ser	Asp	Asn	Lys	Gln	Pro	His	Thr		
		225			230					235					240		
acg	gct	gca	ctt	gat	aca	acc	caa	acc	gga	gcc	att	gaa	act	gca	ccc		768
Thr	Ala	Ala	Leu	Asp	Thr	Thr	Gln	Thr	Gly	Ala	Ile	Glu	Thr	Ala	Pro		
				245					250					255			
aga	aag	tcc	att	gac	act	ttt	gga	cag	aga	act	tct	atc	tac	cgt	ggg		816
Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly		
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gta	aca	agg	cat	agg	tgg	acg	ggg	agg	tat	gag	gct	cac	ctg	tgg	gat		864
Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp		
		275					280					285					
aat	agt	tgt	aga	aga	gag	gga	caa	act	cgc	aaa	gga	agg	caa	gtt	tac		912
Asn	Ser	Cys	Arg	Arg	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Val	Tyr		
		290				295					300						
ttg	gga	ggg	tat	gac	aaa	gaa	gaa	aag	gca	gct	aga	gcc	tac	gat	ttg		960
Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu		
		305			310					315					320		
gca	gca	cta	aaa	tac	tgg	gga	aca	act	acg	aca	aca	aat	ttt	cca	att		1008
Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Thr	Thr	Thr	Thr	Thr	Asn	Phe	Pro	Ile		
				325					330					335			
agc	cac	tat	gag	aaa	gag	ttg	gaa	gaa	atg	aag	cac	atg	act	agg	caa		1056
Ser	His	Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln		
			340					345					350				
gag	tac	gtt	gcg	tca	ttg	aga	agg	aag	agt	agt	ggg	ttt	tct	cgc	ggg		1104
Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly		
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Sequence Listing from Patent scope

gca tcc att tat cga ggt gtg acg aga cac cat caa cat gga aga tgg Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp 370 375 380	1152
caa gcg agg att gga aga gtt gct ggc aac aag gat ct c t ac ttg gga Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly 385 390 395 400	1200
act ttc agc acc caa gag gag gca gca gaa gca tat gat gta gca gca Thr Phe Ser Thr Gln Gu Gu Ala Ala Gu Ala Tyr Asp Val Ala Ala 405 410 415	1248
atc aaa ttc aga gga cta agt gct gtt aca aac ttt gac atg agc aga Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn Phe Asp Met Ser Arg 420 425 430	1296
tat gac gtg aaa agc ata ctt gag agc acc act ttg cca att ggt ggt Tyr Asp Val Lys Ser Ile Leu Gu Ser Thr Thr Leu Pro Ile Gly Gly 435 440 445	1344
gct gca aag cgt ttg aag gat atg gag cag gtg gaa ctg agg gtg gag Ala Ala Lys Arg Leu Lys Asp Met Gu Gn Val Gu Leu Arg Val Gu 450 455 460	1392
aat gtt cat aga gca gat caa gaa gat cat agt agc atc atg aac tct Asn Val His Arg Ala Asp Gln Gu Asp His Ser Ile Met Asn Ser 465 470 475 480	1440
cac tta act caa gga atc att aac aac tat gca gca gga gga aca aca His Leu Thr Gln Gly Ile Ile Asn Asn Tyr Ala Ala Gly Gly Thr Thr 485 490 495	1488
gcg act cat cat cat aac tgg cac aat gct ctt gca ttc cac caa cct Ala Thr His His His Asn Trp His Asn Ala Leu Ala Phe His Gln Pro 500 505 510	1536
caa cct tgc acc acc ata cac tac cct tat gga caa aga att aat tgg Gln Pro Cys Thr Thr Ile His Tyr Pro Tyr Gly Gln Arg Ile Asn Trp 515 520 525	1584
tgc aag caa gaa caa gac aac tct gat gcc tct cac tct ttg tct tat Cys Lys Gln Gu Gln Asp Asn Ser Asp Ala Ser His Ser Leu Ser Tyr 530 535 540	1632
tca gat att cat caa cta cag cta ggg aac aat ggc aca cac aac ttc Ser Asp Ile His Gln Leu Gn Leu Gly Asn Asn Gly Thr His Asn Phe 545 550 555 560	1680
ttt cac aca aat tca ggg ttg cac cct atg tta agc atg gat tct gct Phe His Thr Asn Ser Gly Leu His Pro Met Leu Ser Met Asp Ser Ala 565 570 575	1728
tcc att gac aat agc tct tca tct aac tct gtt gtt tat gat ggt tat Ser Ile Asp Asn Ser Ser Ser Asn Ser Val Val Tyr Asp Gly Tyr 580 585 590	1776
gga ggt ggt ggg ggc tat aat gtg att cct atg ggg act act act act Gly Gly Gly Gly Gly Tyr Asn Val Ile Pro Met Gly Thr Thr Thr Thr 595 600 605	1824
gtt gtt gca aat gat ggt gat caa aat cca aga agc aat cat ggt ttt Val Val Ala Asn Asp Gly Asp Gln Asn Pro Arg Ser Asn His Gly Phe 610 615 620 625 630 635 640 645	1872

Sequence Listing from Patent scope

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	ata Ile	aag Lys 630	gca Ala
	ctt Leu	ggt Gly	tat Tyr
		gaa Glu 635	agt Ser
		gtg Val	tat Tyr
		ggt Gly	tct Ser 640
			1920
aca Thr	act Thr	gat Asp	cct Pro
		tat Tyr 645	cat His
		gca Ala	cat His
		gca Ala	agg Arg 650
		aac Asn	ttg Leu
		tat Tyr	tat Tyr
		ctt Leu 655	act Thr
			1968
caa Gln	cag Gln	caa Gln	cca Pro 660
		tct Ser	tct Ser
		gtt Val	gat Asp
		gca Ala 665	gtg Val
		aag Lys	gct Ala
		agt Ser	gca Ala 670
		tat Tyr	gat Asp
			2016
caa Gln	gga Gly	tct Ser 675	gca Ala
		tgc Cys	aat Asn
		act Thr	tgg Trp 680
		gtt Val	cca Pro
		act Thr	gct Ala
		att Ile 685	cca Pro
		act Thr	cat His
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gca Ala	cca Pro 690	agg Arg	tct Ser
		agt Ser	act Thr
		agt Ser 695	atg Met
		gct Ala	ctc Leu
		tgc Cys	cat His 700
		ggt Gly	gct Ala
		acg Thr	ccc Pro
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ttc Phe 705	tct Ser	tta Leu	ttg Leu
		cat His	gaa Glu 710
		t ag	
			2133

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 <211> 710
 <212> PRT
 <213> Glycine max

<400> 2

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

Sequence Listing from Patent scope

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Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly
Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp
Asn	Ser	Cys	Arg	Arg	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Val	Tyr
Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu
Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Thr	Thr	Thr	Thr	Thr	Asn	Phe	Pro	Ile
Ser	His	Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln
Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly
Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp
Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly
Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Val	Ala	Ala
Ile	Lys	Phe	Arg	Gly	Leu	Ser	Ala	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg
Tyr	Asp	Val	Lys	Ser	Ile	Leu	Glu	Ser	Thr	Thr	Leu	Pro	Ile	Gly	Gly
Ala	Ala	Lys	Arg	Leu	Lys	Asp	Met	Glu	Gln	Val	Glu	Leu	Arg	Val	Glu
Asn	Val	His	Arg	Ala	Asp	Gln	Glu	Asp	His	Ser	Ser	Ile	Met	Asn	Ser
His	Leu	Thr	Gln	Gly	Ile	Ile	Asn	Asn	Tyr	Ala	Ala	Gly	Gly	Thr	Thr
Ala	Thr	His	His	His	Asn	Trp	His	Asn	Ala	Leu	Ala	Phe	His	Gln	Pro
Gln	Pro	Cys	Thr	Thr	Ile	His	Tyr	Pro	Tyr	Gly	Gln	Arg	Ile	Asn	Trp
Cys	Lys	Gln	Glu	Gln	Asp	Asn	Ser	Asp	Ala	Ser	His	Ser	Leu	Ser	Tyr
Ser	Asp	Ile	His	Gln	Leu	Gln	Leu	Gly	Asn	Asn	Gly	Thr	His	Asn	Phe
Phe	His	Thr	Asn	Ser	Gly	Leu	His	Pro	Met	Leu	Ser	Met	Asp	Ser	Ala
Ser	Ile	Asp	Asn	Ser	Ser	Ser	Ser	Asn	Ser	Val	Val	Tyr	Asp	Gly	Tyr
Gly	Gly	Gly	Gly	Gly	Tyr	Asn	Val	Ile	Pro	Met	Gly	Thr	Thr	Thr	Thr
Val	Val	Ala	Asn	Asp	Gly	Asp	Gln	Asn	Pro	Arg	Ser	Asn	His	Gly	Phe
Gly	Asp	Asn	Glu	Ile	Lys	Ala	Leu	Gly	Tyr	Glu	Ser	Val	Tyr	Gly	Ser
Thr	Thr	Asp	Pro	Tyr	His	Ala	His	Ala	Arg	Asn	Leu	Tyr	Tyr	Leu	Thr
Gln	Gln	Gln	Pro	Ser	Ser	Val	Asp	Ala	Val	Lys	Ala	Ser	Ala	Tyr	Asp
Gln	Gly	Ser	Ala	Cys	Asn	Thr	Trp	Val	Pro	Thr	Ala	Ile	Pro	Thr	His
Ala	Pro	Arg	Ser	Ser	Thr	Ser	Met	Ala	Leu	Cys	His	Gly	Ala	Thr	Pro
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Sequence Listing from Patent scope

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<212> DNA

<213> Sorghum bicolor

<220>

<221> CDS

<222> (1)... (2112)

<400> 3

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ctg ccg ccc acc cag acg gac tcc acc ctg atc tct gcc gcc acc acc	96
Leu Pro Pro Thr Gln Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr Thr	
20 25 30	
gac gat gtc tcc ggc gat gtc tgc ttc aac atc ccc caa gat tgg agc	144
Asp Asp Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp Ser	
35 40 45	
atg agg gga tcc gag ctt tcg gcg ctg gtc gcc gag ccg aag ctg gag	192
Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu Glu	
50 55 60	
gac ttc ctg ggc gga atc tcc ttc tcc gag cag cac cac aag gcc aac	240
Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ala Asn	
65 70 75 80	
tgc aac atg atc ccc agc act agc agc aca gct tgc tac gcg agc tcg	288
Cys Asn Met Ile Pro Ser Thr Ser Ser Thr Ala Cys Tyr Ala Ser Ser	
85 90 95	
ggg gct acc gcc ggc tac cat cac cag ctg tac cac cag ccc acc agc	336
Gly Ala Thr Ala Gly Tyr His His Gln Leu Tyr His Gln Pro Thr Ser	
100 105 110	
tcc gcg ctg cac ttc gct gac tcc gtc atg gtg gcc tcc tcg gcc ggc	384
Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala Gly	
115 120 125	
ggc gtc cac gac gga ggt gcc atg ctg agc gcg gcc agc gct aat ggt	432
Gly Val His Asp Gly Gly Ala Met Leu Ser Ala Ala Ser Ala Asn Gly	
130 135 140	
agc gct ggc gct ggc gct gcc agt gcc aat ggc agc ggc agc atc ggg	480
Ser Ala Gly Ala Gly Ala Ala Ser Ala Asn Ala Gly Ser Gly Ser Ile Gly	
145 150 155 160	
ctg tcc atg atc aag aac tgg ctg cgg agc caa cca gct ccc atg cag	528
Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln	
165 170 175	
ccg agg gtg gcg gcg gct gag agc gtg cag ggg ctg tct ttg tcc atg	576
Pro Arg Val Ala Ala Ala Glu Ser Val Gln Gly Leu Ser Leu Ser Met	
180 185 190	
aac atg gcg ggg gcg acg caa ggc gcc gct ggc atg cca ctt ctt gct	624
Asn Met Ala Gly Ala Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala	
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Sequence Listing from Patent scope

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ggc gcg tcg gct gac aac acg gca agg aag acg gtg gac acg ttc ggg 816 Gly Ala Ser Ala Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly 260 265 270			
cag cgc acg tcg att tac cgt ggc gtg aca agg cat aga tgg act ggg 864 Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly 275 280 285			
aga tat gaa gca cat ctg tgg gac aac agt tgc aga agg gaa gga caa 912 Arg Tyr Gu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Gu Gly Gln 290 295 300			
act cgc aag ggt cgt caa gtc tat tta ggt ggc tat gat aaa gag gag 960 Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Gu Gu 305 310 315 320			
aaa gct gct agg gct tat gat ctg gct gct ctt aag tac tgg ggt ccc 1008 Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro 325 330 335			
acg aca aca aca aat ttt cca gtg aat aac tac gaa aag gag ctg gag 1056 Thr Thr Thr Thr Asn Phe Pro Val Asn Asn Tyr Gu Lys Gu Leu Gu 340 345 350			
gat atg aag cac atg aca agg cag gag ttt gta gcg tct ctg aga agg 1104 Asp Met Lys His Met Thr Arg Gln Gu Phe Val Ala Ser Leu Arg Arg 355 360 365			
aag agc agt ggt ttc tcc aga ggt gca tcc att tac agg gga gtg act 1152 Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr 370 375 380			
agg cat cac cag cat gga aga tgg caa gca cgg att gga cga gtt gca 1200 Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala 385 390 395 400			
ggg aac aag gat ctg tac ttg ggc acc ttc agc acg cag gag gag gca 1248 Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Gu Gu Ala 405 410 415			
gcg gag gca tac gac att gcg gcg atc aag ttc cgc ggc ctg aac gcc 1296 Ala Gu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala 420 425 430			
gtc aca aac ttc gac atg agc cgc tac gac gtc aag agc atc ctg gac 1344 Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp 435 440 445			
agc agt gcg ctg ccc atc ggc agc gcc gcc aag cgt ctg aag gag gcc 1392 Ser Ser Ala Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Gu Ala 450 455 460			
gag gcc gcc gcg tcc gca cag cac cat gcc gcc gtg gtg agc tac gac 1440			

Sequence Listing from Patent scope															
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gcg Al a	t ac Tyr	ggc G y	gcg Al a 500	cac H i s	t ac Tyr	cat H i s	ggc G y	gcc Al a 505	t gg Trp	ccg Pro	acc Thr	at c I l e	gcg Al a 510	t t c Phe	cag G n
ccg Pro	agc Ser	gcg Al a 515	gcc Al a	acg Thr	ggc G y	ct g Leu	t ac Tyr 520	cac H i s	ccg Pro	t ac Tyr	gcg Al a	cag G n 525	ccg Pro	at g Met	cgc Arg
ggg G y	t gg Trp 530	t gc Cys	aag Lys	cag G n	gag G u	cag G n 535	gac Asp	cac H i s	gcg Al a	gt g Val	at c I l e 540	gcg Al a	gcc Al a	gcg Al a	cac H i s
agc Ser 545	ct g Leu	cag G n	gag G u	ct c Leu	cac H i s 550	cac H i s	ct g Leu	aac Asn	ct g Leu	ggt G y 555	gct Al a	gcc Al a	gcc Al a	ggc G y	gcg Al a 560
cac H i s	gac Asp	t t c Phe	t t c Phe	t cg Ser 565	gcg Al a	ggg G y	cag G n	cag G n	gcg Al a 570	gcg Al a	at g Met	cac H i s	ggc G y	ct g Leu 575	ggt G y
agc Ser	at g Met	gac Asp	aat Asn 580	gca Al a	t ca Ser	ct c Leu	gag G u	cac H i s 585	agc Ser	acc Thr	ggc G y	t cc Ser	aac Asn 590	t cc Ser	gt c Val
gt g Val	t ac Tyr	aac Asn 595	ggt G y	gt t Val	ggt G y	gat Asp	agc Ser 600	aac Asn	ggc G y	agc Ser	acc Thr	gt c Val 605	gt c Val	ggc G y	agt Ser
ggt G y 610	ggc G y	t ac Tyr	at g Met	at g Met	cct Pro	at g Met 615	agc Ser	gct Al a	gcc Al a	acg Thr	gcg Al a 620	acg Thr	gct Al a	acc Thr	acg Thr
gca Al a 625	at g Met	gt g Val	agc Ser	cac H i s	gag G u 630	cag G n	gt g Val	cat H i s	gca Al a	cgg Arg 635	gca Al a	cag G n	ggt G y	gat Asp	cac H i s 640
cac H i s	gac Asp	gaa G u	gcc Al a	aag Lys 645	cag G n	gct Al a	gct Al a	cag G n	at g Met 650	ggg G y	t ac Tyr	gag G u	agc Ser	t ac Tyr 655	ct g Leu
gt g Val	aac Asn	gca Al a	gag G u 660	aac Asn	t at Tyr	ggc G y	ggc G y	ggg G y 665	agg Arg	at g Met	t ct Ser	gcg Al a	gcc Al a 670	t gg Trp	gcg Al a
act Thr	gt c Val	t ca Ser 675	gcg Al a	cca Pro	ccg Pro	gcg Al a	gca Al a 680	agc Ser	agc Ser	aac Asn	gat Asp	aac Asn 685	at g Met	gcg Al a	gac Asp
gt c Val 690	ggc G y	cat H i s	ggc G y	ggc G y	gca Al a	cag G n 695	ct c Leu	t t c Phe	agt Ser	gt c Val	t gg Trp 700	aac Asn	gat Asp	act Thr	t aa

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Sequence Listing from Patent scope

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<213> Sorghum bicolor

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Cys	Asn	Met	Ile	Pro	Ser	Thr	Ser	Ser	Thr	Ala	Cys	Tyr	Ala	Ser	Ser
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Ser	Ala	Leu	His	Phe	Ala	Asp	Ser	Val	Met	Val	Ala	Ser	Ser	Ala	Gly
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Gly	Val	His	Asp	Gly	Gly	Ala	Met	Leu	Ser	Ala	Ala	Ser	Ala	Asn	Gly
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Pro	Arg	Val	Ala	Ala	Ala	Glu	Ser	Val	Gln	Gly	Leu	Ser	Leu	Ser	Met
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Ala	Ala	Thr	Gly	Ala	Leu	Val	Ala	Val	Ser	Thr	Asp	Thr	Gly	Gly	Ser
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Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	Glu	Gly	Gln
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Thr	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu
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Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro
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Thr	Thr	Thr	Thr	Asn	Phe	Pro	Val	Asn	Asn	Tyr	Glu	Lys	Glu	Leu	Glu
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Asp	Met	Lys	His	Met	Thr	Arg	Gln	Glu	Phe	Val	Ala	Ser	Leu	Arg	Arg
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Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr
	370					375					380				
Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala
385					390					395					400
Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala
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Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala
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Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Lys	Ser	Ile	Leu	Asp
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Ser	Ser	Ala	Leu	Pro	Ile	Gly	Ser	Ala	Ala	Lys	Arg	Leu	Lys	Glu	Ala
	450					455					460				
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Sequence Listing from Patent scope

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 Ala Tyr Gly Ala His Tyr His Gly Ala Trp Pro Thr Ile Ala Phe Gln
 485 490 495
 Pro Ser Ala Ala Thr Gly Leu Tyr His Pro Tyr Ala Gln Pro Met Arg
 500 505 510
 Gly Trp Cys Lys Gln Gln Asp His Ala Val Ile Ala Ala Ala His
 515 520 525
 Ser Leu Gln Gln Leu His His Leu Asn Leu Gly Ala Ala Ala Gly Ala
 530 535 540
 545 His Asp Phe Phe Ser Ala Gly Gln Gln Ala Met His Gly Leu Gly
 550 555 560
 Ser Met Asp Asn Ala Ser Leu Gln His Ser Thr Gly Ser Asn Ser Val
 565 570 575
 Val Tyr Asn Gly Val Gly Asp Ser Asn Gly Ser Thr Val Gly Ser
 580 585 590
 Gly Gly Tyr Met Met Pro Met Ser Ala Ala Thr Ala Thr Thr Thr
 595 600 605
 Ala Met Val Ser His Gln Gln Val His Ala Arg Ala Gln Gly Asp His
 610 615 620
 625 His Asp Gln Ala Lys Gln Ala Ala Gln Met Gly Tyr Gln Ser Tyr Leu
 630 635 640
 Val Asn Ala Gln Asn Tyr Gly Gly Gly Arg Met Ser Ala Ala Trp Ala
 645 650 655
 Thr Val Ser Ala Pro Pro Ala Ala Ser Ser Asn Asp Asn Met Ala Asp
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 690 695 700

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 1 5 10 15
 ctt cca cca cag cct gaa aat cac tca cag aac agt gtc tct aga ctt 96
 Leu Pro Pro Gln Pro Gln Asn His Ser Gln Asn Ser Val Ser Arg Leu
 20 25 30
 ggt ttc aac tct gat gaa atc tct ggg act gat gtg tca ggt gag tgt 144
 Gly Phe Asn Ser Asp Gln Ile Ser Gly Thr Asp Val Ser Gly Gln Cys
 35 40 45
 ttt gat ctg act tca gat tcc act gct ccc tct ctg aac ctg cct ccc 192
 Phe Asp Leu Thr Ser Asp Ser Thr Ala Pro Ser Leu Asn Leu Pro Pro
 50 55 60
 cct ttt ggg ata ctt gaa gca ttc aac agg aat aat cag ccc caa gat 240
 Pro Phe Gly Ile Leu Gln Ala Phe Asn Arg Asn Asn Gln Pro Gln Asp
 65 70 75 80
 act aac tac aaa acc acc act tct gag ctg tcc atg ctg atg ggt agt 288
 Thr Asn Tyr Lys Thr Thr Thr Ser Gln Leu Ser Met Leu Met Gly Ser
 85 90 95

Sequence Listing from Patent scope

85

90

95

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			100					105					110			
aat	ttc	ctg	ggc	tgc	cgc	tct	ttt	gct	gat	cat	gag	cag	aaa	ctt	caa	384
Asn	Phe	Leu	Gly	Cys	Arg	Ser	Phe	Ala	Asp	His	Glu	Gln	Lys	Leu	Gln	
		115					120					125				
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Gly	Tyr	Tyr	Ile	Ser	Ile	Gly	Leu	Ser	Met	Ile	Lys	Thr	Trp	Leu	Arg	
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Gly	Pro	Val	Gly	Gly	Ala	Ala	Ala	Gly	Asn	Leu	Pro	Asn	Ala	Gln	Thr	
			165						170					175		
tta	tgc	tig	tcc	atg	agc	acc	ggc	tgc	cac	cag	acc	ggt	gcc	att	gaa	576
Leu	Ser	Leu	Ser	Met	Ser	Thr	Gly	Ser	His	Gln	Thr	Gly	Ala	Ile	Glu	
			180					185					190			
acg	gtg	cca	agg	aag	tcc	att	gat	aca	ttt	gga	cag	agg	aca	tcc	ata	624
Thr	Val	Pro	Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile	
		195					200					205				
tac	cgt	ggt	gta	aca	agg	cat	aga	tgg	acg	ggt	aga	tat	gag	gct	cat	672
Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	
	210					215					220					
cta	tgg	gac	aac	agt	tgc	aga	aga	gaa	gga	caa	act	cga	aag	gga	agg	720
Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	
225					230					235				240		
caa	gtt	tat	tta	ggt	ggt	tat	gac	aaa	gaa	gaa	aag	gca	gct	agg	gct	768
Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala	
				245					250					255		
tac	gat	tta	gca	gca	ctg	aag	tat	tgg	ggt	acc	acc	acc	aca	aca	aat	816
Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Thr	Thr	Thr	Thr	Thr	Asn	
			260					265					270			
ttc	cct	att	agc	aac	tat	gaa	aaa	gag	ata	gag	gag	atg	aag	cac	atg	864
Phe	Pro	Ile	Ser	Asn	Tyr	Glu	Lys	Glu	Ile	Glu	Glu	Met	Lys	His	Met	
		275					280					285				
aca	agg	cag	gag	tac	gta	gca	tct	ctg	cga	agg	aag	agt	agc	ggg	ttt	912
Thr	Arg	Gln	Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	
	290					295					300					
tct	cgt	gga	gca	tcc	ata	tat	aga	gga	gtg	acc	aga	cac	cat	cag	cat	960
Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	
305					310					315				320		
ggg	aga	tgg	cag	gca	agg	att	gga	aga	gtc	gca	ggc	aac	aaa	gat	ctt	1008
Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	
				325					330					335		
tac	tig	gga	act	ttc	agc	acc	caa	gag	gaa	gca	gca	gag	gcc	tat	gac	1056

Sequence Listing from Patent scope															
Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	
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Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp
		355					360					365			1104
atg	agt	aga	tat	gat	gtt	aat	agc	att	cta	gag	agc	agt	acc	tig	ccg
Met	Ser	Arg	Tyr	Asp	Val	Asn	Ser	Ile	Leu	Glu	Ser	Ser	Thr	Leu	Pro
	370					375					380				1152
att	ggt	gga	gct	gca	aag	cgg	tig	aaa	gat	gct	gag	cag	gct	gaa	atg
Ile	Gly	Gly	Ala	Ala	Lys	Arg	Leu	Lys	Asp	Ala	Glu	Gln	Ala	Glu	Met
385					390					395					1200
act	ata	gat	gga	cag	agg	aca	gac	gat	gag	atg	agc	tca	cag	ctg	act
Thr	Ile	Asp	Gly	Gln	Arg	Thr	Asp	Asp	Glu	Met	Ser	Ser	Gln	Leu	Thr
				405					410					415	1248
gat	gga	atc	aac	aac	tat	gga	gca	cac	cac	cat	ggc	tgg	cct	act	gtt
Asp	Gly	Ile	Asn	Asn	Tyr	Gly	Ala	His	His	His	Gly	Trp	Pro	Thr	Val
			420					425					430		1296
gca	ttc	caa	caa	gct	cag	cca	ttt	agc	atg	cac	tac	cct	tat	ggc	cat
Ala	Phe	Gln	Gln	Ala	Gln	Pro	Phe	Ser	Met	His	Tyr	Pro	Tyr	Gly	His
		435					440					445			1344
cag	cag	agg	gct	gtt	tgg	tgt	aag	caa	gag	caa	gac	cct	gat	ggc	aca
Gln	Gln	Arg	Ala	Val	Trp	Cys	Lys	Gln	Glu	Gln	Asp	Pro	Asp	Gly	Thr
	450					455					460				1392
cac	aac	ttt	caa	gat	ctt	cac	caa	cta	caa	tig	gga	aac	act	cac	aac
His	Asn	Phe	Gln	Asp	Leu	His	Gln	Leu	Gln	Leu	Gly	Asn	Thr	His	Asn
465					470					475					1440
ttc	ttc	cag	cct	aat	gtt	ctg	cac	aac	ctc	atg	agc	atg	gac	tct	tct
Phe	Phe	Gln	Pro	Asn	Val	Leu	His	Asn	Leu	Met	Ser	Met	Asp	Ser	Ser
				485					490					495	1488
tca	atg	gac	cat	agc	tca	ggc	tcc	aat	tca	gtc	atc	tat	agc	ggt	ggt
Ser	Met	Asp	His	Ser	Ser	Gly	Ser	Asn	Ser	Val	Ile	Tyr	Ser	Gly	Gly
			500					505					510		1536
gga	gcc	gct	gat	ggc	agc	gct	gca	act	ggc	ggc	agt	ggc	agt	ggg	agc
Gly	Ala	Ala	Asp	Gly	Ser	Ala	Ala	Thr	Gly	Gly	Ser	Gly	Ser	Gly	Ser
		515					520					525			1584
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Phe	Gln	Gly	Val	Gly	Tyr	Gly	Asn	Asn	Ile	Gly	Phe	Val	Met	Pro	Ile
		530				535					540				1632
agc	acc	gtc	atc	gct	cat	gaa	ggc	ggc	cat	ggc	cag	gga	aat	ggt	ggc
Ser	Thr	Val	Ile	Ala	His	Glu	Gly	Gly	His	Gly	Gln	Gly	Asn	Gly	Gly
545					550					555					1680
ttt	gga	gat	agc	gaa	gtg	aag	gcg	att	ggt	tac	gac	aac	atg	ttt	gga
Phe	Gly	Asp	Ser	Glu	Val	Lys	Ala	Ile	Gly	Tyr	Asp	Asn	Met	Phe	Gly
				565					570					575	1728
tcg	aca	gat	cct	tac	cat	gct	agg	agc	tig	tac	tat	ctt	tca	cag	caa
Ser	Thr	Asp	Pro	Tyr	His	Ala	Arg	Ser	Leu	Tyr	Tyr	Leu	Ser	Gln	Gln
			580					585					590		1776

Sequence Listing from Patent scope

tca	tct	gca	ggc	atg	gtg	aag	ggc	agt	agt	gca	tat	gat	cag	ggg	tca	1824
Ser	Ser	Ala	Gly	Met	Val	Lys	Gly	Ser	Ser	Ala	Tyr	Asp	Gln	Gly	Ser	
		595					600					605				
ggg	tgt	aac	aac	tgg	gtt	cca	act	gca	gtt	cca	acc	cta	gct	cca	agg	1872
Gly	Cys	Asn	Asn	Trp	Val	Pro	Thr	Ala	Val	Pro	Thr	Leu	Ala	Pro	Arg	
	610					615					620					
act	aac	agc	tig	gca	gta	tcg	cat	gga	aca	cct	aca	ttc	aca	gta	tgg	1920
Thr	Asn	Ser	Leu	Ala	Val	Cys	His	Gly	Thr	Pro	Thr	Phe	Thr	Val	Trp	
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Asn	Asp	Thr														

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

Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu
				325					330					335	
Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp
			340					345					350		
Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp
		355					360					365			
Met	Ser	Arg	Tyr	Asp	Val	Asn	Ser	Ile	Leu	Glu	Ser	Ser	Thr	Leu	Pro
	370					375					380				
Ile	Gly	Gly	Ala	Ala	Lys	Arg	Leu	Lys	Asp	Ala	Glu	Gln	Ala	Glu	Met
385					390					395					400
Thr	Ile	Asp	Gly	Gln	Arg	Thr	Asp	Asp	Glu	Met	Ser	Ser	Gln	Leu	Thr
				405					410					415	
Asp	Gly	Ile	Asn	Asn	Tyr	Gly	Ala	His	His	His	Gly	Trp	Pro	Thr	Val
			420					425					430		
Ala	Phe	Gln	Gln	Ala	Gln	Pro	Phe	Ser	Met	His	Tyr	Pro	Tyr	Gly	His
		435					440					445			
Gln	Gln	Arg	Ala	Val	Trp	Cys	Lys	Gln	Glu	Gln	Asp	Pro	Asp	Gly	Thr
	450					455					460				
His	Asn	Phe	Gln	Asp	Leu	His	Gln	Leu	Gln	Leu	Gly	Asn	Thr	His	Asn
465					470					475					480
Phe	Phe	Gln	Pro	Asn	Val	Leu	His	Asn	Leu	Met	Ser	Met	Asp	Ser	Ser
				485					490					495	
Ser	Met	Asp	His	Ser	Ser	Gly	Ser	Asn	Ser	Val	Ile	Tyr	Ser	Gly	Gly
			500					505					510		
Gly	Ala	Ala	Asp	Gly	Ser	Ala	Ala	Thr	Gly	Gly	Ser	Gly	Ser	Gly	Ser
		515					520					525			
Phe	Gln	Gly	Val	Gly	Tyr	Gly	Asn	Asn	Ile	Gly	Phe	Val	Met	Pro	Ile
	530					535					540				
Ser	Thr	Val	Ile	Ala	His	Glu	Gly	Gly	His	Gly	Gln	Gly	Asn	Gly	Gly
545					550					555					560
Phe	Gly	Asp	Ser	Glu	Val	Lys	Ala	Ile	Gly	Tyr	Asp	Asn	Met	Phe	Gly
				565					570					575	
Ser	Thr	Asp	Pro	Tyr	His	Ala	Arg	Ser	Leu	Tyr	Tyr	Leu	Ser	Gln	Gln
			580					585					590		
Ser	Ser	Ala	Gly	Met	Val	Lys	Gly	Ser	Ser	Ala	Tyr	Asp	Gln	Gly	Ser
		595					600					605			
Gly	Cys	Asn	Asn	Trp	Val	Pro	Thr	Ala	Val	Pro	Thr	Leu	Ala	Pro	Arg
	610					615					620				
Thr	Asn	Ser	Leu	Ala	Val	Cys	His	Gly	Thr	Pro	Thr	Phe	Thr	Val	Trp
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Asn	Asp	Thr													

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	15
cat cca tca aca caa gat caa acg gtg gct tcc cgt ttt ggg ttc aac	96
His Pro Ser Thr 20 Gln Asp Gln Thr Val 25 Ala Ser Arg Phe Gly Phe Asn	
	30
cct aat gaa atc tca ggc tct gat gtt caa gga gat cac tgc tat gat	144

Sequence Listing from Patent scope															
Pro	Asn	Glu	Ile	Ser	Gly	Ser	Asp	Val	Gln	Gly	Asp	His	Cys	Tyr	Asp
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ctc	tct	tct	cac	aca	act	cct	cat	cat	tca	ctc	aac	ctt	tct	cat	cct
Leu	Ser	Ser	His	Thr	Thr	Pro	His	His	Ser	Leu	Asn	Leu	Ser	His	Pro
	50					55					60				192
ttt	tcc	att	tat	gaa	gct	ttc	cac	aca	aat	aac	aac	att	cac	acc	act
Phe	Ser	Ile	Tyr	Glu	Ala	Phe	His	Thr	Asn	Asn	Asn	Ile	His	Thr	Thr
65				70						75					240
caa	gat	tgg	aag	gag	aac	tac	aac	aac	caa	aac	cta	cta	tig	gga	aca
Gln	Asp	Trp	Lys	Glu	Asn	Tyr	Asn	Asn	Gln	Asn	Leu	Leu	Leu	Gly	Thr
				85					90					95	288
tca	tgc	atg	aac	caa	aat	gtg	aac	aac	aac	aac	caa	caa	gca	caa	cca
Ser	Cys	Met	Asn	Gln	Asn	Val	Asn	Asn	Asn	Asn	Gln	Gln	Ala	Gln	Pro
			100				105						110		336
aag	cta	gaa	aac	ttc	ctc	ggt	gga	cac	tct	ttc	acc	gac	cat	caa	gaa
Lys	Leu	Glu	Asn	Phe	Leu	Gly	Gly	His	Ser	Phe	Thr	Asp	His	Gln	Glu
		115				120					125				384
tac	ggt	ggt	agc	aac	tca	tac	tct	tca	tta	cac	ctc	cca	cct	cat	cag
Tyr	Gly	Gly	Ser	Asn	Ser	Tyr	Ser	Ser	Leu	His	Leu	Pro	Pro	His	Gln
	130					135					140				432
ccg	gaa	gca	tcc	tgt	ggc	ggt	ggt	gat	ggt	agt	aca	agt	aac	aat	aac
Pro	Glu	Ala	Ser	Cys	Gly	Gly	Gly	Asp	Gly	Ser	Thr	Ser	Asn	Asn	Asn
145				150					155						480
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Ser	Ile	Gly	Leu	Ser	Met	Ile	Lys	Thr	Trp	Leu	Arg	Asn	Gln	Pro	Pro
			165						170					175	528
cca	cca	gaa	aac	aac	aac	aat	aac	aac	aat	gaa	agt	ggt	gca	cgt	gtg
Pro	Pro	Glu	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Glu	Ser	Gly	Ala	Arg	Val
			180				185						190		576
cag	aca	cta	tca	ctt	tct	atg	agt	act	ggc	tca	cag	tca	agt	tca	tct
Gln	Thr	Leu	Ser	Leu	Ser	Met	Ser	Thr	Gly	Ser	Gln	Ser	Ser	Ser	Ser
		195					200				205				624
gtg	cct	ctt	ctc	aat	gca	aat	gtg	atg	agt	ggt	gag	att	tcc	tca	tcg
Val	Pro	Leu	Leu	Asn	Ala	Asn	Val	Met	Ser	Gly	Glu	Ile	Ser	Ser	Ser
	210					215					220				672
gaa	aac	aaa	caa	cca	ccc	aca	act	gca	gtt	gta	ctt	gat	agc	aac	caa
Glu	Asn	Lys	Gln	Pro	Pro	Thr	Thr	Ala	Val	Val	Leu	Asp	Ser	Asn	Gln
225					230				235						720
aca	agt	gtc	gtt	gaa	agt	gct	gtg	cct	aga	aaa	tcc	gtt	gat	aca	ttt
Thr	Ser	Val	Val	Glu	Ser	Ala	Val	Pro	Arg	Lys	Ser	Val	Asp	Thr	Phe
				245					250					255	768
gga	caa	aga	act	tcc	att	tac	cgt	ggt	gta	aca	agg	cat	aga	tgg	aca
Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr
			260				265						270		816
ggg	aga	tat	gaa	gct	cac	ctt	tgg	gat	aat	agt	tgt	aga	aga	gag	ggg
Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	Glu	Gly
		275					280					285			864

Sequence Listing from Patent scope																
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gaa G u 305	aaa Lys	gca Ala	gct Ala	aga Arg	gcc Ala 310	tat Tyr	gat Asp	tig Leu	gca Ala	gca Ala 315	cta Leu	aaa Lys	tat Tyr	tgg Trp	gga G y 320	960
aca Thr	act Thr	act Thr	aca Thr	aca Thr 325	aat Asn	ttt Phe	cca Pro	att Ile	agc Ser 330	cat His	tat Tyr	gaa G u	aaa Lys	gaa G u 335	gtg Val	1008
gaa G u	gaa G u	atg Met	aag Lys 340	cat His	atg Met	aca Thr	agg Arg	caa G n 345	gag G u	tac Tyr	gtt Val	gcg Ala	tca Ser 350	tig Leu	aga Arg	1056
agg Arg	aaa Lys	agt Ser 355	agt Ser	ggt G y	ttt Phe	tca Ser	cga Arg 360	ggt G y	gca Ala	tcc Ser	att Ile	tac Tyr 365	cga Arg	gga G y	gta Val	1104
aca Thr	aga Arg 370	cat His	cat His	caa G n	cat His	ggt G y 375	aga Arg	tgg Trp	caa G n	gct Ala	agg Arg 380	att Ile	gga G y	aga Arg	gtt Val	1152
gca Ala 385	ggc G y	aac Asn	aaa Lys	gat Asp	ctc Leu 390	tac Tyr	cta Leu	gga G y	act Thr	ttc Phe 395	agc Ser	act Thr	caa G n	gaa G u	gag G u 400	1200
gca Ala	gca Ala	gag G u	gca Ala	tat Tyr 405	gat Asp	gtg Val	gca Ala	gca Ala	ata Ile 410	aaa Lys	ttc Phe	aga Arg	gga G y	ctg Leu 415	agt Ser	1248
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atg Met	gag G u 450	caa G n	gtt Val	gaa G u	tig Leu	aat Asn 455	cat His	gtg Val	aat Asn	gtt Val	gat Asp 460	att Ile	agc Ser	cat His	aga Arg	1392
act Thr 465	gaa G u	caa G n	gat Asp	cat His	agc Ser 470	atc Ile	atc Ile	aac Asn	aac Asn	act Thr 475	tcc Ser	cat His	tta Leu	aca Thr	gaa G u 480	1440
caa G n	gcc Ala	atc Ile	tat Tyr	gca Ala 485	gca Ala	aca Thr	aat Asn	gca Ala	tct Ser 490	aat Asn	tgg Trp	cat His	gca Ala	ctt Leu 495	tca Ser	1488
ttc Phe	caa G n	cat His	caa G n 500	caa G n	cca Pro	cat His	cat His	cat His 505	tac Tyr	aat Asn	gcc Ala	aac Asn	aac Asn 510	atg Met	cag G n	1536
tta Leu	cag G n	aat Asn 515	tat Tyr	cct Pro	tat Tyr	gga G y 520	act Thr	caa G n	act Thr	caa G n	aag Lys	ctt Leu 525	tgg Trp	tgc Cys	aaa Lys	1584
caa G n	gaa G u 530	caa G n	gat Asp	tct Ser	gat Asp	gat Asp 535	cat His	agt Ser	act Thr	tat Tyr	act Thr 540	act Thr	gct Ala	act Thr	gat Asp	1632

Sequence Listing from Patent scope

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ttt Phe	ggt Gly	tta Leu	caa Gln	aat Asn 565	atc Ile	atg Met	agt Ser	atg Met	gat Asp 570	tct Ser	gct Ala	tcc Ser	atg Met	gat Asp 575	aat Asn	1728
agt Ser	tct Ser	gga Gly	tct Ser 580	aat Asn	tct Ser	gtt Val	gtt Val	tat Tyr 585	ggg Gly	ggg Gly	gga Gly	gat Asp	cat His 590	ggg Gly	ggg Gly	1776
tat Tyr	gga Gly	gga Gly 595	aat Asn	ggg Gly	gga Gly	tat Tyr	atg Met 600	att Ile	cca Pro	atg Met	gct Ala	att Ile 605	gca Ala	aat Asn	gat Asp	1824
ggg Gly 610	aac Asn	caa Gln	aat Asn	cca Pro	aga Arg	agc Ser 615	aac Asn	aac Asn	aat Asn	ttt Phe	ggg Gly 620	gag Glu	agt Ser	gag Glu	att Ile	1872
aaa Lys 625	gga Gly	ttt Phe	ggg Gly	tat Tyr	gaa Glu 630	aat Asn	gtt Val	ttt Phe	ggg Gly	act Thr 635	act Thr	act Thr	gat Asp	cct Pro	tat Tyr 640	1920
cat His	gca Ala	cag Gln	gca Ala	gca Ala 645	agg Arg	aac Asn	ttg Leu	tac Tyr	tat Tyr 650	cag Gln	cca Pro	caa Gln	caa Gln	tta Leu 655	tct Ser	1968
gtt Val	gat Asp	caa Gln	gga Gly 660	tca Ser	aat Asn	tgg Trp	gtt Val	cca Pro 665	act Thr	gct Ala	att Ile	cca Pro	aca Thr 670	ctt Leu	gct Ala	2016
cca Pro	agg Arg	act Thr 675	acc Thr	aat Asn	gtc Val	tct Ser	cta Leu 680	tgt Cys	cct Pro	cct Pro	ttc Phe	act Thr 685	ttg Leu	ttg Leu	cat His	2064
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<212> PRT

<213> Medi cago t r u n c a t u l a

<400> 8

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Pro	Asn	Glu 35	Ile	Ser	Gly	Ser	Asp 40	Val	Gln	Gly	Asp	His 45	Cys	Tyr	Asp
Leu	Ser 50	Ser	His	Thr	Thr	Pro 55	His	His	Ser	Leu	Asn 60	Leu	Ser	His	Pro
Phe 65	Ser	Ile	Tyr	Glu	Ala 70	Phe	His	Thr	Asn	Asn 75	Asn	Ile	His	Thr	Thr 80
Gln	Asp	Trp	Lys	Glu 85	Asn	Tyr	Asn	Asn 90	Gln	Asn	Leu	Leu	Leu	Gly 95	Thr
Ser	Cys	Met	Asn 100	Gln	Asn	Val	Asn	Asn 105	Asn	Asn	Gln	Gln	Ala 110	Gln	Pro
Lys	Leu	Glu	Asn	Phe	Leu	Gly	Gly	His	Ser	Phe	Thr	Asp	His	Gln	Glu

Sequence Listing from Patent scope

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Pro	Glu	Ala	Ser	Cys	Gly	Gly	Gly	Asp	Gly	Ser	Thr	Ser	Asn	Asn	Asn		
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Ser	Ile	Gly	Leu	Ser	Met	Ile	Lys	Thr	Trp	Leu	Arg	Asn	Gln	Pro	Pro		
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Pro	Pro	Glu	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Glu	Ser	Gly	Ala	Arg	Val		
			180					185					190				
Gln	Thr	Leu	Ser	Leu	Ser	Met	Ser	Thr	Gly	Ser	Gln	Ser	Ser	Ser	Ser		
	195					200						205					
Val	Pro	Leu	Leu	Asn	Ala	Asn	Val	Met	Ser	Gly	Glu	Ile	Ser	Ser	Ser		
	210					215					220						
Glu	Asn	Lys	Gln	Pro	Pro	Thr	Thr	Ala	Val	Val	Leu	Asp	Ser	Asn	Gln		
225				230						235					240		
Thr	Ser	Val	Val	Glu	Ser	Ala	Val	Pro	Arg	Lys	Ser	Val	Asp	Thr	Phe		
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Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr		
			260					265					270				
Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	Glu	Gly		
	275						280					285					
Gln	Thr	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu		
	290					295					300						
Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly		
305				310					315						320		
Thr	Thr	Thr	Thr	Asn	Phe	Pro	Ile	Ser	His	Tyr	Glu	Lys	Glu	Val			
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Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln	Glu	Tyr	Val	Ala	Ser	Leu	Arg		
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Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val		
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Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val		
	370					375					380						
Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu		
385				390						395					400		
Ala	Ala	Glu	Ala	Tyr	Asp	Val	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Ser		
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Ala	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Lys	Thr	Ile	Leu		
			420					425					430				
Glu	Ser	Ser	Thr	Leu	Pro	Ile	Gly	Gly	Ala	Ala	Lys	Arg	Leu	Lys	Asp		
	435					440					445						
Met	Glu	Gln	Val	Glu	Leu	Asn	His	Val	Asn	Val	Asp	Ile	Ser	His	Arg		
	450					455					460						
Thr	Glu	Gln	Asp	His	Ser	Ile	Ile	Asn	Asn	Thr	Ser	His	Leu	Thr	Glu		
465				470						475					480		
Gln	Ala	Ile	Tyr	Ala	Ala	Thr	Asn	Ala	Ser	Asn	Trp	His	Ala	Leu	Ser		
				485					490					495			
Phe	Gln	His	Gln	Gln	Pro	His	His	His	Tyr	Asn	Ala	Asn	Asn	Met	Gln		
			500					505				510					
Leu	Gln	Asn	Tyr	Pro	Tyr	Gly	Thr	Gln	Thr	Gln	Lys	Leu	Trp	Cys	Lys		
	515						520					525					
Gln	Glu	Gln	Asp	Ser	Asp	Asp	His	Ser	Thr	Tyr	Thr	Thr	Ala	Thr	Asp		
	530					535					540						
Ile	His	Gln	Leu	Gln	Leu	Gly	Asn	Asn	Asn	Asn	Asn	Thr	His	Asn	Phe		
545				550						555					560		
Phe	Gly	Leu	Gln	Asn	Ile	Met	Ser	Met	Asp	Ser	Ala	Ser	Met	Asp	Asn		
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Ser	Ser	Gly	Ser	Asn	Ser	Val	Val	Tyr	Gly	Gly	Gly	Asp	His	Gly	Gly		
	580							585					590				
Tyr	Gly	Gly	Asn	Gly	Gly	Tyr	Met	Ile	Pro	Met	Ala	Ile	Ala	Asn	Asp		
	595						600					605					
Gly	Asn	Gln	Asn	Pro	Arg	Ser	Asn	Asn	Asn	Phe	Gly	Glu	Ser	Glu	Ile		
	610					615					620						

Sequence Listing from Patent scope

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His	Ala	Gln	Ala	Ala 645	Arg	Asn	Leu	Tyr	Tyr 650	Gln	Pro	Gln	Gln	Leu	Ser 655
Val	Asp	Gln	Gly 660	Ser	Asn	Trp	Val	Pro 665	Thr	Ala	Ile	Pro	Thr 670	Leu	Ala
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Leu Pro Pro Ser Gln Thr Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr	
20 25 30	
gcc gac cat gtg tcc ggc gat gtg tgc ttc aac atc ccc caa gat tgg	144
Ala Asp His Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp	
35 40 45	
agc atg agg gga tca gag ctt tcc gcg ctg gtg gcg gag ccg aag ctg	192
Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu	
50 55 60	
gag gac ttc ctg ggc ggc atc tcc ttc tcc gag cag cat cac aag tcc	240
Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ser	
65 70 75 80	
aac tgc aac ttg ata ccc agc act agc agc aca gtt tgc tac gcg agc	288
Asn Cys Asn Leu Ile Pro Ser Thr Ser Ser Thr Val Cys Tyr Ala Ser	
85 90 95	
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Ser Ala Ala Ser Thr Gly Tyr His His Gln Leu Tyr Gln Pro Thr Ser	
100 105 110	
tcc gcg ctg cac ttc gcg gac tcc gtg atg gtg gcc tcc tcc gcc ggt	384
Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala Gly	
115 120 125	
gtg cac gac ggc ggt tcc atg ctg agc gcg gcc gcc gct aac ggt gtg	432
Val His Asp Gly Gly Ser Met Leu Ser Ala Ala Ala Ala Asn Gly Val	
130 135 140	
gct ggc gct gcc agt gcc aac ggc ggc ggc atc ggg ctg tcc atg atc	480
Ala Gly Ala Ala Ser Ala Asn Gly Gly Gly Ile Gly Leu Ser Met Ile	
145 150 155 160	
aag aac tgg ctg cgg agc caa ccg gcg ccc atg cag ccg agg gcg gcg	528

Sequence Listing from Patent scope															
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624															
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672															
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720															
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768															
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816															
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864															
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912															
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960															
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1008															
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1056															
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1104															
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1152															
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1200															
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1248															

Sequence Listing from Patent scope																	
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ccc Pro	atc Ile 450	ggc Gly	agc Ser	gcc Ala	gcc Ala	aag Lys 455	cgt Arg	ctc Leu	aag Lys	gag Glu	gcc Ala 460	gag Glu	gcc Ala	gca Ala	gcg Ala	1392	
tcc Ser 465	gcg Ala	cag Gln	cac His	cac His	cac His 470	gcc Ala	ggc Gly	gtg Val	gtg Val	agc Ser 475	tac Tyr	gac Asp	gtc Val	ggc Gly	cgc Arg 480	1440	
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agc Ser	tac Tyr	ctg Leu	gtg Val 660	aac Asn	gcg Ala	gag Glu	aac Asn	aat Asn 665	ggt Gly	ggc Gly	gga Gly	agg Arg	atg Met 670	tct Ser	gca Ala	2016	

Sequence Listing from Patent scope

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Asp	Asn	Ile	Ala	Ala	Asp	Val	Gly	His	Gly	Gly	Ala	Gln	Leu	Phe	Ser	
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gtc	tgg	aac	gac	act	taa											2130
Val	Trp	Asn	Asp	Thr												
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<400> 10

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Ala	Asp	His	Val	Ser	Gly	Asp	Val	Cys	Phe	Asn	Ile	Pro	Gln	Asp	Trp	
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Ser	Met	Arg	Gly	Ser	Glu	Leu	Ser	Ala	Leu	Val	Ala	Glu	Pro	Lys	Leu	
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Glu	Asp	Phe	Leu	Gly	Gly	Ile	Ser	Phe	Ser	Glu	Gln	His	His	Lys	Ser	
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Asn	Cys	Asn	Leu	Ile	Pro	Ser	Thr	Ser	Ser	Thr	Val	Cys	Tyr	Ala	Ser	
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Ser	Ala	Ala	Ser	Thr	Gly	Tyr	His	His	Gln	Leu	Tyr	Gln	Pro	Thr	Ser	
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Ser	Ala	Leu	His	Phe	Ala	Asp	Ser	Val	Met	Val	Ala	Ser	Ser	Ala	Gly	
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Val	His	Asp	Gly	Gly	Ser	Met	Leu	Ser	Ala	Ala	Ala	Ala	Asn	Gly	Val	
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Val	Thr	Ala	Pro	Lys	Glu	Asp	Ser	Gly	Gly	Ser	Gly	Val	Ala	Gly	Ala	
225					230					235					240	
Leu	Val	Ala	Val	Ser	Thr	Asp	Thr	Gly	Gly	Ser	Gly	Gly	Ala	Ser	Ala	
			245						250					255		
Asp	Asn	Thr	Ala	Arg	Lys	Thr	Val	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	
			260					265					270			
Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	
		275					280					285				
His	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	Glu	Gly	Gln	Thr	Arg	Lys	Gly	
	290					295					300					
Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	
305				310						315					320	
Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Ala	Thr	Thr	Thr	Thr	
			325						330					335		
Asn	Phe	Pro	Val	Ser	Asn	Tyr	Glu	Lys	Glu	Leu	Glu	Asp	Met	Lys	His	

Sequence Listing from Patent scope

Met Thr Arg 340 Gln Glu Phe Val Ala 345 Ser Leu Arg Arg Lys 350 Ser Ser Gly
 Phe 355 Arg Gly Ala Ser Ile 360 Tyr Arg Gly Val Thr 365 Arg His His Gln
 His 370 Gly Arg Trp Gln Ala 375 Ile Gly Arg Val 380 Ala Gly Asn Lys Asp
 385 Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr
 Asp Ile Ala Ala 405 Ile Lys Phe Arg Gly 410 Leu Asn Ala Val Thr 415 Asn Phe
 Asp Met Ser 420 Arg Tyr Asp Val Lys 425 Ser Ile Leu Asp Ser 430 Ala Leu
 Pro Ile Gly Ser Ala Ala Lys 440 Arg Leu Lys Glu Ala Glu Ala Ala Ala
 450 Ser Ala Gln His His His 455 Ala Gly Val Val Ser Tyr Asp Val Gly Arg
 465 Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala Ala Tyr Gly
 485 Ala His Tyr His Gly Ala Ala Trp Pro Thr Ile Ala Phe Gln Pro Gly
 500 Ala Ala Thr Thr Gly Leu Tyr His 505 Pro Tyr Ala Gln Gln Pro Met Arg
 515 Gly Gly Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala
 530 Ala His Ser Leu Gln Asp 535 Leu His His Leu Asn Leu Gly Ala Ala Gly
 545 Ala His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Ala Ala Ala Ala
 565 Met His Gly Leu Ala Ser Ile Asp Ser 570 Ala Ser Leu Glu His Ser Thr
 580 Gly Ser Asn Ser Val Val Tyr Asn 585 Gly Gly Val Gly Asp 590 Ser Asn Gly
 595 Ala Ser Ala Val Gly Ser Gly Gly Tyr Met Met Pro Met Ser Ala
 610 Ala Gly Ala Thr Thr Thr Ser Ala Met Val Ser 620 His Glu Gln Met His
 625 Ala Arg Ala Tyr Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr Glu
 645 Ser Tyr Leu Val Asn Ala Glu Asn Asn Gly Gly Gly Arg Met Ser Ala
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Sequence Listing from Patent scope																
aac Asn	ccg Pro	cag Gln	cct Pro 20	aac Asn	cag Gln	gat Asp	agc Ser	tcg Ser 25	cct Pro	gcc Ala	gcc Ala	ggt Gly	atc Ile 30	gac Asp	atc Ile	96
tcc Ser	ggc Gly	gcc Ala 35	agc Ser	gac Asp	ttc Phe	tat Tyr	ggc Gly 40	ctg Leu	ccc Pro	acg Thr	cag Gln	cag Gln 45	ggc Gly	tcc Ser	gac Asp	144
ggg Gly	cat His 50	ctc Leu	ggc Gly	gtg Val	ccg Pro	ggc Gly 55	ctg Leu	cgg Arg	gac Asp	gat Asp	cac His 60	gct Ala	tct Ser	tat Tyr	ggt Gly	192
atc Ile 65	atg Met	gag Glu	gcc Ala	tac Tyr	aac Asn 70	agg Arg	gtt Val	cct Pro	caa Gln	gaa Glu 75	acc Thr	caa Gln	gat Asp	tgg Trp	aac Asn 80	240
atg Met	agg Arg	ggc Gly	ttg Leu	gac Asp 85	tac Tyr	aac Asn	ggc Gly	ggt Gly	ggc Gly 90	tcg Ser	gag Glu	ctc Leu	tcg Ser	atg Met 95	ctt Leu	288
gtg Val	ggg Gly	tcc Ser	agc Ser 100	ggc Gly	ggc Gly	ggc Gly	ggg Gly	ggc Gly 105	aac Asn	ggc Gly	aag Lys	agg Arg	gcc Ala 110	gtg Val	gaa Glu	336
gac Asp	agc Ser	gag Glu 115	ccc Pro	aag Lys	ctc Leu	gaa Glu	gat Asp 120	ttc Phe	ctc Leu	ggc Gly	ggc Gly	aac Asn 125	tcg Ser	ttc Phe	gtc Val	384
tcc Ser	gat Asp 130	caa Gln	gat Asp	cag Gln	tcc Ser	ggc Gly 135	ggt Gly	tac Tyr	ctg Leu	ttc Phe	tct Ser 140	gga Gly	gtc Val	ccg Pro	ata Ile	432
gcc Ala 145	agc Ser	agc Ser	gcc Ala	aac Asn	agc Ser 150	aac Asn	agc Ser	ggg Gly	agc Ser	aac Asn 155	acc Thr	atg Met	gag Glu	ctc Leu	tcc Ser 160	480
atg Met	atc Ile	aag Lys	acc Thr 165	tgg Trp	cta Leu	cgg Arg	aac Asn	aac Asn	cag Gln 170	gtg Val	gcc Ala	cag Gln	ccc Pro	cag Gln 175	ccg Pro	528
cca Pro	gct Ala	cca Pro	cat His 180	cag Gln	ccg Pro	cag Gln	cct Pro	gag Glu 185	gaa Glu	atg Met	agc Ser	acc Thr	gac Asp 190	gcc Ala	agc Ser	576
ggc Gly	agc Ser	agc Ser 195	ttt Phe	gga Gly	tgc Cys	tcg Ser	gat Asp 200	tcg Ser	atg Met	gga Gly	agg Arg	aac Asn 205	agc Ser	atg Met	gtg Val	624
gcg Ala	gct Ala 210	ggt Gly	ggg Gly	agc Ser	tcg Ser	cag Gln 215	agc Ser	ctg Leu	gcg Ala	ctc Leu	tcg Ser 220	atg Met	agc Ser	acg Thr	ggc Gly	672
tcg Ser 225	cac His	ctg Leu	ccc Pro	atg Met	gtt Val 230	gtg Val	ccc Pro	agc Ser	ggc Gly	gcc Ala 235	gcc Ala	agc Ser	gga Gly	gcg Ala	gcc Ala 240	720
tcg Ser	gag Glu	agc Ser	aca Thr	tcg Ser 245	tcg Ser	gag Glu	aac Asn	aag Lys	cga Arg 250	gcg Ala	agc Ser	ggt Gly	gcc Ala	atg Met 255	gat Asp	768
tcg Ser	ccc Pro	ggc Gly	agc Ser 260	gcg Ala	gta Val	gaa Glu	gcc Ala	gta Val 265	ccg Pro	agg Arg	aag Lys	tcc Ser	atc Ile 270	gac Asp	acg Thr	816

Sequence Listing from Patent scope

t t c	g g g	c a a	a g g	a c c	t c t	a t a	t a t	c g a	g g t	g t a	a c a	a g g	c a t	a g a	t g g	864
Phe	G y	G n	Arg	Thr	Ser	I l e	Tyr	Arg	G y	Val	Thr	Arg	H i s	Arg	Trp	
		275					280					285				
a c a	g g g	c g g	t a t	g a g	g c t	c a t	c t a	t g g	g a t	a a t	a g t	t g t	a g a	a g g	g a a	912
Thr	G y	Arg	Tyr	G u	Al a	H i s	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	G u	
	290					295					300					
g g g	c a g	a g t	c g c	a a g	g g t	a g g	c a a	g t t	t a c	c t t	g g t	g g c	t a t	g a c	a a g	960
G y	G n	Ser	Arg	Lys	G y	Arg	G n	Val	Tyr	Leu	G y	G y	Tyr	Asp	Lys	
305					310					315					320	
g a g	g a c	a a g	g c a	g c a	a g g	g c t	t a t	g a t	t t g	g c a	g c t	c t c	a a g	t a t	t g g	1008
G u	Asp	Lys	Al a	Al a	Arg	Al a	Tyr	Asp	Leu	Al a	Al a	Leu	Lys	Tyr	Trp	
				325					330					335		
g g c	a c t	a c g	a c a	a c a	a c a	a a t	t t c	c c t	a t a	a g c	a a c	t a c	g a a	a a g	g a g	1056
G y	Thr	Thr	Thr	Thr	Thr	Asn	Phe	Pro	I l e	Ser	Asn	Tyr	G u	Lys	G u	
			340					345					350			
c t a	g a a	g a a	a t g	a a a	c a t	a t g	a c t	a g a	c a g	g a g	t a c	a t t	g c a	t a c	c t a	1104
Leu	G u	G u	Met	Lys	H i s	Met	Thr	Arg	G n	G u	Tyr	I l e	Al a	Tyr	Leu	
		355					360					365				
a g a	a g a	a a t	a g c	a g t	g g a	t t t	t c t	c g t	g g g	g c g	t c a	a a g	t a t	c g t	g g a	1152
Arg	Arg	Asn	Ser	Ser	G y	Phe	Ser	Arg	G y	Al a	Ser	Lys	Tyr	Arg	G y	
	370					375					380					
g t a	a c t	a g a	c a t	c a t	c a g	c a t	g g g	a g a	t g g	c a a	g c a	a g g	a t a	g g g	a g a	1200
Val	Thr	Arg	H i s	H i s	G n	H i s	G y	Arg	Trp	G n	Al a	Arg	I l e	G y	Arg	
385					390					395					400	
g t t	g c a	g g a	a a c	a a g	g a t	c t c	t a c	t t g	g g c	a c a	t t c	a g c	a c c	g a g	g a g	1248
Val	Al a	G y	Asn	Lys	Asp	Leu	Tyr	Leu	G y	Thr	Phe	Ser	Thr	G u	G u	
				405				410						415		
g a g	g c g	g c g	g a g	g c c	t a c	g a c	a t c	g c c	g c g	a t c	a a g	t t c	c g c	g g t	c t c	1296
G u	Al a	Al a	G u	Al a	Tyr	Asp	I l e	Al a	Al a	I l e	Lys	Phe	Arg	G y	Leu	
			420					425					430			
a a c	g c c	g t c	a c c	a a c	t t c	g a c	a t g	a g c	c g c	t a c	g a c	g t g	a a g	a g c	a t c	1344
Asn	Al a	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Lys	Ser	I l e	
		435					440					445				
c t c	g a g	a g c	a g c	a c a	c t g	c c t	g t c	g g c	g g t	g c g	g c c	a g g	c g c	c t c	a a g	1392
Leu	G u	Ser	Ser	Thr	Leu	Pro	Val	G y	G y	Al a	Al a	Arg	Arg	Leu	Lys	
	450					455					460					
g a c	g c c	g t g	g a c	c a c	g t g	g a g	g c c	g g c	g c c	a c c	a t c	t g g	c g c	g c c	g a c	1440
Asp	Al a	Val	Asp	H i s	Val	G u	Al a	G y	Al a	Thr	I l e	Trp	Arg	Al a	Asp	
465					470					475					480	
a t g	g a c	g g c	g c c	g t g	a t c	t c c	c a g	c t g	g c c	g a a	g c c	g g g	a t g	g g c	g g c	1488
Met	Asp	G y	Al a	Val	I l e	Ser	G n	Leu	Al a	G u	Al a	G y	Met	G y	G y	
				485				490						495		
t a c	g c c	t c g	t a c	g g c	c a c	c a c	g g c	t g g	c c g	a c c	a t c	g c g	t t c	c a g	c a g	1536
Tyr	Al a	Ser	Tyr	G y	H i s	H i s	G y	Trp	Pro	Thr	I l e	Al a	Phe	G n	G n	
			500					505					510			
c c g	t c g	c c g	c t c	t c c	g t c	c a c	t a c	c c g	t a c	g g c	c a g	c c g	t c c	c g c	g g g	1584
Pro	Ser	Pro	Leu	Ser	Val	H i s	Tyr	Pro	Tyr	G y	G n	Pro	Ser	Arg	G y	

Sequence Listing from Patent scope

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cag gac ctg cag cag ctg cac ctg ggc agc gcg gcc cac aac ttc ttc Gln Asp Leu Gln Gln Leu His Leu Gly Ser Ala Ala His Asn Phe Phe 545	550	555	1680
cag gcg tgc tgc agc tcc aca gtc tac aac ggc ggc gcc ggc gcc agt Gln Ala Ser Ser Ser Thr Val Tyr Asn Gly Gly Ala Gly Ala Ser 565	570	575	1728
ggg ggg tac cag ggc ctg ggt ggt ggc agc tct ttc ctg atg ccg tgc Gly Gly Tyr Gln Gly Leu Gly Gly Gly Ser Ser Phe Leu Met Pro Ser 580	585	590	1776
agc act gtc gtg gcg gcg gcc gac cag ggg cac agc agc acg gcc aac Ser Thr Val Val Ala Ala Ala Asp Gln Gly His Ser Ser Thr Ala Asn 595	600	605	1824
cag ggg agc acg tgc agc tac ggg gac gac cac cag gag ggg aag ctg Gln Gly Ser Thr Cys Ser Tyr Gly Asp Asp His Gln Glu Gly Lys Leu 610	615	620	1872
atc ggt tac gac gcc gcc atg gtg gcg acc gca gct ggt gga gac ccg Ile Gly Tyr Asp Ala Ala Met Val Ala Thr Ala Ala Gly Gly Asp Pro 625	630	635	1920
tac gct gcg gcg agg aac ggg tac cag ttc tgc cag ggc tgc gga tcc Tyr Ala Ala Ala Arg Asn Gly Tyr Gln Phe Ser Gln Gly Ser Gly Ser 645	650	655	1968
acg gtg agc atc gcg agg gcg aac ggg tac gct aac aac tgg agc tct Thr Val Ser Ile Ala Arg Ala Asn Gly Tyr Ala Asn Asn Trp Ser Ser 660	665	670	2016
cct ttc aac aac ggc atg ggg tga Pro Phe Asn Asn Gly Met Gly 675			2040

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Ser Gly Ala Ser Asp Phe Tyr Gly Leu Pro Thr Gln Gln Gly Ser Asp
35 40 45
Gly His Leu Gly Val Pro Gly Leu Arg Asp Asp His Ala Ser Tyr Gly
50 55 60
Ile Met Glu Ala Tyr Asn Arg Val Pro Gln Glu Thr Gln Asp Trp Asn
65 70 75 80
Met Arg Gly Leu Asp Tyr Asn Gly Gly Gly Ser Glu Leu Ser Met Leu
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Val Gly Ser Ser Gly Gly Gly Gly Asn Gly Lys Arg Ala Val Glu
100 105 110

Sequence Listing from Patent scope

Asp	Ser	Glu	Pro	Lys	Leu	Glu	Asp	Phe	Leu	Gly	Gly	Asn	Ser	Phe	Val
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Ser	Asp	Gln	Asp	Gln	Ser	Gly	Gly	Tyr	Leu	Phe	Ser	Gly	Val	Pro	Ile
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Ala	Ser	Ser	Ala	Asn	Ser	Asn	Ser	Gly	Ser	Asn	Thr	Met	Glu	Leu	Ser
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Met	Ile	Lys	Thr	Trp	Leu	Arg	Asn	Asn	Gln	Val	Ala	Gln	Pro	Gln	Pro
				165					170					175	
Pro	Ala	Pro	His	Gln	Pro	Gln	Pro	Glu	Glu	Met	Ser	Thr	Asp	Ala	Ser
			180					185					190		
Gly	Ser	Ser	Phe	Gly	Cys	Ser	Asp	Ser	Met	Gly	Arg	Asn	Ser	Met	Val
		195					200					205			
Ala	Ala	Gly	Gly	Ser	Ser	Gln	Ser	Leu	Ala	Leu	Ser	Met	Ser	Thr	Gly
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Ser	His	Leu	Pro	Met	Val	Val	Pro	Ser	Gly	Ala	Ala	Ser	Gly	Ala	Ala
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Ser	Glu	Ser	Thr	Ser	Ser	Glu	Asn	Lys	Arg	Ala	Ser	Gly	Ala	Met	Asp
				245					250					255	
Ser	Pro	Gly	Ser	Ala	Val	Glu	Ala	Val	Pro	Arg	Lys	Ser	Ile	Asp	Thr
			260					265					270		
Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp
		275					280					285			
Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg	Glu
	290					295					300				
Gly	Gln	Ser	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys
305					310					315					320
Glu	Asp	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp
			325						330					335	
Gly	Thr	Thr	Thr	Thr	Thr	Asn	Phe	Pro	Ile	Ser	Asn	Tyr	Glu	Lys	Glu
			340					345					350		
Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln	Glu	Tyr	Ile	Ala	Tyr	Leu
		355					360					365			
Arg	Arg	Asn	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	Lys	Tyr	Arg	Gly
	370					375					380				
Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg
385					390					395					400
Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Glu	Glu
			405						410					415	
Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu
		420						425				430			
Asn	Ala	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Lys	Ser	Ile
	435						440					445			
Leu	Glu	Ser	Ser	Thr	Leu	Pro	Val	Gly	Gly	Ala	Ala	Arg	Arg	Leu	Lys
	450					455					460				
Asp	Ala	Val	Asp	His	Val	Glu	Ala	Gly	Ala	Thr	Ile	Trp	Arg	Ala	Asp
465					470					475					480
Met	Asp	Gly	Ala	Val	Ile	Ser	Gln	Leu	Ala	Glu	Ala	Gly	Met	Gly	Gly
			485						490					495	
Tyr	Ala	Ser	Tyr	Gly	His	His	Gly	Trp	Pro	Thr	Ile	Ala	Phe	Gln	Gln
		500						505					510		
Pro	Ser	Pro	Leu	Ser	Val	His	Tyr	Pro	Tyr	Gly	Gln	Pro	Ser	Arg	Gly
		515					520					525			
Trp	Cys	Lys	Pro	Glu	Gln	Asp	Ala	Ala	Ala	Ala	Ala	Ala	His	Ser	Leu
	530					535						540			
Gln	Asp	Leu	Gln	Gln	Leu	His	Leu	Gly	Ser	Ala	Ala	His	Asn	Phe	Phe
545					550					555					560
Gln	Ala	Ser	Ser	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Gly	Ala	Gly	Ala	Ser
			565						570					575	
Gly	Gly	Tyr	Gln	Gly	Leu	Gly	Gly	Gly	Ser	Ser	Phe	Leu	Met	Pro	Ser
		580						585					590		
Ser	Thr	Val	Val	Ala	Ala	Ala	Asp	Gln	Gly	His	Ser	Ser	Thr	Ala	Asn
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Gln	Gly	Ser	Thr	Cys	Ser	Tyr	Gly	Asp	Asp	His	Gln	Glu	Gly	Lys	Leu

Sequence Listing from Patent scope

Ile	Gly	Tyr	Asp	Ala	Ala	Met	Val	Ala	Thr	Ala	Ala	Gly	Gly	Asp	Pro
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Tyr	Ala	Ala	Ala	Arg	Asn	Gly	Tyr	Gln	Phe	Ser	Gln	Gly	Ser	Gly	Ser
				645					650					655	
Thr	Val	Ser	Ile	Ala	Arg	Ala	Asn	Gly	Tyr	Ala	Asn	Asn	Trp	Ser	Ser
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Pro	Phe	Asn	Asn	Gly	Met	Gly									
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1 5 10 15																	
cag ct c ccg ccg tct cag acc aac tcc act ct c at c tcc gcc gcc gcc																	96
Gln Leu Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala																	
20 25 30																	
acc acc acc acc gcc ggc gac tcc tcc acc ggc gac gt c tgc ttc aac																	144
Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Cys Phe Asn																	
35 40 45																	
at c ccc caa gat tgg agc atg agg gga tcg gag ct c tcg gcg ct c gt c																	192
Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Gln Leu Ser Ala Leu Val																	
50 55 60																	
gcc gag ccg aag ct g gag gac ttc ct c ggc ggc at c tcc ttc tcg gag																	240
Ala Gu Pro Lys Leu Gu Asp Phe Leu Gly Gly Ile Ser Phe Ser Gu																	
65 70 75 80																	
cag cag cat cat cac ggc ggc aag ggc ggc gt g at c ccg agc agc gcc																	288
Gln Gln His His His Gly Gly Lys Gly Gly Val Ile Pro Ser Ser Ala																	
85 90 95																	
gcc gct tgc t ac gcg agc tcc ggc agc gt c ggc t ac ct g t ac cct																	336
Ala Ala Cys Tyr Ala Ser Ser Gly Ser Val Gly Tyr Leu Tyr Pro																	
100 105 110																	
cct cca agc t ca tcc t cg ct c cag ttc gcc gac tcc gt c at g gt g gcc																	384
Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala																	
115 120 125																	
acc tcc t cg ccc gt c gt c gcc cac gac ggc gt c agc ggc ggc ggc at g																	432
Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met																	
130 135 140																	
gt g agc gcc gcc gcc gcc gcg gcg gcc agt ggc aac ggc ggc at t ggc																	480
Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly																	
145 150 155 160																	
ct g tcc at g at c aag aac tgg ct c cgg agc cag ccg gcg ccg cag ccg																	528
Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro																	

Sequence Listing from Patent scope

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tct Ser	ctg Leu	tcc Ser	atg Met
aac Asn 185	atg Met	gcg Ala	ggg Gly
acg Thr 190	acg Thr	acg Thr	gcg Ala
576			
cag Gln	ggc Gly 195	ggc Gly	ggc Gly
gcc Ala	atg Met	gcg Ala	ctc Leu 200
ctc Leu	gcc Ala	ggc Gly	gca Ala
ggg Gly 205	gag Glu	cga Arg	ggc Gly
624			
cgg Arg	acg Thr 210	acg Thr	ccc Pro
gcg Ala	tca Ser	gag Glu 215	agc Ser
ctg Leu	tcc Ser	acg Thr	tcg Ser 220
gcg Ala	cac His	gga Gly	gcg Ala
672			
acg Thr 225	acg Thr	gcg Ala	acg Thr
atg Met	gct Ala 230	ggt Gly	ggt Gly
cgc Arg	aag Lys	gag Glu 235	att Ile
aac Asn	gag Glu	gaa Glu	ggc Gly 240
720			
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ggc Gly 245	gcc Ala	gtg Val	gtt Val
gcc Ala	gtc Val 250	ggc Gly	tcg Ser
gag Glu	tca Ser	ggc Gly 255	ggc Gly
768			
agc Ser	ggc Gly	gcc Ala	gtg Val 260
gtg Val	gag Glu	gcc Ala	ggc Gly
gcg Ala 265	gcg Ala	gcg Ala	gcg Ala
gcg Ala	gcg Ala	gcg Ala	agg Arg
aag Lys			
816			
tcc Ser	gtc Val	gac Asp 275	acg Thr
ttc Phe	ggc Gly	cag Gln	aga Arg 280
aca Thr	tcg Ser	atc Ile	tac Tyr
cgc Arg 285	ggc Gly	gtg Val	aca Thr
864			
agg Arg	cat His 290	aga Arg	tgg Trp
aca Thr	ggg Gly	agg Arg 295	tat Tyr
gag Glu	gct Ala	cat His	ctt Leu 300
tgg Trp	gac Asp	aac Asn	agc Ser
912			
tgc Cys 305	aga Arg	aga Arg	gag Glu
ggc Gly	caa Gln 310	act Thr	cgc Arg
aag Lys	ggt Gly	cgt Arg 315	caa Gln
gtc Val	tat Tyr	cta Leu	ggt Gly 320
960			
ggt Gly	tat Tyr	gac Asp	aaa Lys
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gct Ala	aga Arg 330	gct Ala	tat Tyr
gat Asp	tig Leu	gct Ala 335	gct Ala
1008			
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ggc Gly	ccg Pro	acg Thr	acg Thr 345
aca Thr	aat Asn	ttt Phe	ccg Pro
gta Val 350	aat Asn	aac Asn	
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ctg Leu	gag Glu	atg Met 360	aag Lys
cac His	atg Met	aca Thr	agg Arg 365
cag Gln	ggg Gly	aga Arg	gag Glu
ttc Phe	tcc Ser 380	aga Arg	ggt Gly
gca Ala	tcc Ser		
1152			
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gta Val 390	act Thr	agg Arg	cat His
cac His	cag Gln	cat His 395	ggg Gly
aga Arg	tgg Trp	caa Gln	gca Ala 400
1200			
agg Arg	ata Ile	gga Gly	aga Arg
gtt Val 405	gca Ala	ggg Gly	aac Asn
aag Lys	gac Asp 410	ctc Leu	tac Tyr
tig Leu	ggc Gly	acc Thr	ttc Phe
1248			
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gag Glu	gcg Glu	gcg Glu	atc Aag
1296			

Sequence Listing from Patent scope																
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			420					425					430			
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Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	
		435					440					445				
g t c	a a g	a g c	a t c	c t c	g a c	a g c	g c t	g c c	c t c	c c c	g t c	g g c	a c c	g c c	g c c	1392
Val	Lys	Ser	Ile	Leu	Asp	Ser	Ala	Ala	Leu	Pro	Val	Gly	Thr	Ala	Ala	
	450					455					460					
a a g	c g c	c t c	a a g	g a c	g c c	g a g	g c c	g c c	g c c	g c c	t a c	g a c	g t c	g g c	c g c	1440
Lys	Arg	Leu	Lys	Asp	Ala	Glu	Ala	Ala	Ala	Ala	Tyr	Asp	Val	Gly	Arg	
465					470					475					480	
a t c	g c c	t c g	c a c	c t c	g g c	g g c	g a c	g g c	g c c	t a c	g c c	g c g	c a t	t a c	g g c	1488
Ile	Ala	Ser	His	Leu	Gly	Gly	Asp	Gly	Ala	Tyr	Ala	Ala	His	Tyr	Gly	
				485					490					495		
c a c	c a c	c a c	c a c	t c g	g c c	g c c	g c c	g c c	t g g	c c g	a c c	a t c	g c g	t t c	c a g	1536
His	His	His	His	Ser	Ala	Ala	Ala	Ala	Trp	Pro	Thr	Ile	Ala	Phe	Gln	
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g c g	g c g	g c g	g c g	c c g	c c g	c c g	c a c	g c c	g c c	g g g	c t t	t a c	c a c	c c g	t a c	1584
Ala	Ala	Ala	Ala	Pro	Pro	Pro	His	Ala	Ala	Gly	Leu	Tyr	His	Pro	Tyr	
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g c g	c a g	c c g	c t g	c g t	g g g	t g g	t g c	a a g	c a g	g a g	c a g	g a c	c a c	g c c	g t g	1632
Ala	Gln	Pro	Leu	Arg	Gly	Trp	Cys	Lys	Gln	Glu	Gln	Asp	His	Ala	Val	
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a t c	g c g	g c g	g c g	c a c	a g c	c t g	c a g	g a t	c t c	c a c	c a c	c t c	a a c	c t c	g g c	1680
Ile	Ala	Ala	Ala	His	Ser	Leu	Gln	Asp	Leu	His	His	Leu	Asn	Leu	Gly	
	545				550					555					560	
g c c	g c c	g c c	g c c	g c g	c a t	g a c	t t c	t t c	t c g	c a g	g c g	a t g	c a g	c a g	c a g	1728
Ala	Ala	Ala	Ala	Ala	His	Asp	Phe	Phe	Ser	Gln	Ala	Met	Gln	Gln	Gln	
				565					570					575		
c a c	g g c	c t c	g g c	a g c	a t c	g a c	a a c	g c g	t c g	c t c	g a g	c a c	a g c	a c c	g g c	1776
His	Gly	Leu	Gly	Ser	Ile	Asp	Asn	Ala	Ser	Leu	Glu	His	Ser	Thr	Gly	
			580					585					590			
t c c	a a c	t c c	g t c	g t c	t a c	a a c	g g c	g a c	a a t	g g c	g g c	g g a	g g c	g g c	g g c	1824
Ser	Asn	Ser	Val	Val	Tyr	Asn	Gly	Asp	Asn	Gly	Gly	Gly	Gly	Gly	Gly	
		595					600					605				
t a c	a t c	a t g	g c g	c c g	a t g	a g c	g c c	g t g	t c g	g c c	a c g	g c c	a c c	g c g	g t g	1872
Tyr	Ile	Met	Ala	Pro	Met	Ser	Ala	Val	Ser	Ala	Thr	Ala	Thr	Ala	Val	
	610					615					620					
g c g	a g c	a g c	c a c	g a t	c a c	g g c	g g c	g a c	g g c	g g g	a a g	c a g	g t g	c a g	a t g	1920
Ala	Ser	Ser	His	Asp	His	Gly	Gly	Asp	Gly	Gly	Lys	Gln	Val	Gln	Met	
	625				630					635					640	
g g g	t a c	g a c	a g c	t a c	c t c	g t c	g g c	g c a	g a c	g c c	t a c	g g c	g g c	g g c	g g c	1968
Gly	Tyr	Asp	Ser	Tyr	Leu	Val	Gly	Ala	Asp	Ala	Tyr	Gly	Gly	Gly	Gly	
				645					650					655		
g c c	g g g	a g g	a t g	c c a	t c c	t g g	g c g	a t g	a c g	c c g	g c g	t c g	g c g	c c g	g c c	2016
Ala	Gly	Arg	Met	Pro	Ser	Trp	Ala	Met	Thr	Pro	Ala	Ser	Ala	Pro	Ala	
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Sequence Listing from Patent scope

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Phe	Ser	Val	Trp	Asn	Asp	Thr										
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<400> 14

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			20					25					30			
Thr	Thr	Thr	Thr	Ala	Gly	Asp	Ser	Ser	Thr	Gly	Asp	Val	Cys	Phe	Asn	
			35				40					45				
Ile	Pro	Gln	Asp	Trp	Ser	Met	Arg	Gly	Ser	Glu	Leu	Ser	Ala	Leu	Val	
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Ala	Glu	Pro	Lys	Leu	Glu	Asp	Phe	Leu	Gly	Gly	Ile	Ser	Phe	Ser	Glu	
65					70					75					80	
Gln	Gln	His	His	His	Gly	Gly	Lys	Gly	Val	Ile	Pro	Ser	Ser	Ser	Ala	
				85					90				95			
Ala	Ala	Cys	Tyr	Ala	Ser	Ser	Gly	Ser	Ser	Val	Gly	Tyr	Leu	Tyr	Pro	
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Pro	Pro	Ser	Ser	Ser	Ser	Leu	Gln	Phe	Ala	Asp	Ser	Val	Met	Val	Ala	
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Thr	Ser	Ser	Pro	Val	Val	Ala	His	Asp	Gly	Val	Ser	Gly	Gly	Gly	Met	
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Val	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Gly	Asn	Gly	Gly	Ile	Gly	
145				150						155					160	
Leu	Ser	Met	Ile	Lys	Asn	Trp	Leu	Arg	Ser	Gln	Pro	Ala	Pro	Gln	Pro	
				165					170					175		
Ala	Gln	Ala	Leu	Ser	Leu	Ser	Met	Asn	Met	Ala	Gly	Thr	Thr	Thr	Ala	
			180					185					190			
Gln	Gly	Gly	Gly	Ala	Met	Ala	Leu	Leu	Ala	Gly	Ala	Gly	Glu	Arg	Gly	
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Arg	Thr	Thr	Pro	Ala	Ser	Glu	Ser	Leu	Ser	Thr	Ser	Ala	His	Gly	Ala	
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Thr	Thr	Ala	Thr	Met	Ala	Gly	Gly	Arg	Lys	Glu	Ile	Asn	Glu	Glu	Gly	
225				230						235					240	
Ser	Gly	Ser	Ala	Gly	Ala	Val	Val	Ala	Val	Gly	Ser	Glu	Ser	Gly	Gly	
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Ser	Gly	Ala	Val	Val	Glu	Ala	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Arg	Lys	
			260					265					270			
Ser	Val	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly	Val	Thr	
		275					280					285				
Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	
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Cys	Arg	Arg	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly	
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Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	
			325						330					335		
Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Thr	Thr	Asn	Phe	Pro	Val	Asn	Asn		
			340					345				350				
Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln	Glu	Phe	
		355					360					365				
Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	
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Sequence Listing from Patent scope

Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala
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Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe
				405					410					415	
Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys
				420				425						430	
Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Met	Ser		Tyr	Asp
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Val	Lys	Ser	Ile	Leu	Asp	Ser	Ala	Ala	Leu	Pro	Val	Gly	Thr	Ala	Ala
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Lys	Arg	Leu	Lys	Asp	Ala	Glu	Ala	Ala	Ala	Ala	Tyr	Asp	Val	Gly	Arg
465					470					475					480
Ile	Ala	Ser	His	Leu	Gly	Gly	Asp	Gly	Ala	Tyr	Ala	Ala	His	Tyr	Gly
				485					490					495	
His	His	His	His	Ser	Ala	Ala	Ala	Ala	Trp	Pro	Thr	Ile	Ala	Phe	Gln
			500					505					510		
Ala	Ala	Ala	Ala	Pro	Pro	Pro	His	Ala	Ala	Gly	Leu	Tyr	His	Pro	Tyr
			515				520						525		
Ala	Gln	Pro	Leu	Arg	Gly	Trp	Cys	Lys	Gln	Glu	Gln	Asp	His	Ala	Val
	530					535						540			
Ile	Ala	Ala	Ala	His	Ser	Leu	Gln	Asp	Leu	His	His	Leu	Asn	Leu	Gly
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Ala	Ala	Ala	Ala	Ala	His	Asp	Phe	Phe	Ser	Gln	Ala	Met	Gln	Gln	Gln
				565					570					575	
His	Gly	Leu	Gly	Ser	Ile	Asp	Asn	Ala	Ser	Leu	Glu	His	Ser	Thr	Gly
			580					585					590		
Ser	Asn	Ser	Val	Val	Tyr	Asn	Gly	Asp	Asn	Gly	Gly	Gly	Gly	Gly	Gly
		595					600						605		
Tyr	Ile	Met	Ala	Pro	Met	Ser	Ala	Val	Ser	Ala	Thr	Ala	Thr	Ala	Val
	610					615					620				
Ala	Ser	Ser	His	Asp	His	Gly	Gly	Asp	Gly	Gly	Lys	Gln	Val	Gln	Met
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Gly	Tyr	Asp	Ser	Tyr	Leu	Val	Gly	Ala	Asp	Ala	Tyr	Gly	Gly	Gly	Gly
				645					650					655	
Ala	Gly	Arg	Met	Pro	Ser	Trp	Ala	Met	Thr	Pro	Ala	Ser	Ala	Pro	Ala
			660					665					670		
Ala	Thr	Ser	Ser	Ser	Asp	Met	Thr	Gly	Val	Cys	His	Gly	Ala	Gln	Leu
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Gly Ala Gly Ala Asp Pro Val Leu Pro His Pro Pro Leu Gln Gu Trp	
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Gly Ser Ala Tyr Glu Gly Gly Gly Thr Val Ala Ala Ala Gly Gly Gly	
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Sequence Listing from Patent scope

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cag Gln 65	gag G u	acg Thr	gcc Ala	gcc Ala	gcg Ala 70	gcg Ala	gcg Ala	ggg Gly	cac His	ggc Gly 75	cgt Arg	gga Gly	ggc Gly	agc Ser	tcg Ser 80	240
tcg Ser	gtc Val	gtt Val	ggg Gly	ctg Leu 85	tcc Ser	atg Met	atc Ile	aag Lys	aac Asn 90	tgg Trp	cta Leu	cgc Arg	agc Ser	cag Gln 95	ccg Pro	288
ccg Pro	ccc Pro	gcg Ala	gtg Val 100	gtt Val	ggg Gly	gga Gly	gaa G u	gac Asp 105	gct Ala	atg Met	atg Met	gcg Ala	ctc Leu 110	gcg Ala	gtg Val	336
tcg Ser	acg Thr	tcg Ser 115	gcg Ala	tcg Ser	ccg Pro	ccg Pro	gtg Val 120	gac Asp	gcg Ala	acg Thr	gtg Val	ccg Pro 125	gcc Ala	tgc Cys	att Ile	384
tcg Ser	ccg Pro 130	gat Asp	ggg Gly	atg Met	ggg Gly	tcg Ser 135	aag Lys	gcg Ala	gcc Ala	gac Asp	ggc Gly 140	ggc Gly	ggc Gly	gcg Ala	gcc Ala	432
gag G u 145	gcg Ala	gcg Ala	gcg Ala	gcg Ala	gcg Ala 150	gcg Ala	gcg Ala	cag Gln	agg Arg	atg Met 155	aag Lys	gcg Ala	gcc Ala	atg Met	gac Asp 160	480
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tgg Trp	aca Thr	gga Gly	agg Arg 180	tat Tyr	gaa G u	gcc Ala	cat His	ctt Leu 185	tgg Trp	gat Asp	aac Asn	agc Ser	tgc Cys 190	aga Arg	aga Arg	576
gaa G u 195	ggt Gly	cag Gln	act Thr	cgc Arg	aaa Lys	ggc Gly	aga Arg 200	caa Gln	gta Val	tat Tyr	ctt Leu	gga Gly 205	gga Gly	tat Tyr	gat Asp	624
aag Lys 210	gaa G u	gaa G u	aaa Lys	gct Ala	gct Ala	agg Arg 215	gct Ala	tat Tyr	gat Asp	ttg Leu	gct Ala 220	gcc Ala	ctt Leu	aaa Lys	tac Tyr	672
tgg Trp 225	ggc Gly	act Thr	aca Thr	acg Thr 230	acg Thr	aat Asn	ttt Phe	ccg Pro	gta Val 235	agc Ser	aac Asn	tac Tyr	gaa G u 240	aaa Lys		720
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ctt Leu	aga Arg	aga Arg	aaa Lys 260	agc Ser	agt Ser	gga Gly	ttt Phe	tca Ser 265	cgt Arg	ggt Gly	gct Ala	tcc Ser	ata Ile 270	tat Tyr	cgt Arg	816
ggt Gly	gtt Val	aca Thr 275	aga Arg	cac His	cat His	cag Gln 280	cat His	gga Gly	agg Arg	tgg Trp	caa Gln	gca Ala 285	agg Arg	ata Ile	gga Gly	864
cgg Arg	gtg Val	gca Ala	gga Gly	aac Asn	aag Lys	gat Asp	ctg Leu	tat Tyr	ttg Leu	ggc Gly	aca Thr	ttt Phe	ggc Gly	acc Thr	caa Gln	912

Sequence Listing from Patent scope

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	Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser			325 330		335
	atc att gaa agc agc aat ctc cca att ggt act gga acc acc cgg cga					1056
	Ile Ile Gu Ser Ser Asn Leu Pro Ile Gy Thr Gy Thr Thr Arg Arg			340 345		350
	ttg aag gac tcc tct gat cac act gat aat gt c atg gac atc aat gt c					1104
	Leu Lys Asp Ser Ser Asp His Thr Asp Asn Val Met Asp Ile Asn Val			355 360		365
	aat acc gaa ccc aat aat gtg gta tca tcc cac ttc acc aat ggg gt t					1152
	Asn Thr Gu Pro Asn Asn Val Val Ser Ser His Phe Thr Asn Gy Val			370 375		380
	ggc aac tat ggt tcg cag cat tat ggt tac aat gga tgg tcg cca att					1200
	Gy Asn Tyr Gy Ser Gn His Tyr Gy Tyr Asn Gy Trp Ser Pro Ile			385 390		400
	agc atg cag ccg atc ccc tcg cag tac gcc aac ggc cag ccc agg gca					1248
	Ser Met Gn Pro Ile Pro Ser Gn Tyr Ala Asn Gy Gn Pro Arg Ala			405 410		415
	tgg ttg aaa caa gag cag gac agc tct gtg gtt aca gcg gcg cag aac					1296
	Trp Leu Lys Gn Gu Gn Asp Ser Ser Val Val Thr Ala Ala Gn Asn			420 425		430
	ctg cac aat cta cat cat ttt agt tcc ttg ggc tac acc cac aac ttc					1344
	Leu His Asn Leu His His Phe Ser Ser Leu Gy Tyr Thr His Asn Phe			435 440		445
	ttc cag caa tct gat gtt cca gac gt c aca ggt ttc gtt gat gcg cct					1392
	Phe Gn Gn Ser Asp Val Pro Asp Val Thr Gy Phe Val Asp Ala Pro			450 455		460
	tcg agg tcc agt gac tca tac tcc ttc agg tac aat gga aca aat ggc					1440
	Ser Arg Ser Ser Asp Ser Tyr Ser Phe Arg Tyr Asn Gy Thr Asn Gy			465 470		480
	ttt cat ggt ctc ccg ggt gga atc agc tat gct atg ccg gtt gcg aca					1488
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	gcg gtg gac caa ggt cag ggc atc cat ggc tat gga gaa gat ggt gt g					1536
	Ala Val Asp Gn Gy Gn Gy Ile His Gy Tyr Gy Gu Asp Gy Val			500 505		510
	gca ggc att gac acc aca cat gac ctg tat ggc agc cgt aat gtg tac					1584
	Ala Gy Ile Asp Thr Thr His Asp Leu Tyr Gy Ser Arg Asn Val Tyr			515 520		525
	tac ctt tcc gag ggt tcg ctt ctt gcc gat gt c gaa aaa gaa ggc gac					1632
	Tyr Leu Ser Gu Gy Ser Leu Leu Ala Asp Val Gu Lys Gu Gy Asp			530 535		540
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Sequence Listing from Patent scope

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Gln	Glu	Thr	Ala	Ala	Ala	Ala	Ala	Gly	His	Gly	Arg	Gly	Gly	Ser	Ser
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Pro	Pro	Ala	Val	Val	Gly	Gly	Glu	Asp	Ala	Met	Met	Ala	Leu	Ala	Val
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Ser	Thr	Ser	Ala	Ser	Pro	Pro	Val	Asp	Ala	Thr	Val	Pro	Ala	Cys	Ile
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Ser	Pro	Asp	Gly	Met	Gly	Ser	Lys	Ala	Ala	Asp	Gly	Gly	Gly	Ala	Ala
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Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gln	Arg	Met	Lys	Ala	Ala	Met	Asp
145				150					155					160	
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			165					170						175	
Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Arg	Arg
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Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr
	210					215					220				
Trp	Gly	Thr	Thr	Thr	Thr	Thr	Asn	Phe	Pro	Val	Ser	Asn	Tyr	Glu	Lys
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Glu	Leu	Asp	Glu	Met	Lys	His	Met	Asn	Arg	Gln	Glu	Phe	Val	Ala	Ser
			245					250						255	
Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg
		260						265					270		
Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly
		275					280					285			
Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Gly	Thr	Gln
	290				295						300				
Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly
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Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Lys	Ser
			325					330						335	
Ile	Ile	Glu	Ser	Ser	Asn	Leu	Pro	Ile	Gly	Thr	Gly	Thr	Thr	Arg	Arg
		340						345					350		
Leu	Lys	Asp	Ser	Ser	Asp	His	Thr	Asp	Asn	Val	Met	Asp	Ile	Asn	Val
		355					360					365			
Asn	Thr	Glu	Pro	Asn	Asn	Val	Val	Ser	Ser	His	Phe	Thr	Asn	Gly	Val
	370				375						380				
Gly	Asn	Tyr	Gly	Ser	Gln	His	Tyr	Gly	Tyr	Asn	Gly	Trp	Ser	Pro	Ile
385				390						395				400	
Ser	Met	Gln	Pro	Ile	Pro	Ser	Gln	Tyr	Ala	Asn	Gly	Gln	Pro	Arg	Ala
			405						410					415	

Sequence Listing from Patent scope

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

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 <212> DNA
 <213> Oryza sativa

<220>
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 aat ccg cag cct cac cag gat agc tcc cct ccg gca gcc atc gac gtc 96
 Asn Pro Gln Pro His Gln Asp Ser Ser Pro Pro Ala Ala Ile Asp Val
 20 25 30
 tcc ggc gcc ggc gac ttc tat ggc ctg ccg acg tcc cag ccg acg gcg 144
 Ser Gly Ala Gly Asp Phe Tyr Gly Leu Pro Thr Ser Gln Pro Thr Ala
 35 40 45
 gcc gac gcg cac ctg ggc gtg gcg ggg cat cat cac aac gcc tcc tat 192
 Ala Asp Ala His Leu Gly Val Ala Gly His His His Asn Ala Ser Tyr
 50 55 60
 ggc atc atg gag gcc ttc aat agg gga gct caa gag gca caa gat tgg 240
 Gly Ile Met Glu Ala Phe Asn Arg Gly Ala Gln Glu Ala Gln Asp Trp
 65 70 75 80
 aac atg agg ggg ctg gac tac aac ggc ggc gcc tcc gag ctg tcc atg 288
 Asn Met Arg Gly Leu Asp Tyr Asn Gly Gly Ala Ser Glu Leu Ser Met
 85 90 95
 ctg gtc ggc tcc agc ggc ggc aag agg gcg gcg gcg gtg gag gag acc 336
 Leu Val Gly Ser Ser Gly Gly Lys Arg Ala Ala Ala Val Glu Glu Thr
 100 105 110
 gag ccg aag ctg gag gac ttc ctg ggc ggc aac tcc ttc gtc tcc gag 384
 Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn Ser Phe Val Ser Glu
 115 120 125
 caa gat cat cac gcg gcg ggg ggc ttc ctg ttc tcc ggc gtc ccg atg 432

Sequence Listing from Patent scope															
Gln	Asp	His	His	Ala	Ala	Gly	Gly	Phe	Leu	Phe	Ser	Gly	Val	Pro	Met
130						135					140				
gcc Ala 145	agc Ser	agc Ser	acc Thr	aac Asn	agc Ser 150	aac Asn	agc Ser	ggg Gly	agc Ser	aac Asn 155	act Thr	atg Met	gag Glu	ctc Leu	tcc Ser 160
atg Met	atc Ile	aag Lys	acc Thr	tgg Trp 165	ctc Leu	cgg Arg	aac Asn	aac Asn	ggc Gly 170	cag Gln	gtg Val	ccc Pro	gcc Ala	ggc Gly 175	cac His
cag Gln	ccg Pro	cag Gln	cag Gln 180	cag Gln	cag Gln	ccg Pro	gcg Ala	gcc Ala 185	gcg Ala	gcc Ala	gcc Ala	gcc Ala	gcg Ala 190	cag Gln	cag Gln
cag Gln	gcg Ala	cac His 195	gag Glu	gcg Ala	gcg Ala	gag Glu	atg Met 200	agc Ser	acc Thr	gac Asp	gcg Ala	agc Ser 205	gcg Ala	agc Ser	agc Ser
ttc Phe 210	ggg Gly	tgc Cys	tcc Ser	tcc Ser	gac Asp	gcg Ala 215	atg Met	ggg Gly	agg Arg	agt Ser	aac Asn 220	aac Asn	ggc Gly	ggc Gly	gcg Ala
gtc Val 225	tgc Ser	gcg Ala	gcg Ala	gcc Ala	ggc Gly 230	ggg Gly	acg Thr	agc Ser	tgc Ser	cag Gln 235	agc Ser	ctg Leu	gcg Ala	ctc Leu	tgc Ser 240
atg Met	agc Ser	acg Thr	ggc Gly	tgc Ser 245	cac His	tgc Ser	cac His	ctg Leu	cct Pro 250	atc Ile	gtc Val	gtc Val	gcc Ala	ggc Gly 255	ggc Gly
ggg Gly	aac Asn	gcc Ala	agc Ser 260	ggc Gly	gga Gly	gcg Ala	gcc Ala	gag Glu 265	agc Ser	aca Thr	tgc Ser	tgc Ser	gag Glu 270	aac Asn	aag Lys
cgg Arg	gcc Ala	agc Ser 275	ggc Gly	gcc Ala	atg Met	gat Asp	tgc Ser 280	ccg Pro	ggc Gly	ggt Gly	ggc Gly	gcg Ala 285	ata Ile	gag Glu	gcc Ala
gtg Val 290	ccg Pro	agg Arg	aag Lys	tcc Ser	atc Ile	gac Asp 295	acg Thr	ttc Phe	ggg Gly	caa Gln	agg Arg 300	acc Thr	tgc Ser	ata Ile	tat Tyr
cga Arg 305	ggt Gly	gta Val	aca Thr	agg Arg	cat His 310	aga Arg	tgg Trp	aca Thr	ggg Gly	cga Arg 315	tat Tyr	gag Glu	gct Ala	cat His	ctc Leu 320
tgg Trp	gat Asp	aat Asn	agc Ser	tgt Cys 325	aga Arg	aga Arg	gaa Glu	ggg Gly	cag Gln 330	agt Ser	cgc Arg	aag Lys	ggt Gly	agg Arg 335	caa Gln
gtt Val	tat Tyr	ctt Leu	ggt Gly 340	ggc Gly	tat Tyr	gac Asp	aag Lys	gag Glu 345	gat Asp	aaa Lys	gca Ala	gcg Ala	aga Arg 350	gct Ala	tat Tyr
gat Asp	tig Leu	gca Ala 355	gct Ala	ctg Leu	aag Lys	tat Tyr	tgg Trp 360	ggc Gly	aca Thr	aca Thr	aca Thr 365	aca Thr	aca Thr	aat Asn	ttc Phe
cca Pro	ata Ile 370	agt Ser	aac Asn	tat Tyr	gaa Glu	aaa Lys 375	gag Glu	cta Leu	gat Asp	gaa Glu	atg Met 380	aaa Lys	cat His	atg Met	acc Thr

Sequence Listing from Patent scope																
agg Arg 385	cag Gln	gag Glu	tat Tyr	att Ile	gca Ala 390	tac Tyr	cta Leu	aga Arg	agg Arg	aat Asn 395	agc Ser	agt Ser	gga Gly	ttt Phe	tct Ser 400	1200
cgt Arg	ggt Gly	gca Ala	tcg Ser	aaa Lys 405	tat Tyr	cgt Arg	ggt Gly	gta Val	acc Thr 410	agg Arg	cac His	cat His	cag Gln	cat His 415	ggg Gly	1248
aga Arg	tgg Trp	caa Gln	gca Ala 420	agg Arg	ata Ile	ggg Gly	agg Arg	gtt Val 425	gca Ala	gga Gly	aac Asn	aag Lys	gac Asp 430	ctc Leu	tac Tyr	1296
tta Leu	ggc Gly	acc Thr 435	ttc Phe	agc Ser	acc Thr	gag Glu	gag Glu 440	gag Glu	gcg Ala	gcg Ala	gag Glu	gcg Ala 445	tac Tyr	gac Asp	atc Ile	1344
gcg Ala 450	gcg Ala	atc Ile	aag Lys	ttc Phe	cgg Arg	ggg Gly 455	ctc Leu	aac Asn	gcc Ala	gtc Val	acc Thr 460	aac Asn	ttt Phe	gac Asp	atg Met	1392
agc Ser 465	cgc Arg	tac Tyr	gac Asp	gtc Val	aag Lys 470	agc Ser	atc Ile	ctg Leu	gag Glu	agc Ser 475	agc Ser	acg Thr	ctg Leu	ccg Pro	gtg Val 480	1440
ggc Gly	ggc Gly	gcg Ala	gcg Ala	agg Arg 485	cgg Arg	ctg Leu	aag Lys	gag Glu	gcg Ala 490	gcg Ala	gac Asp	cac His	gcg Ala 495	gag Glu 495	gcg Ala	1488
gcc Ala	ggc Gly	gcc Ala	acc Thr 500	atc Ile	tgg Trp	cgc Arg	gcc Ala	gcc Ala 505	gac Asp	atg Met	gac Asp	ggc Gly	gcc Ala 510	ggc Gly	gtc Val	1536
atc Ile	tcc Ser	ggc Gly 515	ctg Leu	gcc Ala	gac Asp	gtc Val	ggg Gly 520	atg Met	ggc Gly	gcc Ala	tac Tyr	gcc Ala 525	gcc Ala	tcg Ser	tac Tyr	1584
cac His 530	cac His	cac His	cac His	cac His	cac His	ggc Gly 535	tgg Trp	ccg Pro	acc Thr	atc Ile	gcg Ala 540	ttc Phe	cag Gln	cag Gln	ccg Pro	1632
ccg Pro 545	ccg Pro	ctc Leu	gcc Ala	gtg Val	cac His 550	tac Tyr	ccg Pro	tac Tyr	ggc Gly 555	cag Gln 555	gcg Ala	ccg Pro	gcg Ala	gcg Ala	ccg Pro 560	1680
tcg Ser	cgc Arg	ggg Gly	tgg Trp	tgc Cys 565	aag Lys	ccc Pro	gag Glu	cag Gln	gac Asp 570	gcc Ala	gcc Ala	gtc Val	gct Ala	gcc Ala 575	gcc Ala	1728
gcg Ala	cac His	agc Ser	ctc Leu 580	cag Gln	gac Asp	ctc Leu	cag Gln	cag Gln 585	ctg Leu	cac His	ctc Leu	ggc Gly	agc Ser 590	gcc Ala	gcc Ala	1776
gcc Ala	cac His	aac Asn 595	ttc Phe	ttc Phe	cag Gln	gcg Ala	tcg Ser 600	tcg Ser	agc Ser	tcg Ser	acg Thr	gtc Val 605	tac Tyr	aac Asn	ggc Gly	1824
ggc Gly 610	ggc Gly	ggc Gly	ggg Gly	tac Tyr	cag Gln	ggc Gly 615	ctc Leu	ggt Gly	ggc Gly	aac Asn	gcc Ala 620	ttc Phe	tig Leu	atg Met	ccg Pro	1872
gcg Ala 625	agc Ser	acc Thr	gtc Val	gtg Val	gcc Ala 630	gac Asp	cag Gln	ggg Gly	cac His	agc Ser 635	agc Ser	acg Thr	gcc Ala	acc Thr	aac Asn 640	1920

Sequence Listing from Patent scope

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His	Gly	Asn	Thr	Cys	Ser	Tyr	Gly	Asn	Glu	Glu	Gln	Gly	Lys	Leu	Ile	
				645					650					655		
ggg	tac	gac	gcc	atg	gcg	atg	gcg	agc	ggc	gcc	gcc	ggc	ggc	ggg	tac	2016
Gly	Tyr	Asp	Ala	Met	Ala	Met	Ala	Ser	Gly	Ala	Ala	Gly	Gly	Gly	Tyr	
			660					665					670			
cag	ctg	tcg	cag	ggc	tcg	gcg	tcg	acg	gtg	agc	atc	gcg	agg	gcg	aac	2064
Gln	Leu	Ser	Gln	Gly	Ser	Ala	Ser	Thr	Val	Ser	Ile	Ala	Arg	Ala	Asn	
			675				680					685				
ggc	tac	tcg	gcc	aac	tgg	agc	tcg	cct	ttc	aat	ggc	gcc	atg	gga	tga	2112
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 <212> PRT
 <213> Oryza sativa

<400> 18

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Ser	Gly	Ala	Gly	Asp	Phe	Tyr	Gly	Leu	Pro	Thr	Ser	Gln	Pro	Thr	Ala
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Ala	Asp	Ala	His	Leu	Gly	Val	Ala	Gly	His	His	His	Asn	Ala	Ser	Tyr
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Gly	Ile	Met	Glu	Ala	Phe	Asn	Arg	Gly	Ala	Gln	Glu	Ala	Gln	Asp	Trp
65					70				75					80	
Asn	Met	Arg	Gly	Leu	Asp	Tyr	Asn	Gly	Gly	Ala	Ser	Glu	Leu	Ser	Met
				85				90						95	
Leu	Val	Gly	Ser	Ser	Gly	Gly	Lys	Arg	Ala	Ala	Ala	Val	Glu	Glu	Thr
			100					105					110		
Glu	Pro	Lys	Leu	Glu	Asp	Phe	Leu	Gly	Gly	Asn	Ser	Phe	Val	Ser	Glu
		115					120					125			
Gln	Asp	His	His	Ala	Ala	Gly	Gly	Phe	Leu	Phe	Ser	Gly	Val	Pro	Met
	130					135					140				
Ala	Ser	Ser	Thr	Asn	Ser	Asn	Ser	Gly	Ser	Asn	Thr	Met	Glu	Leu	Ser
	145			150					155					160	
Met	Ile	Lys	Thr	Trp	Leu	Arg	Asn	Asn	Gly	Gln	Val	Pro	Ala	Gly	His
				165				170						175	
Gln	Pro	Gln	Gln	Gln	Gln	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gln	Gln
			180					185					190		
Gln	Ala	His	Glu	Ala	Ala	Glu	Met	Ser	Thr	Asp	Ala	Ser	Ala	Ser	Ser
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Phe	Gly	Cys	Ser	Ser	Asp	Ala	Met	Gly	Arg	Ser	Asn	Asn	Gly	Gly	Ala
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Val	Ser	Ala	Ala	Ala	Gly	Gly	Thr	Ser	Ser	Gln	Ser	Leu	Ala	Leu	Ser
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Met	Ser	Thr	Gly	Ser	His	Ser	His	Leu	Pro	Ile	Val	Val	Ala	Gly	Gly
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Gly	Asn	Ala	Ser	Gly	Gly	Ala	Ala	Glu	Ser	Thr	Ser	Ser	Glu	Asn	Lys
			260					265					270		
Arg	Ala	Ser	Gly	Ala	Met	Asp	Ser	Pro	Gly	Gly	Gly	Ala	Ile	Glu	Ala
	275						280					285			
Val	Pro	Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr
	290					295					300				

Sequence Listing from Patent scope

Arg 305	Gly	Val	Thr	Arg 310	His	Arg	Trp	Thr	Gly	Arg 315	Tyr	Glu	Ala	His	Leu 320
Trp	Asp	Asn	Ser	Cys 325	Arg	Arg	Glu	Gly	Gln	Ser	Arg	Lys	Gly	Arg	Gln
Val	Tyr	Leu	Gly 340	Gly	Tyr	Asp	Lys	Glu	Asp	Lys	Ala	Ala	Arg	Ala	Tyr
Asp	Leu	Ala 355	Ala	Leu	Lys	Tyr	Trp 360	Gly	Thr	Thr	Thr	Thr	Thr	Asn	Phe
Pro	Ile 370	Ser	Asn	Tyr	Glu	Lys 375	Glu	Leu	Asp	Glu	Met 380	Lys	His	Met	Thr
Arg 385	Gln	Glu	Tyr	Ile	Ala 390	Tyr	Leu	Arg	Arg	Asn 395	Ser	Ser	Gly	Phe	Ser
Arg	Gly	Ala	Ser	Lys 405	Tyr	Arg	Gly	Val	Thr 410	Arg	His	His	Gln	His	Gly
Arg	Trp	Gln	Ala 420	Arg	Ile	Gly	Arg	Val 425	Ala	Gly	Asn	Lys	Asp 430	Leu	Tyr
Leu	Gly	Thr 435	Phe	Ser	Thr	Glu	Glu 440	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile
Ala	Ala	Ile 450	Lys	Phe	Arg	Gly 455	Leu	Asn	Ala	Val	Thr 460	Asn	Phe	Asp	Met
Ser 465	Arg	Tyr	Asp	Val	Lys 470	Ser	Ile	Leu	Glu	Ser 475	Ser	Thr	Leu	Pro	Val
Gly	Gly	Ala	Ala	Arg 485	Arg	Leu	Lys	Glu	Ala	Ala	Asp	His	Ala	Glu	Ala
Ala	Gly	Ala	Thr 500	Ile	Trp	Arg	Ala	Ala 505	Asp	Met	Asp	Gly	Ala	Gly	Val
Ile	Ser	Gly 515	Leu	Ala	Asp	Val	Gly 520	Met	Gly	Ala	Tyr	Ala 525	Ala	Ser	Tyr
His	His 530	His	His	His	His	Gly 535	Trp	Pro	Thr	Ile	Ala 540	Phe	Gln	Gln	Pro
Pro 545	Pro	Leu	Ala	Val	His 550	Tyr	Pro	Tyr	Gly	Gln	Ala	Pro	Ala	Ala	Pro
Ser	Arg	Gly	Trp	Cys 565	Lys	Pro	Glu	Gln	Asp 570	Ala	Ala	Val	Ala	Ala	Ala
Ala	His	Ser	Leu 580	Gln	Asp	Leu	Gln	Gln	Leu	His	Leu	Gly	Ser 590	Ala	Ala
Ala	His	Asn 595	Phe	Phe	Gln	Ala	Ser 600	Ser	Ser	Ser	Thr	Val 605	Tyr	Asn	Gly
Gly	Gly	Gly	Gly	Tyr	Gln	Gly 615	Leu	Gly	Gly	Asn	Ala	Phe	Leu	Met	Pro
Ala 625	Ser	Thr	Val	Val	Ala 630	Asp	Gln	Gly	His	Ser 635	Ser	Thr	Ala	Thr	Asn
His	Gly	Asn	Thr	Cys 645	Ser	Tyr	Gly	Asn	Glu	Glu	Gln	Gly	Lys	Leu	Ile
Gly	Tyr	Asp	Ala 660	Met	Ala	Met	Ala	Ser 665	Gly	Ala	Ala	Gly	Gly	Gly	Tyr
Gln	Leu	Ser 675	Gln	Gly	Ser	Ala	Ser 680	Thr	Val	Ser	Ile	Ala 685	Arg	Ala	Asn
Gly 690	Tyr	Ser	Ala	Asn	Trp	Ser 695	Ser	Pro	Phe	Asn	Gly 700	Ala	Met	Gly	

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 <213> Oryza sativa

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 <222> (1)... (1977)

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 Page 40

Sequence Listing from Patent scope															
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aac Asn	cca Pro	cag Gln	cat His 20	cac His	cag Gln	aac Asn	ggc Gly	tcg Ser 25	ccg Pro	tct Ser	gcc Ala	gcc Ala	ggc Gly 30	gac Asp	gcc Ala
96															
gcc Ala	atc Ile	gac Asp 35	atc Ile	tcc Ser	ggc Gly	tca Ser	ggc Gly 40	gac Asp	ttc Phe	tat Tyr	ggt Gly	ctg Leu 45	cca Pro	acg Thr	ccg Pro
144															
gac Asp	gca Ala 50	cac His	cac His	atc Ile	ggc Gly	atg Met 55	gcg Ala	ggc Gly	gaa Glu	gac Asp	gcg Ala 60	ccc Pro	tat Tyr	ggc Gly	gtc Val
192															
atg Met 65	gat Asp	gct Ala	ttc Phe	aac Asn	aga Arg 70	ggc Gly	acc Thr	cat His	gaa Glu	acc Thr 75	caa Gln	gat Asp	tgg Trp	gcg Ala	atg Met 80
240															
agg Arg	ggt Gly	ttg Leu	gac Asp	tac Tyr 85	ggc Gly	ggc Gly	ggc Gly	tcc Ser	tcc Ser 90	gac Asp	ctc Leu	tcc Ser	atg Met	ctc Leu 95	gtc Val
288															
ggc Gly	tcc Ser	agc Ser	ggc Gly 100	ggc Gly	ggg Gly	agg Arg	agg Arg	acg Thr 105	gtg Val	gcc Ala	ggc Gly	gac Asp	ggc Gly 110	gtc Val	ggc Gly
336															
gag Glu	gcg Ala	ccg Pro 115	aag Lys	ctg Leu	gag Glu	aac Asn	ttc Phe 120	ctc Leu	gac Asp	ggc Gly	aac Asn	tca Ser 125	ttc Phe	tcc Ser	gac Asp
384															
gtg Val	cac His 130	ggc Gly	caa Gln	gcc Ala	gcc Ala	ggc Gly 135	ggg Gly	tac Tyr	ctc Leu	tac Tyr	tcc Ser 140	gga Gly	agc Ser	gct Ala	gtc Val
432															
ggc Gly 145	ggc Gly	gcc Ala	ggt Gly	ggt Gly	tac Tyr 150	agt Ser	aac Asn	ggc Gly	gga Gly	tgc Cys 155	ggc Gly	ggc Gly	gga Gly	acc Thr	ata Ile 160
480															
gag Glu	ctg Leu	tcc Ser	atg Met	atc Ile 165	aag Lys	acg Thr	tgg Trp	ctc Leu	cgg Arg 170	agc Ser	aac Asn	cag Gln	tcc Ser	cag Gln 175	cag Gln
528															
cag Gln	cca Pro	tcc Ser	ccg Pro 180	ccg Pro	cag Gln	cac His	gct Ala	gat Asp 185	cag Gln	ggc Gly	atg Met	agc Ser	acc Thr 190	gac Asp	gcc Ala
576															
agc Ser	gcg Ala	agc Ser 195	agc Ser	tac Tyr	gcg Ala	tgc Cys	tcc Ser 200	gac Asp	gtg Val	ctg Leu	gtg Val	ggg Gly 205	agc Ser	tgc Cys	ggc Gly
624															
ggc Gly	ggc Gly 210	ggc Gly	gcc Ala	ggg Gly	ggc Gly	acg Thr 215	gcg Ala	agc Ser	tcc Ser	cat His	ggg Gly 220	cag Gln	ggc Gly	ctg Leu	gcg Ala
672															
ctg Leu 225	tcc Ser	atg Met	agc Ser	acg Thr	ggg Gly 230	tcc Ser	gtg Val	gcc Ala	gcc Ala	gcc Ala 235	gga Gly	ggg Gly	ggc Gly	ggc Gly	gcc Ala 240
720															
gtc Val	gtc Val	gcg Ala	gcc Ala	gag Glu 245	agc Ser	tcc Ser	tcc Ser	tcc Ser	gag Glu 250	aac Asn	aag Lys	cgg Arg	gtg Val	gat Asp 255	tcc Ser
768															

Sequence Listing from Patent scope																
ccg Pro	ggc Gly	ggc Gly	gcc Ala 260	gtg Val	gac Asp	ggc Gly	gcc Ala 265	gtc Val	ccg Pro	agg Arg	aaa Lys	tcc Ser 270	atc Ile	gac Asp	acc Thr	816
ttc Phe	ggg Gly	caa Gln 275	agg Arg	acg Thr	tct Ser	ata Ile	tac Tyr 280	cga Arg	ggt Gly	gta Val	aca Thr	agg Arg 285	cat His	aga Arg	tgg Trp	864
aca Thr	gga Gly 290	aga Arg	tat Tyr	gaa Glu	gct Ala	cat His 295	ctg Leu	tgg Trp	gat Asp	aat Asn	agc Ser 300	tgt Cys	agg Arg	aga Arg	gaa Glu	912
ggc Gly 305	caa Gln	agt Ser	cgc Arg	aag Lys	ggg Gly 310	aga Arg	cag Gln	gtt Val	tat Tyr	tig Leu 315	ggc Gly	ggt Gly	tat Tyr	gac Asp	aaa Lys 320	960
gaa Glu	gat Asp	aag Lys	gcg Ala	gct Ala 325	cgg Arg	gct Ala	tat Tyr	gat Asp	tig Leu 330	gca Ala	gct Ala	cta Leu	aaa Lys	tac Tyr 335	tgg Trp	1008
ggc Gly	acg Thr	acc Thr	aca Thr 340	aca Thr	aca Thr	aat Asn	ttc Phe	cca Pro 345	atg Met	agt Ser	aat Asn	tat Tyr	gaa Glu 350	aag Lys	gag Glu	1056
cta Leu	gag Glu	gaa Glu 355	atg Met	aaa Lys	cac His	atg Met	acc Thr 360	agg Arg	cag Gln	gag Glu	tac Tyr	att Ile 365	gca Ala	cat His	ctt Leu	1104
aga Arg	agg Arg 370	aat Asn	agc Ser	agt Ser	gga Gly	ttt Phe 375	tct Ser	cgt Arg	ggt Gly	gca Ala	tcc Ser 380	aaa Lys	tat Tyr	cgt Arg	ggt Gly	1152
gtt Val 385	act Thr	agg Arg	cat His	cat His	cag Gln 390	cat His	ggg Gly	aga Arg	tgg Trp	cag Gln 395	gca Ala	agg Arg	ata Ile	ggg Gly	cga Arg 400	1200
gtt Val	gca Ala	ggc Gly	aac Asn	aag Lys 405	gat Asp	atc Ile	tac Tyr	cta Leu	ggc Gly 410	acc Thr	ttc Phe	agc Ser	acc Thr	gag Glu 415	gag Glu	1248
gag Glu	gcc Ala	gcc Ala	gag Glu 420	gcg Ala	tac Tyr	gac Asp	atc Ile	gcc Ala 425	gcc Ala	atc Ile	aag Lys	ttc Phe	cgc Arg 430	ggg Gly	ctc Leu	1296
aac Asn	gcc Ala 435	gtc Val	acc Thr	aac Asn	ttc Phe	gac Asp	atg Met 440	agc Ser	cgg Arg	tac Tyr	gac Asp 445	gtc Val	aag Lys	agc Ser	atc Ile	1344
ctg Leu	gac Asp 450	agc Ser	agc Ser	acg Thr	ctg Leu	ccg Pro 455	gtc Val	ggc Gly	ggc Gly	gcg Ala	gcg Ala 460	cgg Arg	cgg Arg	ctc Leu	aag Lys	1392
gag Glu 465	gcg Ala	gag Glu	gtc Val	gcc Ala 470	gcc Ala	gcc Ala	gcc Ala	gcg Ala	ggc Gly	ggc Gly 475	ggc Gly	gtg Val	atc Ile	gtc Val	tcc Ser 480	1440
cac His	ctg Leu	gcc Ala	gac Asp	ggc Gly 485	ggt Gly	gtg Val	ggt Gly	ggg Gly	tac Tyr 490	tac Tyr	tac Tyr	ggg Gly	tgc Cys	ggc Gly 495	ccg Pro	1488
acc Thr	atc Ile	gcg Ala	ttc Phe 500	ggc Gly	ggc Gly	ggc Gly	ggc Gly	cag Gln 505	cag Gln	ccg Pro	gcg Ala	ccg Pro	ctc Leu 510	gcc Ala	gtg Val	1536

Sequence Listing from Patent scope

cac His	tac Tyr	ccg Pro 515	tcg Ser	tac Tyr	ggc Gly	cag Gln	gcc Ala 520	agc Ser	ggg Gly	tgg Trp	tgc Cys	aag Lys 525	ccg Pro	gag Glu	cag Gln	1584
gac Asp	gcg Ala 530	gtg Val	atc Ile	gcg Ala	gcc Ala	ggg Gly 535	cac His	tgc Cys	gcg Ala	acg Thr	gac Asp 540	ctc Leu	cag Gln	cac His	ctg Leu	1632
cac His 545	ctc Leu	ggg Gly	agc Ser	ggc Gly	ggc Ala 550	gcc Ala	gcc Ala	gcc Ala	acc Thr	cac His 555	aac Asn	ttc Phe	ttc Phe	cag Gln	cag Gln 560	1680
ccg Pro	gcg Ala	tca Ser	agc Ser	tcg Ser 565	gcc Ala	gtc Val	tac Tyr	ggc Gly	aac Asn 570	ggc Gly	ggc Gly	ggc Gly	ggc Gly	ggc Gly	ggc Gly	1728
aac Asn	gcg Ala	ttc Phe	atg Met 580	atg Met	ccg Pro	atg Met	ggc Gly	gcc Ala 585	gtg Val	gtg Val	gcc Ala	gcc Ala	gcc Ala 590	gat Asp	cac His	1776
ggc Gly	ggg Gly	cag Gln 595	agc Ser	agc Ser	gcc Ala	tac Tyr	ggc Gly 600	ggt Gly	ggc Gly	gac Asp	gag Glu	agc Ser 605	ggg Gly	agg Arg	ctc Leu	1824
gtc Val 610	gtg Val	ggg Gly	tac Tyr	gac Asp	ggc Gly	gtc Val 615	gtc Val	gac Asp	ccg Pro	tac Tyr	gcg Ala 620	gcc Ala	atg Met	aga Arg	agc Ser	1872
gcg Ala 625	tac Tyr	gag Glu	ctc Leu	tcg Ser	cag Gln 630	ggc Gly	tcg Ser	tcg Ser	tcg Ser	tcg Ser 635	tcg Ser	gtg Val	agc Ser	gtc Val	gcg Ala 640	1920
aag Lys	gcg Ala	gcg Ala	aac Asn	ggg Gly 645	tac Tyr	ccg Pro	gac Asp	aac Asn	tgg Trp 650	agc Ser	tcg Ser	ccg Pro	ttc Phe	aac Asn 655	ggc Gly	1968
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 Asp Ala His His Ile Gly Met Ala Gly Glu Asp Ala Pro Tyr Gly Val
 50 55 60
 Met Asp Ala Phe Asn Arg Gly Thr His Glu Thr Gln Asp Trp Ala Met
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 Arg Gly Leu Asp Tyr Gly Gly Gly Ser Ser Asp Leu Ser Met Leu Val
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 Glu Ala Pro Lys Leu Glu Asn Phe Leu Asp Gly Asn Ser Phe Ser Asp

Sequence Listing from Patent scope

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

Sequence Listing from Patent scope

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 Lys Ala Ala Asn Gly Tyr Pro Asp Asn Trp Ser Ser Pro Phe Asn Gly
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 caa aat cat cac cgt acg gat gtt gac tcc tcc acc acc aga acc gcc 96
 Gln Asn His His Arg Thr Asp Val Asp Ser Ser Thr Thr Arg Thr Ala
 20 25 30
 gta gat gtt gcc gga ggg tac tgt ttt gat ctg gcc gct ccc tcc gat 144
 Val Asp Val Ala Gly Gly Tyr Cys Phe Asp Leu Ala Ala Pro Ser Asp
 35 40 45
 gaa tct tct gcc gtt caa aca tct ttt ctt tct cct ttc ggt gtc acc 192
 Glu Ser Ser Ala Val Gln Thr Ser Phe Leu Ser Pro Phe Gly Val Thr
 50 55 60
 ctg gaa gct ttc acc aga gac aat aat agt cac tcc cga gat tgg gac 240
 Leu Glu Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp
 65 70 75 80
 atc aat ggt ggt gca tgc aat aca tta acc aat aac gaa caa aat gga 288
 Ile Asn Gly Gly Ala Cys Asn Thr Leu Thr Asn Asn Glu Gln Asn Gly
 85 90 95
 cca aag ctt gag aat ttc ctg ggc cgc acc acc acg att tac aat acc 336
 Pro Lys Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr
 100 105 110
 aac gag acc gtt gta gat gga aat ggc gat tgt gga gga gga gac ggt 384
 Asn Glu Thr Val Val Asp Gly Asn Gly Asp Cys Gly Gly Gly Asp Gly
 115 120 125
 ggt ggt ggc ggc tca cta ggc ctt tcg atg ata aaa aca tgg ctg agt 432
 Gly Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Ser
 130 135 140
 aat cat tcg gtt gct aat gct aat cat caa gac aat ggt aac ggt gca 480
 Asn His Ser Val Ala Asn Ala Asn His Gln Asp Asn Gly Asn Gly Ala
 145 150 155 160
 cga ggc ttg tcc ctg tct atg aat tca tct act agt gat agc aac aac 528
 Arg Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Asp Ser Asn Asn
 165 170 175
 tac aac aac aat gat gat gtc gtc caa gag aag act att gtt gat gtc 576

Sequence Listing from Patent scope															
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Val	Glu	Thr	Thr	Pro	Lys	Lys	Thr	Ile	Glu	Ser	Phe	Gly	Gln	Arg	Thr
		195					200					205			
tct	ata	tac	cgc	ggc	gtt	aca	agg	cat	cgg	tgg	aca	ggc	aga	tac	gag
Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu
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Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Lys	Arg	Glu	Gly	Gln	Thr	Arg	Lys
225					230					235					240
gga	aga	caa	gtt	tat	ctg	gga	ggc	tat	gac	aaa	gaa	gaa	aaa	gca	gct
Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala
				245					250					255	
agg	gct	tac	gat	tta	gcc	gca	cta	aag	tat	tgg	gga	ccc	acc	act	act
Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Thr	Thr
			260					265					270		
act	aac	ttc	ccc	ttg	agt	gaa	tat	gag	aaa	gag	gta	gaa	gag	atg	aag
Thr	Asn	Phe	Pro	Leu	Ser	Glu	Tyr	Glu	Lys	Glu	Val	Glu	Glu	Met	Lys
		275					280					285			
cac	atg	acg	agg	caa	gag	tat	gtt	gcc	tct	ctg	cgc	agg	aaa	agt	agt
His	Met	Thr	Arg	Gln	Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser
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ggc	ttc	tct	cgt	ggc	gca	tgc	att	tat	cga	gga	gta	aca	agg	cat	cac
Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His
305					310					315					320
caa	cat	gga	agg	tgg	caa	gct	agg	atc	gga	aga	gtc	gcc	ggc	aac	aaa
Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys
				325					330					335	
gac	ctc	tac	ttg	gga	act	ttc	ggc	aca	cag	gaa	gag	gct	gct	gag	gct
Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Gly	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala
			340					345					350		
tat	gac	att	gca	gcc	att	aaa	ttc	aga	gga	tta	agc	gca	gtg	act	aac
Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Ser	Ala	Val	Thr	Asn
		355					360					365			
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Phe	Asp	Met	Asn	Arg	Tyr	Asn	Val	Lys	Ala	Ile	Leu	Glu	Ser	Pro	Ser
	370					375					380				
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Leu	Pro	Ile	Gly	Ser	Ser	Ala	Lys	Arg	Leu	Lys	Asp	Val	Asn	Asn	Pro
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gtt	cca	gct	atg	atg	att	agt	aat	aac	gtt	tca	gag	agt	gca	aat	aat
Val	Pro	Ala	Met	Met	Ile	Ser	Asn	Asn	Val	Ser	Glu	Ser	Ala	Asn	Asn
				405					410					415	
gtt	agc	ggc	tgg	caa	aac	act	gcg	ttt	cag	cat	cat	cag	gga	atg	gat
Val	Ser	Gly	Trp	Gln	Asn	Thr	Ala	Phe	Gln	His	His	Gln	Gly	Met	Asp
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Sequence Listing from Patent scope

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gga gga aac ttg tct acc gag agt act agg gtt tgt ttc aaa caa gag	1392
G y G y Asn Leu Ser Thr G u Ser Thr Arg Val Cys Phe Lys G n G u	
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gag gaa caa caa cac ttc ttg aga aac tcg ccg agt cac atg act aat	1440
G u G u G n G n H s Phe Leu Arg Asn Ser Pro Ser H s Met Thr Asn	
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ggt gat cat cat agc tcg acc tct gat gat tct gtt acc gtt tgt gga	1488
Val Asp H s H s Ser Ser Thr Ser Asp Asp Ser Val Thr Val Cys G y	
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	490
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aat gtt gtt agt tat ggt ggt tat caa gga ttc gca atc cct gtt gga	1536
Asn Val Val Ser Tyr G y G y Tyr G n G y Phe Ala Ile Pro Val G y	
	500
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aca tcg gtt aat tac gat ccc ttt act gct gct gag att gct tac aac	1584
Thr Ser Val Asn Tyr Asp Pro Phe Thr Ala Ala G u Ile Ala Tyr Asn	
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gca aga aat cat tat tac tat gct cag cat cag caa caa cag cag att	1632
Ala Arg Asn H s Tyr Tyr Tyr Ala G n H s G n G n G n G n Ile	
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agc tct aac atg tac ttt cac ggg gaa ggt ggt gga gaa ggg gct cca	1728
Ser Ser Asn Met Tyr Phe H s G y G u G y G y G y G u G y Ala Pro	
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<400> 22

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G u Ser Ser Ala Val G n Thr Ser Phe Leu Ser Pro Phe G y Val Thr	
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Leu G u Ala Phe Thr Arg Asp Asn Asn Ser H s Ser Arg Asp Trp Asp	
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Ile Asn G y G y Ala Cys Asn Thr Leu Thr Asn Asn G u G n Asn G y	
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Pro Lys Leu G u Asn Phe Leu G y Arg Thr Thr Thr Ile Tyr Asn Thr	
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Asn G u Thr Val Val Asp G y Asn G y Asp Cys G y G y Asp G y	
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Sequence Listing from Patent scope

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Arg	Gly	Leu	Ser	Leu	Ser	Met	Asn	Ser	Ser	Thr	Ser	Asp	Ser	Asn	Asn
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Tyr	Asn	Asn	Asn	Asp	Asp	Val	Val	Gln	Glu	Lys	Thr	Ile	Val	Asp	Val
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Val	Glu	Thr	Thr	Pro	Lys	Lys	Thr	Ile	Glu	Ser	Phe	Gly	Gln	Arg	Thr
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Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu
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Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Lys	Arg	Glu	Gly	Gln	Thr	Arg	Lys
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Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala
				245					250					255	
Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Thr	Thr
			260					265					270		
Thr	Asn	Phe	Pro	Leu	Ser	Glu	Tyr	Glu	Lys	Glu	Val	Glu	Glu	Met	Lys
		275					280					285			
His	Met	Thr	Arg	Gln	Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser
	290					295					300				
Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His
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Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys
				325					330					335	
Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Gly	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala
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Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Ser	Ala	Val	Thr	Asn
		355					360					365			
Phe	Asp	Met	Asn	Arg	Tyr	Asn	Val	Lys	Ala	Ile	Leu	Glu	Ser	Pro	Ser
	370					375					380				
Leu	Pro	Ile	Gly	Ser	Ser	Ala	Lys	Arg	Leu	Lys	Asp	Val	Asn	Asn	Pro
385					390					395					400
Val	Pro	Ala	Met	Met	Ile	Ser	Asn	Asn	Val	Ser	Glu	Ser	Ala	Asn	Asn
				405					410					415	
Val	Ser	Gly	Trp	Gln	Asn	Thr	Ala	Phe	Gln	His	His	Gln	Gly	Met	Asp
			420					425					430		
Leu	Ser	Leu	Leu	Gln	Gln	Gln	Gln	Glu	Arg	Tyr	Val	Gly	Tyr	Tyr	Asn
		435					440					445			
Gly	Gly	Asn	Leu	Ser	Thr	Glu	Ser	Thr	Arg	Val	Cys	Phe	Lys	Gln	Glu
	450					455					460				
Glu	Glu	Gln	Gln	His	Phe	Leu	Arg	Asn	Ser	Pro	Ser	His	Met	Thr	Asn
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Val	Asp	His	His	Ser	Ser	Thr	Ser	Asp	Asp	Ser	Val	Thr	Val	Cys	Gly
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Asn	Val	Val	Ser	Tyr	Gly	Gly	Tyr	Gln	Gly	Phe	Ala	Ile	Pro	Val	Gly
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Thr	Ser	Val	Asn	Tyr	Asp	Pro	Phe	Thr	Ala	Ala	Glu	Ile	Ala	Tyr	Asn
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Ala	Arg	Asn	His	Tyr	Tyr	Tyr	Ala	Gln	His	Gln	Gln	Gln	Gln	Gln	Ile
	530					535						540			
Gln	Gln	Ser	Pro	Gly	Gly	Asp	Phe	Pro	Val	Ala	Ile	Ser	Asn	Asn	His
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Ser	Ser	Asn	Met	Tyr	Phe	His	Gly	Glu	Gly	Gly	Gly	Glu	Gly	Ala	Pro
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Sequence Listing from Patent scope

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gtc gcc gga gag tac tgt tac gat ccg acc gct gcc tcc gat gag tct	144
Val Ala Gly Gu Tyr Oys Tyr Asp Pro Thr Ala Ala Ser Asp Gu Ser	
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tca gcc atc caa aca tcg ttt cct tct ccc ttt ggt gtc gtc gtc gat	192
Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Val Asp	
50 55 60	
gct ttc acc aga gac aac aat agt cac tcc cga gat tgg gac atc aat	240
Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn	
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ggt tgt gca tgc aat aac atc cac aac gat gag caa gat gga cca aag	288
Gly Oys Ala Oys Asn Asn Ile His Asn Asp Gu Gln Asp Gly Pro Lys	
85 90 95	
ctt gag aat ttc ctt ggc cgc acc acc acg att tac aac acc aac gaa	336
Leu Gu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Gu	
100 105 110	
aac gtt gga gat gga agt gga agt ggc tgt tat gga gga gga gac ggt	384
Asn Val Gly Asp Gly Ser Gly Ser Gly Cys Tyr Gly Gly Gly Asp Gly	
115 120 125	
ggt ggt ggc tca cta gga ctt tcg atg ata aag aca tgg ctg aga aat	432
Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn	
130 135 140	
caa ccc gtg gat aat gtt gat aat caa gaa aat ggc aat gct gca aaa	480
Gln Pro Val Asp Asn Val Asp Asn Gln Gu Asn Gly Asn Ala Ala Lys	
145 150 155 160	
ggc ctg tcc ctg tca atg aac tca tct act tct tgt gat aac aac aac	528
Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Oys Asp Asn Asn Asn	
165 170 175	
gac agc aat aac aac gtt gtt gcc caa ggg aag act att gat gat agc	576
Asp Ser Asn Asn Asn Val Val Ala Gln Gly Lys Thr Ile Asp Asp Ser	
180 185 190	
gtt gaa gct aca ccg aag aaa act att gag agt ttt gga cag agg acg	624
Val Gu Ala Thr Pro Lys Lys Thr Ile Gu Ser Phe Gly Gln Arg Thr	
195 200 205	
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Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Gu	
210 215 220	

Sequence Listing from Patent scope																
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gga Gly	aga Arg	caa Gln	gtt Val	tat Tyr 245	tig Leu	gga Gly	ggt Gly	tat Tyr	gac Asp 250	aaa Lys	gaa Glu	gaa Glu	aaa Lys	gca Ala 255	gct Ala	768
agg Arg	gct Ala	tat Tyr	gat Asp 260	tta Leu	gcc Ala	gca Ala	ctc Leu	aag Lys 265	tat Tyr	tgg Trp	gga Gly	acc Thr	acc Thr 270	act Thr	act Thr	816
act Thr	aac Asn	ttc Phe 275	ccc Pro	atg Met	agc Ser	gaa Glu	tat Tyr 280	gaa Glu	aaa Lys	gag Glu	gta Val	gaa Glu 285	gag Glu	atg Met	aag Lys	864
cac His 290	atg Met	aca Thr	agg Arg	caa Gln	gag Glu	tat Tyr 295	gtt Val	gcc Ala	tca Ser	ctg Leu	cgc Arg 300	agg Arg	aaa Lys	agt Ser	agt Ser	912
ggt Gly 305	ttc Phe	tct Ser	cgt Arg	ggt Gly	gca Ala 310	tct Ser	att Ile	tat Tyr	cgt Arg	gga Gly 315	gta Val	aca Thr	aga Arg	cat His	cac His 320	960
caa Gln	cat His	gga Gly	aga Arg	tgg Trp 325	caa Gln	gct Ala	agg Arg	ata Ile	gga Gly 330	aga Arg	gtc Val	gcc Ala	ggt Gly 335	aac Asn 335	aaa Lys	1008
gac Asp	ctc Leu	tac Tyr	tig Leu 340	gga Gly	act Thr	ttt Phe	ggc Gly	aca Thr 345	caa Gln	gaa Glu	gaa Glu	gct Ala	gca Ala 350	gag Glu	gca Ala	1056
tac Tyr	gac Asp	att Ile 355	gcg Ala	gcc Ala	atc Ile	aaa Lys	ttc Phe 360	aga Arg	gga Gly	tta Leu	acc Thr	gca Ala 365	gtg Val	act Thr	aac Asn	1104
ttc Phe 370	gac Asp	atg Met	aac Asn	aga Arg	tac Tyr	aac Asn 375	gtt Val	aaa Lys	gca Ala	atc Ile	ctc Leu 380	gaa Glu	agc Ser	cct Pro	agt Ser	1152
ctt Leu 385	cct Pro	att Ile	ggt Gly	agc Ser	gcc Ala 390	gca Ala	aaa Lys	cgt Arg	ctc Leu	aag Lys 395	gag Glu	gct Ala	aac Asn	cgt Arg	ccg Pro 400	1200
gtt Val	cca Pro	agt Ser	atg Met	atg Met 405	atg Met	atc Ile	agt Ser	aat Asn	aac Asn 410	gtt Val	tca Ser	gag Glu	agt Ser	gag Glu 415	aat Asn	1248
agt Ser	gct Ala	agc Ser	ggt Gly 420	tgg Trp	caa Gln	aac Asn	gct Ala	gcg Ala 425	gtt Val	cag Gln	cat His	cat His	cag Gln 430	gga Gly	gta Val	1296
gat Asp	tig Leu	agc Ser 435	tta Leu	tig Leu	cac His	caa Gln	cat His 440	caa Gln	gag Glu	agg Arg	tac Tyr	aat Asn 445	ggt Gly	tat Tyr	tat Tyr	1344
tac Tyr 450	aat Asn	gga Gly	gga Gly	aac Asn	tig Leu	tct Ser 455	tct Ser	gag Glu	agt Ser	gct Ala	agg Arg 460	gct Ala	tgt Cys	ttc Phe	aaa Lys	1392
caa Gln 465	gag Glu	gat Asp	gat Asp	caa Gln	cac His 470	cat His	ttc Phe	tig Leu	agc Ser	aac Asn 475	acg Thr	cag Gln	agc Ser	ctc Leu	atg Met 480	1440

Sequence Listing from Patent scope

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tgt Cys	gga Gly	aat Asn	gtt Val 500	gtt Val	ggg Gly	tat Tyr	ggg Gly	ggg Gly 505	tat Tyr	caa Gln	gga Gly	ttt Phe	gca Ala 510	gcc Ala	ccg Pro	1536
gtt Val	aac Asn	tgc Cys 515	gat Asp	gcc Ala	tac Tyr	gct Ala	gct Ala 520	agt Ser	gag Glu	ttt Phe	gat Asp	tat Tyr 525	aac Asn	gca Ala	aga Arg	1584
aac Asn	cat His 530	tat Tyr	tac Tyr	ttt Phe	gct Ala	cag Gln 535	cag Gln	cag Gln	cag Gln	acc Thr	cag Gln 540	cag Gln	tcg Ser	cca Pro	ggg Gly	1632
gga Gly 545	gat Asp	ttt Phe	ccc Pro	gcg Ala	gca Ala 550	atg Met	acg Thr	aat Asn	aat Asn	gtt Val 555	ggc Gly	tct Ser	aat Asn	atg Met	tat Tyr 560	1680
tac Tyr	cat His	ggg Gly	gaa Glu	ggg Gly 565	ggg Gly	gga Gly	gaa Glu	gtt Val	gct Ala 570	cca Pro	aca Thr	ttt Phe	aca Thr	gtt Val 575	tgg Trp	1728
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 35 40
 Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Val Asp
 50 55 60
 Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
 65 70 75 80
 Gly Oys Ala Oys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
 85 90 95
 Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Glu
 100 105 110
 Asn Val Gly Asp Gly Ser Gly Ser Gly Cys Tyr Gly Gly Asp Gly
 115 120 125
 Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
 130 135 140
 Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Ala Ala Lys
 145 150 155 160
 Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Oys Asp Asn Asn Asn
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 Asp Ser Asn Asn Asn Val Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
 180 185 190
 Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
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 Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu

Sequence Listing from Patent scope

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Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala
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Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Thr	Thr	Thr	Thr
			260					265					270		
Thr	Asn	Phe	Pro	Met	Ser	Glu	Tyr	Glu	Lys	Glu	Val	Glu	Glu	Met	Lys
		275					280					285			
His	Met	Thr	Arg	Gln	Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser
	290					295					300				
Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His
305					310					315					320
Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys
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Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Gly	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala
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Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Thr	Ala	Val	Thr	Asn
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Phe	Asp	Met	Asn	Arg	Tyr	Asn	Val	Lys	Ala	Ile	Leu	Glu	Ser	Pro	Ser
	370					375					380				
Leu	Pro	Ile	Gly	Ser	Ala	Ala	Lys	Arg	Leu	Lys	Glu	Ala	Asn	Arg	Pro
385					390					395					400
Val	Pro	Ser	Met	Met	Met	Ile	Ser	Asn	Asn	Val	Ser	Glu	Ser	Glu	Asn
				405					410					415	
Ser	Ala	Ser	Gly	Trp	Gln	Asn	Ala	Ala	Val	Gln	His	His	Gln	Gly	Val
			420				425						430		
Asp	Leu	Ser	Leu	Leu	His	Gln	His	Gln	Glu	Arg	Tyr	Asn	Gly	Tyr	Tyr
		435				440						445			
Tyr	Asn	Gly	Gly	Asn	Leu	Ser	Ser	Glu	Ser	Ala	Arg	Ala	Cys	Phe	Lys
	450					455					460				
Gln	Glu	Asp	Asp	Gln	His	His	Phe	Leu	Ser	Asn	Thr	Gln	Ser	Leu	Met
465					470					475					480
Thr	Asn	Ile	Asp	His	Gln	Ser	Ser	Val	Ser	Asp	Asp	Ser	Val	Thr	Val
			485						490					495	
Oys	Gly	Asn	Val	Val	Gly	Tyr	Gly	Gly	Tyr	Gln	Gly	Phe	Ala	Ala	Pro
			500					505					510		
Val	Asn	Cys	Asp	Ala	Tyr	Ala	Ala	Ser	Glu	Phe	Asp	Tyr	Asn	Ala	Arg
		515					520					525			
Asn	His	Tyr	Tyr	Phe	Ala	Gln	Gln	Gln	Gln	Thr	Gln	Gln	Ser	Pro	Gly
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Gly	Asp	Phe	Pro	Ala	Ala	Met	Thr	Asn	Asn	Val	Gly	Ser	Asn	Met	Tyr
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Tyr	His	Gly	Glu	Gly	Gly	Gly	Glu	Val	Ala	Pro	Thr	Phe	Thr	Val	Trp
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Sequence Listing from Patent scope																
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gtc	gcc	gga	gag	tac	tgt	tac	gat	ccg	acc	gct	gcc	tcc	gat	gag	tct	144
Val	Ala	Gly 35	Glu	Tyr	Cys	Tyr	Asp 40	Pro	Thr	Ala	Ala	Ser 45	Asp	Glu	Ser	
tca	gcc	atc	caa	aca	tgc	ttt	cct	tct	ccc	ttt	ggt	gtc	gtc	ctc	gat	192
Ser	Ala 50	Ile	Gln	Thr	Ser	Phe 55	Pro	Ser	Pro	Phe	Gly 60	Val	Val	Leu	Asp	
gct	ttc	acc	aga	gac	aac	aat	agt	cac	tcc	cga	gat	tgg	gac	atc	aat	240
Ala 65	Phe	Thr	Arg	Asp	Asn 70	Asn	Ser	His	Ser	Arg 75	Asp	Trp	Asp	Ile	Asn 80	
ggt	agt	gca	tgt	aat	aac	atc	cac	aat	gat	gag	caa	gat	gga	cca	aaa	288
Gly	Ser	Ala	Cys	Asn 85	Asn	Ile	His	Asn	Asp 90	Glu	Gln	Asp	Gly	Pro 95	Lys	
ctt	gag	aat	ttc	ctt	ggc	cgc	acc	acc	acg	att	tac	aac	acc	aac	gaa	336
Leu	Glu	Asn	Phe 100	Leu	Gly	Arg	Thr	Thr 105	Thr	Ile	Tyr	Asn	Thr 110	Asn	Glu	
aac	gtt	gga	gat	atc	gat	gga	agt	ggg	tgt	tat	gga	gga	gga	gac	ggt	384
Asn	Val	Gly 115	Asp	Ile	Asp	Gly	Ser 120	Gly	Cys	Tyr	Gly	Gly 125	Gly	Asp	Gly	
ggt	ggt	ggc	tca	cta	gga	ctt	tgc	atg	ata	aag	aca	tgg	ctg	aga	aat	432
Gly	Gly 130	Gly	Ser	Leu	Gly	Leu 135	Ser	Met	Ile	Lys	Thr 140	Trp	Leu	Arg	Asn	
caa	ccc	gtg	gat	aat	gtt	gat	aat	caa	gaa	aat	ggc	aat	ggt	gca	aaa	480
Gln 145	Pro	Val	Asp	Asn	Val 150	Asp	Asn	Gln	Glu	Asn 155	Gly	Asn	Gly	Ala 160	Lys	
ggc	ctg	tcc	ctc	tca	atg	aac	tca	tct	act	tct	tgt	gat	aac	aac	aac	528
Gly	Leu	Ser	Leu	Ser 165	Met	Asn	Ser	Ser	Thr 170	Ser	Cys	Asp	Asn	Asn 175	Asn	
tac	agc	agt	aac	aac	ctt	gtt	gcc	caa	ggg	aag	act	att	gat	gat	agc	576
Tyr	Ser	Ser	Asn 180	Asn	Leu	Val	Ala 185	Gln 185	Gly	Lys	Thr	Ile	Asp 190	Asp	Ser	
gtt	gaa	gct	aca	ccg	aag	aaa	act	att	gag	agt	ttt	gga	cag	agg	acg	624
Val	Glu 195	Ala	Thr	Pro	Lys	Lys	Thr 200	Ile	Glu	Ser	Phe	Gly 205	Gln	Arg	Thr	
tct	ata	tac	cgc	ggt	gtt	aca	agg	cat	cgg	tgg	aca	gga	aga	tat	gag	672
Ser	Ile 210	Tyr	Arg	Gly	Val	Thr 215	Arg	His	Arg	Trp	Thr 220	Gly	Arg	Tyr	Glu	
gca	cat	tta	tgg	gat	aat	agt	tgt	aaa	cga	gaa	ggc	caa	acg	cgc	aaa	720
Ala 225	His	Leu	Trp	Asp	Asn 230	Ser	Cys	Lys	Arg	Glu 235	Gly	Gln	Thr	Arg	Lys 240	
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Gly	Arg	Gln	Val	Tyr 245	Leu	Gly	Gly	Tyr	Asp 250	Lys	Glu	Glu	Lys	Ala 255	Ala	
agg	gct	tat	gat	tta	gcc	gca	ctc	aag	tat	tgg	gga	acc	acc	act	act	816
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Sequence Listing from Patent scope

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cac H i s	at g Met 290	aca Thr	agg Arg	caa G n	gag G u	t at Tyr 295	gt t Val	gcc Al a	t ca Ser	ct t Leu	cgc Arg 300	agg Arg	aaa Lys	agt Ser	agt Ser	912
gg t G y 305	t t c Phe	t ct Ser	cgt Arg	gg t G y	gca Al a 310	t cg Ser	att I l e	t at Tyr	cgt Arg	gga G y 315	gt a Val	aca Thr	aga Arg	cat H i s	cac H i s 320	960
caa G n	cat H i s	gga G y	aga Arg	t gg Tr p 325	caa G n	gct Al a	agg Arg	at a I l e	gga G y 330	aga Arg	gt c Val	gcc Al a	gg t G y	aac Asn 335	aaa Lys	1008
gac Asp	ct c Leu	t ac Tyr	t t g Leu 340	gga G y	act Thr	t t t Phe	ggc G y	aca Thr 345	caa G n	gaa G u	gaa G u	gct Al a	gca Al a 350	gag G u	gca Al a	1056
t ac Tyr	gac Asp	att I l e 355	gcg Al a	gcc Al a	at c I l e	aaa Lys	t t c Phe 360	aga Arg	gga G y	t t a Leu	acc Thr	gca Al a 365	gt g Val	act Thr	aac Asn	1104
t t c Phe 370	gac Asp	at g Met	aac Asn	aga Arg	t ac Tyr	aac Asn 375	gt t Val	aaa Lys	gca Al a	at c I l e	ct c Leu 380	gaa G u	agc Ser	cct Pro	agt Ser	1152
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gt t Val	cca Pro	agt Ser	at g Met	at g Met 405	at g Met	at c I l e	agt Ser	aat Asn	aac Asn 410	gt t Val	t ca Ser	gag G u	agt Ser	gag G u 415	aat Asn	1248
aat Asn	gct Al a	agc Ser	gg t G y 420	t gg Tr p	caa G n	aac Asn	gct Al a	gcg Al a 425	gt t Val	cag G n	cat H i s	cat H i s	cag G n 430	gga G y	gt a Val	1296
gat Asp	t t g Leu	agc Ser	t t a Leu	t t g Leu	cag G n	caa G n	cat H i s 440	caa G n	gag G u	agg Arg	t ac Tyr	aat Asn 445	gg t G y	t at Tyr	t at Tyr	1344
t ac Tyr 450	aat Asn	gga G y	gga G y	aac Asn	t t g Leu	t ct Ser 455	t cg Ser	gag G u	agt Ser	gct Al a	agg Arg 460	gct Al a	t gt Cys	t t c Phe	aaa Lys	1392
caa G n 465	gag G u	gat Asp	gat Asp	caa G n	cac H i s 470	cat H i s	t t c Phe	t t g Leu	agc Ser	aac Asn 475	acg Thr	cag G n	agc Ser	ct c Leu	at g Met 480	1440
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t gt Cys	gga G y	aat Asn	gt t Val 500	gt t Val	gg t G y	t at Tyr	gg t G y	gg t G y 505	t at Tyr	caa G n	gga G y	t t t Phe	gca Al a 510	gcc Al a	ccg Pro	1536
gt t Val	aac Asn	t gc Cys	gat Asp	gcc Al a	t ac Tyr	gct Al a	gct Al a	agt Ser	gag G u	t t t Phe	gac Asp	t at Tyr	aac Asn	gca Al a	aga Arg	1584

Sequence Listing from Patent scope

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Ser	Ala	Ile	Gln	Thr	Ser	Phe	Pro	Ser	Pro	Phe	Gly	Val	Val	Leu	Asp
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Ala	Phe	Thr	Arg	Asp	Asn	Asn	Ser	His	Ser	Arg	Asp	Trp	Asp	Ile	Asn
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Gly	Ser	Ala	Cys	Asn	Asn	Ile	His	Asn	Asp	Glu	Gln	Asp	Gly	Pro	Lys
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Leu	Glu	Asn	Phe	Leu	Gly	Arg	Thr	Thr	Thr	Ile	Tyr	Asn	Thr	Asn	Glu
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Gly	Gly	Gly	Ser	Leu	Gly	Leu	Ser	Met	Ile	Lys	Thr	Trp	Leu	Arg	Asn
		130				135						140			
Gln	Pro	Val	Asp	Asn	Val	Asp	Asn	Gln	Glu	Asn	Gly	Asn	Gly	Ala	Lys
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Gly	Leu	Ser	Leu	Ser	Met	Asn	Ser	Ser	Thr	Ser	Cys	Asp	Asn	Asn	Asn
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Tyr	Ser	Ser	Asn	Asn	Leu	Val	Ala	Gln	Gly	Lys	Thr	Ile	Asp	Asp	Ser
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Val	Glu	Ala	Thr	Pro	Lys	Lys	Thr	Ile	Glu	Ser	Phe	Gly	Gln	Arg	Thr
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Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu
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Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Lys	Arg	Glu	Gly	Gln	Thr	Arg	Lys
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Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala
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Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Thr	Thr	Thr	Thr
			260					265					270		
Thr	Asn	Phe	Pro	Met	Ser	Glu	Tyr	Glu	Lys	Glu	Ile	Glu	Glu	Met	Lys
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His	Met	Thr	Arg	Gln	Glu	Tyr	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser
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Sequence Listing from Patent scope

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gat Asp	tgg Trp	aac Asn	atg Met	agg Arg 85	gga Gly	ttg Leu	gac Asp	tac Tyr	aac Asn 90	ggc Gly	ggt Gly	ggc Gly	tcg Ser	gaa Glu 95	ctc Leu	288
tcg Ser	atg Met	ctt Leu	gtg Val 100	ggg Gly	tcc Ser	agc Ser	ggc Gly 105	ggc Gly 105	ggc Gly	ggg Gly	ggc Gly	ggc Gly 110	ggc Gly 110	aag Lys	agg Arg	336
gcc Ala	gtg Val	gaa Glu 115	gac Asp	agc Ser	gag Glu	ccc Pro	aag Lys 120	ctc Leu	gaa Glu	gat Asp	ttc Phe	ctc Leu 125	ggc Gly	ggc Gly	aac Asn	384
tcg Ser 130	ttc Phe	gtc Val	tcc Ser	gag Glu	cat His	gat Asp 135	cag Gln	tcc Ser	ggc Gly	ggt Gly	tac Tyr 140	ctg Leu	ttc Phe	tct Ser	gga Gly	432
gtc Val 145	ccg Pro	atg Met	gcc Ala	agc Ser	agc Ser 150	acc Thr	aac Asn	agc Ser	aac Asn	agc Ser 155	ggg Gly	agc Ser	aac Asn	acc Thr	atg Met 160	480
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agc Ser	acc Thr	gac Asp 195	gcc Ala	aac Asn	gcc Ala	agc Ser	gcc Ala 200	agc Ser	agc Ser	ttt Phe	ggc Gly	tgc Cys 205	tcg Ser	gat Asp	tcg Ser	624
atg Met 210	ggg Gly	agg Arg	aac Asn	ggc Gly	acg Thr	gtg Val 215	gcg Ala	gct Ala	gct Ala	ggg Gly	agc Ser 220	tcc Ser	cag Gln	agc Ser	ctg Leu	672
gcg Ala 225	ctc Leu	tcg Ser	atg Met	agc Ser	acg Thr 230	ggc Gly	tcg Ser	cac His	ctg Leu	ccg Pro 235	atg Met	gtt Val	gtg Val	gcc Ala	ggc Gly 240	720
ggc Gly	ggc Gly	gcc Ala	agc Ser	gga Gly 245	gcg Ala	gcc Ala	tcg Ser	gag Glu	agc Ser 250	acg Thr	tca Ser	tcg Ser	gag Glu 255	aac Asn 255	aag Lys	768
cga Arg	gcg Ala	agc Ser	ggc Gly 260	gcc Ala	atg Met	gat Asp	tcg Ser	ccc Pro 265	ggc Gly	agc Ser	gcg Ala	gta Val	gaa Glu 270	gcc Ala	gtc Val	816
ccg Pro	agg Arg	aag Lys 275	tcc Ser	atc Ile	gac Asp	acg Thr	ttc Phe 280	ggg Gly	caa Gln	agg Arg	acc Thr	tct Ser 285	ata Ile	tat Tyr	cga Arg	864
ggt Gly 290	gta Val	aca Thr	aga Arg	cat His	aga Arg	tgg Trp 295	aca Thr	ggg Gly	cga Arg	tat Tyr	gag Glu 300	gct Ala	cat His	cta Leu	tgg Trp	912
gat Asp	aat Asn	agt Ser	tgt Cys	aga Arg	aga Arg	gaa Glu	ggg Gly	cag Gln	agt Ser	cgc Arg	aag Lys	ggt Gly	agg Arg	caa Gln	gtt Val	960

Sequence Listing from Patent scope

305	310															315															320															
tac Tyr	ctt Leu	ggt Gly	ggc Gly	tat Tyr 325	gac Asp	aag Lys	gaa Glu	gac Asp	aag Lys 330	gca Ala	gca Ala	agg Arg	gct Ala	tat Tyr 335	gat Asp	1008																														
ttg Leu	gca Ala	gct Ala	ctc Leu 340	aag Lys	tat Tyr	tgg Trp	ggc Gly	act Thr 345	act Thr	aca Thr	aca Thr	aca Thr	aat Asn 350	ttc Phe	cct Pro	1056																														
ata Ile	agc Ser	aac Asn 355	tat Tyr	gaa Glu	aag Lys	gag Glu	cta Leu 360	gag Glu	gaa Glu	atg Met	aaa Lys	cat His 365	atg Met	act Thr	agg Arg	1104																														
cag Gln	gag Glu 370	tat Tyr	att Ile	gca Ala	tac Tyr	cta Leu 375	aga Arg	aga Arg	aat Asn	agc Ser	agt Ser 380	gga Gly	ttt Phe	tct Ser	cgt Arg	1152																														
ggc Gly 385	gca Ala	tca Ser	aaa Lys	tat Tyr	cgt Arg 390	gga Gly	gta Val	act Thr	aga Arg	cat His 395	cat His	cag Gln	cat His	ggg Gly	aga Arg 400	1200																														
tgg Trp	caa Gln	gca Ala	agg Arg	ata Ile 405	ggg Gly	aga Arg	gtt Val	gca Ala	gga Gly 410	aac Asn	aag Lys	gat Asp	ctc Leu	tac Tyr 415	ttg Leu	1248																														
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gcg Ala	atc Ile	aag Lys 435	ttc Phe	cgc Arg	ggt Gly	ctg Leu	aac Asn 440	gcc Ala	gtc Val	acc Thr	aac Asn	ttc Phe 445	gac Asp	atg Met	agc Ser	1344																														
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ggc Gly 465	gcg Ala	gcc Ala	agg Arg	cgc Arg	ctc Leu 470	aag Lys	gat Asp	gcc Ala	gtg Val	gac Asp 475	cac His	gtg Val	gag Glu	gcc Ala	ggc Gly 480	1440																														
gcc Ala	acc Thr	atc Ile	tgg Trp	cgc Arg 485	gcc Ala	gac Asp	atg Met	gac Asp	ggc Gly 490	ggc Gly	gtg Val	atc Ile	tcc Ser	cag Gln 495	ctc Leu	1488																														
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ccg Pro	acc Thr	atc Ile 515	gcg Ala	ttc Phe	cag Gln	cag Gln	ccg Pro 520	tcg Ser	ccg Pro	ctc Leu	tcc Ser	gtc Val 525	cac His	tac Tyr	ccg Pro	1584																														
tac Tyr	ggg Gly 530	cag Gln	ccg Pro	ccg Pro	tcc Ser	cgc Arg 535	ggg Gly	tgg Trp	tgc Cys	aag Lys	ccc Pro 540	gag Glu	cag Gln	gac Asp	gcg Ala	1632																														
gcc Ala 545	gtc Val	gcc Ala	gcc Ala	gcc Ala	gcg Ala 550	cac His	agc Ser	ctg Leu	cag Gln	gac Asp 555	ctc Leu	cag Gln	cag Gln	ctg Leu	cac His 560	1680																														
ctc	ggc	agc	gcg	gca	cac	aac	ttc	ttc	cag	gcg	tcg	tcg	agc	tcg	gca	1728																														

Sequence Listing from Patent scope

Leu	Gly	Ser	Ala	Ala	His	Asn	Phe	Phe	Gln	Ala	Ser	Ser	Ser	Ala			
				565					570					575			
gtc	tac	aac	agc	ggc	ggc	ggc	ggc	gct	agc	ggc	ggg	tac	cac	cag	ggc	1776	
Val	Tyr	Asn	Ser	Gly	Gly	Gly	Gly	Ala	Ser	Gly	Gly	Tyr	His	Gln	Gly		
			580					585					590				
ctc	ggt	ggc	ggc	agc	agc	tcc	ttc	ctc	atg	ccg	tcg	agc	act	gtc	gtg	1824	
Leu	Gly	Gly	Gly	Ser	Ser	Ser	Phe	Leu	Met	Pro	Ser	Ser	Thr	Val	Val		
			595				600					605					
gcg	ggg	gcc	gac	cag	ggg	cac	agc	agc	agc	acg	gcc	aac	cag	ggg	agc	1872	
Ala	Gly	Ala	Asp	Gln	Gly	His	Ser	Ser	Ser	Thr	Ala	Asn	Gln	Gly	Ser		
	610					615					620						
acg	tgc	agc	tac	ggg	gac	gat	cac	cag	gaa	ggg	aag	ctc	atc	ggg	tac	1920	
Thr	Cys	Ser	Tyr	Gly	Asp	Asp	His	Gln	Glu	Gly	Lys	Leu	Ile	Gly	Tyr		
	625				630					635					640		
gac	gcc	atg	gtg	gcg	gcg	acc	gca	gcc	ggc	ggg	gac	ccg	tac	gcc	gcg	1968	
Asp	Ala	Met	Val	Ala	Ala	Thr	Ala	Ala	Gly	Gly	Asp	Pro	Tyr	Ala	Ala		
				645					650					655			
gcg	agg	agc	ggg	tac	cag	ttc	tgc	tgc	cag	ggc	tgc	gga	tcc	acg	gtg	2016	
Ala	Arg	Ser	Gly	Tyr	Gln	Phe	Ser	Ser	Gln	Gly	Ser	Gly	Ser	Thr	Val		
			660				665						670				
agc	atc	gcg	agg	gcg	aac	ggg	tac	tct	aac	aac	tgg	agc	tct	cct	ttc	2064	
Ser	Ile	Ala	Arg	Ala	Asn	Gly	Tyr	Ser	Asn	Asn	Trp	Ser	Ser	Pro	Phe		
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aac	ggc	ggc	atg	ggg	tga											2082	
Asn	Gly	Gly	Met	Gly													
	690																

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 <211> 693
 <212> PRT
 <213> Sorghum bicolor

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

Sequence Listing from Patent scope

Pro	Gln	Pro	Pro	165 Ala	Ala	Pro	His	Gln	170 Ala	Pro	Gln	Thr	Glu	175 Glu	Met
Ser	Thr	Asp	180 Ala	Asn	Ala	Ser	Ala	185 Ser	Ser	Phe	Gly	Cys	190 Ser	Asp	Ser
Met	Gly	195 Arg	Asn	Gly	Thr	Val	200 Ala	Ala	Ala	Gly	Ser	205 Ser	Gln	Ser	Leu
Ala	Leu	Ser	Met	Ser	Thr	Gly	215 Ser	His	Leu	Pro	Met	Val	Val	Ala	Gly
225 Gly	Gly	Ala	Ser	Gly	230 Ala	Ala	Ser	Glu	Ser	235 Thr	Ser	Ser	Glu	Asn	Lys
Arg	Ala	Ser	Gly	245 Ala	Met	Asp	Ser	Pro	250 Gly	Ser	Ala	Val	Glu	255 Ala	Val
Pro	Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg
Gly	Val	275 Thr	Arg	His	Arg	Trp	280 Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp
Asp	Asn	Ser	Cys	Arg	Arg	Glu	Gly	Gln	Ser	Arg	Lys	Gly	Arg	Gln	Val
305 Tyr	Leu	Gly	Gly	Tyr	310 Asp	Lys	Glu	Asp	Lys	Ala	Ala	Arg	Ala	Tyr	Asp
Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Thr	Thr	Thr	Thr	Asn	335 Phe	Pro	
Ile	Ser	Asn	Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg
Gln	Glu	Tyr	Ile	Ala	Tyr	Leu	Arg	Arg	Asn	Ser	Ser	Gly	Phe	Ser	Arg
Gly	Ala	Ser	Lys	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg
385 Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu
Gly	Thr	Phe	Ser	Thr	Glu	Glu	Glu	Ala	410 Ala	Glu	Ala	Tyr	Asp	Ile	Ala
Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	425 Val	Thr	Asn	Phe	Asp	Met	Ser
Arg	Tyr	435 Asp	Val	Lys	Ser	Ile	Leu	Glu	Ser	Ser	Thr	Leu	Pro	Val	Gly
Gly	Ala	Ala	Arg	Arg	Leu	Lys	Asp	Ala	Val	Asp	His	Val	Glu	Ala	Gly
465 Ala	Thr	Ile	Trp	Arg	Ala	Asp	Met	Asp	Gly	Gly	Val	Ile	Ser	Gln	Leu
Ala	Glu	Ala	Gly	Met	Gly	Gly	Tyr	Ala	Ser	Tyr	Gly	His	His	Ala	Trp
Pro	Thr	Ile	Ala	Phe	Gln	Gln	Pro	Ser	Pro	Leu	Ser	Val	His	Tyr	Pro
Tyr	Gly	Gln	Pro	Pro	Ser	Arg	Gly	Trp	Cys	Lys	Pro	Glu	Gln	Asp	Ala
Ala	Val	Ala	Ala	Ala	Ala	His	Ser	Leu	Gln	Asp	Leu	Gln	Gln	Leu	His
545 Leu	Gly	Ser	Ala	Ala	His	Asn	Phe	Phe	Gln	Ala	Ser	Ser	Ser	Ser	Ala
Val	Tyr	Asn	Ser	Gly	Gly	Gly	Gly	Ala	Ser	Gly	Gly	Tyr	His	Gln	Gly
Leu	Gly	Gly	Gly	Ser	Ser	Ser	Phe	Leu	Met	Pro	Ser	Ser	Thr	Val	Val
Ala	Gly	Ala	Asp	Gln	Gly	His	Ser	Ser	Ser	Thr	Ala	Asn	Gln	Gly	Ser
Thr	Cys	Ser	Tyr	Gly	Asp	His	Gln	Glu	Gly	Lys	Leu	Ile	Gly	Tyr	
Asp	Ala	Met	Val	Ala	Ala	Thr	Ala	Ala	Gly	Gly	Asp	Pro	Tyr	Ala	Ala
Ala	Arg	Ser	Gly	Tyr	Gln	Phe	Ser	Ser	Gln	Gly	Ser	Gly	Ser	Thr	Val
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Sequence Listing from Patent scope

Ser Ile Ala Arg Ala Asn Gly Tyr Ser Asn Asn Trp Ser Ser Pro Phe
675 680 685

Asn Gly Gly Met Gly
690

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<211> 508
<212> DNA
<213> Zea mays

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tcttctttta ataatat tgaatttta tgtat taaatgttatgc agttcgctct 180
ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg 240
cctgcattga ataatggatg agcaccggt aaatccgcgt acccaacttt cgagaagaac 300
cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg 360
cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac 420
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taaatggcgg catcgaccgt cacctgct 508

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<211> 665
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter construct comprising Zea mays Rab17
promoter and attB1 site

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accctcctgt tttaaaatag ttggcattat cgaattatca ttttagtctt taaatgttttc 120
tcttctttta ataatat tgaatttta tgtat taaatgttatgc agttcgctct 180
ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg 240
cctgcattga ataatggatg agcaccggt aaatccgcgt acccaacttt cgagaagaac 300
cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg 360
cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac 420
accctgccg tggcgcgcc agatcctaat cctttcgccg ttctgcactt ctgctgccta 480
taaatggcgg catcgaccgt cacctgcttc accaccggcg agccacatcg agaacacgat 540
cgagcacaca agcacgaaga ctggttagg agaaaccaca aaccaccaag ccgtgcaagc 600
accaagcttg gt caccgggt ccgggcctag aaggccagct tcaagtttgt acaaaaaagc 660
aggct 665

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> attachment B1 site

<400> 31
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<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> attachment B2 site

Sequence Listing from Patent scope

<400> 32
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<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> attachment B3 site

<400> 33
acaactttgt ataataaagt tg 22

<210> 34
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> attachment B4 site

<400> 34
acaactttgt atagaaaagt tg 22

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<211> 95
<212> DNA
<213> Zea mays

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ggagaaacca caaaccacca agccgtgcaa gcacc 95

<210> 36
<211> 133
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid linker sequence

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agaaggccag ctt 133

<210> 37
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid linker sequence

<400> 37
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<210> 38
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<212> DNA

Sequence Listing from Patent scope

<213> Artificial Sequence

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<223> Pnll terminator

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tagttatctg aataaaagag aaagagatca tccatatttc ttatcctaaa tgaatgtcac 180
gtgtctttat aattctttga tgaaccagat gcatttcat t aaccaaattcc atat acat at 240
aaatattaat catat ataat taat at caat tgggttagca aaacaaatct agtct aggt g 300
tgttttgcga attgcggc 318
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<210> 39

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid linker sequence

<400> 39

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<210> 40

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid linker sequence

<400> 40

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<210> 41

<211> 1272

<212> DNA

<213> Artificial Sequence

<220>

<223> Maize optimized FLP coding sequence

<220>

<221> CDS

<222> (1)...(1272)

<400> 41

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1 5 10 15

agg cag ttc gtg gag agg ttc gag agg ccc tcc ggc gag aag atc gcc 96
Arg Gl n Phe Val Gl u Arg Phe Gl u Arg Pro Ser Gl y Gl u Lys lle Ala
20 25 30

ctc tgc gcc gcc gag ctc acc tac ctc tgc tgg atg atc acc cac aac 144
Leu Cys Ala Ala Gl u Leu Thr Tyr 40 Leu Cys Trp Met lle Thr His Asn
35 45

ggc acc gcc att aag agg gcc acc ttc atg tca tac aac acc atc atc 192
Gl y Thr Ala lle Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr lle lle
50 55 60
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Sequence Listing from Patent scope

tcc Ser 65	aac Asn	tcc Ser	ctc Leu	tcc Ser	ttc Phe 70	gac Asp	atc Ile	gtg Val	aac Asn	aag Lys 75	tcc Ser	ctc Leu	cag Gln	ttc Phe	aaa Lys 80	240
tac Tyr	aag Lys	acc Thr	cag Gln	aag Lys 85	gcc Ala	acc Thr	atc Ile	ctc Leu	gag Glu 90	gcc Ala	tcc Ser	ctc Leu	aag Lys	aag Lys 95	ctc Leu	288
atc Ile	ccc Pro	gcc Ala	tgg Trp 100	gag Glu	ttc Phe	acc Thr	atc Ile	atc Ile 105	ccc Pro	tac Tyr	tac Tyr	ggc Gly 110	cag Gln	aag Lys	cac His	336
cag Gln	tcc Ser	gac Asp 115	atc Ile	acc Thr	gac Asp	atc Ile	gtg Val 120	tca Ser	tcc Ser	ctc Leu	cag Gln	ctt Leu 125	cag Gln	ttc Phe	gag Glu	384
tcc Ser 130	tcc Ser	gag Glu	gag Glu	gct Ala	gac Asp	aag Lys 135	ggc Gly	aac Asn	tcc Ser	cac His	tcc Ser 140	aag Lys	aag Lys	atg Met	ctg Leu	432
aag Lys 145	gcc Ala	ctc Leu	ctc Leu	tcc Ser	gag Glu 150	ggc Gly	gag Glu	tcc Ser	atc Ile	tgg Trp 155	gag Glu	atc Ile	acc Thr	gag Glu	aag Lys 160	480
atc Ile	ctc Leu	aac Asn	tcc Ser	ttc Phe 165	gag Glu	tac Tyr	acc Thr	tcc Ser	agg Arg 170	ttc Phe	act Thr	aag Lys	acc Thr	aag Lys 175	acc Thr	528
ctc Leu	tac Tyr	cag Gln	ttc Phe 180	ctc Leu	ttc Phe	ctc Leu	gcc Ala	acc Thr 185	ttc Phe	atc Ile	aac Asn	tgc Cys	ggc Gly 190	agg Arg	ttc Phe	576
tca Ser	gac Asp	atc Ile 195	aag Lys	aac Asn	gtg Val	gac Asp	ccc Pro 200	aag Lys	tcc Ser	ttc Phe	aag Lys	ctc Leu 205	gtg Val	cag Gln	aac Asn	624
aag Lys 210	tac Tyr	ctc Leu	ggc Gly	gtg Val	atc Ile	atc Ile 215	cag Gln	tgc Cys	ctc Leu	gtg Val	acc Thr 220	gag Glu	acc Thr	aag Lys	acc Thr	672
tcc Ser 225	gtg Val	tcc Ser	agg Arg	cac His	atc Ile 230	tac Tyr	ttc Phe	ttc Phe	tcc Ser	gct Ala 235	cgc Arg	ggc Gly	agg Arg	atc Ile	gac Asp 240	720
ccc Pro	ctc Leu	gtg Val	tac Tyr	ctc Leu 245	gac Asp	gag Glu	ttc Phe	ctc Leu	agg Arg 250	aac Asn	tca Ser	gag Glu	ccc Pro	gtg Val 255	ctc Leu	768
aag Lys	agg Arg	gtg Val	aac Asn 260	agg Arg	acc Thr	ggc Gly	aac Asn	tcc Ser 265	tcc Ser	tcc Ser	aac Asn	aag Lys	cag Gln 270	gag Glu	tac Tyr	816
cag Gln	ctc Leu	ctc Leu 275	aag Lys	gac Asp	aac Asn	ctc Leu	gtg Val 280	agg Arg	tcc Ser	tac Tyr	aac Asn	aag Lys 285	gcc Ala	ctc Leu	aag Lys	864
aag Lys 290	aac Asn	gcc Ala	ccc Pro	tac Tyr	tcc Ser	atc Ile 295	ttc Phe	gcc Ala	atc Ile	aag Lys	aac Asn 300	ggc Gly	ccc Pro	aag Lys	tcc Ser	912
cac His	atc Ile	ggg Gly	agg Arg	cac His	ctc Leu	atg Met	acc Thr	tcc Ser	ttc Phe	ctc Leu	tca Ser	atg Met	aag Lys	ggc Gly	ctc Leu	960

Sequence Listing from Patent scope

305	310	315	320	
acc gag ct c acc aac gt g gt g ggc aac t gg t cc gac aag agg gcc t cc	Thr Gu Leu Thr Asn Val Val Gy Asn Trp Ser Asp Lys Arg Ala Ser	1008		
	325	330	335	
gcc gt g gcc agg acc acc t ac acc cac cag at c acc gcc at c ccc gac	Ala Val Ala Arg Thr Thr Tyr Thr His Gn Ile Thr Ala Ile Pro Asp	1056		
	340	345	350	
cac t ac t t c gcc ct c gt g t ca agg t ac t ac gcc t ac gac ccc at c t cc	His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser	1104		
	355	360	365	
aag gag at g at c gcc ct c aag gac gag act aac ccc at c gag gag t gg	Lys Gu Met Ile Ala Leu Lys Asp Gu Thr Asn Pro Ile Gu Gu Trp	1152		
	370	375	380	
cag cac at c gag cag ct c aag ggc t cc gcc gag ggc t cc at c agg t ac	Gn His Ile Gu Gn Leu Lys Gy Ser Ala Gu Gy Ser Ile Arg Tyr	1200		
	385	390	395	400
ccc gcc t gg aac ggc at c at c t cc cag gag gt g ct c gac t ac ct c t cc	Pro Ala Trp Asn Gy Ile Ile Ser Gn Gu Val Leu Asp Tyr Leu Ser	1248		
	405	410	415	
t cc t ac at c aac agg agg at c t ga	Ser Tyr Ile Asn Arg Arg Ile	1272		
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<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> FLP

<400> 42

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			20					25					30		
Leu	Oys	Ala	Ala	Gy	Leu	Thr	Tyr	Leu	Oys	Trp	Met	Ile	Thr	His	Asn
			35				40					45			
Gy	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr	Asn	Thr	Ile	Ile
			50			55					60				
Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys	Ser	Leu	Gn	Phe	Lys
					70					75				80	
Tyr	Lys	Thr	Gn	Lys	Ala	Thr	Ile	Leu	Gu	Ala	Ser	Leu	Lys	Lys	Leu
			85						90				95		
Ile	Pro	Ala	Trp	Gy	Phe	Thr	Ile	Ile	Pro	Tyr	Tyr	Gy	Gn	Lys	His
			100					105					110		
Gn	Ser	Asp	Ile	Thr	Asp	Ile	Val	Ser	Ser	Leu	Gn	Leu	Gn	Phe	Gu
			115				120					125			
Ser	Ser	Gu	Gu	Ala	Asp	Lys	Gy	Asn	Ser	His	Ser	Lys	Lys	Met	Leu
			130			135					140				
Lys	Ala	Leu	Leu	Ser	Gy	Gy	Gu	Ser	Ile	Trp	Gu	Ile	Thr	Gu	Lys
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Ile	Leu	Asn	Ser	Phe	Gy	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr
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Leu	Tyr	Gn	Phe	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gy	Arg	Phe

Ser	Asp	Ile	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn
Lys	Tyr	Leu	Gly	Val	Ile	Ile	Gln	Oys	Leu	Val	Thr	Glu	Thr	Lys	Thr
Ser 225	Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp
Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	Leu
Lys	Arg	Val	Asn	Arg	Thr	Gly	Asn	Ser	Ser	Ser	Asn	Lys	Gln	Glu	Tyr
Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	Ala	Leu	Lys
Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn	Gly	Pro	Lys	Ser
His 305	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu	Ser	Met	Lys	Gly	Leu
Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp	Ser	Asp	Lys	Arg	Ala	Ser
Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His	Gln	Ile	Thr	Ala	Ile	Pro	Asp
His	Tyr	Phe	Ala	Leu	Val	Ser	Arg	Tyr	Tyr	Ala	Tyr	Asp	Pro	Ile	Ser
Lys	Glu	Met	Ile	Ala	Leu	Lys	Asp	Glu	Thr	Asn	Pro	Ile	Glu	Glu	Trp
Gln 385	His	Ile	Glu	Gln	Leu	Lys	Gly	Ser	Ala	Glu	Gly	Ser	Ile	Arg	Tyr
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Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg		
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Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val		
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Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe		
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Sequence Listing from Patent scope															
Pro 65	Ala	Glu	Pro	Glu	Asp 70	Val	Arg	Asp	Tyr	Leu 75	Leu	Tyr	Leu	Gln	Ala 80
cgc Arg	ggg Gly	ctg Leu	gca Ala	gtg Val 85	aag Lys	acc Thr	atc Ile	cag Gln 90	caa Gln 90	cac His	ctt Leu	gga Gly	caa Gln 95	ctg Leu 95	aac Asn
atg Met	ctt Leu	cac His	agg Arg 100	cgc Arg	tcc Ser	ggc Gly	ctc Leu	ccg Pro 105	cgc Arg	ccc Pro	agc Ser	gac Asp	tcg Ser 110	aac Asn	gcc Ala
gtg Val	agc Ser	ctc Leu 115	gtc Val	atg Met	cgc Arg	cgc Arg	atc Ile 120	agg Arg	aag Lys	gaa Glu	aac Asn	gtc Val 125	gat Asp	gcc Ala	ggc Gly
gaa Glu 130	agg Arg	gca Ala	aag Lys	cag Gln	gcc Ala	ctc Leu 135	gcg Ala	ttc Phe	gag Glu	agg Arg	acc Thr 140	gat Asp	ttc Phe	gac Asp	cag Gln
gtc Val 145	cgc Arg	agc Ser	ctg Leu	atg Met	gag Glu 150	aac Asn	agc Ser	gac Asp	agg Arg	tgc Cys 155	cag Gln	gac Asp	att Ile	agg Arg	aac Asn 160
ctg Leu	gcg Ala	ttc Phe	ctc Leu	gga Gly 165	att Ile	gca Ala	tac Tyr	aac Asn	acg Thr 170	ctc Leu	ctc Leu	agg Arg	atc Ile	gcg Ala 175	gaa Glu
att Ile	gcc Ala	cgc Arg	att Ile 180	cgc Arg	gtg Val	aag Lys	gac Asp	att Ile 185	agc Ser	cgc Arg	acc Thr	gac Asp	ggc Gly 190	ggc Gly	agg Arg
atg Met	ctt Leu	atc Ile 195	cac His	att Ile	ggc Gly	agg Arg	acc Thr 200	aag Lys	acg Thr	ctc Leu	gtt Val	tcc Ser 205	acc Thr	gca Ala	ggc Gly
gtc Val 210	gaa Glu	aag Lys	gcc Ala	ctc Leu	agc Ser	ctc Leu 215	gga Gly	gtg Val	acc Thr	aag Lys	ctc Leu 220	gtc Val	gaa Glu	cgc Arg	tgg Trp
atc Ile 225	tcc Ser	gtg Val	tcc Ser	ggc Gly 230	gtc Val 230	gcg Ala	gac Asp	gac Asp	cca Pro	aac Asn 235	aac Asn	tac Tyr	ctc Leu	ttc Phe	tgc Cys 240
cgc Arg	gtc Val	cgc Arg	aag Lys	aac Asn 245	ggg Gly	gtg Val	gct Ala	gcc Ala	cct Pro 250	agc Ser	gcc Ala	acc Thr	agc Ser	caa Gln 255	ctc Leu
agc Ser	acg Thr	agg Arg	gcc Ala 260	tig Leu	gaa Glu	ggt Gly	att Ile	ttc Phe 265	gag Glu	gcc Ala	acc Thr	cac His	cgc Arg 270	ctg Leu	atc Ile
tac Tyr	ggc Gly	gcg Ala 275	aag Lys	gat Asp	gac Asp	agc Ser	ggt Gly 280	caa Gln	cgc Arg	tac Tyr	ctc Leu	gca Ala 285	tgg Trp	tcc Ser	ggg Gly
cac His 290	tcc Ser	gcc Ala	cgc Arg	gtt Val	gga Gly 295	gct Ala 295	gct Ala	agg Arg	gac Asp	atg Met 300	gcc Ala	cgc Arg	gcc Ala	ggt Gly	gtt Val
tcc Ser 305	atc Ile	ccc Pro	gaa Glu	atc Ile	atg Met 310	cag Gln	gcg Ala	ggt Gly	gga Gly	tgg Trp 315	acg Thr	aac Asn	gtg Val	aac Asn	att Ile 320

Sequence Listing from Patent scope

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Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe
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65					70				75						80
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn
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Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala
			100					105					110		
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly
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Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln
			130			135					140				
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn
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Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu
			165						170					175	
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg
			180					185					190		
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly
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Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp
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Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys
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Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu
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Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile
			260					265					270		
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly
			275				280					285			
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val
			290			295					300				
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile
305					310					315					320
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val
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Sequence Listing from Patent scope

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<211> 1198
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<213> Artificial Sequence

<220>
<223> Expression cassette comprising Zea mays rab17 promoter, attB1 site, and FLPm coding sequence

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t c t t c t t t t a a t a t a t t t t a t g a a t t t t a a t g t a t t t t a a a a t g t t a t g c a g t t c g c t c t 180
g g a c t t t t c t g c t g c g c c t a c a c t t g g g t g t a c t g g g c c t a a a t t c a g c c t g a c c g a c c g 240
c c t g c a t t g a a t a a t g g a t g a g c a c c g g t a a a t c c g c g t a c c c a a c t t t c g a g a a g a a c 300
c g a g a c g t g g c g g g c c g g g c c a c c g a c g c a c g g c a c c g a c t g c a c a c g t c c c g c c g g 360
c g t a c g t g t a c g t g c t g t t c c c t c a c t g g c c g c c c a a t c c a c t c a t g c a t g c c c a c g t a c 420
a c c c c t g c c g t g g c g c g c c c a g a t c c t a a t c c t t t c g c c g t t c t g c a c t t c t g c t g c c t a 480
t a a t g g c g g c a t c g a c c g t c a c c t g c t t c a c c a c c g g c g a g c c a c a t c g a g a a c a c g a t 540
c g a g c a c a c a a g c a c g a a g a c t c g t t t a g g a g a a a c c a c a a a c c a c c a a g c c g t g c a a g c 600
a c c a a g c t t g g t c a c c c g g t c c g g c c t a g a a g g c c a g c t t c a a g t t t g t a c a a a a a a g c 660
a g g c t t c g a a g g a g a t a g a a c c a a t t c t c t a a g g a a a t a c t t a a c c a t g g t c g a c t g g a t 720
c c a a c a a t g c c c c a g t t c g a c a t c c t c t g c a a g a c c c c c c c a a g g t g c t c g t g a g g c a g 780
t t c g t g g a g a g g t t c g a g a g g c c c c t c g g c g a g a a g a t c g c c c t c t g c g c c g c c g a g c t c 840
a c c t a c c t c t g c t g g a t g a t c a c c c a c a a c g g c a c c g c c a t t a a g a g g g c c a c c t t c a t g 900
t c a t a c a a c a c c a t c a t c t c c a a c t c c c t c t c c t t c g a c a t c g t g a a c a a g t c c c t c c a g 960
t t c a a a t a c a a g a c c c a g a a g g c c a c c a t c c t c g a g g c c t c c c t c a a g a a g c t c a t c c c c 1020
g c c t g g g a g t t c a c c a t c a t c c c c t a c t a c g g c c a g a a g c a c c a g t c c g a c a t c a c c g a c 1080
a t c g t g t c a t c c c t c c a g c t t c a g t t c g a g t c c t c c g a g g a g g c t g a c a a g g g c a a c t c c 1140
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t c t t c t t t t a a t a t a t t t t a t g a a t t t t a a t g t a t t t t a a a a t g t t a t g c a g t t c g c t c t 180
g g a c t t t t c t g c t g c g c c t a c a c t t g g g t g t a c t g g g c c t a a a t t c a g c c t g a c c g a c c g 240
c c t g c a t t g a a t a a t g g a t g a g c a c c g g t a a a t c c g c g t a c c c a a c t t t c g a g a a g a a c 300
c g a g a c g t g g c g g g c c g g g c c a c c g a c g c a c g g c a c c g a c t g c a c a c g t c c c g c c g g 360
c g t a c g t g t a c g t g c t g t t c c c t c a c t g g c c g c c c a a t c c a c t c a t g c a t g c c c a c g t a c 420
a c c c c t g c c g t g g c g c g c c c a g a t c c t a a t c c t t t c g c c g t t c t g c a c t t c t g c t g c c t a 480
t a a t g g c g g c a t c g a c c g t c a c c t g c t t c a c c a c c g g c g a g c c a c a t c g a g a a c a c g a t 540
c g a g c a c a c a a g c a c g a a g a c t c g t t t a g g a g a a a c c a c a c a a a c c a c c a a g c c g t g c a a g c 600
a c c a a g c t t g g t c a c c c g g t c c g g c c t a g a a g g c c a g c t t c a a g t t t g t a c a a a a a a g c 660
a g g c t t c g a a g g a g a t a g a a c c a a t t c t c t a a g g a a a t a c t t a a c c a t g g t c g a c t g g a t 720
c c a a c a a t g c c c c a g t t c g a c a t c c t c t g c a a g a c c c c c c c a a g g t g c t c g t g a g g c a g 780
t t c g t g g a g a g g t t c g a g a g g c c c c t c g g c g a g a a g a t c g c c c t c t g c g c c g c c g a g c t c 840
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t c a t a c a a c a c c a t c a t c t c c a a c t c c c t c t c c t t c g a c a t c g t g a a c a a g t c c c t c c a g 960
t t c a a a t a c a a g a c c c a g a a g g c c a c c a t c c c c t a c t a c g g c c a g a a g c a c c a g t c c g a c a t c a c c g a c 1020
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g a g a a g a t c c t c a a c t c c t t c g a g t a c a c t c c a g g t t c a c t a a g a c c a a g a c c c t c t a c 1260
c a g t t c c t c t t c c t c g c c a c c t t c a t c a a c t g c g g c a g g t t c t c a g a c a t c a a g a a c g t g 1320
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gt t aacggat	ccagact t gt	ccat ct t ct g	gat t ggccaa	ct t aat t aat	gt at gaaat a	2100
aaaggat gca	cacat agt ga	cat gct aat c	act at aat gt	gggcat caaa	gt t gt gt gt t	2160
at gt gt aat t	act agt t at c	t gaat aaaag	agaaagagat	cat ccat at t	t ct t at cct a	2220
aat gaat gt c	acgt gt ct t t	at aat t ct t t	gat gaaccag	at gcat t t ca	t t aaccaa	2280
ccat at acat	at aaat at t a	at cat at at a	at t aat at ca	at t gggg t ag	caaaacaaat	2340
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<212> DNA

<213> Artificial Sequence

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cgagcacaca	agcacgaaga	ct cgt t t agg	agaaaccaca	aaccaccaag	ccgt gcaagc	600
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gccgagct ca	cct acct ct g	ct ggat gat c	accacaacg	gcaccgccat	t aagagggcc	780
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t cct ccat	t caaat acaa	gacccagaag	gccaccat cc	t cgaggcct c	cct caagaag	900
ct cat ccccg	cct gggagt t	cacat cat c	ccct act acg	gccagaagca	ccagt ccgac	960
at caccgaca	t cgt gt cat c	cct ccagct t	cagt t cgagt	cct ccgagga	ggct gacaag	1020
ggcaact ccc	act ccaagaa	gat gct gaag	gcccct cct ct	ccgagggcga	gt ccat ct gg	1080
gagat caccg	agaagat cct	caact cct t c	gagt acacct	ccaggt t cac	t aagaccaag	1140
accct ct acc	agt t cct ct t	cct cgccacc	t t cat caact	gcggcagggt t	ct cagacat c	1200
aagaacgt gg	accccaagt c	ct t caagct c	gt gcagaaca	agt acct cgg	cgt gat cat c	1260
cagt gcct cg	t gaccgagac	caagacct cc	gt gt ccaggc	acat ct act t	ct t ct ccgct	1320
cgcgccagga	t cgacccccct	cgt gt acct c	gacgagt t cc	t caggaact c	agagcccgt g	1380
ct caagaggg	t gaacaggac	cggcaact cc	t cct ccaaca	agcaggagt a	ccagct cct c	1440
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t t cgccat ca	agaacggccc	caagt cccac	at cggg aggc	acct cat gac	ct cct t cct c	1560
t caat gaagg	gcct caccga	gct caccaac	gt ggt gggca	act ggt ccga	caagagggcc	1620
t ccgccgt gg	ccaggaccac	ct acaccac	cagat caccg	ccat ccccgga	ccact act t c	1680
gccct cgt gt	caaggt act a	cgct acgac	cccat ct cca	aggagat gat	cgccct caag	1740
gacgagact a	acccccat cga	ggagt ggcag	cacat cgagc	agct caaggg	ct ccgccgag	1800
ggct ccat ca	ggt accccgc	ct ggaacggc	at cat ct ccc	aggaggt gct	cgact acct c	1860
t cct cct aca	t caacaggag	gat ct gagi t	ct agt t cgaa	t gt gagt t ga	t ccccgccgg	1920
t gt ccccccac	t gaagaaact	at gt gct gt a	gt at agccgc	t ggct agct a	gct agt t gag	1980
t cat t t agcg	gcgat gat t g	agt aat aat g	t gt cacgcat	cacat gcat	gggt ggcagt	2040
ct cagt gt ga	gcaat gacct	gaat gaacaa	t t gaaat gaa	aagaaaaaag	t at t gt t cca	2100

Sequence Listing from Patent scope

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tgtctaat ttt gttatcatcc atttagat at agacgaaaaa aaatctaaga actaaaacaa 2220
atgctaat ttt gaaatgaagg gagt at at at tgggat aat g t cgat gagat ccctcgt aat 2280
atcaccgaca t cacacgtgt ccagttaat g t atcagt gat acgtgtattc acatttgttg 2340
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<210> 48

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<220>

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<222> 10

<223> Xaa = His or Asn

<220>

<221> VARI ANT

<222> 16

<223> Xaa = Phe or Tyr

<220>

<221> VARI ANT

<222> 17

<223> Xaa = Val or Ile

<220>

<221> VARI ANT

<222> 19

<223> Xaa = Ser or His

<400> 48

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Tyr  G u Lys  G u  Leu  G u  G u  Met  Lys  Xaa  Met  Thr  Arg  G n  G u  Xaa
1      5      10      15
Xaa  Al a  Xaa  Leu  Arg  Arg  Lys  Ser  Ser  Gly  Phe  Ser  Arg  Gly  Al a
      20      25      30

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<210> 49

<211> 63

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 2

<220>

<221> VARI ANT

<222> 2

<223> Xaa = Ile or Met

<220>

<221> VARI ANT

<222> 36

<223> Xaa = Gln or Glu

<220>

<221> VARI ANT

<222> 45

<223> Xaa = Ile or Val

Sequence Listing from Patent scope

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 <222> 60
 <223> Xaa = Asp or Glu

<220>
 <221> VARI ANT
 <222> 61
 <223> Xaa = Met or Ile

<220>
 <221> VARI ANT
 <222> (62) ... (62)
 <223> Xaa = Ser or Asn

<400> 49
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 Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr
 20 25 30
 Phe Ser Thr Xaa Glu Glu Ala Ala Glu Ala Tyr Asp Xaa Ala Ala Ile
 35 40 45
 Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Xaa Xaa Xaa Arg
 50 55 60

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<220>
 <223> Consensus sequence motif 3

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 <223> Xaa = Ile or Gln

<220>
 <221> VARI ANT
 <222> 26
 <223> Xaa = Arg or Lys

<220>
 <221> VARI ANT
 <222> 30, 59
 <223> Xaa = Ser or Thr

<220>
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 <222> 33
 <223> Xaa = Val or Gly

<220>
 <221> VARI ANT
 <222> 34
 <223> Xaa = Tyr or Arg

Sequence Listing from Patent scope

<220>
 <221> VARI ANT
 <222> (35) . . . (35)
 <223> Xaa = Leu or G n

<220>
 <221> VARI ANT
 <222> (42) . . . (42)
 <223> Xaa = G u or Asp

<220>
 <221> VARI ANT
 <222> (58) . . . (58)
 <223> Xaa = Pr o or Thr

<220>
 <221> VARI ANT
 <222> (61) . . . (61)
 <223> Xaa = Thr or Hi s

<220>
 <221> VARI ANT
 <222> (62) . . . (62)
 <223> Xaa = Thr or I l e

<220>
 <221> VARI ANT
 <222> (66) . . . (66)
 <223> Xaa = I l e, Val , or Leu

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 Al a Hi s Leu Trp Asp Asn Ser Cys Arg Xaa Gl u Gly Gl n Xaa Arg Lys
 20 25 30
 Xaa Xaa Xaa Gly Gly Tyr Asp Lys Gl u Xaa Lys Al a Al a Arg Al a Tyr
 35 40 45
 Asp Leu Al a Al a Leu Lys Tyr Trp Gly Xaa Xaa Thr Xaa Xaa Asn Phe
 50 55 60
 Pro Xaa Ser Asn
 65

<210> 51
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 <212> PRT
 <213> Art i f i c i a l Sequence

<220>
 <223> Consensus sequence motif 4

<220>
 <221> VARI ANT
 <222> 3
 <223> Xaa = Leu or Val

<220>

Sequence Listing from Patent scope

<221> VARI ANT

<222> 4

<223> Xaa = Glu or Ala

<220>

<221> VARI ANT

<222> 5

<223> Xaa = Asp or Asn

<400> 51

Pro Lys Xaa Xaa Xaa Phe Leu Gly
1 5

<210> 52

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 5

<220>

<221> VARI ANT

<222> 6

<223> Xaa = Ile or Val

<220>

<221> VARI ANT

<222> 9

<223> Xaa = Ala or Leu

<220>

<221> VARI ANT

<222> 11, 12

<223> Xaa = Lys or Arg

<220>

<221> VARI ANT

<222> 13

<223> Xaa = Leu or Arg

<400> 52

Ser Ser Thr Leu Pro Xaa Gly Gly Xaa Ala Xaa Xaa Xaa
1 5 10

<210> 53

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 6

<220>

<221> VARI ANT

<222> 4

<223> Xaa = Gly or Ser

<400> 53

Asn Trp Leu Xaa Phe Ser Leu Ser Pro
1 5

Sequence Listing from Patent scope

<210> 54
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence motif 7

 <220>
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 <222> 1
 <223> Xaa = Gly or Glu

 <220>
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 <222> 7
 <223> Xaa = Thr or Asn

 <400> 54
 Xaa Leu Ser Met Ile Lys Xaa Trp Leu Arg
 1 5 10

 <210> 55
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 <220>
 <223> Consensus sequence motif 8

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 <222> 2, 4, 5
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 1 5

 <210> 56
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence motif 9

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 <223> Xaa = Ser, Thr, or Ala

 <400> 56
 Leu Xaa Leu Ser Met
 1 5

 <210> 57
 <211> 7

Sequence Listing from Patent scope

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 10

<220>

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<222> 4

<223> Xaa = G n or Pro

<400> 57

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1 5

<210> 58

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 14

<400> 58

Trp Pro Thr Ile Ala Phe G n
1 5

<210> 59

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 15

<220>

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<222> 2

<223> Xaa = Ser or Thr

<400> 59

Ser Xaa Gly Ser Asn Ser Val Val Tyr Asn Gly
1 5 10

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence motif 19

<220>

<221> VARI ANT

<222> 4

<223> Xaa = Ser or Asn

<400> 60

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1 5

Sequence Listing from Patent scope

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<212> DNA
<213> Zea mays

<220>
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cac ggg cag gac gac ggc ggg tcc ccg ccg atg tcc ccg gcc tcc gcc 96
His Gly Glu Asp Asp Gly Gly Ser Pro Pro Met Ser Pro Ala Ser Ala
20 25 30

gcg gcg gcg gcg ctg gcg aac gcg ccg tgg aac ccg acc aag gag cag 144
Ala Ala Ala Ala Leu Ala Asn Ala Arg Trp Asn Pro Thr Lys Glu Glu
35 40 45

gtg gcc gtg ctg gag ggc ctg tac gag cac ggc ctg cgc acc ccc agc 192
Val Ala Val Leu Glu Gly Leu Tyr Glu His Gly Leu Arg Thr Pro Ser
50 55 60

gcg gag cag ata cag cag atc acg ggc agg ctg ccg gag cac ggc gcc 240
Ala Glu Glu Ile Glu Glu Ile Thr Gly Arg Leu Arg Glu His Gly Ala
65 70 75 80

atc gag ggc aag aac gtc ttc tac tgg ttc cag aac cac aag gcc cgc 288
Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Glu Asn His Lys Ala Arg
85 90 95

cag cgc cag agg cag aag cag gac agc ttc gcc tac ttc agc agg ctg 336
Glu Arg Glu Arg Glu Lys Glu Asp Ser Phe Ala Tyr Phe Ser Arg Leu
100 105 110

ctc cgc ccg ccc ccg ccg ctg ccc gtg ctc tcc atg ccc ccc gcg cca 384
Leu Arg Arg Pro Pro Pro Leu Val Leu Ser Met Pro Pro Ala Pro
115 120 125

ccg tac cat cac gcc cgc gtc ccg gcg ccg ccc gcg ata ccg atg ccg 432
Pro Tyr His His Ala Arg Val Pro Ala Pro Pro Ala Ile Pro Met Pro
130 135 140

atg gcg ccg ccg ccg ccc gct gca tgc aac gac aac ggc ggc gcg cgt 480
Met Ala Pro Pro Pro Pro Ala Ala Cys Asn Asp Asn Gly Gly Ala Arg
145 150 155 160

gtg atc tac agg aac cca ttc tac gtg gct gcg ccg cag gcg ccc cct 528
Val Ile Tyr Arg Asn Pro Phe Tyr Val Ala Ala Pro Glu Ala Pro Pro
165 170 175

gca aat gcc gcc tac tac tac cca cag cca cag cag cag cag cag cag 576
Ala Asn Ala Ala Tyr Tyr Tyr Pro Glu Pro Glu Glu Glu Glu Glu Glu
180 185 190

cag gtg aca gtc atg tac cag tac ccg aga atg gag gta gcc ggc cag 624
Glu Val Thr Val Met Tyr Glu Tyr Pro Arg Met Glu Val Ala Gly Glu
195 200 205

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Sequence Listing from Patent scope

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ctc Leu	cag Gln	ctg Leu	ttc Phe	ccg Pro 245	ctc Leu	cag Gln	ccc Pro	acc Thr	ttc Phe 250	gtg Val	ctg Leu	cgg Arg	cac His	gac Asp 255	aag Lys	768
ggg Gly	cgc Arg	gcc Ala	gcc Ala 260	aac Asn	ggc Gly	agt Ser	aat Asn	aac Asn 265	gac Asp	tcc Ser	ctg Leu	acg Thr	tcc Ser 270	acg Thr	tcc Ser	816
acg Thr	gcg Ala	act Thr 275	gcg Ala	aca Thr	gcg Ala	aca Thr	gcg Ala 280	aca Thr	gcg Ala	aca Thr	gcg Ala	tcc Ser 285	gct Ala	tcc Ser	atc Ile	864
tcc Ser	gag Glu 290	gac Asp	tcc Ser	gat Asp	ggc Gly	ctg Leu 295	gag Glu	agc Ser	ggc Gly	agc Ser	tcc Ser 300	ggc Gly	aag Lys	ggc Gly	gtc Val	912
gag Glu 305	gag Glu	gcg Ala	ccc Pro	gcg Ala	ctg Leu 310	ccg Pro	ttc Phe	tat Tyr	gac Asp	ttc Phe 315	ttc Phe	ggg Gly	ctc Leu	cag Gln	tcc Ser 320	960
tcc Ser	gga Gly	ggc Gly	cgc Arg	tga												975

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<400> 62

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

G n	Val	Thr	180 Val	Met	Tyr	G n	Tyr	Pro	Arg	Met	G u	Val	Al a	G y	G n
Asp	Lys	Met	195 Met	Thr	Arg	Al a	Al a	Al a	Hi s	G n	G n	G n	G n	Hi s	Asn
G y	Al a	G y	210 G n	G n	Pro	Al a	Arg	Al a	G y	Hi s	Pro	Ser	Arg	G u	Thr
Leu	G n	Leu	225 Phe	Pro	Leu	G n	Pro	Thr	Phe	Val	Leu	Arg	Hi s	Asp	Lys
G y	Arg	Al a	240 Al a	Asn	G y	Ser	Asn	Asn	Asp	Ser	Leu	Thr	Ser	Thr	Ser
Thr	Al a	Thr	260 Al a	Thr	Al a	Thr	Al a	Thr	Al a	Thr	Al a	Ser	Al a	Ser	I le
Ser	G u	Asp	275 Ser	Asp	G y	Leu	G u	Ser	G y	Ser	Ser	G y	Lys	G y	Val
G u	G u	Al a	290 Al a	Pro	Al a	Leu	Pro	Phe	Tyr	Asp	Phe	G y	Leu	G n	Ser
Ser	G y	G y	305 Arg			310					315				320

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Met	Al a	Al a	Asn	Al a	G l y	G l y	G l y	G l y	Al a	G l y	G l y	G l y	Ser	G l y	Ser			
1				5					10					15				
g g c	a g c	g t g	g c t	g c g	c c g	g c g	g t g	t g c	c g c	c c c	a g c	g g c	t c g	c g g	t g g			96
G l y	Ser	Val	Al a	Al a	Pro	Al a	Val	O y s	Arg	Pro	Ser	G l y	Ser	Arg	Tr p			
			20					25					30					
a c g	c c g	a c g	c c g	g a g	c a g	a t c	a g g	a t g	c t g	a a g	g a g	c t c	t a c	t a c	g g c			144
Thr	Pro	Thr	Pro	G u	G n	I l e	Arg	Met	Leu	Lys	G u	Leu	Tyr	Tyr	G l y			
			35				40						45					
t g c	g g c	a t c	c g g	t c g	c c c	a g c	t c g	g a g	c a g	a t c	c a g	c g c	a t c	a c c	g c c			192
O y s	G l y	I l e	Arg	Ser	Pro	Ser	Ser	G u	G n	I l e	G n	Arg	I l e	Thr	Al a			
	50					55					60							
a t g	c t g	c g g	c a g	c a c	g g c	a a g	a t c	g a g	g g c	a a g	a a c	g t c	t t c	t a c	t g g			240
Met	Leu	Arg	G n	H i s	G l y	Lys	I l e	G u	G l y	Lys	Asn	Val	Phe	Tyr	Tr p			
65					70					75					80			
t t c	c a g	a a c	c a c	a a g	g c c	c g c	g a g	c g c	c a g	a a g	c g c	c g c	c t c	a c c	a g c			288
Phe	G n	Asn	H i s	Lys	Al a	Arg	G u	Arg	G n	Lys	Arg	Arg	Leu	Thr	Ser			
				85					90					95				
c t c	g a c	g t c	a a c	g t g	c c c	g c c	g c c	g g c	g c g	g c c	g a c	g c c	a c c	a c c	a g c			336
Leu	Asp	Val	Asn	Val	Pro	Al a	Al a	G l y	Al a	Al a	Asp	Al a	Thr	Thr	Ser			
			100					105					110					
c a a	c t c	g g c	g t c	c t c	t c g	c t g	t c g	t c g	c c g	c c g	c c t	t c a	g g c	g c g	g c g			384
G n	Leu	G l y	Val	Leu	Ser	Leu	Ser	Ser	Pro	Pro	Pro	Ser	G l y	Al a	Al a			
		115					120					125						

Sequence Listing from Patent scope

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gcc Ala	at g Met	gcc Ala	acc Thr	gag Glu 165	aca Thr	t gc Cys	t t c Phe	ct g Leu	cag Gln 170	gac Asp	t ac Tyr	at g Met	ggc Gly	gt g Val 175	acg Thr	528
gac Asp	acg Thr	ggc Gly	agc Ser 180	t cg Ser	t cg Ser	cag Gln	t gg Trp	cca Pro 185	cgc Arg	t t c Phe	t cg Ser	t cg Ser	t cg Ser 190	gac Asp	acg Thr	576
at a Ile	at g Met	gcg Ala 195	gcg Ala	gcc Ala	gcg Ala	gcg Ala	cgg Arg 200	gcg Ala	gcg Ala	acg Thr	acg Thr	cgg Arg 205	gcg Ala	ccc Pro	gag Glu	624
acg Thr 210	ct c Leu	cct Pro	ct c Leu	t t c Phe	ccg Pro	acc Thr 215	t gc Cys	ggc Gly	gac Asp	gac Asp	ggc Gly 220	ggc Gly	agc Ser	ggt Gly	agc Ser	672
agc Ser 225	agc Ser	t ac Tyr	t t g Leu	ccg Pro	t t c Phe 230	t gg Trp	ggt Gly	gcc Ala	gcg Ala	t cc Ser 235	aca Thr	act Thr	ggc Ala	ggc Gly	gcc Ala 240	720
act Thr	t ct Ser	t cc Ser	gt t Val	gcg Ala 245	at c Ile	cag Gln	cag Gln	caa Gln	cac His 250	cag Gln	ct g Leu	cag Gln	gag Glu	cag Gln 255	t ac Tyr	768
agc Ser	t t t Phe	t ac Tyr	agc Ser 260	aac Asn	agc Ser	aac Asn	agc Ser	acc Thr 265	cag Gln	ct g Leu	gcc Ala	ggc Gly	acc Thr 270	ggc Gly	aac Asn	816
caa Gln	gac Asp	gt a Val 275	t cg Ser	gca Ala	aca Thr	gca Ala	gca Ala 280	gca Ala	gcc Ala	gcc Ala	gcc Ala	ct g Leu 285	gag Glu	ct g Leu	agc Ser	864
ct c Leu 290	agc Ser	t ca Ser	t gg Trp	t gc Cys	t cc Ser	cct Pro 295	t ac Tyr	cct Pro	gct Ala	gca Ala	ggg Gly 300	agt Ser	at g Met	t ga		909

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 <212> PRT
 <213> Zea mays

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 Gly 16 Ser 17 Val 18 Ala 19 Ala 20 Pro 21 Ala 22 Val 23 Cys 24 Arg 25 Pro 26 Ser 27 Gly 28 Ser 29 Arg 30 Trp
 Thr 31 Pro 32 Thr 33 Pro 34 Glu 35 Gln 36 Ile 37 Arg 38 Met 39 Leu 40 Lys 41 Glu 42 Leu 43 Tyr 44 Tyr 45 Gly
 Cys 46 Gly 47 Ile 48 Arg 49 Ser 50 Pro 51 Ser 52 Ser 53 Glu 54 Gln 55 Ile 56 Gln 57 Arg 58 Ile 59 Thr 60 Ala
 Met 61 Leu 62 Arg 63 Gln 64 His 65 Gly 66 Lys 67 Ile 68 Glu 69 Gly 70 Lys 71 Asn 72 Val 73 Phe 74 Tyr 75 Trp
 Phe 76 Gln 77 Asn 78 His 79 Lys 80 Ala 81 Arg 82 Glu 83 Arg 84 Gln 85 Lys 86 Arg 87 Arg 88 Leu 89 Thr 90 Ser

Sequence Listing from Patent scope

Leu	Asp	Val	Asn	Val	Pro	Ala	Ala	Gly	Ala	Ala	Asp	Ala	Thr	Thr	Ser
Gln	Leu	Gly	Val	Leu	Ser	Leu	Ser	Ser	Pro	Pro	Pro	Ser	Gly	Ala	Ala
Pro	Pro	Ser	Pro	Thr	Leu	Gly	Phe	Tyr	Ala	Ala	Gly	Asn	Gly	Gly	Gly
Ser	Ala	Val	Leu	Leu	Asp	Thr	Ser	Ser	Asp	Trp	Gly	Ser	Ser	Gly	Ala
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Gln	Asp	Val	Ser	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Glu	Leu	Ser
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Sequence Listing from Patent scope

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Sequence Listing from Patent scope

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505

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Sequence Listing from Patent scope

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Sequence Listing from Patent scope

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<213> Zea mays

<400> 68

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<212> DNA

<213> Sorghum bicolor

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Sequence Listing from Patent scope

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

Sequence Listing from Patent scope

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Gly 65	Gly 70	Ser 75	Ala 80	Ala 85	Thr 90	Ala 95	Thr 100	Thr 105	Val 110	Ala 115	Oys 120	Ala 125	Pro 130	Pro 135	Gln 140
Leu 65	Pro 70	Gln 75	Phe 80	Ser 85	Thr 90	Asp 95	Asn 100	Asn 105	Asn 110	His 115	Leu 120	Tyr 125	Asp 130	Ser 135	Glu 140
Leu 65	Lys 70	Ser 75	Thr 80	Ile 85	Ala 90	Ala 95	Oys 100	Phe 105	Pro 110	Arg 115	Ala 120	Leu 125	Ala 130	Ala 135	Glu 140
Gln 65	Ser 70	Thr 75	Glu 80	Pro 85	Gln 90	Lys 95	Lys 100	Ser 105	Pro 110	Lys 115	Lys 120	Thr 125	Val 130	Asp 135	Thr 140
Phe 145	Gly 150	Gln 155	Arg 160	Thr 165	Ser 170	Ile 175	Tyr 180	Arg 185	Gly 190	Val 195	Thr 200	Arg 205	His 210	Arg 215	Trp 220
Thr 145	Gly 150	Arg 155	Tyr 160	Glu 165	Ala 170	His 175	Leu 180	Trp 185	Asp 190	Asn 195	Ser 200	Oys 205	Arg 210	Arg 215	Glu 220
Gly 145	Gln 150	Ser 155	Arg 160	Lys 165	Gly 170	Arg 175	Gln 180	Val 185	Tyr 190	Leu 195	Gly 200	Gly 205	Tyr 210	Asp 215	Lys 220
Glu 145	Asp 150	Lys 155	Ala 160	Ala 165	Arg 170	Ala 175	Tyr 180	Asp 185	Leu 190	Ala 195	Ala 200	Leu 205	Lys 210	Tyr 215	Trp 220
Gly 145	Pro 150	Thr 155	Thr 160	Thr 165	Thr 170	Asn 175	Phe 180	Pro 185	Ile 190	Ser 195	Asn 200	Tyr 205	Glu 210	Lys 215	Glu 220
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Arg 225	Arg 230	Lys 235	Ser 240	Ser 245	Gly 250	Phe 255	Ser 260	Arg 265	Gly 270	Ala 275	Ser 280	Ile 285	Tyr 290	Arg 295	Gly 300
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Val 225	Ala 230	Gly 235	Asn 240	Lys 245	Asp 250	Leu 255	Tyr 260	Leu 265	Gly 270	Thr 275	Phe 280	Ser 285	Thr 290	Gln 295	Glu 300
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Gln 305	Pro 310	Ser 315	Ser 320	Ser 325	Asn 330	Leu 335	Phe 340	Phe 345	Ala 350	Ile 355	Pro 360	Ile 365	Lys 370	Gln 375	Asp 380
Pro 385	Ser 390	Asp 395	Tyr 400	Trp 405	Ser 410	Ile 415	Leu 420	Gly 425	Tyr 430	His 435	Asn 440	Thr 445	Pro 450	Leu 455	Asp 460
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Pro 385	Ser 390	Ser 395	Asn 400	Asn 405	Gly 410	Thr 415	Ala 420	Ser 425	Ser 430	Leu 435	Thr 440	Pro 445	Phe 450	Asn 455	Met 460
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Sequence Listing from Patent scope

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<400> 71

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20      25      30      35      40      45      50      55      60      65      70      75      80      85      90      95      100      105      110      115
His Ser Phe Thr Tyr Pro Ser Leu Thr Gly Ser His Thr Ala
35      40      45      50      55      60      65      70      75      80      85      90      95      100      105      110      115      120      125      130
Asp Ala Pro Pro Glu Pro Ile Ala Gly Gly Gly Ala Thr Asn Leu Ser
50      55      60      65      70      75      80      85      90      95      100      105      110      115      120      125      130      135      140      145
Ile Phe Thr Gly Ala Pro Lys Phe Glu Asp Phe Leu Gly Gly Ser Ser
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Ala Thr Ala Thr Ala Thr Thr Cys Ala Pro Pro Gln Leu Pro Gln Phe
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Ser Thr Asp Asn Asn Asn His Leu Tyr Asp Ser Glu Leu Lys Thr Thr
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Ile Ala Ala Cys Phe Pro Arg Ala Phe Ala Ala Glu Pro Thr Thr Glu
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Pro Gln Lys Pro Ser Pro Lys Lys Thr Val Asp Thr Phe Gly Gln Arg
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Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
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Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg
165      170      175      180      185      190      195      200      205      210      215      220      225      230      235      240      245      250      255      260      265
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180      185      190      195      200      205      210      215      220      225      230      235      240      245      250      255      260      265      270      275      280
Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr
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Lys Asn Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser
225      230      235      240      245      250      255      260      265      270      275      280      285      290      295      300      305      310      315      320      325
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His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn
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Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu
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Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr
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Leu Pro Ile Gly Gly Leu Ser Gly Lys Asn Lys Asn Ser Thr Asp Ser
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Ala Ser Glu Ser Lys Ser His Glu Ala Ser Arg Ser Asp Glu Arg Asp
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Pro Ser Ala Ala Ser Ser Val Thr Phe Ala Ser Gln Gln Gln Pro Ser
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Ser Ser Thr Leu Ser Phe Ala Ile Pro Ile Lys Gln Asp Pro Ser Asp
370      375      380      385      390      395      400      405      410      415      420      425      430      435      440      445      450      455      460      465      470
Tyr Trp Ser Ile Leu Gly Tyr His Asn Ser Pro Leu Asp Asn Thr Gly
385      390      395      400      405      410      415      420      425      430      435      440      445      450      455      460      465      470      475      480      485
Ile Arg Asn Thr Thr Ser Val Thr Ala Thr Ser Phe Pro Ser Ser Asn
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Asn Gly Thr Thr Ser Ser Leu Thr Pro Phe His Met Glu Phe Ser Asn
420      425      430      435      440      445      450      455      460      465      470      475      480      485      490      495      500      505      510      515      520
Ala Pro Thr Ser Thr Gly Ser Asp Asn Asp Ala Ala Phe Phe Ser Gly
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Gly Gly Ile Phe Val Gln Gln Gln Ser Gly His Gly Asn Gly His Gly
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Sequence alignment of the protein with the reference sequence																
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				545	Lys	Pro	Ser	Leu	Phe	550	G n	Thr	Pro	I le	Phe	555
				560	Lys	Pro	Ser	Leu	Phe	565	G n	Thr	Pro	I le	Phe	570
				575	Lys	Pro	Ser	Leu	Phe	580	G n	Thr	Pro	I le	Phe	585
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				665	Lys	Pro	Ser	Leu	Phe	670	G n	Thr	Pro	I le	Phe	675
				680	Lys	Pro	Ser	Leu	Phe	685	G n	Thr	Pro	I le	Phe	690
				695	Lys	Pro	Ser	Leu	Phe	700	G n	Thr	Pro	I le	Phe	705
				710	Lys	Pro	Ser	Leu	Phe	715	G n	Thr	Pro	I le	Phe	720
				725	Lys	Pro	Ser	Leu	Phe	730	G n	Thr	Pro	I le	Phe	735
				740	Lys	Pro	Ser	Leu	Phe	745	G n	Thr	Pro	I le	Phe	750
				755	Lys	Pro	Ser	Leu	Phe	760	G n	Thr	Pro	I le	Phe	765
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				830	Lys	Pro	Ser	Leu	Phe	835	G n	Thr	Pro	I le	Phe	840
				845	Lys	Pro	Ser	Leu	Phe	850	G n	Thr	Pro	I le	Phe	855
				860	Lys	Pro	Ser	Leu	Phe	865	G n	Thr	Pro	I le	Phe	870
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				905	Lys	Pro	Ser	Leu	Phe	910	G n	Thr	Pro	I le	Phe	915
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Pro	Arg 50	Thr	Val	Gly	Asp	Phe 55	Leu	Gly	Gly	Val	Gly 60	Gly	Al a	Gly	Al a
Pro 65	Pro	Gly	Pro	Al a	Al a 70	Al a	Al a	Asp	Gly	Asp 75	His	Gly	Leu	Val	Cys 80
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Al a	Met	Ser 115	Ser	Thr	Asp	Val	Al a 120	Gly	Al a	Gly	Ser	Asp 125	Gly	Al a	Arg
Arg	Pro 130	Al a	Gly	Thr	Phe	Gly 135	Gly	Arg	Thr	Ser	Ile 140	Tyr	Arg	Gly	Val
Thr 145	Arg	His	Arg	Trp	Thr 150	Gly	Arg	Tyr	Gly	Al a 155	His	Leu	Trp	Asp	Asn 160
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Al a	Leu	Lys 195	Tyr	Trp	Gly	Pro	Thr 200	Thr	Thr	Thr	Asn	Phe 205	Pro	Val	Ser
Asn	Tyr 210	Gly	Lys	Gly	Leu	Gly 215	Gly	Met	Lys	Ser	Met 220	Thr	Arg	Gly	Gly
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Phe	Ser	Thr 275	Gly	Gly	Gly	Al a	Al a 280	Gly	Al a	Tyr	Asp	Ile 285	Al a	Al a	Ile
Lys	Phe 290	Arg	Gly	Leu	Asn	Al a 295	Val	Thr	Asn	Phe	Asp 300	Met	Ser	Arg	Tyr
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Ser	Gly	Arg	Al a	Pro 325	Al a	Lys	Phe	Pro	Leu 330	Asp	Ser	Leu	Gly	Pro 335	Gly
Ser	Al a	Al a	Al a 340	Met	Met	Leu	Al a	Gly 345	Al a	Al a	Al a	Al a	Ser 350	Gly	Al a
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Sequence Listing from Patent scope

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Ala	Thr	Thr	Gly	Ala	Val	Val	Val	Gly	Gln	Gln	Asp	Ser	Ser	Gly	Lys
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 <212> PRT
 <213> Oryza sativa

<400> 73

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Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala
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Phe	Pro	Val	Ala	Glu	Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met
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Tyr	Leu	Gly	Thr	Phe	Gly	Thr	Glu	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp
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Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Glu
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Sequence Listing from Patent scope

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Pro	Ser	Ser	Ser	Ala	340	Pro	Ser	Thr	Leu	345	Ala	Phe	Thr	Ala	Leu	Pro	Met	Lys	
Gly	Val	Ala	355	Gln	Ala	Asp	Tyr	Leu	Ser	360	Tyr	Leu	Ala	Leu	Gln	His	His	Gln	
Tyr	Asp	370	Gly	Asn	Leu	Gln	Gly	Leu	Gly	Phe	Gly	Leu	Tyr	Ser	Ser	Gly	Val		
385	Asn	Leu	Asp	Phe	Ala	405	Asn	Ala	Asn	Gly	Asn	410	Gly	Ala	Met	Ser	Asn	Cys	
Tyr	Thr	Asn	Val	Ser	Leu	His	Glu	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Gln			
His	Gln	Gln	435	Glu	Gln	Gln	Gln	Asp	440	Gln	Gln	Asp	Asp	Gln	445	Ser	Gln	Ser	
Ser	Asn	Asn	Ser	Cys	Gly	Ser	Ile	Pro	Phe	Ala	Thr	Pro	Ile	Ala	Phe				
450	Ser	Gly	Ser	Tyr	Glu	Ser	Ser	Met	Thr	Ala	Ala	475	Gly	Thr	Phe	Gly	Tyr		
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<210> 74

<211> 558

<212> PRT

<213> Arabidopsis thaliana

<400> 74

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				20				25					30						
Phe	Ser	Leu	Ser	Asn	Asn	Asn	Asn	Asn	Phe	Asn	Ser	Ser	45	Ser	Asn	Pro			
				35				40											
Asn	Leu	Thr	Ser	Ser	Thr	Ser	Asp	His	His	His	Pro	His	Pro	Ser	His				
				50				55					60						
Leu	Ser	Leu	Phe	Gln	Ala	Phe	Ser	Thr	Ser	Pro	Val	Glu	Arg	Gln	Asp				
65				70															
Gly	Ser	Pro	Gly	Val	Ser	Pro	Ser	Asp	Ala	Thr	Ala	Val	Leu	Ser	Val				
				85				90											
Tyr	Pro	Gly	Gly	Pro	Lys	Leu	Glu	Asn	Phe	Leu	Gly	Gly	Gly	Ala	Ser				
				100				105											
Thr	Thr	Thr	Thr	Arg	Pro	Met	Gln	Gln	Val	Gln	Ser	Leu	Gly	Gly	Val				
				115				120											
Val	Phe	Ser	Ser	Asp	Leu	Gln	Pro	Pro	Leu	His	Pro	Pro	Ser	Ala	Ala				
				130				135											
Glu	Ile	Tyr	Asp	Ser	Glu	Leu	Lys	Ser	Ile	Ala	Ala	Ser	Phe	Leu	Gly				
145				150															
Asn	Tyr	Ser	Gly	Gly	His	Ser	Ser	Glu	Val	Ser	Ser	Val	His	Lys	Gln				
				165				170											
Gln	Pro	Asn	Pro	Leu	Ala	Val	Ser	Glu	Ala	Ser	Pro	Thr	Pro	Lys	Lys				
				180				185											
Asn	Val	Glu	Ser	Phe	Gly	Gln	Arg	Thr	Ser	Ile	Tyr	Arg	Gly	Val	Thr				
				195				200											
Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser				
				210				215											
Cys	Arg	Arg	Glu	Gly	Gln	Ser	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly				
225				230															
Gly	Tyr	Asp	Lys	Glu	Asp	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala				
				245					250										

Sequence Listing from Patent scope

Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Thr	Thr	Asn	Phe	Pro	Ile	Ser	Asn
			260					265				270		
Tyr	Glu	Ser	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln	Glu
		275					280					285		
Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala
	290					295					300			
Met	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln
305					310					315				320
Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr
				325					330					335
Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile
			340					345					350	
Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile	Ser	Arg	Tyr
		355					360					365		
Val	Lys	Ser	Ile	Ala	Ser	Cys	Asn	Leu	Pro	Val	Gly	Gly	Leu	Met
	370					375					380			
Lys	Pro	Ser	Pro	Ala	Thr	Ala	Ala	Ala	Asp	Lys	Thr	Val	Asp	Leu
385					390					395				400
Pro	Ser	Asp	Ser	Pro	Ser	Leu	Thr	Thr	Pro	Ser	Leu	Thr	Phe	Asn
				405					410					415
Ala	Thr	Pro	Val	Asn	Asp	His	Gly	Gly	Thr	Phe	Tyr	His	Thr	Gly
			420				425						430	
Pro	Ile	Lys	Pro	Asp	Pro	Ala	Asp	His	Tyr	Trp	Ser	Asn	Ile	Phe
		435					440					445		
Phe	Gln	Ala	Asn	Pro	Lys	Ala	Glu	Met	Arg	Pro	Leu	Ala	Asn	Phe
	450					455					460			
Ser	Asp	Leu	His	Asn	Pro	Ser	Pro	Gly	Tyr	Ala	Ile	Met	Pro	Val
465					470					475				480
Gln	Glu	Gly	Glu	Asn	Asn	Phe	Gly	Gly	Ser	Phe	Val	Gly	Ser	Asp
				485					490					495
Tyr	Asn	Asn	His	Ser	Ala	Ala	Ser	Asn	Pro	Val	Ser	Ala	Ile	Pro
			500					505					510	
Ser	Ser	Thr	Thr	Thr	Met	Ser	Asn	Gly	Asn	Glu	Gly	Tyr	Gly	Gly
		515					520					525		
Ile	Asn	Trp	Ile	Asn	Asn	Asn	Ile	Ser	Ser	Ser	Tyr	Gln	Thr	Ala
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<210> 75

<211> 568

<212> PRT

<213> Arabidopsis thaliana

<400> 75

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

	130					135					140				
G u 145	Val	Al a	Thr	Val	Lys 150	Al a	Ser	Pro	Al a	G u 155	Thr	Ser	Al a	Asp	Asn 160
Ser	Ser	Ser	Thr	Thr 165	Asn	Thr	Ser	G y	G y 170	Al a	I le	Val	G u	Al a	Thr 175
Pro	Arg	Arg	Thr 180	Leu	G u	Thr	Phe	G y 185	G n	Arg	Thr	Ser	I le	Tyr	Arg
G y	Val	Thr 195	Arg	Hi s	Arg	Trp	Thr 200	G y	Arg	Tyr	G u	Al a	Hi s	Leu	Trp
Asp	Asn 210	Ser	Oys	Arg	Arg	G u 215	G y	G n	Ser	Arg	Lys 220	G y	Arg	G n	Val
Tyr 225	Leu	G y	G y	Tyr	Asp 230	Lys	G u	G u	Lys	Al a 235	Al a	Arg	Al a	Tyr	Asp 240
Leu	Al a	Al a	Leu	Lys 245	Tyr	Trp	G y	Pro	Ser 250	Thr	Thr	Thr	Asn	Phe 255	Pro
I le	Thr	Asn	Tyr 260	G u	Lys	G u	Val	G u 265	G u	Met	Lys	Asn	Met 270	Thr	Arg
G n	G u	Phe 275	Val	Al a	Ser	I le	Arg 280	Arg	Lys	Ser	Ser	G y 285	Phe	Ser	Arg
G y	Al a 290	Ser	Met	Tyr	Arg	G y 295	Val	Thr	Arg	Hi s	Hi s 300	G n	Hi s	G y	Arg
Trp 305	G n	Al a	Arg	I le	G y 310	Arg	Val	Al a	G y	Asn 315	Lys	Asp	Leu	Tyr	Leu 320
G y	Thr	Phe	Ser	Thr 325	G u	G u	G u	Al a	Al a 330	G u	Al a	Tyr	Asp	I le	Al a 335
Al a	I le	Lys	Phe 340	Arg	G y	Leu	Asn	Al a 345	Val	Thr	Asn	Phe	G u 350	I le	Asn
Arg	Tyr	Asp 355	Val	Lys	Al a	I le	Leu 360	G u	Ser	Asn	Thr	Leu 365	Pro	I le	G y
G y	G y 370	Al a	Al a	Lys	Arg	Leu 375	Lys	G u	Al a	G n	Al a 380	Leu	G u	Ser	Ser
Arg 385	Lys	Arg	G u	G u	Met 390	I le	Al a	Leu	G y	Ser 395	Asn	Phe	Hi s	G n	Tyr 400
G y	Al a	Al a	Ser	G y 405	Ser	Ser	Ser	Val	Al a 410	Ser	Ser	Ser	Arg	Leu 415	G n
Leu	G n	Pro	Tyr 420	Pro	Leu	Ser	I le	G n 425	G n	Pro	Phe	G u	Hi s 430	Leu	Hi s
Hi s	Hi s	G n 435	Pro	Leu	Leu	Thr	Leu 440	G n	Asn	Asn	Asn	Asp 445	I le	Ser	G n
Tyr	Hi s 450	Asp	Ser	Phe	Ser	Tyr 455	I le	G n	Thr	G n	Leu 460	Hi s	Leu	Hi s	G n
G n 465	G n	Thr	Asn	Asn	Tyr 470	Leu	G n	Ser	Ser	Ser 475	Hi s	Thr	Ser	G n	Leu 480
Tyr	Asn	Al a	Tyr	Leu 485	G n	Ser	Asn	Pro	G y 490	Leu	Leu	Hi s	G y	Phe 495	Val
Ser	Asp	Asn	Asn 500	Asn	Thr	Ser	G y	Phe 505	Leu	G y	Asn	Asn	G y 510	I le	G y
I le	G y	Ser 515	Ser	Ser	Thr	Val	G y 520	Ser	Ser	Al a	G u	G u 525	G u	Phe	Pro
Al a	Val 530	Lys	Val	Asp	Tyr	Asp 535	Met	Pro	Pro	Ser	G y 540	G y	Al a	Thr	G y
Tyr 545	G y	G y	Trp	Asn	Ser 550	G y	G u	Ser	Al a	G n 555	G y	Ser	Asn	Pro	G y 560
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<210> 76
<211> 474
<212> PRT
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<400> 76

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Ala 65	Pro	Pro	Ala	Ala	Ala 70	Thr	Ala	Ala	Glu	Asp 75	His	Gln	Leu	Val	Cys 80
Gly	Glu	Leu	Gly	Ser 85	Ile	Thr	Ala	Gly	Phe 90	Leu	Arg	His	Tyr	Pro 95	Ala
Pro	Gly	Thr	Thr 100	Val	Glu	Asn	Pro	Gly 105	Ala	Val	Thr	Val	Ala 110	Ala	Met
Ser	Thr	Asp 115	Val	Ala	Glu	Ser	Asp 120	Gln	Ala	Arg	Arg	Pro 125	Ala	Glu	Thr
Phe	Gly 130	Gln	Arg	Thr	Ser	Ile 135	Tyr	Arg	Gly	Val	Thr 140	Arg	His	Arg	Trp
Thr 145	Gly	Arg	Tyr	Glu	Ala 150	His	Leu	Trp	Asp	Asn 155	Ser	Cys	Arg	Arg	Glu 160
Gly	Gln	Ser	Arg	Lys 165	Gly	Arg	Gln	Val	Tyr 170	Leu	Gly	Gly	Tyr	Asp 175	Lys
Glu	Glu	Lys	Ala 180	Ala	Arg	Ala	Tyr	Asp 185	Leu	Ala	Ala	Leu	Lys 190	Tyr	Trp
Gly	Ala	Thr 195	Thr	Thr	Thr	Asn	Phe 200	Pro	Val	Ser	Asn	Tyr 205	Glu	Lys	Glu
Leu	Glu 210	Glu	Met	Lys	Ser	Met 215	Thr	Arg	Gln	Glu	Phe 220	Ile	Ala	Ser	Leu
Arg 225	Arg	Lys	Ser	Ser	Gly 230	Phe	Ser	Arg	Gly	Ala 235	Ser	Ile	Tyr	Arg	Gly 240
Val	Thr	Arg	His	His 245	Gln	His	Gly	Arg	Trp 250	Gln	Ala	Arg	Ile	Gly 255	Arg
Val	Ala	Gly	Asn 260	Lys	Asp	Leu	Tyr	Leu 265	Gly	Thr	Phe	Ser	Thr 270	Gln	Glu
Glu	Ala	Ala 275	Glu	Ala	Tyr	Asp	Ile 280	Ala	Ala	Ile	Lys	Phe 285	Arg	Gly	Leu
Asn	Ala 290	Val	Thr	Asn	Phe	Asp 295	Met	Ser	Arg	Tyr	Asp 300	Val	Asp	Ser	Ile
Leu 305	Asn	Ser	Asp	Leu	Pro 310	Val	Gly	Gly	Gly	Ala 315	Ala	Gly	Arg	Ala	Ser 320
Lys	Phe	Pro	Leu	Asp 325	Ser	Leu	Gln	Pro	Gly 330	Ser	Ala	Ala	Ala	Met 335	Ile
Ala	Gly	Ala	Ala 340	Ser	Gln	Ala	Met	Pro 345	Pro	Ser	Glu	Lys	Asp 350	Tyr	Trp
Ser	Leu	Leu 355	Ala	Leu	His	Tyr	Gln 360	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Phe
Pro	Ala 370	Ser	Ala	Tyr	Glu	Ala 375	Tyr	Gly	Ser	Gly	Val 380	Asn	Val	Asp	Phe
Thr 385	Met	Gly	Thr	Ser	Ser	His	Ser	Ser	Ser	Asn 395	Thr	Gly	Ser	Gly	Val 400
Met	Trp	Gly	Thr 405	Thr	Thr	Gly	Ala	Met	Gly 410	Gln	Gln	Asp	Ser	Ser	Ser
Ser	Lys	Gln	Gly 420	Asn	Gly	Tyr	Ala	Ser 425	Asn	Ile	Pro	Tyr	Ala 430	Ala	Ala
Ala	Ala	Ala 435	Met	Val	Ser	Gly	Ser 440	Ala	Gly	Tyr	Glu	Gly 445	Ser	Thr	Gly
Asn	Asn 450	Gly	Thr	Trp	Val	Thr 455	Ser	Ser	Thr	Ser	Thr 460	Ser	Thr	Ala	Pro
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<211> 549

<212> PRT

<213> Oryza sativa

<400> 77

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Gly 3  Asp  Gly  Ser  Cys  Ser  Ser  Pro  Val  Ala  Ala  Ser  Pro  Leu  Val  Ala
Met 4  Pro  Leu  His  Ser  Asp  Gly  Ser  Val  His  Tyr  Asp  Ala  Pro  Asp  Trp
Arg 5  His  Ala  Glu  Ala  Lys  Asp  Pro  Lys  Leu  Glu  Asp  Phe  Met  Ser  Val
Ser 6  Tyr  Ser  Asn  Lys  Ser  Ser  Ser  Asn  Leu  Tyr  Gly  Ser  Ser  Ser  Ser
Ser 7  Ser  Cys  Gly  His  Ala  Asp  Gln  Ile  Lys  Tyr  His  His  Val  His  Asp
Val 8  Gln  Ala  Phe  Ser  Thr  Pro  Tyr  Phe  Tyr  Gly  His  Gly  Gly  Ser  Gly
Val 9  Gly  Ile  Asp  Ile  Asn  Met  Asn  Ala  Pro  Pro  Ala  Gly  Cys  Thr  Gly
Val 10 Leu  Pro  Asp  His  Arg  Pro  Pro  Pro  Pro  Gln  Gln  Asp  His  Ile  Phe
Leu 11 Pro  Pro  His  Gly  Gln  Tyr  Phe  Leu  Gly  Pro  Pro  Asn  Pro  Met  Ala
Pro 12 Ala  Pro  Met  Tyr  Asn  Ala  Gly  Gly  Gly  Gly  Gly  Gly  Val  Val  Asp
Gly 13 Ser  Met  Ser  Ile  Ser  Gly  Ile  Lys  Ser  Trp  Leu  Arg  Gln  Ala  Met
Tyr 14 Val  Pro  Glu  Arg  Ser  Ala  Ala  Ala  Leu  Ser  Leu  Ser  Val  Pro  Ala
Ala 15 Pro  Pro  Ser  Glu  Ala  Pro  Leu  Pro  Pro  Ala  Ala  Met  Pro  Val  Val
Arg 16 Lys  Pro  Ala  Gln  Thr  Phe  Gly  Gln  Arg  Thr  Ser  Gln  Phe  Arg  Gly
Val 17 Thr  Arg  His  Arg  Trp  Thr  Gly  Arg  Tyr  Glu  Ala  His  Leu  Trp  Asp
Asn 18 Thr  Cys  Arg  Lys  Glu  Gly  Gln  Thr  Arg  Lys  Gly  Arg  Gln  Val  Tyr
Leu 19 Gly  Gly  Tyr  Asp  Lys  Glu  Lys  Ala  Ala  Arg  Ala  Tyr  Asp  Leu
Ala 20 Ala  Leu  Lys  Tyr  Trp  Gly  Pro  Thr  Thr  His  Ile  Asn  Phe  Pro  Leu
Ser 21 Thr  Tyr  Glu  Lys  Glu  Leu  Glu  Glu  Met  Lys  His  Met  Thr  Arg  Gln
Glu 22 Phe  Ile  Ala  His  Leu  Arg  Arg  Asn  Ser  Ser  Gly  Phe  Ser  Arg  Gly
Ala 23 Ser  Met  Tyr  Arg  Gly  Val  Thr  Arg  His  His  Gln  His  Gly  Arg  Trp
Gln 24 Ala  Arg  Ile  Gly  Arg  Val  Ala  Gly  Asn  Lys  Asp  Leu  Tyr  Leu  Gly
Thr 25 Phe  Ser  Thr  Gln  Glu  Glu  Ala  Ala  Glu  Ala  Tyr  Asp  Ile  Ala  Ala
Ile 26 Lys  Phe  Arg  Gly  Leu  Asn  Ala  Val  Thr  Asn  Phe  Asp  Ile  Ser  Lys
Tyr 27 Asp  Val  Lys  Arg  Ile  Cys  Ser  Ser  Thr  His  Leu  Ile  Gly  Gly  Asp
Leu 28 Ala  Cys  Arg  Arg  Ser  Pro  Thr  Arg  Met  Leu  Pro  Pro  Asp  Ala  Pro
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Sequence Listing from Patent scope

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 485 490 495
 His Ala Met Lys Phe Gu Ala Gly Gu Ser Ser Gly Gly Gly Gly
 500 505 510
 Asp Gly Ala Thr Thr Asn Trp Met Ala Ala Ala Ala Ala Arg
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 530 535 540
 Ala Leu Trp Asn Asp
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 <212> PRT
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<400> 78
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 35 40 45
 Asn Leu Ile Asn Thr His Ser Ser Asn Gu Ile Pro Lys Val Ala Asp
 50 55 60
 Phe Leu Gly Val Ser Lys Ser Gu Asn Gln Ser Asp Leu Ala Ala Leu
 65 70 75 80
 Asn Gu Ile His Ser Asn Asp Ser Asp Tyr Leu Phe Thr Asn Asn Ser
 85 90 95
 Leu Val Pro Met Gln Asn Pro Val Leu Asp Thr Pro Ser Asn Gu Tyr
 100 105 110
 Gln Gu Asn Ala Asn Ser Asn Leu Gln Ser Leu Thr Leu Ser Met Gly
 115 120 125
 Ser Gly Lys Asp Ser Thr Cys Gu Thr Ser Gly Gu Asn Ser Thr Asn
 130 135 140
 Thr Thr Val Gu Val Ala Pro Arg Arg Thr Leu Asp Thr Phe Gly Gln
 145 150 155 160
 Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg
 165 170 175
 Tyr Gu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Gu Gly Gln Ser
 180 185 190
 Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Gu Gu Lys
 195 200 205
 Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Ser
 210 215 220
 Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Gu Lys Gu Leu Asp Gu
 225 230 235 240
 Met Lys His Met Thr Arg Gln Gu Phe Val Ala Ala Ile Arg Arg Lys
 245 250 255
 Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly Val Thr Arg
 260 265 270
 His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly
 275 280 285
 Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gu Gu Gu Ala Ala
 290 295 300
 Gu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val
 305 310 315 320
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 325 330 335
 Asn Thr Leu Pro Ile Gly Gly Gly Ala Ala Lys Arg Leu Lys Gu Ala

Sequence Listing from Patent scope

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His	370 Ala	Tyr	Pro	Leu	Met	375 Gln	His	His	His	Gln	380 Phe	Glu	Gln	Pro	Gln
385 Pro	Leu	Leu	Thr	Leu	Gln	390 Asn	His	Asp	Ile	Ser	Ser	Ser	His	Phe	Ser
His	Gln	Gln	Asp	405 Pro	Leu	His	His	Gln	410 Gly	Tyr	Ile	Gln	Thr	Gln	Leu
Gln	Leu	His	420 Gln	Gln	Ser	Gly	Ala	425 Ser	Ser	Tyr	Ser	Phe	Gln	Asn	Asn
Ala	435 Gln	Phe	Tyr	Asn	Gly	Tyr	440 Leu	Gln	Asn	His	Pro	445 Ala	Leu	Leu	Gln
Gly	450 Met	Met	Asn	Met	Gly	455 Ser	Ser	Ser	Ser	Ser	460 Ser	Ser	Val	Leu	Glu
465 Asn	Asn	Asn	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Val	Gly	Gly	Phe	Val	Gly
Ser	Gly	Phe	Gly	485 Met	Ala	Ser	Asn	Ala	490 Thr	Ala	Gly	Asn	Thr	Val	Gly
Thr	Ala	Glu	500 Glu	Leu	Gly	Leu	Val	505 Lys	Val	Asp	Tyr	Asp	510 Met	Pro	Ala
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<211> 509

<212> PRT

<213> Medicago truncatula

<400> 79

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Ser	Ile	Ile	Pro	Pro	Ser	Leu	Thr	Leu	Thr	Gly	Ser	60 Asn	Asn	Pro	Val
Glu	Ala	Ser	Pro	Glu	Ala	Thr	Asp	Gly	Gly	Thr	Thr	Asn	Leu	Ser	Ile
65	Phe	Thr	Gly	Gly	His	Lys	Phe	Glu	Asp	90 Phe	Leu	Gly	Ser	Ser	Val
Pro	Thr	Arg	Thr	Ala	Ala	Ala	Thr	Cys	105 Ala	Pro	Thr	Gln	Leu	Gln	Gln
Phe	Ser	Thr	Asp	Asn	Asp	Val	Tyr	120 Asn	Ser	Glu	Leu	Lys	Lys	Thr	Ile
Ala	Ala	Cys	Phe	Pro	Gly	Gly	Tyr	Pro	Thr	Glu	Pro	125 Asn	Ser	Glu	Pro
Gln	Lys	Pro	Ser	Pro	Lys	Lys	Thr	Val	Asp	Thr	Phe	Gly	Gln	Arg	Thr
145	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr
Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	185 Arg	Arg	Glu	Gly	Gln	Ser	Arg	Lys
Gly	Arg	Gln	Gly	Gly	Tyr	Asp	Lys	200 Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr
Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Thr	Thr	Asn	Phe	
210					215										

Sequence Listing from Patent scope

Pro 225	Ile	Ser	Asn	Tyr	Glu 230	Lys	Glu	Ile	Asp 235	Met	Lys	Asn	Met	Thr 240	
Arg	Gln	Glu	Phe	Val 245	Ala	Ser	Leu	Arg	Arg 250	Lys	Ser	Ser	Gly	Phe 255	Ser
Arg	Gly	Ala	Ser 260	Ile	Tyr	Arg	Gly	Val 265	Thr	Arg	His	His	Gln	His	Gly
Arg	Trp	Gln 275	Ala	Arg	Ile	Gly	Arg 280	Val	Ala	Gly	Asn	Lys 285	Asp	Leu	Tyr
Leu	Gly 290	Thr	Phe	Ser	Thr	Gln 295	Glu	Glu	Ala	Ala	Glu 300	Ala	Tyr	Asp	Ile
Ala 305	Ala	Ile	Lys	Phe	Arg 310	Gly	Leu	Asn	Ala	Val 315	Thr	Asn	Phe	Asp	Met 320
Ser	Arg	Tyr	Asp	Val 325	Lys	Ser	Ile	Ala	Asn 330	Cys	Ser	Leu	Pro	Ile	Gly
Gly	Leu	Ser	Asn 340	Lys	Asn	Asn	Lys	Asn 345	Ser	Thr	Asp	Cys	Val 350	Ser	Glu
Thr	Lys	Ile 355	Asn	Glu	Pro	Ile	Gln 360	Ser	Asp	Glu	Ile	Asp 365	His	Pro	Ser
Ser	Thr 370	Ser	Ser	Ala	Thr	Thr 375	Leu	Ser	Phe	Ala	Leu 380	Pro	Ile	Lys	Gln
Asp 385	Pro	Ser	Thr	Asp	Tyr 390	Trp	Ser	Asn	Ile	Leu 395	Gly	Phe	His	Asn	Asn 400
Pro	Ser	Ala	Val	Thr 405	Thr	Thr	Thr	Ile	Pro 410	Phe	Asn	Met	Asp	Phe	Ser
Ala	His	Val	Pro 420	Ser	Asn	Thr	Asn	Ser 425	Asp	Asn	Pro	His	Asn 430	Ala	Ala
Phe	Phe	Ser 435	Gly	Ser	Gly	Ile	Phe 440	Val	Gln	Gln	Gln	Asn 445	Met	Asn	Gly
Ser	Ser 450	Gly	Ser	Asn	Ser	Ser	Ser	Ser	Ser	Ala 460	Ser	Thr	Ser	Ser	
Ile 465	Pro	Phe	Ala	Thr	Pro 470	Ile	Phe	Ser	Leu	Asn 475	Ser	Asn	Ser	Ser	Ser 480
Tyr	Gly	Asn	Gly	Asn 485	Asn	Trp	Ile	Gly	His 490	Thr	Phe	Gln	Thr	His 495	Ala
Lys	Pro	Ser	Leu 500	Phe	Gln	Thr	Pro	Ile 505	Phe	Gly	Met	Glu			

<210> 80
 <211> 492
 <212> PRT
 <213> Zea mays

<400> 80

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

Sequence Listing from Patent scope

145	Val	Tyr	Leu	Gly	Gly	150	Tyr	Asp	Lys	Glu	Glu	155	Lys	Ala	Ala	Arg	Ala	160	Tyr
				165	Leu	Lys	Tyr	Trp	Gly	Ser	Ser	Thr	Thr	Thr	Thr	Asn	Phe		
Asp	Leu	Ala	Ala	180	Tyr	Glu	Lys	Glu	185	Val	Glu	Glu	Met	Lys	Asn	Met	Thr		
Pro	Val	Ala	Glu	195	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser			
Arg	Gln	Glu	Phe	210	Gly	Ala	Ser	Ile	215	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His
Arg	Gly	Ala	Ser	225	Arg	Ile	Gly	Arg	Val	Ala	235	Gly	Asn	Lys	Asp	Leu	240	Tyr	
Arg	Trp	Gln	Ala	245	Ser	Thr	Glu	Glu	Glu	Ala	250	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	
Leu	Gly	Thr	Phe	260	Leu	Arg	Gly	Leu	Asn	Ala	265	Ala	Val	Thr	Asn	Phe	Glu	Ile	
Ala	Ala	Ile	Lys	275	Val	Glu	Thr	Ile	Met	Ser	Ser	Asn	Leu	Pro	Val	Ala			
Ser	Arg	Tyr	Asn	290	Ser	Ala	Ala	Ala	Ala	Ala	300	Gly	Gly	Arg	Ser	Ser	Lys		
Ser	Met	Ser	Ser	305	Ala	Ala	Ala	Ala	Ala	Ala	315	Gly	Gly	Arg	Ser	Ser	Lys		
Ala	Leu	Glu	Ser	325	Pro	Ser	Gly	Ser	Leu	330	Asp	Gly	Gly	Gly	Gly	Met			
Pro	Val	Val	Glu	340	Ala	Ser	Thr	Ala	Pro	Pro	Leu	Phe	Ile	Pro	Val	Lys			
Tyr	Asp	Gln	Gln	355	Gln	Gln	Glu	Tyr	Leu	Ser	Met	Leu	Ala	Leu	Gln	Gln			
His	His	Gln	Gln	370	Gln	Gln	Ala	Gly	Asn	Leu	Leu	Gln	Gly	Pro	Leu	Val			
Gly	Phe	Gly	Gly	385	Leu	Tyr	Ser	Ser	Gly	Val	Asn	Leu	Asp	Phe	Ala	Asn			
Ser	His	Gly	Thr	405	Ala	Pro	Ser	Ser	Met	Ala	410	His	His	Cys	Tyr	Ala			
Asn	Gly	Thr	Ala	420	Ser	Ala	Ser	His	Glu	His	Gln	His	Gln	Met	Gln	Gln			
Gly	Gly	Glu	Asn	435	Glu	Thr	Gln	Pro	Gln	Pro	Gln	Gln	Ser	Ser	Ser	Ser			
Cys	Ser	Ser	Leu	450	Pro	Phe	Ala	Thr	Pro	Val	Ala	Phe	Asn	Gly	Ser	Tyr			
Glu	Ser	Ser	Ile	465	Thr	Ala	Ala	Gly	Pro	Phe	Gly	Tyr	Ser	Tyr	Pro	Asn			
Val	Ala	Ala	Phe	485	Thr	Pro	Ile	Tyr	Gly	Met	Glu					480			

<210> 81
 <211> 469
 <212> PRT
 <213> Oryza sativa

<400> 81

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

Sequence Listing from Patent scope

Asn	Ala	Gly	Gly	Val	Thr	Ile	Ala	Met	Ala	Thr	Asp	Ala	Ala	Ala	Glu
Leu	Ala	Asp	Pro	Ala	Arg	Arg	Thr	Ala	Glu	Thr	Phe	Gly	Gln	Arg	Thr
Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu
Ala	His	Leu	Trp	Asp	Asn	Ser	Oys	Arg	Arg	Glu	Gly	Gln	Ser	Arg	Lys
Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala
Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Thr	Thr
Thr	Asn	Phe	Pro	Val	Ala	Asn	Tyr	Glu	Thr	Glu	Leu	Glu	Glu	Met	Lys
Ser	Met	Thr	Arg	Gln	Glu	Phe	Ile	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser
Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His
Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys
Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala
Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn
Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Asp	Ser	Ile	Leu	Asn	Ser	Asp	Leu
Pro	Val	Gly	Gly	Gly	Ala	Ala	Thr	Arg	Ala	Ser	Lys	Phe	Pro	Ser	Asp
Pro	Ser	Leu	Pro	Leu	Pro	Ser	Pro	Ala	Met	Pro	Pro	Ser	Glu	Lys	Asp
Tyr	Trp	Ser	Leu	Leu	Ala	Leu	His	Tyr	His	His	His	Gln	Gln	Gln	Gln
Gln	Gln	Gln	Gln	Phe	Pro	Ala	Ser	Ala	Phe	Asp	Thr	Tyr	Gly	Oys	Ser
Ser	Gly	Val	Asn	Val	Asp	Phe	Thr	Met	Gly	Thr	Ser	Ser	His	Ser	Gly
Ser	Asn	Ser	Asn	Ser	Ser	Ser	Ser	Ser	Ala	Ile	Trp	Gly	Thr	Ala	Ala
Gly	Ala	Ala	Met	Gly	Arg	Gln	Gln	Asn	Gly	Gly	Ser	Ser	Asn	Lys	Gln
Ser	Asn	Ser	Tyr	Ser	Gly	Asn	Asn	Ile	Pro	Tyr	Ala	Ala	Ala	Ala	Ala
Met	Thr	Ser	Gly	Ser	Ala	Leu	Tyr	Gly	Gly	Ser	Thr	Gly	Ser	Asn	Gly
Thr	Trp	Val	Ala	Ser	Asn	Thr	Ser	Thr	Ala	Pro	His	Phe	Tyr	Asn	Tyr
Leu	Phe	Gly	Met	Glu											

<210> 82
 <211> 562
 <212> PRT
 <213> Glycine max

<400> 82
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 Leu Pro Ala His Asp Leu Gln Ala Thr Gln Tyr His Gln Phe Ser Leu
 20 25 30
 Gly Leu Val Asn Glu Asn Met Glu Asn Pro Phe Gln Asn His Asp Trp
 35 40 45
 Ser Leu Ile Asn Thr His Ser Ser Ser Glu Val Pro Lys Val Ala Asp

Sequence Listing from Patent scope

	50					55				60					
Phe 65	Leu	G y	Val	Ser	Lys 70	Ser	G u	Asn	G u	Ser 75	Asp	Leu	Al a	Al a	Ser 80
Leu	Asn	G u	I le	G n 85	Ser	Asn	Asp	Ser	Asp 90	Tyr	Leu	Phe	Thr	Asn 95	Asn
Ser	Leu	Val	Pro 100	Met	G n	Asn	Pro	Al a 105	Val	Asp	Thr	Pro	Ser 110	Asn	G u
Tyr	G n	G u 115	Asn	Al a	Asn	Ser	Ser 120	Leu	G n	Ser	Leu	Thr 125	Leu	Ser	Met
G y	Ser 130	G y	Lys	Asp	Ser	Thr 135	Oys	G u	Thr	Ser	G y 140	Asp	Asn	Ser	Thr
Asn 145	Thr	Thr	Thr	Thr	Thr 150	Thr	Val	G u	Al a	Al a 155	Pro	Arg	Arg	Thr	Leu 160
Asp	Thr	Phe	G y	G n 165	Arg	Thr	Ser	I le	Tyr 170	Arg	G y	Val	Thr	Arg 175	Hi s
Arg	Trp	Thr	G y 180	Arg	Tyr	G u	Al a	Hi s 185	Leu	Trp	Asp	Asn	Ser 190	Oys	Arg
Arg	G u	G y 195	G n	Ser	Arg	Lys	G y 200	Arg	G n	Val	Tyr	Leu 205	G y	G y	Tyr
Asp	Lys 210	G u	G u	Lys	Al a	Al a 215	Arg	Ser	Tyr	Asp	Leu 220	Al a	Al a	Leu	Lys
Tyr 225	Trp	G y	Thr	Ser	Thr 230	Thr	Thr	Asn	Phe	Pro 235	I le	Ser	Asn	Tyr	G u 240
Lys	G u	Leu	Asp	G u 245	Met	Lys	Hi s	Met	Thr 250	Arg	G n	G u	Phe	Val 255	Al a
Al a	I le	Arg	Arg 260	Lys	Ser	Ser	G y	Phe 265	Ser	Arg	G y	Al a	Ser 270	Met	Tyr
Arg	G y	Val 275	Thr	Arg	Hi s	Hi s	G n 280	Hi s	G y	Arg	Trp	G n 285	Al a	Arg	I le
G y	Arg 290	Val	Al a	G y	Asn	Lys 295	Asp	Leu	Tyr	Leu	G y 300	Thr	Phe	Ser	Thr
G u 305	G u	G u	Al a	Al a	G u 310	Al a	Tyr	Asp	I le	Al a 315	Al a	I le	Lys	Phe	Arg 320
G y	Leu	Asn	Al a	Val 325	Thr	Asn	Phe	Asp	Met 330	Ser	Arg	Tyr	Asp	Val 335	Lys
Al a	I le	Leu	G u 340	Ser	Asn	Thr	Leu	Pro 345	I le	G y	G y	G y	Al a 350	Al a	Lys
Arg	Leu	Lys 355	G u	Al a	G n	Al a	Leu 360	G u	Ser	Ser	Arg	Lys 365	Arg	G u	G u
Met	I le 370	Al a	Leu	G y	Ser	Ser 375	Thr	Phe	G n	Tyr	G y 380	Thr	Thr	Ser	Ser
Asn 385	Ser	Arg	Leu	Hi s	Al a 390	Tyr	Pro	Leu	Met	G n 395	Hi s	Hi s	Hi s	G n	Phe 400
G u	G n	Pro	G n	Pro 405	Leu	Leu	Thr	Leu	G n 410	Asn	Hi s	Asp	I le	Ser 415	Ser
Hi s	Phe	Ser	Hi s 420	G n	G n	Asp	Pro	Leu 425	Hi s	G n	G y	Tyr	I le 430	G n	Thr
G n	Leu	G n	Leu 435	Hi s	G n	G n	G n 440	Ser	G y	G y	Ser	Ser 445	Ser	Tyr	Ser
Phe	G n 450	Asn	Asn	Asn	I le	Asn 455	Asn	Al a	G n	Phe	Tyr 460	Asn	G y	Tyr	Asn
Leu 465	G n	Asn	Hi s	Pro	Al a 470	Leu	Leu	G n	G y	Met 475	I le	Asn	Met	G y	Ser 480
Ser	Ser	Ser	Ser	Ser 485	Val	Leu	G u	Asn	Asn 490	Asn	Ser	Asn	Asn	Asn 495	Asn
Val	G y	G y	Phe 500	Val	G y	Ser	G y	Phe 505	G y	Met	Al a	Ser	Asn 510	Al a	Thr
Ser	G y	Asn 515	Thr	Val	G y	Thr	Al a 520	G u	G u	Leu	G y	Leu 525	Val	Lys	Val
Asp	Tyr 530	Asp	Met	Pro	Thr	G y 535	G y	Tyr	G y	G y	Trp 540	Ser	Al a	Al a	Al a
Al a 545	Al a	G u	Ser	Met	G n 550	Thr	Ser	Asn	Ser	G y 555	Val	Phe	Thr	Met	Trp 560

Sequence Listing from Patent scope

Asn Asp

<210> 83
<211> 574
<212> PRT
<213> Arabidopsis thaliana

<400> 83
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Ser Leu Pro Pro His Gu Tyr Asn Leu Gly Leu Val Ser Asp His Met
20 25 30
Asp Asn Pro Phe Gn Thr Gn Gu Trp Asn Met Ile Asn Pro His Gly
35 40 45
Gly Gly Gly Asp Gu Gly Gly Gu Val Pro Lys Val Ala Asp Phe Leu
50 55 60
Gly Val Ser Lys Pro Asp Gu Asn Gn Ser Asn His Leu Val Ala Tyr
65 70 75 80
Asn Asp Ser Asp Tyr Thr Phe His Thr Asn Ser Leu Met Pro Ser Val
85 90 95
Gn Ser Asn Asp Val Val Val Ala Ala Cys Asp Ser Asn Thr Pro Asn
100 105 110
Asn Ser Ser Tyr His Gu Leu Gn Gu Ser Ala His Asn Leu Gn Ser
115 120 125
Leu Thr Leu Ser Met Gly Thr Thr Ala Gly Asn Asn Val Val Asp Lys
130 135 140
Ala Ser Pro Ser Gu Thr Thr Gly Asp Asn Ala Ser Gly Gly Ala Leu
145 150 155 160
Ala Val Val Gu Thr Ala Thr Pro Arg Arg Ala Leu Asp Thr Phe Gly
165 170 175
Gn Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly
180 185 190
Arg Tyr Gu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Gu Gly Gn
195 200 205
Ser Arg Lys Gly Arg Gn Val Tyr Leu Gly Gly Tyr Asp Lys Gu Asp
210 215 220
Lys Ala Ala Arg Ser Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro
225 230 235 240
Ser Thr Thr Thr Asn Phe Pro Ile Thr Asn Tyr Gu Lys Gu Val Gu
245 250 255
Gu Met Lys His Met Thr Arg Gn Gu Phe Val Ala Ala Ile Arg Arg
260 265 270
Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly Val Thr
275 280 285
Arg His His Gn His Gly Arg Trp Gn Ala Arg Ile Gly Arg Val Ala
290 295 300
Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gu Gu Gu Ala
305 310 315 320
Ala Gu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala
325 330 335
Val Thr Asn Phe Gu Ile Asn Arg Tyr Asp Val Lys Ala Ile Leu Gu
340 345 350
Ser Ser Thr Leu Pro Ile Gly Gly Gly Ala Ala Lys Arg Leu Lys Gu
355 360 365
Ala Gn Ala Leu Gu Ser Ser Arg Lys Arg Gu Ala Gu Met Ile Ala
370 375 380
Leu Gly Ser Ser Phe Gn Tyr Gly Gly Gly Ser Ser Thr Gly Ser Gly
385 390 395 400
Ser Thr Ser Ser Arg Leu Gn Leu Gn Pro Tyr Pro Leu Ser Ile Gn
405 410 415
Gn Pro Leu Gu Pro Phe Leu Ser Leu Gn Asn Asn Asp Ile Ser His

Sequence Listing from Patent scope

			420					425					430				
Tyr	Asn	Asn	Asn	Asn	Ala	His	Asp	Ser	Ser	Ser	Phe	Asn	His	His	Ser		
		435					440					445					
Tyr	Ile	Gln	Thr	Gln	Leu	His	Leu	His	Gln	Gln	Thr	Asn	Asn	Tyr	Leu		
	450					455					460						
Gln	Gln	Gln	Ser	Ser	Gln	Asn	Ser	Gln	Gln	Leu	Tyr	Asn	Ala	Tyr	Leu		
465					470					475					480		
His	Ser	Asn	Pro	Ala	Leu	Leu	His	Gly	Leu	Val	Ser	Thr	Ser	Ile	Val		
				485					490					495			
Asp	Asn	Asn	Asn	Asn	Asn	Gly	Gly	Ser	Ser	Gly	Ser	Tyr	Asn	Thr	Ala		
		500						505					510				
Ala	Phe	Leu	Gly	Asn	His	Gly	Ile	Gly	Ile	Gly	Ser	Ser	Ser	Thr	Val		
		515					520					525					
Gly	Ser	Thr	Glu	Glu	Phe	Pro	Thr	Val	Lys	Thr	Asp	Tyr	Asp	Met	Pro		
	530					535					540						
Ser	Ser	Asp	Gly	Thr	Gly	Gly	Tyr	Ser	Gly	Trp	Thr	Ser	Glu	Ser	Val		
545					550					555					560		
Gln	Gly	Ser	Asn	Pro	Gly	Gly	Val	Phe	Thr	Met	Trp	Asn	Glu				
				565					570								

<210> 84

<211> 543

<212> PRT

<213> Medicago truncatula

<400> 84

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

Sequence Listing from Patent scope

Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Glu	Glu	Glu	Ala	Ala	Glu
290	290					295				300	300				
Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr
305				310						315					320
Asn	Phe	Asp	Met	Thr	Arg	Tyr	Asp	Val	Lys	Ala	Ile	Leu	Glu	Ser	Asn
				325					330					335	
Thr	Leu	Pro	Ile	Gly	Gly	Gly	Ala	Ala	Lys	Arg	Leu	Lys	Glu	Ala	Gln
			340				345						350		
Ala	Leu	Glu	Thr	Ser	Arg	Lys	Arg	Glu	Glu	Met	Leu	Ala	Leu	Asn	Ser
		355					360					365			
Ser	Ser	Phe	Gln	Tyr	Gly	Thr	Ser	Ser	Ser	Ser	Asn	Thr	Arg	Leu	Gln
		370				375					380				
Pro	Tyr	Pro	Leu	Met	Gln	Tyr	His	His	Gln	Phe	Glu	Gln	Pro	Gln	Pro
385					390					395					400
Leu	Leu	Thr	Leu	Gln	Asn	Asn	His	Glu	Ser	Leu	Asn	Ser	Gln	Gln	Phe
				405					410					415	
Ser	Gln	His	Gln	Gly	Gly	Gly	Tyr	Phe	Gln	Thr	Gln	Leu	Glu	Leu	Cys
			420					425					430		
Gln	Gln	Gln	Asn	Gln	Gln	Pro	Ser	Gln	Asn	Ser	Asn	Ile	Gly	Ser	Phe
		435					440					445			
Tyr	Asn	Gly	Tyr	Tyr	Gln	Asn	His	Pro	Gly	Leu	Phe	Gln	Met	Asn	Asn
		450				455					460				
Ile	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Val	Met	Gly	Asn	Asn	Gly	Gly	Gly
465					470					475					480
Ser	Ser	Gly	Ile	Tyr	Ser	Asn	Ser	Gly	Gly	Leu	Ile	Ser	Asn	Asn	Ala
				485					490					495	
Val	Glu	Glu	Phe	Val	Pro	Val	Lys	Val	Asp	Tyr	Asp	Met	Gln	Gly	Asp
			500					505					510		
Gly	Ser	Gly	Phe	Gly	Gly	Trp	Ser	Ala	Ala	Gly	Glu	Asn	Met	Gln	Thr
		515					520					525			
Ala	Asp	Leu	Phe	Thr	Met	Trp	Asn	Asp	Tyr	Glu	Thr	Arg	Glu	Asn	
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 <212> PRT
 <213> Zea mays

<400> 85

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

Ala	Met	Pro	Met	Tyr	Asn	Ala	Gly	Gly	Gly	Ser	Val	Val	Gly	Gly	Ser
Met	Ser	Ile	Ser	Gly	Ile	Lys	Ser	Trp	Leu	Arg	Glu	Ala	Met	Tyr	Val
Pro	Pro	Glu	Arg	Pro	Ala	Ala	Ala	Leu	Ser	Leu	Ala	Val	Thr	Asp	
225	Val	Pro	Pro	Ala	Glu	Pro	Pro	Gln	Leu	Leu	Pro	Ala	Pro	Leu	Pro
Asp	Val	Pro	Pro	Ala	Glu	Pro	Pro	Gln	Leu	Leu	Pro	Ala	Pro	Leu	Pro
Val	His	Arg	Lys	Pro	Ala	Gln	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Phe
Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu
Trp	Asp	Asn	Thr	Cys	Arg	Lys	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln
Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Arg	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr
305	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Ile	Asn	Phe
Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Ile	Asn	Phe
Pro	Leu	Ser	His	Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Ser
Arg	Gln	Glu	Phe	Ile	Ala	His	Leu	Arg	Arg	Asn	Ser	Ser	Gly	Phe	Ser
Arg	Gly	Ala	Ser	Met	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly
Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr
385	Leu	Gly	Thr	Phe	Ser	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile
Leu	Gly	Thr	Phe	Ser	Gln	Glu	Glu	Ala	Ala	Ala	Glu	Ala	Tyr	Asp	Ile
Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile
Ser	Lys	Tyr	Asp	Val	Lys	Arg	Ile	Cys	Ala	Ser	Thr	His	Leu	Ile	Gly
Gly	Gly	Asp	Ala	Cys	Arg	Arg	Ser	Pro	Thr	Arg	Pro	Pro	Asp	Ala	Ala
Pro	Ala	Leu	Ala	Gly	Gly	Ala	Asp	Arg	Ser	Ser	Asp	Ala	Pro	Gly	Asp
465	Gln	Ala	Ala	Ser	Asn	Ser	Asp	Thr	Ser	Asp	Gly	His	Arg	Gly	Ala
Gln	Ala	Ala	Ser	Asp	Asn	Ser	Asp	Thr	Ser	Asp	Gly	His	Arg	Gly	Ala
His	Leu	Leu	His	Gly	Leu	Gln	Tyr	Gly	His	Pro	Met	Lys	Leu	Glu	Ala
Gly	Glu	Gly	Ser	Ser	Trp	Met	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Arg	Pro
Pro	Gly	Val	His	Gln	Leu	Pro	Met	Phe	Ala	Leu	Trp	Asn	Asp	Cys	
530	Val	His	Gln	Leu	Pro	Met	Ala	Phe	Ala	Leu	Trp	Asn	Asp	Cys	
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<211>	512
<212>	PRT
<213>	Glycine max

<400> 86															
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			20					25					30		
Phe	Glu	Lys	Lys	Lys	Thr	Lys	Trp	Arg	Tyr	Asp	Ser	Ala	Ile	Gly	Gly
		35					40					45			
Gly	Asn	Ser	Asn	Glu	Glu	Gly	Pro	Lys	Leu	Glu	Asp	Phe	Leu	Gly	Cys
	50					55					60				
Tyr	Ser	Asn	Ser	Pro	Ala	Lys	Val	Phe	Cys	Gln	Asp	Ser	Gln	Pro	Asp
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Sequence Listing from Patent scope

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Asp	Asn	Leu	Thr	Asn	Pro	Ser	Ser	Leu	Leu	His	Ser	Phe	His	Ala	Tyr	
Asn	Asp	Asn	Ser	His	Ala	Leu	Ile	Pro	Thr	Asn	Gly	Met	Tyr	Lys	Ser	
Trp	Leu	Ala	Gln	Thr	Gln	Phe	Ser	Ser	Asp	Gly	Lys	Pro	Ser	Asn	Glu	
Ala	Asn	Gly	Oys	Asn	Phe	Gln	Ser	Leu	Ser	Leu	Thr	Met	Ser	Pro	Ser	
Val	Gln	Asn	Gly	Val	Gly	Ala	Ile	Ser	Ser	Val	Gln	Val	Asn	Glu	Asp	
Ser	Arg	Lys	Arg	Val	Met	Ala	Lys	Ser	His	Ala	Arg	Glu	Pro	Val	Pro	
Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Tyr	Arg	Gly	
Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	
Asn	Ser	Oys	Arg	Lys	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Gly	Gly	
Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Lys	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	
Lys	Tyr	Trp	Gly	Pro	Thr	Thr	His	Ile	Asn	Phe	Pro	Leu	Ser	Thr	Tyr	
Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln	Glu	Phe	Val	
Ala	Asn	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	Val	
Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	
Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	
Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	
Arg	Gly	Thr	Ser	Ala	Val	Thr	Asn	Phe	Asp	Ile	Ser	Arg	Tyr	Asp	Val	
Lys	Arg	Ile	Oys	Ser	Ser	Ser	Thr	Leu	Ile	Ala	Gly	Asp	Leu	Ala	Lys	
Arg	Ser	Pro	Lys	Glu	Ser	Pro	Ala	Pro	Pro	Pro	Pro	Leu	Ala	Ile	Thr	
Asp	Gly	Glu	His	Ser	Asp	Glu	Leu	Ser	Asn	Met	Met	Trp	Asn	Ala	Asn	
Asn	Ser	Asp	Glu	Gln	Ala	Gln	Asn	Glu	Ser	Gly	Gly	Ala	Glu	Phe	Asn	
Asn	Asn	Val	Thr	Glu	Ser	Ser	Ser	Ser	Gln	Gln	Val	Ser	Pro	Ser	Ser	
Asn	Lys	Asp	Ala	Leu	Asn	Pro	Gln	Ser	Pro	Asn	Glu	Phe	Gly	Val	Ser	
Gly	Ala	Asp	Tyr	Gly	His	Gly	Tyr	Phe	Thr	Leu	Asp	Gly	Pro	Lys	Tyr	
Asp	Asp	Gly	Asn	Asn	Glu	Asn	Asp	His	Met	Ser	Thr	Asn	Arg	Leu	Gly	
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 <211> 485
 <212> PRT
 <213> Sorghum bicolor

<400> 87
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Sequence Listing from Patent scope

[illegible]

Sequence Listing from Patent scope

<210> 88
 <211> 507
 <212> PRT
 <213> Glycine max

<400> 88

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			20					25					30		
Ala	Thr	Ser	Ser	His	His	Tyr	Tyr	Leu	Asp	Asn	Leu	Tyr	Thr	Asn	Gly
		35					40					45			
Trp	Gly	Asn	Gly	Ser	Leu	Lys	Phe	Glu	Gln	Asn	Leu	Asn	His	Ser	Asp
	50					55					60				
Val	Ser	Phe	Val	Glu	Ser	Ser	Ser	Gln	Ser	Val	Gly	His	Val	Pro	Pro
65					70					75				80	
Pro	Pro	Pro	Lys	Leu	Glu	Asp	Phe	Leu	Gly	Asp	Ser	Ser	Ala	Val	Met
			85						90					95	
Arg	Tyr	Ser	Asp	Ser	Gln	Thr	Glu	Thr	Gln	Asp	Ser	Ser	Leu	Thr	His
			100					105					110		
Ile	Tyr	Asp	His	His	His	His	His	His	His	His	His	Gly	Ser	Thr	Ser
		115					120					125			
Tyr	Phe	Gly	Gly	Asp	Gln	Gln	Asp	Leu	Lys	Ala	Ile	Thr	Gly	Phe	Gln
	130					135					140				
Ala	Phe	Ser	Thr	Asn	Ser	Gly	Ser	Glu	Val	Asp	Asp	Ser	Ala	Ser	Ile
145					150					155				160	
Gly	Lys	Ala	Gln	Ala	Ser	Glu	Phe	Gly	Thr	His	Ser	Ile	Glu	Ser	Ser
			165					170						175	
Gly	Asn	Glu	Phe	Ala	Ala	Phe	Ser	Gly	Gly	Thr	Thr	Gly	Thr	Leu	Ser
			180					185					190		
Leu	Ala	Val	Ala	Leu	Ser	Ser	Glu	Lys	Ala	Val	Val	Ala	Ala	Glu	Ser
		195					200					205			
Asn	Ser	Ser	Lys	Lys	Ile	Val	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Ile
	210				215						220				
Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His
225					230					235				240	
Leu	Trp	Asp	Asn	Ser	Oys	Arg	Arg	Glu	Gly	Gln	Ala	Arg	Lys	Gly	Arg
			245						250					255	
Gln	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu
			260					265					270		
Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Thr	Ala	Thr	Thr	Asn	Phe	Pro	Val
		275					280					285			
Ser	Asn	Tyr	Ser	Lys	Glu	Val	Glu	Glu	Met	Lys	His	Val	Thr	Lys	Gln
	290					295					300				
Glu	Phe	Ile	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly
305					310					315				320	
Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	Gln	Gly	Arg	Trp
			325						330					335	
Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly
			340					345					350		
Thr	Phe	Ala	Thr	Glu	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala
		355					360					365			
Ile	Lys	Phe	Arg	Gly	Ala	Asn	Ala	Val	Thr	Asn	Phe	Glu	Met	Asn	Arg
	370					375					380				
Tyr	Asp	Val	Glu	Ala	Ile	Met	Lys	Ser	Ser	Leu	Pro	Val	Gly	Gly	Ala
385					390					395				400	
Ala	Lys	Arg	Leu	Arg	Leu	Ser	Leu	Glu	Ser	Glu	Gln	Lys	Ala	Pro	Pro
			405						410					415	
Val	Asn	Ser	Ser	Ser	Gln	Gln	Gln	Asn	Pro	Gln	Oys	Gly	Asn	Val	Ser
			420					425					430		
Gly	Ser	Ile	Asn	Phe	Ser	Ala	Ile	His	Gln	Pro	Ile	Ala	Ser	Ile	Pro
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Oys	Gly	Ile	Pro	Phe	Asp	Ser	Thr	Thr	Ala	Tyr	Tyr	Pro	His	Asn	Leu

Sequence Listing from Patent scope

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465
Thr Ser A l a Asn A l a Thr A l a Leu Thr A l a Leu Pro A l a Ser A l a A l a
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485
500
505

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<211> 569
<212> PRT
<213> Arabidopsis thaliana

<400> 89
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35
Leu A l a A l a A l a Ser Met A l a Asp Ser Thr I l e Leu Thr Thr Phe
50
Val Asp Pro G n Ser H i s H i s Ser G n Asn H i s I l e Pro Lys Leu G u
65
Asp Phe Leu G l y Asp Ser Ser Ser I l e Val Arg Tyr Ser Asp Asn Ser
85
G n Thr Asp Thr G n Asp Ser Ser Leu Thr G n I l e Tyr Asp Pro Arg
100
H i s H i s H i s Asn G n Thr G l y Phe Tyr Ser Asp H i s H i s Asp Phe Lys
115
Thr Met A l a G l y Phe G n Ser A l a Phe Ser Thr Asn Ser G l y Ser G u
130
Val Asp Asp Ser A l a Ser I l e G l y Arg Thr H i s Leu A l a G l y Asp Tyr
145
Leu G l y H i s Val Val G u Ser Ser G l y Pro G u Leu G l y Phe H i s G l y
165
G l y Ser Thr G l y A l a Leu Ser Leu G l y Val Asn Val Asn Asn Thr
180
Asn H i s Arg Asn Asp Asn Asp Asn H i s Tyr Arg G l y Asn Asn Asn G l y
195
G u Arg I l e Asn Asn Asn Asn Asn Asn Asp Asn G u Lys Thr Asp Ser
210
G u Lys G u Lys A l a Val Val A l a Val G u Thr Ser Asp Cys Ser Asn
225
Lys Lys I l e A l a Asp Thr Phe G l y G n Arg Thr Ser I l e Tyr Arg G l y
245
Val Thr Arg H i s Arg Trp Thr G l y Arg Tyr G u A l a H i s Leu Trp Asp
260
Asn Ser Cys Arg Arg G u G l y G n A l a Arg Lys G l y Arg G n Val Tyr
275
Leu G l y G l y Tyr Asp Lys G u Asp Lys A l a A l a Arg A l a Tyr Asp Leu
290
A l a A l a Leu Lys Tyr Trp Asn A l a Thr A l a Thr Thr Asn Phe Pro I l e
305
Thr Asn Tyr Ser Lys G u Val G u G u Met Lys H i s Met Thr Lys G n
325
G u Phe I l e A l a Ser Leu Arg Arg Lys Ser Ser G l y Phe Ser Arg G l y
340
A l a Ser I l e Tyr Arg G l y Val Thr Arg H i s H i s G n G n G l y Arg Trp
355
G n A l a Arg I l e G l y Arg Val A l a G l y Asn Lys Asp Leu Tyr Leu G l y
370
375

Sequence Listing from Patent scope

Thr 385	Phe	Ala	Thr	Glu	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	400
Ile	Lys	Phe	Arg	Gly	Ile	Asn	Ala	Val	Thr	Asn	Phe	Glu	Met	Asn	Arg	415
Tyr	Asp	Val	Glu	Ala	Ile	Met	Lys	Ser	Ala	Leu	Pro	Ile	Gly	Gly	Ala	430
Ala	Lys	Arg	Leu	Lys	Leu	Ser	Leu	Glu	Ala	Ala	Ala	Ser	Ser	Glu	Gln	445
Lys	Pro	Ile	Leu	Gly	His	His	Gln	Leu	His	His	Phe	Gln	Gln	Gln	Gln	460
Gln	Gln	Gln	Gln	Leu	Gln	Leu	Gln	Ser	Ser	Pro	Asn	His	Ser	Ser	Ile	480
Asn	Phe	Ala	Leu	Cys	Pro	Asn	Ser	Ala	Val	Gln	Ser	Gln	Gln	Ile	Ile	495
Pro	Cys	Gly	Ile	Pro	Phe	Glu	Ala	Ala	Ala	Leu	Tyr	His	His	His	Gln	510
Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Asn	Phe	Phe	Gln	525
His	Phe	Pro	Ala	Asn	Ala	Ala	Ser	Asp	Ser	Thr	Gly	Ser	Asn	Asn	Asn	540
Ser	Asn	Val	Gln	Gly	Thr	Met	Gly	Leu	Met	Ala	Pro	Asn	Pro	Ala	Glu	560
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<211> 574

<212> PRT

<213> Medicago truncatula

<400> 90

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			20					25					30			
Glu	Gly	Ser	Glu	Ile	Gly	Arg	Asn	Tyr	Val	Thr	Pro	Ser	Ser	His	Pro	
		35					40					45				
His	Pro	His	His	Leu	Ser	Ile	Met	Pro	Leu	Arg	Ser	Asp	Gly	Ser	Leu	
	50				55						60					
Cys	Val	Ser	Asp	Ser	Phe	Thr	Pro	Gln	Glu	Trp	Arg	Tyr	Glu	Asn	Ala	
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Ile	Thr	Asp	Gly	Asn	Ser	Asn	Glu	Glu	Gly	Pro	Lys	Leu	Glu	Asp	Phe	
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Leu	Gly	Cys	Tyr	Ser	Asn	Gln	Asn	Gln	Asn	Ser	Thr	Thr	Thr	Ser	Thr	
		100						105					110			
Met	Ser	Lys	Ile	Asn	Val	Asn	Val	Ser	Pro	Ser	Phe	Cys	Thr	Asn	Asn	
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Asn	Pro	Glu	Ile	Asp	Thr	Arg	Glu	Asn	Leu	Thr	Asn	Gln	Ser	Leu	Ile	
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145					150					155					160	
Leu	Ile	His	Asp	Asn	Ser	Met	Tyr	Lys	Ser	Trp	Met	Thr	Gln	Thr	Gln	
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Phe	Ser	Ser	Glu	Gly	Lys	Thr	Thr	Ser	Ser	Asp	Gly	Asn	Gly	Phe	Gln	
		180						185					190			
Ser	Leu	Asn	Leu	Thr	Met	Ser	Pro	Cys	Val	Gln	Asn	Gly	Val	Gly	Gly	
		195					200					205				
Gly	Val	Gly	Ser	Ala	Ile	Ser	Asn	Val	Gln	Val	Asn	Glu	Asp	Pro	Arg	
	210					215					220					
Lys	Arg	Ser	Leu	Ser	Lys	Ser	Asn	Ala	Arg	Glu	Pro	Val	Pro	Arg	Lys	
225					230					235					240	
Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Tyr	Arg	Gly	Val	Thr	

Sequence Listing from Patent scope

Arg	His	Arg	Trp	245	Thr	Gly	Arg	Tyr	Glu	250	Ala	His	Leu	Trp	255	Asp	Asn	Ser
Oys	Arg	Lys	260	Glu	Gly	Gln	Thr	Arg	265	Lys	Gly	Arg	Gln	Gly	270	Gly	Tyr	Asp
Lys	Glu	275	Lys	Ala	Ala	Lys	280	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr		
Trp	Gly	290	Pro	Thr	Thr	His	295	Ile	Asn	Phe	Pro	Leu	Ser	Thr	Tyr	Asp	Lys	
305	Glu	Leu	Glu	Glu	Met	Lys	310	His	Met	Thr	Arg	Gln	Glu	Phe	Val	Ala	Asn	
Leu	Arg	Arg	Lys	325	Ser	Ser	Gly	Phe	Ser	330	Arg	Gly	Ala	Ser	Val	335	Tyr	
Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly			
Arg	Val	355	Ala	Gly	Asn	Lys	Asp	360	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	
Glu	Glu	370	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly		
385	Thr	Ser	Ala	Val	Thr	Asn	Phe	Asp	Ile	Ser	Arg	Tyr	Asp	Val	Lys	Arg		
Ile	Oys	Ser	Ser	405	Thr	Leu	Ile	Thr	410	Gly	Asp	Leu	Ala	Lys	Arg	Ser		
Pro	Lys	Asp	Ser	420	Thr	Pro	Pro	Ala	425	Thr	Thr	Ala	Glu	Asp	Phe	Asn	Ser	
Oys	Gly	435	Ser	Ser	Thr	Leu	Ser	Gln	440	Pro	Pro	Pro	Leu	Thr	Ile	Thr		
Asp	Gly	450	Glu	Gln	His	Ser	Asp	Glu	455	Leu	Ser	Asn	Met	Val	Trp	Asn	Ser	
465	Asn	Asn	Asp	Glu	Gln	Lys	Pro	Gln	470	Asn	Gly	Thr	Asn	Ile	Thr	Glu	Ser	
Ser	Gln	His	Gly	485	Ser	Pro	Ser	Asn	490	Asn	Glu	Met	Asn	Pro	Gln	Ser		
Pro	Lys	Oys	Ser	500	Leu	Gly	Leu	Pro	505	Asn	Glu	Phe	Gly	Val	Ser	Gly	Ala	
Asp	Tyr	515	Gly	His	Gly	Tyr	Phe	Thr	520	Leu	His	Gly	Pro	Lys	Phe	Asp	Asp	
Gly	Ser	530	Asn	Glu	Asn	Asp	His	Met	535	Asn	Asn	Asn	Arg	Leu	Gly	Asn	Leu	
545	Gly	Leu	Val	Asn	Gln	Val	Pro	Met	550	Phe	Ala	Leu	Trp	Asn	Glu		560	
				565					570									

<210> 91
 <211> 541
 <212> PRT
 <213> Sorghum bicolor

<400> 91
 Met Asp Met Asn Asn Gly Trp Leu Gly Phe Ser Leu Ser Pro Ser Ala
 1 5 10 15
 Gly Arg Gly Gly Tyr Gly Asp Gly Gly Ala Ser Ala Ser Gly Asp Gly
 20 25 30
 Gly Asp Gly Ser Oys Ser Ser Pro Ala Ala Ala Ala Ser Pro Val Pro
 35 40 45
 Leu Val Ala Met Pro Leu Gln Pro Asp Gly Ser Leu His Tyr Thr Ser
 50 55 60
 Ala Pro Asp Trp Arg His Gly Ala Ala Glu Ala Asn Gly Pro Lys Leu
 65 70 75 80
 Glu Asp Phe Met Ser Val Thr Oys Ser Ser Asn Asn Lys Arg Ser Ser
 85 90 95
 Ser Ser Ser Ser Phe Tyr Asp Arg Oys Ser His Ala Glu Gln Ala Asn
 100 105 110

Sequence Listing from Patent scope

Lys	Tyr	His	Glu	Val	His	Asp	Leu	Gln	Pro	Leu	Ser	Cys	Gly	Ser	Tyr
		115					120					125			
Tyr	His	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Asn	Gly	Ile	Ala	Leu	Gly	Ile
	130					135					140				
Asn	Met	Asn	Ala	Pro	Pro	Cys	Ser	Gly	Gly	Gly	Phe	Pro	Asp	His	His
145					150					155					160
His	His	His	Gln	Phe	Val	Ser	Ser	His	His	Gly	Gln	Tyr	Phe	Leu	Gly
			165						170					175	
Ala	Pro	Leu	Asn	Ala	Ser	Pro	Pro	Gly	Ala	Val	Pro	Met	Tyr	Ser	Ala
			180					185					190		
Gly	Gly	Gly	Gly	Val	Gly	Gly	Ser	Met	Ser	Ile	Ser	Gly	Ile	Lys	Ser
		195					200					205			
Trp	Leu	Arg	Glu	Ala	Met	Tyr	Val	Pro	Pro	Glu	Arg	Pro	Val	Ala	Ala
	210					215					220				
Ala	Ala	Ala	Leu	Ser	Leu	Ala	Val	Thr	Asp	Asp	Val	Gly	Ala	Glu	Pro
225					230					235					240
Pro	Gln	Leu	Leu	Pro	Ala	Ala	Pro	Met	Pro	Pro	Val	His	Arg	Lys	Pro
				245					250					255	
Ala	Gln	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Phe	Arg	Gly	Val	Thr	Arg
			260					265					270		
His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Thr	Cys
		275					280					285			
Arg	Lys	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Gly	Gly	Tyr	Asp	Arg
	290					295					300				
Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp
305					310					315					320
Gly	Pro	Ser	Thr	His	Ile	Asn	Phe	Pro	Leu	Ser	His	Tyr	Glu	Lys	Glu
				325					330					335	
Leu	Glu	Glu	Met	Lys	His	Met	Ser	Arg	Gln	Glu	Phe	Ile	Ala	His	Leu
			340					345					350		
Arg	Arg	Asn	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	Met	Tyr	Arg	Gly
		355					360					365			
Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg
	370					375					380				
Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu
385					390					395					400
Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu
				405					410					415	
Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile	Ser	Lys	Tyr	Asp	Val	Lys	Arg	Ile
			420					425					430		
Cys	Ala	Ser	Thr	His	Leu	Ile	Gly	Gly	Gly	Asp	Ala	Cys	Arg	Arg	Ser
		435					440					445			
Pro	Thr	Gln	Pro	Pro	Asp	Ala	Pro	Ala	Leu	Ala	Ile	Asp	Ala	Ala	Gly
	450				455						460				
Ala	Asp	Arg	Ser	Ser	Asp	Ala	Pro	Gly	Gly	Gly	Asp	Gln	Ala	Val	Ser
465					470					475					480
Asp	Asn	Ser	Asp	Thr	Ser	Ala	Gly	His	Arg	Gly	Ala	His	Leu	Leu	His
				485					490					495	
Gly	Leu	Gln	Tyr	Gly	His	Pro	Met	Lys	Leu	Glu	Ala	Gly	Glu	Gly	Ser
			500					505					510		
Ser	Trp	Met	Ala	Ala	Ala	Thr	Ala	Ala	Ala	Ala	Arg	Pro	Val	Ala	Gly
		515					520					525			
Val	His	Gln	Leu	Pro	Val	Phe	Ala	Leu	Trp	Asn	Asp	Cys			
	530					535					540				

<210> 92
 <211> 555
 <212> PRT
 <213> Arabidopsis thaliana

<400> 92
 Met Lys Ser Phe Cys Asp Asn Asp Asp Asn Asn His Ser Asn Thr Thr

Sequence Listing from Patent scope

1	Asn	Leu	Leu	Gly	5	Phe	Ser	Leu	Ser	Ser	10	Asn	Met	Met	Lys	15	Met	Gly	Gly
			20							25						30			
	Arg	Gly	Gly	Arg	Glu	Ala	Ile	Tyr	Ser	Ser	Ser	Thr	Ser	Ser	Ala	Ala			
			35					40							45				
	Thr	Ser	Ser	Ser	Val	Pro	55	Pro	Gln	Leu	Val	Val	Gly	Asp	Asn	Thr			
			50																
	Ser	Asn	Phe	Gly	Val	Cys	Tyr	Gly	Ser	Asn	Pro	Asn	Gly	Gly	Ile	Tyr			
65					70											80			
	Ser	His	Met	Ser	Val	Met	Pro	Leu	Arg	Ser	Asp	Gly	Ser	Leu	Cys	Leu			
					85					90					95				
	Met	Glu	Ala	Leu	Asn	Arg	Ser	Ser	His	Ser	Asn	His	His	Gln	Asp	Ser			
			100						105										
	Ser	Pro	Lys	Val	Glu	Asp	Phe	Phe	Gly	Thr	His	His	Asn	Asn	Thr	Ser			
			115						120										
	His	Lys	Glu	Ala	Met	Asp	Leu	Ser	Leu	Asp	Ser	Leu	Phe	Tyr	Asn	Thr			
			130						135										
	Thr	His	Glu	Pro	Asn	Thr	Thr	Thr	Asn	Phe	Gln	Glu	Phe	Phe	Ser	Phe			
145					150											160			
	Pro	Gln	Thr	Arg	Asn	His	Glu	Glu	Glu	Thr	Arg	Asn	Tyr	Gly	Asn	Asp			
					165										175				
	Pro	Ser	Leu	Thr	His	Gly	Gly	Ser	Phe	Asn	Val	Gly	Val	Tyr	Gly	Glu			
					180				185										
	Phe	Gln	Gln	Ser	Leu	Ser	Leu	Ser	Met	Ser	Pro	Gly	Ser	Gln	Ser	Ser			
			195						200										
	Cys	Ile	Thr	Gly	Ser	His	His	His	Gln	Gln	Asn	Gln	Asn	Gln	Asn	His			
			210						215										
	Gln	Ser	Gln	Asn	His	Gln	Gln	Ile	Ser	Glu	Ala	Leu	Val	Glu	Thr	Ser			
225					230											240			
	Val	Gly	Phe	Glu	Thr	Thr	Thr	Met	Ala	Ala	Ala	Lys	Lys	Lys	Arg	Gly			
					245										255				
	Gln	Glu	Asp	Val	Val	Val	Gly	Gln	Thr	Ser	Gln	Tyr	Arg	Gly	Val	Thr			
					260				265										
	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Tyr	Arg	Gly	Val	Thr			
			275						280										
	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp	Asp	Asn	Ser			
									295										
	Phe	Lys	Lys	Glu	Gly	His	Ser	Arg	Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly			
305					310											320			
	Gly	Tyr	Asp	Met	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala			
					325					330					335				
	Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Thr	Asn	Phe	Ser	Ala	Glu	Asn			
					340					345					350				
	Tyr	Gln	Lys	Glu	Ile	Glu	Asp	Met	Lys	Asn	Met	Thr	Arg	Gln	Glu	Tyr			
					355				360						365				
	Val	Ala	His	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser			
					370														
	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala			
385					390											400			
	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe			
					405					410					415				
	Gly	Thr	Gln	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Val	Ala	Ala	Ile	Lys				
					420					425									
	Phe	Arg	Gly	Thr	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile	Thr	Arg	Tyr	Asp			
					435				440										
	Val	Asp	Arg	Ile	Met	Ser	Ser	Asn	Thr	Leu	Leu	Ser	Gly	Glu	Leu	Ala			
	Arg	Arg	Asn	Asn	Asn	Ser	Ile	Val	Val	Arg	Asn	Thr	Glu	Asp	Gln	Thr			
465					470											480			
	Ala	Leu	Asn	Ala	Val	Val	Glu	Gly	Gly	Ser	Asn	Lys	Glu	Val	Ser	Thr			
					485					490					495				
	Pro	Glu	Arg	Leu	Ser	Phe	Pro	Ala	Ile	Phe	Ala	Leu	Pro	Gln	Val				
					500				505					510					

Sequence Listing from Patent scope

Asn	Gln	Lys	Met	Phe	Gly	Ser	Asn	Met	Gly	Gly	Asn	Met	Ser	Pro	Trp
		515					520					525			
Thr	Ser	Asn	Pro	Asn	Ala	Glu	Leu	Lys	Thr	Val	Ala	Leu	Thr	Leu	Pro
	530					535					540				
Gln	Met	Pro	Val	Phe	Ala	Ala	Trp	Ala	Asp	Ser					
545					550					555					

<210> 93
 <211> 678
 <212> PRT
 <213> Sorghum bicolor

<400> 93

Met	Thr	Asn	Asn	Asn	Gly	Asn	Gly	Thr	Asn	Ala	Ala	Ala	Ser	Ser	Trp
1				5					10					15	
Leu	Gly	Phe	Ser	Leu	Ser	Pro	His	Met	Ala	Ser	Ala	Met	Asp	Glu	His
			20					25					30		
His	His	Val	Gln	Gln	Gln	Gln	Gln	His	His	His	His	His	Ser	Leu	Phe
		35					40					45			
Phe	Pro	Ser	Val	Thr	Ala	Ala	Ala	Ala	Ala	Tyr	Gly	Leu	Gly	Gly	
	50					55					60				
Ser	Asp	Gly	Gly	Val	Ala	Thr	Ser	Ala	Ser	Pro	Tyr	Tyr	Thr	Pro	Gln
65					70					75					80
Leu	Ala	Ser	Met	Pro	Leu	Lys	Ser	Asp	Gly	Ser	Leu	Cys	Ile	Met	Glu
				85					90					95	
Ala	Leu	Arg	Arg	Ser	Asp	Gln	Pro	Asp	His	His	Gly	Pro	Lys	Leu	Glu
			100					105					110		
Asp	Phe	Leu	Gly	Ala	Ala	Ala	Ala	Gln	Ser	Gln	Ala	Met	Ala	Leu	Ser
		115					120					125			
Leu	Gln	Asp	Asn	Pro	Ala	Ala	Ala	Ala	Ser	Ser	Phe	Tyr	Tyr	Tyr	Gly
	130					135					140				
Asn	Gly	Gly	Gly	Gly	Gly	Ser	Gly	His	Gln	His	His	Gly	Gly	Phe	Leu
145					150					155					160
Gln	Pro	Cys	Ala	Asp	Leu	Tyr	Gly	Gly	Pro	Ser	Glu	Ala	Ser	Leu	Val
				165					170					175	
Ala	Asp	Asp	Asp	Glu	Ala	Ala	Ala	Ala	Thr	Ala	Met	Ala	Ser	Trp	
			180					185					190		
Val	Ala	Ala	Arg	Ala	Gly	Glu	Ser	Gly	Gly	Val	Leu	Ser	Ala	Ala	Ala
		195					200					205			
Ala	Ala	Ala	Gly	His	Gln	His	His	His	His	Ala	Leu	Ala	Leu	Ser	Met
	210					215					220				
Ser	Ser	Gly	Ser	Leu	Ser	Ser	Cys	Val	Thr	Ala	His	Pro	Gly	Ala	Ala
225					230					235					240
Ala	Ala	Asp	Tyr	Gly	Val	Val	Ala	Ala	Thr	Ala	Ser	Ala	Ser	Leu	Asp
			245						250					255	
Gly	Gly	Arg	Lys	Arg	Gly	Gly	Ala	Ala	Gly	Gln	Lys	Gln	Pro	Val	His
			260					265					270		
His	Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser	Gln	Tyr	Arg
		275					280					285			
Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala	His	Leu	Trp
	290					295					300				
Asp	Asn	Ser	Cys	Lys	Lys	Glu	Gly	Gln	Thr	Arg	Lys	Gly	Arg	Gln	Gly
305					310					315					320
Gly	Tyr	Asp	Met	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala
			325						330					335	
Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Ile	Asn	Phe	Pro	Leu	Glu	Asp
			340					345					350		
Tyr	Gln	Glu	Glu	Leu	Glu	Glu	Met	Lys	Asn	Met	Thr	Arg	Gln	Glu	Tyr
		355					360					365			
Val	Ala	His	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser
	370					375					380				
Met	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala

Sequence Listing from Patent scope

385	Arg	Ile	Gly	Arg	Val	390	Ser	Gly	Asn	Lys	Asp	395	Leu	Tyr	Leu	Gly	Thr	400	Phe
					405		Ala	Ala	Glu	Ala	410	Tyr	Asp	Ile	Ala	Ala	415	Ile	Lys
					420		Asn	Ala	Val	Thr	425	Phe	Asp	Ile	Thr	430	Arg	Tyr	Asp
					435		Val	Asp	Lys	Ile	Met	Ala	Ser	Asn	Thr	440	Leu	Ala	
					450		Arg	Arg	Arg	Lys	Asp	Asp	Pro	Ala	Ala	455	Val	Ile	Ala
					465		Ala	Ser	Asn	Gly	Gly	470	Val	Thr	Thr	475	Ala	Ala	Ala
					485		Val	Gln	Gln	Ala	Ala	Ala	Ala	Ala	Ala	490	Gly	Ala	Gly
					500		Ser	Ala	Ser	Ser	Ser	Glu	Thr	Trp	Ile	505	Lys	Val	Ala
					515		Leu	Gln	Ala	Ala	Gly	Ala	Ala	Pro	Arg	Asp	Gly	Asn	His
					530		His	His	Asp	Val	Leu	Ser	Gly	Glu	Ala	Phe	Ser	Val	Leu
					545		Val	Val	Thr	Ala	Ala	Asp	Gly	Gly	Asn	Gly	550	Gly	Asn
					565		His	His	His	His	Val	His	Asn	Ser	Ala	Ala	570	Thr	Ala
					580		Met	Ser	Ser	Ala	Ser	Ser	Leu	Val	Thr	Ser	585	Leu	Gly
					595		Gly	Ser	Pro	Asp	Arg	Gly	Gly	Gly	Leu	Ser	Met	Leu	Phe
					610		Pro	Ala	Pro	Ala	Pro	Ala	Ala	Ser	Ala	His	Ala	Ala	Asn
					625		Ser	Pro	Leu	Met	Pro	Leu	Gly	Ser	Trp	Ala	630	Ser	Thr
					645		Ala	Arg	Ala	Ala	Ala	Ala	Ala	Val	Ser	Ile	650	Ala	His
					660		Ala	Ala	Ala	Trp	Thr	Asp	Ala				665	Ala	His
					675														

<210> 94
 <211> 509
 <212> PRT
 <213> Glycine max

<400> 94

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

Sequence Listing from Patent scope

Asn 145	Ser	Gly	Ser	Glu	Val 150	Asp	Asp	Ser	Ala	Ser 155	Ile	Gly	Lys	Ala	Gln 160
Gly	Ser	Glu	Phe	Gly 165	Thr	His	Ser	Ile	Glu 170	Ser	Ser	Val	Asn	Glu 175	Phe
Ala	Ala	Phe	Ser 180	Gly	Gly	Thr	Asn	Thr 185	Gly	Gly	Thr	Leu	Ser 190	Leu	Ala
Val	Ala	Gln 195	Ser	Ser	Glu	Lys	Ala 200	Val	Ala	Ala	Ala	Ala 205	Glu	Ser	Asp
Arg	Ser 210	Lys	Lys	Val	Val	Asp 215	Thr	Phe	Gly	Gln	Arg 220	Thr	Ser	Ile	Tyr
Arg 225	Gly	Val	Thr	Arg	His 230	Arg	Trp	Thr	Gly	Arg 235	Tyr	Glu	Ala	His	Leu 240
Trp	Asp	Asn	Ser	Cys 245	Arg	Arg	Glu	Gly	Gln 250	Ala	Arg	Lys	Gly	Arg 255	Gln
Gly	Gly	Tyr	Asp 260	Lys	Glu	Glu	Lys	Ala 265	Ala	Arg	Ser	Tyr	Asp 270	Leu	Ala
Ala	Leu	Lys 275	Tyr	Trp	Gly	Pro	Thr 280	Ala	Thr	Thr	Asn	Phe 285	Pro	Val	Ser
Asn 290	Tyr	Ser	Lys	Glu	Val	Glu 295	Glu	Met	Lys	His	Val 300	Thr	Lys	Gln	Glu
Phe 305	Ile	Ala	Ser	Leu	Arg 310	Arg	Lys	Ser	Ser	Gly 315	Phe	Ser	Arg	Gly	Ala 320
Ser	Ile	Tyr	Arg	Gly 325	Val	Thr	Arg	His	His 330	Gln	Gln	Gly	Arg	Trp 335	Gln
Ala	Arg	Ile	Gly 340	Arg	Val	Ala	Gly	Asn 345	Lys	Asp	Leu	Tyr	Leu 350	Gly	Thr
Phe	Ala	Thr 355	Glu	Glu	Glu	Ala 360	Ala	Glu	Ala	Tyr	Asp 365	Ile	Ala	Ala	Ile
Lys	Phe 370	Arg	Gly	Ala	Asn 375	Ala	Val	Thr	Asn	Phe 380	Glu	Met	Asn	Arg	Tyr
Asp 385	Val	Glu	Ala	Ile	Met 390	Lys	Ser	Ser	Leu	Pro 395	Val	Gly	Gly	Ala	Ala 400
Lys	Arg	Leu	Lys	Leu 405	Ser	Leu	Glu	Ser	Glu 410	Gln	Lys	Ala	Leu	Pro 415	Val
Ser	Ser	Ser	Ser 420	Ser	Ser	Ser	Gln	Gln 425	Gln	Asn	Pro	Gln	Cys 430	Gly	Asn
Val	Ser	Ala 435	Ser	Ile	Asn	Phe	Ser 440	Ser	Ile	His	Gln	Pro 445	Ile	Ala	Ser
Ile	Pro 450	Cys	Gly	Ile	Pro	Phe 455	Asp	Ser	Thr	Thr	Ala 460	Tyr	Tyr	His	His
Asn 465	Leu	Phe	Gln	His	Phe 470	His	Pro	Thr	Asn	Ala 475	Gly	Thr	Ala	Ala	Ser 480
Ala	Val	Thr	Ser	Ala 485	Asn	Ala	Asn	Ala	Leu 490	Thr	Ala	Leu	Pro	Pro 495	Thr
Ala	Ala	Ala	Glu 500	Phe	Phe	Ile	Trp	Pro 505	His	Gln	Ser	Tyr			

<210> 95
 <211> 652
 <212> PRT
 <213> Oryza sativa

<400> 95
 Met Ala Ser Gly Asn Ser Ser Ser Ser Ser Gly Ser Met Ala Ala Thr
 1 5 10 15
 Ala Gly Gly Val Gly Gly Trp Leu Gly Phe Ser Leu Ser Pro His Met
 20 25 30
 Ala Thr Tyr Cys Ala Gly Gly Val Asp Asp Val Gly His His His His
 35 40 45
 His His Val His Gln His Gln Gln Gln His Gly Gly Gly Leu Phe Tyr
 50 55 60
 Asn Pro Ala Ala Val Ala Ser Ser Phe Tyr Tyr Gly Gly Gly His Asp

Sequence Listing from Patent scope

65	Ala	Val	Val	Thr	Ser	70	Ala	Ala	Gly	Gly	Gly	75	Ser	Tyr	Tyr	Gly	80	Ala	Gly
					85							90					95		
Phe	Ser	Ser	Met	Pro	Leu	Lys	Ser	Asp	Gly	Ser	Leu	Cys	Ile	Met	Glu				
			100					105									110		
Ala	Leu	Arg	Gly	Gly	Asp	Gln	Glu	Gln	Gln	Gly	Val	Val	Val	Ser	Ala				
			115					120									125		
Ser	Pro	Lys	Leu	Glu	Asp	Phe	Leu	Gly	Ala	Gly	Pro	Ala	Met	Ala	Leu				
			130			135											140		
Ser	Leu	Asp	Asn	Ser	Ala	Phe	Tyr	Tyr	Gly	Gly	His	Gly	His	His	Gln				
			145			150										160			
Gly	His	Ala	Gln	Asp	Gly	Gly	Ala	Val	Gly	Gly	Asp	Pro	His	His	Gly				
				165												175			
Gly	Gly	Gly	Phe	Leu	Gln	Cys	Ala	Val	Ile	Pro	Gly	Ala	Gly	Ala	Gly				
			180													190			
His	Asp	Ala	Ala	Leu	Val	His	Asp	Gln	Ser	Ala	Ala	Ala	Val	Ala	Ala				
			195				200									205			
Gly	Trp	Ala	Ala	Met	His	Gly	Gly	Gly	Tyr	Asp	Ile	Ala	Asn	Ala	Ala				
			210			215										220			
Ala	Asp	Asp	Val	Cys	Ala	Ala	Gly	Pro	Ile	Ile	Pro	Thr	Gly	Gly	His				
			225			230										240			
Leu	His	Pro	Leu	Thr	Leu	Ser	Met	Ser	Ser	Ala	Gly	Ser	Gln	Ser	Ser				
			245						250							255			
Cys	Val	Thr	Val	Gln	Ala	Ala	Ala	Ala	Gly	Glu	Pro	Tyr	Met	Ala	Met				
			260						265							270			
Asp	Ala	Val	Ser	Lys	Lys	Arg	Gly	Gly	Ala	Asp	Arg	Ala	Gly	Gln	Lys				
			275				280									285			
Gln	Pro	Val	His	Arg	Lys	Ser	Ile	Asp	Thr	Phe	Gly	Gln	Arg	Thr	Ser				
			290			295										300			
Gln	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu	Ala				
			305			310										320			
His	Leu	Trp	Asp	Asn	Ser	Cys	Lys	Lys	Glu	Gly	Gln	Thr	Arg	Lys	Gly				
			325						330							335			
Arg	Gln	Gly	Gly	Tyr	Asp	Met	Glu	Glu	Lys	Ala	Ala	Arg	Ala	Tyr	Asp				
			340						345							350			
Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Ile	Asn	Phe	Pro				
			355				360									365			
Leu	Glu	Asp	Tyr	Gln	Glu	Glu	Leu	Glu	Glu	Met	Lys	Asn	Met	Ser	Arg				
			370			375										380			
Gln	Glu	Tyr	Val	Ala	His	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg				
			385			390										400			
Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg				
			405						410							415			
Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ser	Gly	Asn	Lys	Asp	Leu	Tyr	Leu				
			420						425							430			
Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Val	Ala				
			435				440									445			
Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile	Thr				
			450			455										460			
Arg	Tyr	Asp	Val	Asp	Lys	Ile	Leu	Glu	Ser	Ser	Thr	Leu	Leu	Pro	Gly				
			465			470										480			
Glu	Leu	Ala	Arg	Arg	Lys	Gly	Lys	Val	Gly	Asp	Gly	Gly	Gly	Ala	Ala				
			485						490							495			
Ala	Val	Ala	Asp	Ala	Ala	Ala	Ala	Leu	Val	Gln	Ala	Gly	Asn	Val	Ala				
			500					505								510			
Glu	Trp	Lys	Met	Ala	Thr	Ala	Ala	Ala	Leu	Pro	Ala	Ala	Ala	Arg	Thr				
			515					520								525			
Glu	Gln	Gln	Gln	Gln	His	Gly	His	Gly	Gly	His	Gln	His	His	Asp	Leu				
			530			535										540			
Leu	Pro	Ser	Asp	Ala	Phe	Ser	Val	Leu	Gln	Asp	Ile	Val	Ser	Thr	Val				
			545			550										560			
Asp	Ala	Ala	Gly	Ala	Pro	Pro	Arg	Ala	Pro	His	Met	Ser	Met	Ala	Ala				
				565					570							575			

Sequence Listing from Patent scope

Thr	Ser	Leu	Gly	Asn	Ser	Arg	Glu	Gln	Ser	Pro	Asp	Arg	Gly	Val	Gly
			580					585					590		
Gly	Gly	Gly	Gly	Gly	Gly	Val	Leu	Ala	Thr	Leu	Phe	Ala	Lys	Pro	Ala
		595					600					605			
Ala	Ala	Ser	Lys	Leu	Tyr	Ser	Pro	Val	Pro	Leu	Asn	Thr	Trp	Ala	Ser
	610					615					620				
Pro	Ser	Pro	Ala	Val	Ser	Ser	Val	Pro	Ala	Arg	Ala	Gly	Val	Ser	Ile
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Ala	His	Leu	Pro	Met	Phe	Ala	Ala	Trp	Thr	Asp	Ala				
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 96

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

		355					360					365				
Ser	Ser	Ser	Asp	His	Asn	Leu	Gln	Gln	Gln	Gln	Leu	Leu	Pro	Ser	Ser	
	370					375					380					
Ser	Pro	Ser	Asp	Gln	Asn	Pro	Asn	Ser	Ile	Pro	Cys	Gly	Ile	Pro	Phe	
385					390					395					400	
Glu	Pro	Ser	Val	Leu	Tyr	Tyr	His	Gln	Asn	Phe	Phe	Gln	His	Tyr	Pro	
				405					410					415		
Leu	Val	Ser	Asp	Ser	Thr	Ile	Gln	Ala	Pro	Met	Asn	Gln	Ala	Glu	Phe	
			420					425					430			
Phe	Leu	Trp	Pro	Asn	Gln	Ser	Tyr									
		435					440									

<210> 97
<211> 651
<212> PRT
<213> Zea mays

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

Sequence Listing from Patent scope

Asn	Tyr	Arg	Asp	Glu	Leu	Glu	Glu	Met	Lys	Gly	Met	Thr	Arg	Gln	Glu
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Phe	Val	Ala	His	Leu	Arg	Arg	Arg	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala
	370					375					380				
Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	Gln	Gly	Arg	Trp	Gln
385					390					395					400
Ser	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr
				405					410					415	
Phe	Thr	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile
			420					425					430		
Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile	Ala	Arg	Tyr
		435					440					445			
Asp	Val	Asp	Lys	Ile	Met	Glu	Ser	Ser	Thr	Leu	Leu	Ala	Val	Glu	Glu
	450					455					460				
Ala	Arg	Lys	Val	Lys	Ala	Val	Glu	Ala	Ala	Ser	Ser	Ala	Pro	Met	Thr
465					470					475					480
His	Thr	His	Ser	Gly	Gly	Lys	Glu	Gln	Leu	Asn	Ala	Thr	Thr	Ala	Glu
				485					490					495	
Glu	Thr	Ser	Ser	Ala	Gly	Trp	Arg	Met	Val	Leu	His	Gly	Ser	Pro	His
		500						505					510		
Gln	Leu	Glu	Ala	Ala	Arg	Cys	Pro	Glu	Ala	Ala	Asp	Leu	Gln	Ser	Ala
		515					520					525			
Ile	Met	Asn	Asn	Asp	Ser	His	Pro	Arg	Pro	Ser	Leu	His	Gly	Ile	Ala
	530					535					540				
Gly	Leu	Asp	Ile	Glu	Cys	Ala	Val	His	Asp	His	His	Asp	His	Leu	Asp
545					550				555						560
Val	Pro	Ala	Gly	Ser	Arg	Thr	Thr	Ala	Ala	Gly	Ser	Ile	Asn	Phe	Ser
				565					570					575	
Asn	Ser	Ser	Ser	Gln	Val	Thr	Ser	Leu	Gly	Asn	Ser	Arg	Glu	Gly	Ser
		580						585					590		
Pro	Glu	Arg	Leu	Gly	Leu	Ala	Met	Met	Tyr	Gly	Lys	Gln	Pro	Ser	Ser
		595					600					605			
Ala	Val	Ser	Leu	Ala	Ala	Thr	Met	Ser	Pro	Trp	Thr	Pro	Val	Ala	Ala
	610					615					620				
Gln	Thr	Val	Ala	His	Val	Leu	Lys	Gln	Gln	Pro	Asn	Val	Val	Val	Ser
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<211> 656

<212> PRT

<213> Medicago truncatula

<400> 98

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

	130					135					140				
Ser 145	Leu	Asp	Ser	Met	Phe 150	G n	Asn	G n	I le	G n	G n	Asn	Met	Asn	Met 160
Asn	Asn	G n	G n	H s 165	Leu	Ser	Tyr	Tyr	Asn 170	Ser	Thr	Leu	Arg	Asn 175	H s 160
G u	Leu	Met	Leu 180	G u	G y	Ser	Lys	G n	Ser 185	G n	Thr	Ser	Ser 190	G y	Asn
Phe	H s	G n 195	Ser	Asn	Met	G y	G u 200	Asp	H s	G y	Leu	Ser 205	G y	Leu	Lys
Asn	Trp 210	Val	Leu	Arg	Asn	Phe 215	Pro	Al a	Ser	H s	G y 220	H s	Asp	G n	Ser
Lys 225	Met	I le	Val	Pro	Val 230	Val	G u	G u	Asn	G u 235	G y	G u	Oys	G y	Ser 240
Asn	I le	G y	Ser	Met 245	Al a	Tyr	G y	Asp	Leu 250	H s	Ser	Leu	Ser	Leu 255	Ser
Met	Ser	Pro	Ser 260	Ser	G n	Ser	Ser	Oys 265	Val	Thr	Thr	Ser	G n 270	Asn	Met
Ser	Ser	Al a 275	Val	Val	G u	Asn	Ser 280	Val	Al a	Met	Asp	Thr 285	Lys	Lys	Arg
G y	Ser 290	G u	Lys	Phe	G u	G n 295	Lys	G n	I le	Val	H s 300	Arg	Lys	Ser	I le
Asp 305	Thr	Phe	G y	G n	Arg 310	Thr	Ser	G n	Tyr	Arg 315	G y	Val	Thr	Arg	H s 320
Arg	Trp	Thr	G y	Arg 325	Tyr	G u	Al a	H s	Leu 330	Trp	Asp	Asn	Ser	Oys 335	Lys
Lys	G u	G y	G n 340	Ser	Arg	Lys	G y	Arg 345	G n	G y	G y	Tyr	Asp 350	Met	G u
G u	Lys	Al a 355	Al a	Arg	Al a	Tyr	Asp 360	G n	Al a	Al a	Leu	Lys 365	Tyr	Trp	G y
Pro	Ser 370	Thr	H s	I le	Asn	Phe 375	Pro	Leu	G u	Asn	Tyr 380	G n	Asn	G n	Leu
G u 385	G u	Met	Lys	Asn	Met 390	Thr	Arg	G n	G u	Tyr 395	Val	Al a	H s	Leu	Arg 400
Arg	Lys	Ser	Ser	G y 405	Phe	Ser	Arg	G y	Al a 410	Ser	Met	Tyr	Arg	G y 415	Val
Thr	Ser	Arg	H s 420	H s	G n	H s	G y	Arg 425	Trp	G n	Al a	Arg	I le 430	G y	Arg
Val	Al a	G y 435	Asn	Lys	Asp	Leu	Tyr 440	Leu	G y	Thr	Phe	Ser 445	Thr	G n	G u
G u	Al a 450	Al a	G u	Al a	Tyr	Asp 455	I le	Al a	Al a	I le	Lys 460	Phe	Arg	G y	Al a
Asn 465	Al a	Val	Thr	Asn	Phe 470	Asp	I le	I le	Lys	Tyr 475	Asp	Val	G u	Lys	I le 480
Met	Al a	Ser	Ser	Asn 485	Leu	Leu	Asn	I le	G u 490	G n	Al a	Arg	Arg	Asn 495	Lys
G u	Val	Val	Asp 500	I le	Ser	Ser	Thr	G n 505	Tyr	I le	Asp	G n	Asn 510	Lys	Pro
Ser	Ser	Al a 515	Tyr	Asp	Asn	Asn	Ser 520	Thr	G n	G u	Al a	I le 525	Ser	Met	G n
Lys	Ser 530	Met	Val	Leu	Tyr	G n 535	Ser	Ser	G n	H s	G n 540	G n	Leu	G n	G n
Asn 545	G n	Pro	Arg	Phe	G u 550	Asn	G u	Arg	Thr	H s 555	G n	Thr	Phe	Ser	Ser 560
Val	Ser	Leu	Asp	Asn 565	Met	Phe	H s	G n	G u 570	Val	Val	G u	G u	Al a 575	Ser
Lys	Met	Arg	Thr 580	H s	Val	Ser	Asn	Al a 585	Ser	Ser	Leu	Al a	Thr 590	Ser	Leu
Ser	Ser	Ser 595	Arg	G u	G y	Thr	Pro 600	Asp	Arg	Thr	Ser	Leu 605	G n	Asn	Leu
Ser	G y 610	I le	Met	Pro	Ser	Thr 615	Al a	Ser	Lys	Leu	Leu 620	Val	Thr	Ser	Al a
Pro 625	Asn	Ser	Asn	Leu	Asn 630	Ser	Trp	Asp	Pro	Ser 635	G n	H s	Leu	Arg	Pro 640

Sequence Listing from Patent scope

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<211> 546
<212> PRT
<213> Glycine max

<400> 99
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Ser Ala Ala Thr Val Ser Asp Asn Asn Val Pro Thr Thr Phe Tyr Met
35 40 45
Ser Pro Ser His Met Ser Asn Ser Gly Met Cys Tyr Ser Val Gly G u
50 55 60
Asn Gly Asn Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp
65 70 75 80
Gly Ser Leu Gly Ile Leu G u Ala Leu Asn Arg Ser G n Thr G n Val
85 90 95
Met Val Pro Thr Ser Ser Pro Lys Leu G u Asp Phe Leu Gly Gly Ala
100 105 110
Thr Met Gly Thr His G u Tyr Gly Asn His G u Arg Gly Leu Ser Leu
115 120 125
Asp Ser Ile Tyr Tyr Asn Ser G n Asn Ala G u Ala G n Pro Asn Arg
130 135 140
Asn Leu Leu Ser His Pro Phe Arg G n G n Gly His Ala Pro Ser G u
145 150 155 160
G u G u Ala Thr Lys G u Thr His Val Ser Val Met Pro G n Met Thr
165 170 175
Gly Gly Gly Leu G n Asn Trp Ile Leu G u G n G n Met Asn Cys Gly
180 185 190
Ile Trp Asn G u Arg Ser Gly Val Ser Val Gly Thr Val Gly Cys Gly
195 200 205
G u Leu G n Ser Leu Ser Leu Ser Met Ser Pro Gly Ser G n Ser Ser
210 215 220
Cys Val Thr Ala Pro Ser Gly Thr Asp Ser Val Ala Val Asp Ala Lys
225 230 235 240
Lys Arg Gly His Ala Lys Leu Gly G n Lys G n Pro Val His Arg Lys
245 250 255
Ser Ile Asp Thr Phe Gly G n Arg Thr Ser G n Tyr Arg Gly Val Thr
260 265 270
Arg His Arg Trp Thr Gly Arg Tyr G u Ala His Leu Trp Asp Asn Ser
275 280 285
Cys Lys Lys G u Gly G n Thr Arg Lys Gly Arg G n Gly Tyr Asp
290 295 300
Met G u G u Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
305 310 315 320
Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile G u Asn Tyr G n Val
325 330 335
G n Leu G u G u Met Lys Asn Met Ser Arg G n G u Tyr Val Ala His
340 345 350
Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg
355 360 365
Gly Val Thr Arg His His G n His Gly Arg Trp G n Ala Arg Ile Gly
370 375 380
Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr G n
385 390 395 400
G u G u Ala Ala G u Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
405 410 415
Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val G u Arg

Sequence Listing from Patent scope

Ile	Met	Ala	420 Ser	Ser	Asn	Leu	Leu	425 Ala	Gly	Glu	Leu	Ala	430 Arg	Arg	Asn
Lys	Asp	Asn	435 Asp	Pro	Arg	Asn	440 Glu	Ala	Ile	Asp	Tyr	445 Asn	Lys	Ser	Val
Phe	Lys	Gln	Glu	Thr	Thr	455 Met	Lys	Met	Ile	Arg	460 Ser	Gly	Arg	Cys	Leu
465	Ser	Ser	Ser	Arg	Glu	470 Ala	Ser	Pro	Glu	Lys	475 Met	Gly	Pro	Ser	Leu
Ser	Pro	Lys	Pro	Pro	Pro	Met	Glu	Thr	Lys	Ile	Val	Asn	Pro	Ile	Gly
Thr	Ser	Val	500 Thr	Ser	Trp	Leu	Pro	505 Ser	Pro	Thr	Val	Gln	510 Met	Arg	Pro
Ser	Pro	Ala	Ile	Ser	Leu	Ser	520 His	Leu	Pro	Val	Phe	525 Ala	Ala	Trp	Thr
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<210> 100

<211> 415

<212> PRT

<213> Arabidopsis thaliana

<400> 100

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

Sequence Listing from Patent scope

Arg	Gln	Glu	Phe	Val	Ala	Met	Leu	Arg	Arg	Asn	Ser	Ser	Gly	Phe	Ser
305					310					315					320
Arg	Gly	Ala	Ser	Val	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly
				325					330					335	
Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr
			340					345					350		
Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile
		355					360					365			
Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile
		370				375					380				
Asn	Arg	Tyr	Asp	Val	Lys	Arg	Ile	Cys	Ser	Ser	Ser	Thr	Ile	Val	Asp
385					390					395					400
Ser	Asp	Gln	Ala	Lys	His	Ser	Pro	Thr	Ser	Ser	Gly	Ala	Gly	His	
				405					410					415	

<210> 101

<211> 428

<212> PRT

<213> Zea mays

<400> 101

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

Sequence Listing from Patent scope

Ala	Glu	Asp	Gln	325 Ala	Ala	Leu	Ser	Ala	330 Arg	Ser	Phe	Ser	Gln	335 Ser	Gln
Gln	Ser	Ser	340 Asn	Ser	Leu	Pro	Pro	345 Tyr	Phe	Leu	Thr	Asn	350 Leu	Leu	Gln
Pro	Leu	355 Pro	Ser	Gln	His	Ser	360 Leu	Ala	Gln	Ala	Leu	365 Pro	Ser	Tyr	Asn
Asn	Leu	Gly	Phe	Gly	Glu	375 Pro	Ser	Leu	Tyr	Trp	380 Pro	Cys	Pro	Cys	Gly
385 Asp	Pro	Gly	Glu	Gln	Lys	390 Val	Gln	Leu	Gly	Ser	395 Lys	Leu	Glu	Ile	400 Val
Asp	Gly	Leu	405 Val	Gln	Leu	Ala	Asn	410 Ser	Ala	Ala	Asn			415	
			420					425							

<210> 102

<211> 438

<212> PRT

<213> Arabidopsis thaliana

<400> 102

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

Sequence Listing from Patent scope

Met	Met	Asp	Thr	Gly	Phe	Ser	Pro	Phe	Leu	Thr	Asp	Gln	Asn	Leu	Ala
			340					345					350		
Asn	Glu	Asn	Pro	Ile	Glu	Tyr	Pro	Glu	Leu	Phe	Asn	Glu	Leu	Ala	Phe
		355					360					365			
Glu	Asp	Asn	Ile	Asp	Phe	Met	Phe	Asp	Asp	Gly	Lys	His	Glu	Cys	Leu
	370					375					380				
Asn	Leu	Glu	Asn	Leu	Asp	Cys	Cys	Val	Val	Gly	Arg	Glu	Ser	Pro	Pro
385					390					395					400
Ser	Ser	Ser	Ser	Pro	Leu	Ser	Cys	Leu	Ser	Thr	Asp	Ser	Ala	Ser	Ser
				405						410				415	
Thr	Thr	Thr	Thr	Thr	Thr	Ser	Val	Ser	Cys	Asn	Tyr	Leu	Phe	Gln	Gly
			420					425						430	
Leu	Phe	Val	Gly	Ser	Glu										
		435													

<210> 103

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 103

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

Sequence Listing from Patent scope

G u	Val	Leu	G y	325 Leu	G y	G n	Thr	G y	330 Met	Leu	Asn	Hi s	Thr	335 Pro	Asn
Ser	Asn	Hi s	340 G n	Phe	Pro	G y	Ser	345 Ser	Asn	I l e	G y	Ser	350 G y	G y	G y
Phe	Ser	Leu	Phe	Pro	Al a	Al a	G u	Asn	Hi s	Arg	Phe	Asp	G y	Arg	Al a
Ser	370 Thr	Asn	G n	Val	Leu	390 G n	Asn	Al a	Al a	Al a	395 Ser	Ser	G y	Phe	Ser
385 Pro	Hi s	Hi s	Hi s	Asn	405 Thr	Asn	G y	Phe	G n	410 Pro	Pro	Leu	Met	Arg	415 Pro
Asn	Tr p	Leu	G n	420					425				430		Ser

<210> 104

<211> 449

<212> PRT

<213> Arabi dopsi s t hal i ana

<400> 104

Met 1	Leu	Asp	Leu	Asn 5	Leu	Asn	Ala	Asp	Ser 10	Pro	Glu	Ser	Thr	Gln 15	Tyr
Gly	Gly	Asp	Ser 20	Tyr	Leu	Asp	Arg	Gln 25	Thr	Ser	Asp	Asn 30	Ser	Ala	Gly
Asn	Arg	Val 35	Glu	Glu	Ser	Gly	Thr 40	Ser	Thr	Ser	Ser	Val 45	Ile	Asn	Ala
Asp	Gly	Asp	Glu	Asp	Ser	Cys 55	Ser	Thr	Arg	Ala	Phe 60	Thr	Leu	Ser	Phe
Asp 65	Ile	Leu	Lys	Val 70	Gly	Ser	Ser	Ser	Gly 75	Gly	Asp	Glu	Ser	Pro 80	Ala
Ala	Ser	Ala	Ser	Val 85	Thr	Lys	Glu	Phe	Phe 90	Pro	Val	Ser	Gly	Asp 95	Cys
Gly	His	Leu	Arg 100	Asp	Val	Glu	Gly	Ser 105	Ser	Ser	Ser	Arg	Asn 110	Trp	Ile
Asp	Leu	Ser 115	Phe	Asp	Arg	Ile	Gly 120	Asp	Gly	Glu	Thr	Lys 125	Leu	Val	Thr
Pro	Val 130	Pro	Thr	Pro	Ala	Pro 135	Val	Pro	Ala	Gln	Val 140	Lys	Lys	Ser	Arg
Arg 145	Gly	Pro	Arg	Ser	Arg 150	Ser	Ser	Gln	Tyr	Arg 155	Gly	Val	Thr	Phe	Tyr 160
Arg	Arg	Thr	Gly	Arg 165	Trp	Glu	Ser	His	Ile 170	Trp	Asp	Cys	Gly	Lys 175	Gln
Val	Tyr	Leu	Gly 180	Gly	Phe	Asp	Thr	Ala 185	His	Ala	Ala	Ala	Arg 190	Ala	Tyr
Asp	Arg	Ala 195	Ala	Ile	Lys	Phe	Arg 200	Gly	Val	Asp	Ala	Asp 205	Ile	Asn	Phe
Thr	Leu 210	Gly	Asp	Tyr	Glu	Glu	Asp	Met	Lys	Gln	Val 220	Gln	Asn	Leu	Ser
Lys 225	Glu	Glu	Phe	Val	His 230	Ile	Leu	Arg	Arg	Gln	Ser	Thr	Gly	Phe	Ser 240
Arg	Gly	Ser	Ser	Lys 245	Tyr	Arg	Gly	Val	Thr 250	Leu	His	Lys	Cys	Gly 255	Arg
Trp	Glu	Ala	Arg 260	Met	Gly	Gln	Phe	Leu 265	Gly	Lys	Lys	Ala	Tyr 270	Asp	Lys
Ala	Ala	Ile 275	Asn	Thr	Asn	Gly	Arg 280	Glu	Ala	Val	Thr	Asn 285	Phe	Glu	Met
Ser	Ser 290	Tyr	Gln	Asn	Glu	Ile 295	Asn	Ser	Glu	Ser	Asn 300	Asn	Ser	Glu	Ile
Asp 305	Leu	Asn	Leu	Gly	Ile 310	Ser	Leu	Ser	Thr	Gly 315	Asn	Ala	Pro	Lys	Gln 320
Asn	Gly	Arg	Leu	Phe 325	His	Phe	Pro	Ser	Asn 330	Thr	Tyr	Glu	Thr	Gln 335	Arg

Sequence Listing from Patent scope

Gly	Val	Ser	Leu	Arg	Ile	Asp	Asn	Gly	Tyr	Met	Gly	Lys	Pro	Val	Asn
			340					345					350		
Thr	Pro	Leu	Pro	Tyr	Gly	Ser	Ser	Asp	His	Arg	Leu	Tyr	Trp	Asn	Gly
		355					360					365			
Ala	Cys	Pro	Ser	Tyr	Asn	Asn	Pro	Ala	Gly	Gly	Arg	Ala	Thr	Gly	Lys
	370					375					380				
Arg	Ser	Gly	Ala	Gly	Gly	Met	Met	Ser	Asn	Trp	Gly	Trp	Gly	Arg	Pro
385				390						395					400
Gly	Gly	Thr	Ser	Ala	Val	Arg	Pro	Gly	Pro	Pro	Gly	Pro	Gly	Pro	Pro
				405				410					415		
Pro	Leu	Phe	Ser	Val	Ala	Ala	Ala	Ser	Gly	Phe	Ser	His	Phe	Arg	
			420					425				430			
Pro	Gly	Pro	Pro	Asn	Asp	Asn	Ala	Thr	Arg	Gly	Tyr	Phe	Tyr	Pro	His
		435					440					445			

Pro

<210> 105
 <211> 663
 <212> DNA
 <213> Zea mays
 <220>
 <221> CDS
 <222> (1) ... (663)

<400> 105

atg	gag	gcg	ctg	agc	ggg	cgg	gta	ggc	gtc	aag	tgc	ggg	cgg	tgg	aac	48
Met	Gly	Ala	Leu	Ser	Gly	Arg	Val	Gly	Val	Lys	Cys	Gly	Arg	Trp	Asn	
1				5					10					15		
cct	acg	gcg	gag	cag	gtg	aag	gtc	ctg	acg	gag	ctc	ttc	cgc	gcg	ggg	96
Pro	Thr	Ala	Gly	Gly	Val	Lys	Val	Leu	Thr	Gly	Leu	Phe	Arg	Ala	Gly	
			20					25					30			
ctg	cgg	acg	ccc	agc	acg	gag	cag	atc	cag	cgc	atc	tcc	acc	cac	ctc	144
Leu	Arg	Thr	Pro	Ser	Thr	Gly	Gly	Ile	Gly	Arg	Ile	Ser	Thr	His	Leu	
			35				40					45				
agc	gcc	ttc	ggc	aag	gtg	gag	agc	aag	aac	gtc	ttc	tac	tgg	ttc	cag	192
Ser	Ala	Phe	Gly	Lys	Val	Gly	Ser	Lys	Asn	Val	Phe	Tyr	Trp	Phe	Gly	
	50					55					60					
aac	cac	aag	gcc	cgc	gag	cgc	cac	cac	cac	aag	aag	cgc	cgc	cgc	ggc	240
Asn	His	Lys	Ala	Arg	Gly	Arg	His	His	His	Lys	Lys	Arg	Arg	Arg	Gly	
	65				70					75					80	
gcg	tcg	tcg	tcc	tcc	ccc	gac	agc	ggc	agc	ggc	agg	gga	agc	aac	aac	288
Ala	Ser	Ser	Ser	Ser	Pro	Asp	Ser	Gly	Ser	Gly	Arg	Gly	Ser	Asn	Asn	
				85					90					95		
gag	gaa	gac	ggc	cgt	ggt	gcc	gcc	tcg	cag	tcg	cac	gac	gcc	gac	gcc	336
Gly	Gly	Asp	Gly	Arg	Gly	Ala	Ala	Ser	Gly	Ser	His	Asp	Ala	Asp	Ala	
			100					105					110			
gac	gcc	gac	ctc	gtg	ctg	caa	ccg	cca	gag	agc	aag	cgg	gag	gcc	aga	384
Asp	Ala	Asp	Leu	Val	Leu	Gly	Pro	Pro	Gly	Ser	Lys	Arg	Gly	Ala	Arg	
		115					120					125				
agc	tat	ggc	cac	cat	cac	cgg	ctc	gtg	aca	tgc	tac	gtc	agg	gac	gtg	432
Ser	Tyr	Gly	His	His	His	Arg	Leu	Val	Thr	Cys	Tyr	Val	Arg	Asp	Val	
	130					135					140					

Sequence Listing from Patent scope

gtg gag cag cag gag gcg t c g c c g t c g t g g gag c g g c c g a c g a g g gag 480
Val Glu Glu Glu Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
145 150 155 160

gtg gag acg c t a gag c t c t t c c c c t c a a g t c g t a c g g c g a c c t c gag 528
Val Glu Thr Leu Glu Leu Phe Pro Leu Lys Ser Tyr Gly Asp Leu Glu
165 170 175

gcg gcg gag aag g t c c g g t c g t a c g t c a g a g g c a t c g c c g c c a c c a g c 576
Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
180 185 190

gag cag t g c a g g gag t t g t c c t t c t t c g a c g t c t c c g c c g g c g g a t 624
Glu Glu Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
195 200 205

c c g c c g c t c gag c t c a g g c t c t g c a g c t t c g g t c c c t a g 663
Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro
210 215 220

<210> 106
<211> 220
<212> PRT
<213> Zea mays

<400> 106
Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
1 5 10
Pro Thr Ala Glu Glu Val Lys Val Leu Thr Glu Leu Phe Arg Ala Gly
20 25 30
Leu Arg Thr Pro Ser Thr Glu Glu Ile Glu Arg Ile Ser Thr His Leu
35 40 45
Ser Ala Phe Gly Lys Val Glu Ser Lys Asn Val Phe Tyr Trp Phe Glu
50 55 60
Asn His Lys Ala Arg Glu Arg His His His Lys Lys Arg Arg Arg Gly
65 70 75
Ala Ser Ser Ser Ser Pro Asp Ser Gly Ser Gly Arg Gly Ser Asn Asn
85 90 95
Glu Glu Asp Gly Arg Gly Ala Ala Ser Glu Ser His Asp Ala Asp Ala
100 105 110
Asp Ala Asp Leu Val Leu Glu Pro Pro Glu Ser Lys Arg Glu Ala Arg
115 120 125
Ser Tyr Gly His His His Arg Leu Val Thr Cys Tyr Val Arg Asp Val
130 135 140
Val Glu Glu Glu Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
145 150 155 160
Val Glu Thr Leu Glu Leu Phe Pro Leu Lys Ser Tyr Gly Asp Leu Glu
165 170 175
Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
180 185 190
Glu Glu Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
195 200 205
Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro
210 215 220

<210> 107
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

Sequence Listing from Patent scope

<223> att B1 variant

<400> 107

caagttcgt a caaaaaagca ggct

24

<210> 108

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> att B1 variant

<400> 108

caagtttgt a caaaaaggac tct

23

<210> 109

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> att B1 variant

<400> 109

caagtgcata caaaaaggac tgct

24

<210> 110

<211> 17747

<212> DNA

<213> Artificial Sequence

<220>

<223> PHP32371

<220>

<221> mi sc_ feature

<222> (4310) ... (4817)

<223> Rab17 promoter

<220>

<221> mi sc_ feature

<222> (4818) ... (4912)

<223> Rab17 5' UTR

<220>

<221> mi sc_ feature

<222> (4951) ... (4974)

<223> att B1

<220>

<221> mi sc_ feature

<222> (5036) ... (6496)

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t c t a t t a t a a	t a a c a a g t a	t g t t t t a t a a	t t a t t t t g a t	c t t g a t a t a c	t t g g a t g a t g	2580
g c a t a t g c a g	c a g c t a t a t g	t g g a t t t t t t	t a g c c c t g c c	t t c a t a c g c t	a t t t a t t t g c	2640
t t g g t a c t g t	t t c t t t t g t c	g a t g c t c a c c	c t g t t g t t t g	g t g t t a c t t c	t g c a g g t c g a	2700
c t c t a g a g g a	t c c a c c a t g g	c t a g c a t a a c	t t c g t a t a g c	a t a c a t t a t a	c g a a g t t a t c	2760
c a g a t c t g c c	c t g t c c a a c a	a g t t c a t c g g	c g a c g a c a t g	a a g a t g a c c t	a c c a c a t g g a	2820
c g g c t g c g t g	a a c g g c c a c t	a c t t c a c c g t	g a a g g g c g a g	g g c a g c g g g a	a g c c c t a c g a	2880
g g g c a c c c a g	a c c t c c a c c t	t c a a g g t g a c	c a t g g c c a a c	g g c g g c c c c c	t g g c c t t c t c	2940
c t t c g a c a t c	c t g t c c a c c g	t g t t c a t g t a	c g g c a a c c g c	t g c t t c a c c g	c c t a c c c c a c	3000
c a g c a t g c c c	g a c t a c t t c a	a g c a g g c c t t	c c c c g a c g g c	a t g t c c t a c g	a g a g a a c c t t	3060
c a c c t a c g a g	g a c g g c g g g c	t g g c c a c c g c	c a g c t g g g a g	a t c a g c c t g a	a g g g c a a c t g	3120
c t t c g a g c a c	a a g t c c a c c t	t c c a c g g c g t	g a a c t t c c c c	g c c g a c g g g c	c c g t g a t g g c	3180
c a a g a a g a c c	a c c g g c t g g g	a c c c c t c c t t	c g a g a a g a t g	a c c g t g t g c g	a c g g c a t c t t	3240
g a a g g g c g a c	g t g a c c g c c t	t c c t g a t g c t	g c a g g g c g g c	g g c a a c t a c a	g a t g c c a g t t	3300
c c a c a c c t c c	t a c a a g a c c a	a g a a g c c c g t	g a c c a t g c c c	c c c a a c c a c g	t g g t g g a g c a	3360
c c g c a t c g c c	a g a a c c g a c c	t g g a c a a g g g	c g g c a a c a g c	g t g c a g c t g a	c c g a g c a c g c	3420
c g t g g c c c a c	a t c a c c t c c g	t g g t g c c c t t	c t g a a g c g g c	c g c a a c c t a g	a c t t g t c c a t	3480
c t t c t g g a t t	g g c c a a c t t a	a t t a a t g t a t	g a a a t a a a a g	g a t g c a c a c a	t a g t g a c a t g	3540
c t a a t c a c t a	t a a t g t g g g c	t c t g t t a t g t	t g t g t t a t g t	g t a a t t a c t a	g t t a t c t g a a	3600
t a a a g a g a a	a g a g a t c a t c	c a t a t t t c t t	a t c c t a a a t g	a a t g t c a c g t	g t c t t t a t a a	3660
t t c t t t g a t g	a a c c a g a t g c	a t t t c a t t a a	c c a a a t c c a t	a t a c a t a t a a	a t a t t a a t c a	3720
t a t a t a a t t a	a t a t c a a t t g	g g t t a g c a a a	a c a a a t c t a g	t c t a g g t g t g	t t t t g c g a a t	3780
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a a c a t a c g a g	c c g g a a g c a t	a a a g t g t a a a	g c c t g g g g t g	c c t a a t g a g t	g a g c t a a c t c	3900
a c a t t a a t t g	c g t t g c g c t c	a c t g c c c g c t	t t c c a g t c g g	g a a a c c t g t c	g t g c c a g c t g	3960
c a t t a a t g a a	t c g g c c a a c g	c g c g g g g a g a	g g c g g t t t g c	g t a t t g g g c g	c t c t t c c g c t	4020
g a t c c g a t a t	c g a t g g g c c c	t g g c c g a a g c	t t g g t c a c c c	g g t c c g g g c c	t a g a a g g c c a	4080
g c t t c a a g t t	t g t a c a a a a a	a g c a g g c t c c	g g c c a g a a t g	g c c c g g a c c g	g g t t a c c g a a	4140
t t c g a g c t c g	g t a c c c t g g g	a t c c g a t a t c	g a t g g g c c c t	g g c c g a a g c t	g g g a t a t c g c	4200
t a t c a a c t t t	g t a t a g a a a a	g t t g g g c c g a	a t t c g a g c t c	g g t a c g g c c a	g a a t g g c c c g	4260
g a c c g g g t t a	c c g a a t t c g a	g c t c g g t a c c	c t g g g g a t c c	c t a t a g t a t t	t t a a a a t t g c	4320
a t t a a c a a a c	a t g t c c t a a t	t g g t a c t c c t	g a g a t a c t a t	a c c c t c c t g t	t t t a a a a t a g	4380
t t g g c a t t a t	c g a a t t a t c a	t t t t a c t t t t	t a a t g t t t t c	t c t t c t t t t a	a t a t a t t t t a	4440
t g a a t t t t a a	t g t a t t t t a a	a a t g t t a t g c	a g t t c g c t c t	g g a c t t t t c t	g c t g c g c c t a	4500
c a c t t g g g t g	t a c t g g g c c t	a a a t t c a g c c	t g a c c g a c c g	c c t g c a t t g a	a t a a t g g a t g	4560
a g c a c c g g t a	a a a t c c g c g t	a c c c a a c t t t	c g a g a a g a a c	c g a g a c g t g g	c g g g c c g g g c	4620
c a c c g a c g c a	c g g c a c c a g c	g a c t g c a c a c	g t c c c g c c g g	c g t a c g t g t a	c g t g c t g t t c	4680
c c t c a c t g g c	c g c c c a a t c c	a c t c a t g c a t	g c c c a c g t a c	a c c c c t g c c g	t g g c g c g c c c	4740
a g a t c c t a a t	c c t t t c g c c g	t t c t g c a c t t	c t g c t g c c t a	t a a a t g g c g g	c a t c g a c c g t	4800
c a c c t g c t t c	a c c a c c g g c g	a g c c a c a t c g	g a a c a c a c g a t	c g a g c a c a c a	a g c a c g a a g a	4860
c t c g t t t a g g	a g a a a c c a c a	a a c c a c c a a g	c c g t g c a a g c	a c c a a g c t t g	g t c a c c c g g t	4920
c c g g g c c t a g	a a g g c c a g c t	t c a a g t t t g t	a c a a a a a a g c	a g g c t t c g a a	g g a g a t a g a a	4980
c c g a t c c a c c	a t g t c c a a c c	t g c t c a c g g t	t c a c c a g a a c	c t t c c g g c t c	t t c c a g t g g a	5040
c g c g a c g t c c	g a t g a a g t c a	g g a a g a a c c t	c a t g g a c a t g	t t c c g c g a c a	g g c a a g c g t t	5100
c a g c g a g c a c	a c c t g g a a g a	t g c t g c t c t c	c g t c t g c c c g	t c c t g g g c t g	c a t g g t g c a a	5160
g c t g a a c a a c	a g g a a g t g g t	t c c c c g c t g a	g c c c g a g g a c	g t g a g g g a t t	a c c t t c t g t a	5220
c c t g c a a g c g	c g a g g t t t g t	t t c t g c t t c t	a c c t t t g a t a	t a t a t a t a a t	a a t t a t c a t t	5280
a a t t a g t a g t	a a t a t a a t a t	t t c a a a t a t t	t t t t t c a a a a	t a a a a g a a t g	t a g t a t a t a g	5340
c a a t t g c t t t	t c t g t a g t t t	a t a a g t g t g t	a t a t t t t a a t	t t a t a a c t t t	t c t a a t a t a t	5400
g a c c a a a a c a	t g g t g a t g c c	t a g g t c t g g c	a g t g a a g a c c	a t c a g c a a c	a c c t t g g a c a	5460
a c t g a a c a t g	c t t c a c a g g c	g c t c c g g c c t	c c c g c g c c c c	a g c g a c t c g a	a c g c c g t g a g	5520
c c t c g t c a t g	c g c c g c a t c a	g g a a g g a a a a	c g t c g a t g c c	g g c g a a a g g g	c a a a g c a g g c	5580
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g t g c c a g g a c	a t t a g g a a c c	t g g c g t t c c t	c g g a a t t g c a	t a c a a c a c g c	t c c t c a g g a t	5700
c g c g g a a a t t	g c c c g c a t t c	g c g t g a a g g a	c a t t a g c c g c	a c c g a c g g c g	g c a g g a t g c t	5760

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Sequence Listing from Patent scope

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Sequence Listing from Patent scope

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<212> DNA

<213> Oryza sativa

<400> 117

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Sequence Listing from Patent scope

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Sequence Listing from Patent scope

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Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Oys Phe Asn	
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agg acc aca cca gca tcc gag agc ctg tct act tcc gcg cac gga gcc	672
Arg Thr Thr Pro Ala Ser Glu Ser Leu Ser Thr Ser Ala His Gly Ala	
210 215 220	
acc acg gct aca atg gct ggc ggg agg aaa gag atc aac gag gaa gga	720

Sequence Listing from Patent scope															
Thr 225	Thr	Ala	Thr	Met	Ala 230	Gly	Gly	Arg	Lys	Glu 235	Ile	Asn	Glu	Glu	Gly 240
tct Ser	gga Gly	tcc Ser	gct Ala	ggt Gly 245	gcc Ala	gtg Val	gtt Val	gca Ala	gtt Val 250	ggc Gly	tca Ser	gaa Glu	tca Ser	ggt Gly 255	gga Gly
768															
tcc Ser	ggc Gly	gct Ala	gtt Val 260	gtt Val	gaa Glu	gct Ala	ggt Gly	gcc Ala 265	gct Ala	gcg Ala	gca Ala	gcg Ala	gct Ala 270	cgg Arg	aag Lys
816															
agc Ser	gtt Val	gat Asp 275	act Thr	ttc Phe	ggc Gly	caa Gln	aga Arg 280	acg Thr	agc Ser	atc Ile	tac Tyr	aga Arg 285	ggc Gly	gtt Val	act Thr
864															
cgg Arg	cac His 290	cgc Arg	tgg Trp	acc Thr	ggc Gly	agg Arg 295	tac Tyr	gag Glu	gca Ala	cac His	ttg Leu 300	tgg Trp	gac Asp	aac Asn	agc Ser
912															
tgt Oys 305	cgc Arg	cgc Arg	gag Glu	ggc Gly	caa Gln 310	act Thr	agg Arg	aag Lys	gga Gly	aga Arg 315	cag Gln	gga Gly	gga Gly	tat Tyr	gac Asp 320
960															
aaa Lys	gag Glu	gag Glu	aag Lys	gct Ala 325	gcc Ala	aga Arg	gcg Ala	tac Tyr	gac Asp 330	ctg Leu	gcc Ala	gcg Ala	ttg Leu	aag Lys 335	tac Tyr
1008															
tgg Trp	ggt Gly	cca Pro	aca Thr 340	acg Thr	acg Thr	acc Thr	aac Asn	ttc Phe 345	ccg Pro	gtg Val	aac Asn	aac Asn	tac Tyr 350	gag Glu	aag Lys
1056															
gag Glu	ctg Leu	gaa Glu 355	gag Glu	atg Met	aag Lys	cac His	atg Met 360	acg Thr	cgg Arg	cag Gln	gag Glu	ttc Phe 365	gtc Val	gct Ala	tct Ser
1104															
ctc Leu	agg Arg 370	cgc Arg	aag Lys	tca Ser	tct Ser	ggt Gly 375	ttc Phe	tcc Ser	aga Arg	ggt Gly	gcg Ala 380	tcg Ser	atc Ile	tat Tyr	aga Arg
1152															
gga Gly 385	gtt Val	acc Thr	cgc Arg	cac His	cac His 390	cag Gln	cac His	gga Gly	agg Arg	tgg Trp 395	cag Gln	gca Ala	aga Arg	atc Ile	ggg Gly 400
1200															
aga Arg	gtc Val	gcc Ala	ggt Gly	aac Asn 405	aag Lys	gac Asp	ctg Leu	tac Tyr	ttg Leu 410	gga Gly	acc Thr	ttc Phe	tcg Ser	act Thr 415	cag Gln
1248															
gag Glu	gag Glu	gca Ala	gcg Ala 420	gaa Glu	gcg Ala	tat Tyr	gac Asp	att Ile 425	gcg Ala	gcg Ala	atc Ile	aag Lys	ttc Phe 430	cgc Arg	ggt Gly
1296															
ctc Leu	aat Asn	gcc Ala 435	gtg Val	acc Thr	aac Asn	ttc Phe	gac Asp 440	atg Met	tca Ser	cgc Arg	tat Tyr	gat Asp 445	gtc Val	aag Lys	tcg Ser
1344															
att Ile 450	ctg Leu	gat Asp	agc Ser	gct Ala	gcg Ala	ttg Leu 455	cct Pro	gtg Val	gga Gly	acc Thr	gct Ala 460	gcc Ala	aaa Lys	cgc Arg	ctc Leu
1392															
aag Lys 465	gac Asp	gcg Ala	gaa Glu	gca Ala	gct Ala 470	gcc Ala	gcg Ala	tac Tyr	gat Asp	gtt Val 475	ggc Gly	agg Arg	att Ile	gcc Ala	tca Ser 480
1440															

Sequence Listing from Patent scope

cat	ctc	ggt	gga	gat	gga	gct	tac	gct	gcc	cac	tac	ggg	cat	cat	cac	1488
His	Leu	Gly	Gly	Asp	Gly	Ala	Tyr	Ala	Ala	His	Tyr	Gly	His	His	His	
				485					490						495	
cac	tct	gca	gcc	gca	gct	tgg	cct	aca	ata	gca	ttc	caa	gcg	gca	gcg	1536
His	Ser	Ala	Ala	Ala	Ala	Trp	Pro	Thr	Ile	Ala	Phe	Gln	Ala	Ala	Ala	
			500					505					510			
gct	cct	cct	cca	cac	gct	gct	ggt	ctt	tac	cat	ccg	tac	gcg	caa	cct	1584
Ala	Pro	Pro	Pro	His	Ala	Ala	Gly	Leu	Tyr	His	Pro	Tyr	Ala	Gln	Pro	
		515					520					525				
ctc	cgc	ggt	tgg	tgt	aag	cag	gaa	caa	gat	cat	gcg	gtg	att	gcg	gct	1632
Leu	Arg	Gly	Trp	Cys	Lys	Gln	Glu	Gln	Asp	His	Ala	Val	Ile	Ala	Ala	
	530					535					540					
gca	cac	agc	tig	caa	gat	ctg	cat	cac	ctc	aat	ctg	gga	gcc	gca	gca	1680
Ala	His	Ser	Leu	Gln	Asp	Leu	His	His	Leu	Asn	Leu	Gly	Ala	Ala	Ala	
					550					555					560	
gct	gcc	cat	gac	ttc	ttc	tca	caa	gcc	atg	cag	cag	cag	cat	ggc	ctg	1728
Ala	Ala	His	Asp	Phe	Phe	Ser	Gln	Ala	Met	Gln	Gln	Gln	His	Gly	Leu	
				565					570					575		
ggc	agc	ata	gac	aat	gcg	tct	ctg	gag	cac	tcc	acc	gga	tcg	aac	tcg	1776
Gly	Ser	Ile	Asp	Asn	Ala	Ser	Leu	Glu	His	Ser	Thr	Gly	Ser	Asn	Ser	
			580					585					590			
gtg	gtg	tac	aat	gga	gac	aac	ggc	gga	gga	ggt	gga	ggt	tac	atc	atg	1824
Val	Val	Tyr	Asn	Gly	Asp	Asn	Gly	Gly	Gly	Gly	Gly	Gly	Tyr	Ile	Met	
		595					600					605				
gca	cct	atg	tca	gcg	gtc	tct	gct	acc	gct	acg	gcg	gtg	gcc	tca	tcc	1872
Ala	Pro	Met	Ser	Ala	Val	Ser	Ala	Thr	Ala	Thr	Ala	Val	Ala	Ser	Ser	
	610					615					620					
cac	gac	cac	ggt	gga	gac	ggc	ggc	aag	cag	gtc	caa	atg	ggc	tac	gac	1920
His	Asp	His	Gly	Gly	Asp	Gly	Gly	Lys	Gln	Val	Gln	Met	Gly	Tyr	Asp	
	625				630					635					640	
tcc	tac	ctt	gtg	gga	gct	gac	gct	tac	ggc	gga	gga	gga	gct	ggt	cgc	1968
Ser	Tyr	Leu	Val	Gly	Ala	Asp	Ala	Tyr	Gly	Gly	Gly	Gly	Ala	Gly	Arg	
			645						650					655		
atg	cct	agc	tgg	gcc	atg	acg	cct	gct	tct	gct	cct	gcg	gct	acg	agc	2016
Met	Pro	Ser	Trp	Ala	Met	Thr	Pro	Ala	Ser	Ala	Pro	Ala	Ala	Thr	Ser	
			660				665						670			
tcg	tcg	gat	atg	aca	gga	gtg	tgt	cat	ggc	gcc	caa	ctg	ttc	tcg	gtg	2064
Ser	Ser	Asp	Met	Thr	Gly	Val	Cys	His	Gly	Ala	Gln	Leu	Phe	Ser	Val	
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tgg	aat	gat	aca	tag												2079
Trp	Asn	Asp	Thr													
	690															

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 <211> 692
 <212> PRT
 <213> Oryza sativa

<400> 119

Sequence Listing from Patent scope

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Gln	Leu	Pro	Pro 20	Ser	Gln	Thr	Asn	Ser 25	Thr	Leu	Ile	Ser	Ala 30	Ala	Ala
Thr	Thr	Thr 35	Thr	Ala	Gly	Asp	Ser 40	Ser	Thr	Gly	Asp	Val 45	Cys	Phe	Asn
Ile	Pro 50	Gln	Asp	Trp	Ser	Met 55	Arg	Gly	Ser	Glu	Leu 60	Ser	Ala	Leu	Val
Ala 65	Glu	Pro	Lys	Leu	Glu 70	Asp	Phe	Leu	Gly	Gly 75	Ile	Ser	Phe	Ser	Glu 80
Gln	Gln	His	His 85	His	Gly	Gly	Lys	Gly	Gly 90	Val	Ile	Pro	Ser	Ser 95	Ala
Ala	Ala	Cys	Tyr 100	Ala	Ser	Ser	Gly	Ser 105	Ser	Val	Gly	Tyr	Leu 110	Tyr	Pro
Pro	Pro	Ser 115	Ser	Ser	Ser	Leu	Gln 120	Phe	Ala	Asp	Ser	Val 125	Met	Val	Ala
Thr	Ser 130	Ser	Pro	Val	Val	Ala 135	His	Asp	Gly	Val	Ser 140	Gly	Gly	Gly	Met
Val 145	Ser	Ala	Ala	Ala	Ala 150	Ala	Ala	Ala	Ser	Gly 155	Asn	Gly	Gly	Ile	Gly 160
Leu	Ser	Met	Ile	Lys 165	Asn	Trp	Leu	Arg	Ser 170	Gln	Pro	Ala	Pro	Gln 175	Pro
Ala	Gln	Ala	Leu 180	Ser	Leu	Ser	Met	Asn 185	Met	Ala	Gly	Thr	Thr 190	Thr	Ala
Gln	Gly	Gly 195	Gly	Ala	Met	Ala	Leu 200	Leu	Ala	Gly	Ala	Gly 205	Glu	Arg	Gly
Arg	Thr 210	Thr	Pro	Ala	Ser	Glu 215	Ser	Leu	Ser	Thr	Ser 220	Ala	His	Gly	Ala
Thr 225	Thr	Ala	Thr	Met	Ala 230	Gly	Gly	Arg	Lys	Glu 235	Ile	Asn	Glu	Glu	Gly 240
Ser	Gly	Ser	Ala	Gly 245	Ala	Val	Val	Ala	Val 250	Gly	Ser	Glu	Ser	Gly 255	Gly
Ser	Gly	Ala	Val 260	Val	Glu	Ala	Gly	Ala 265	Ala	Ala	Ala	Ala	Ala 270	Arg	Lys
Ser	Val	Asp 275	Thr	Phe	Gly	Gln	Arg 280	Thr	Ser	Ile	Tyr	Arg 285	Gly	Val	Thr
Arg	His 290	Arg	Trp	Thr	Gly	Arg 295	Tyr	Glu	Ala	His	Leu 300	Trp	Asp	Asn	Ser
Cys 305	Arg	Arg	Glu	Gly	Gln 310	Thr	Arg	Lys	Gly	Arg 315	Gln	Gly	Gly	Tyr	Asp 320
Lys	Glu	Glu	Lys	Ala 325	Ala	Arg	Ala	Tyr	Asp 330	Leu	Ala	Ala	Leu	Lys 335	Tyr
Trp	Gly	Pro	Thr 340	Thr	Thr	Thr	Asn	Phe 345	Pro	Val	Asn	Asn	Tyr 350	Glu	Lys
Glu	Leu	Glu 355	Glu	Met	Lys	His	Met 360	Thr	Arg	Gln	Glu	Phe 365	Val	Ala	Ser
Leu	Arg 370	Arg	Lys	Ser	Ser	Gly 375	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg
Gly 385	Val	Thr	Arg	His	His 390	Gln	His	Gly	Arg	Trp 395	Gln	Ala	Arg	Ile	Gly 400
Arg	Val	Ala	Gly	Asn 405	Lys	Asp	Leu	Tyr	Leu 410	Gly	Thr	Phe	Ser	Thr 415	Gln
Glu	Glu	Ala	Ala 420	Glu	Ala	Tyr	Asp	Ile 425	Ala	Ala	Ile	Lys	Phe 430	Arg	Gly
Leu	Asn 435	Ala	Val	Thr	Asn	Phe	Asp 440	Met	Ser	Arg	Tyr	Asp 445	Val	Lys	Ser
Ile	Leu 450	Asp	Ser	Ala	Ala	Leu 455	Pro	Val	Gly	Thr	Ala	Ala	Lys	Arg	Leu
Lys 465	Asp	Ala	Glu	Ala	Ala 470	Ala	Ala	Tyr	Asp	Val 475	Gly	Arg	Ile	Ala	Ser 480
His	Leu	Gly	Gly	Asp 485	Gly	Ala	Tyr	Ala	Ala 490	His	Tyr	Gly	His	His 495	His
His	Ser	Ala	Ala	Ala	Ala	Trp	Pro	Thr	Ile	Ala	Phe	Gln	Ala	Ala	Ala

Sequence Listing from Patent scope

500
 Ala Pro Pro Pro His Ala Ala Gly 505 Leu Tyr His Pro Tyr 510 Ala Gln Pro
 515
 Leu Arg Gly Trp Cys Lys Gln 520 Gu Gln Asp His Ala 525 Val Ile Ala Ala
 530
 Ala His Ser Leu Gln Asp 535 Leu His His Leu Asn 540 Gly Ala Ala Ala
 545
 Ala Ala His Asp Phe Phe Ser Gln Ala Met 555 Leu Gln Gln Gln His Gly Leu
 560
 Gly Ser Ile Asp 565 Asn Ala Ser Leu Gu His Ser Thr Gly Ser Asn Ser
 580
 Val Val Tyr 595 Asn Gly Asp Asn Gly 600 Gly Gly Gly Gly Tyr 605 Ile Met
 Ala Pro Met Ser Ala Val Ser 615 Ala Thr Ala Thr Ala Val Ala Ser Ser
 610
 His Asp His Gly Gly Asp 630 Gly Gly Lys Gln Val 635 Gln Met Gly Tyr Asp
 625
 Ser Tyr Leu Val Gly Ala Asp Ala Tyr Gly Gly Gly Gly Ala Gly Arg
 645
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 Ser Ser Asp Met Thr Gly Val Cys 680 His Gly Ala Gln Leu 685 Phe Ser Val
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 Trp Asn Asp Thr
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 <212> DNA
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 caa ctg cca ccg tgc cag acc aat agc act ctg atc tcc gct gct gca 96
 Gln Leu Pro Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala
 20 25 30
 acc acc aca acc gca ggc gat tgc tca acg ggc gac gtc tgc ttc aac 144
 Thr Thr Thr Thr Ala Gly Asp Ser Thr Gly Asp Val Cys Phe Asn
 35 40 45
 atc cct caa gac tgg tcc atg cgc gga agc gag ctg agc gct ctg gtc 192
 Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Gu Leu Ser Ala Leu Val
 50 55 60
 gcg gag ccc aag ttg gag gat ttc ttg gga ggc atc tcc ttc tgc gag 240
 Ala Gu Pro Lys Leu Gu Asp Phe Leu Gly Gly Ile Ser Phe Ser Gu
 65 70 75
 caa cag cat cat cac ggc gga aag ggc ggt gtt atc cca agc tct gct 288
 Gln Gln His His His Gly Gly Lys Gly Val Ile Pro Ser Ser Ala
 85 90 95
 gcc gca tgc tat gca agc tcc ggc tcc agc gtg ggc tac ctg tac cct 336
 Ala Ala Cys Tyr Ala Ser Ser Gly Ser Ser Val Gly Tyr Leu Tyr Pro

Sequence Listing from Patent scope

100	105	110	
ccg cct tca tcc tcg tca ctt cag ttt gca gac agc gtg atg gtc gca Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala	115	120	125
acc tca tct cca gtg gtt gcg cac gat ggc gtg agc ggt ggc ggt atg Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met	130	135	140
gtc tca gca gca gcg gct gca gca gct tcg ggt aat ggc ggg att ggc Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly	145	150	155
ctc tcc atg atc aag aac tgg ctg agg agc caa ccg gct ccg caa cct Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro	165	170	175
gcg caa gca ctg agc ctg tcg atg aac atg gct ggt act act acc gct Ala Gln Ala Leu Ser Leu Ser Met Asn Met Ala Gly Thr Thr Thr Ala	180	185	190
caa ggt gga ggc gca atg gca ctt ctg gca ggc gct ggc gaa aga gga Gln Gly Gly Gly Ala Met Ala Leu Leu Ala Gly Ala Gly Gu Arg Gly	195	200	205
agg acc aca cca gca tcc gag agc ctg tct act tcc gcg cac gga gcc Arg Thr Thr Pro Ala Ser Gu Ser Leu Ser Thr Ser Ala His Gly Ala	210	215	220
acc acg gct aca atg gct ggc ggg agg aaa gag atc aac gag gaa gga Thr Thr Ala Thr Met Ala Gly Gly Arg Lys Gu Ile Asn Gu Gu Gly	225	230	235
tct gga tcc gct ggt gcc gtg gtt gca gtt ggc tca gaa tca ggt gga Ser Gly Ser Ala Gly Ala Val Val Ala Val Gly Ser Gu Ser Gly Gly	245	250	255
tcc ggc gct gtt gtt gaa gct ggt gcc gct gcg gca gcg gct cgg aag Ser Gly Ala Val Val Gu Ala Gly Ala Ala Ala Ala Ala Arg Lys	260	265	270
agc gtt gat act ttc ggc caa aga acg agc atc tac aga ggc gtt act Ser Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr	275	280	285
cgg cac cgc tgg acc ggc agg tac gag gca cac ttg tgg gac aac agc Arg His Arg Trp Thr Gly Arg Tyr Gu Ala His Leu Trp Asp Asn Ser	290	295	300
tgt cgc cgc gag ggc caa act agg aag gga aga cag gtg tat cta gga Oys Arg Arg Gu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly	305	310	315
gga tat gac aaa gag gag aag gct gcc aga gcg tac gac ctg gcc gcg Gly Tyr Asp Lys Gu Gu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala	325	330	335
ttg aag tac tgg ggt cca aca acg acg acc aac ttc ccg gtg aac aac Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Asn Asn	340	345	350
tac gag aag gag ctg gaa gag atg aag cac atg acg cgg cag gag ttc			

Sequence Listing from Patent scope																
Tyr	Glu	Lys	Glu	Leu	Glu	Glu	Met	Lys	His	Met	Thr	Arg	Gln	Glu	Phe	
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Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser	
		370				375					380					
atc	tat	aga	gga	gtt	acc	cgc	cac	cac	cag	cac	gga	agg	tgg	cag	gca	1200
Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala	
					390					395					400	
aga	atc	ggg	aga	gtc	gcc	ggt	aac	aag	gac	ctg	tac	tig	gga	acc	ttc	1248
Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe	
				405					410					415		
tcg	act	cag	gag	gag	gca	gcg	gaa	gcg	tat	gac	att	gcg	gcg	atc	aag	1296
Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Ile	Ala	Ala	Ile	Lys	
			420					425					430			
ttc	cgc	ggt	ctc	aat	gcc	gtg	acc	aac	ttc	gac	atg	tca	cgc	tat	gat	1344
Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	Met	Ser	Arg	Tyr	Asp	
		435					440					445				
gtc	aag	tcg	att	ctg	gat	agc	gct	gcg	tig	cct	gtg	gga	acc	gct	gcc	1392
Val	Lys	Ser	Ile	Leu	Asp	Ser	Ala	Ala	Leu	Pro	Val	Gly	Thr	Ala	Ala	
		450				455					460					
aaa	cgc	ctc	aag	gac	gcg	gaa	gca	gct	gcc	gcg	tac	gat	gtt	ggc	agg	1440
Lys	Arg	Leu	Lys	Asp	Ala	Glu	Ala	Ala	Ala	Ala	Tyr	Asp	Val	Gly	Arg	
				470					475					480		
att	gcc	tca	cat	ctc	ggt	gga	gat	gga	gct	tac	gct	gcc	cac	tac	ggg	1488
Ile	Ala	Ser	His	Leu	Gly	Gly	Asp	Gly	Ala	Tyr	Ala	Ala	His	Tyr	Gly	
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cat	cat	cac	cac	tct	gca	gcc	gca	gct	tgg	cct	aca	ata	gca	ttc	caa	1536
His	His	His	His	Ser	Ala	Ala	Ala	Ala	Trp	Pro	Thr	Ile	Ala	Phe	Gln	
				500				505					510			
gcg	gca	gcg	gct	cct	cct	cca	cac	gct	gct	ggt	ctt	tac	cat	ccg	tac	1584
Ala	Ala	Ala	Ala	Pro	Pro	Pro	His	Ala	Ala	Gly	Leu	Tyr	His	Pro	Tyr	
				515			520					525				
gcg	caa	cct	ctc	cgc	ggt	tgg	tgt	aag	cag	gaa	caa	gat	cat	gcg	gtg	1632
Ala	Gln	Pro	Leu	Arg	Gly	Trp	Cys	Lys	Gln	Glu	Gln	Asp	His	Ala	Val	
		530				535					540					
att	gcg	gct	gca	cac	agc	tig	caa	gat	ctg	cat	cac	ctc	aat	ctg	gga	1680
Ile	Ala	Ala	Ala	His	Ser	Leu	Gln	Asp	Leu	His	His	Leu	Asn	Leu	Gly	
					550					555					560	
gcc	gca	gca	gct	gcc	cat	gac	ttc	ttc	tca	caa	gcc	atg	cag	cag	cag	1728
Ala	Ala	Ala	Ala	Ala	His	Asp	Phe	Phe	Ser	Gln	Ala	Met	Gln	Gln	Gln	
				565					570					575		
cat	ggc	ctg	ggc	agc	ata	gac	aat	gcg	tct	ctg	gag	cac	tcc	acc	gga	1776
His	Gly	Leu	Gly	Ser	Ile	Asp	Asn	Ala	Ser	Leu	Glu	His	Ser	Thr	Gly	
			580					585					590			
tcg	aac	tcg	gtg	gtg	tac	aat	gga	gac	aac	ggc	gga	gga	ggt	gga	ggt	1824
Ser	Asn	Ser	Val	Val	Tyr	Asn	Gly	Asp	Asn	Gly	Gly	Gly	Gly	Gly	Gly	
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Sequence Listing from Patent scope

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Tyr	Ile	Met	Ala	Pro	Met	Ser	Ala	Val	Ser	Ala	Thr	Ala	Thr	Ala	Val	
	610					615					620					
gcc	tca	tcc	cac	gac	cac	ggg	gga	gac	ggc	ggc	aag	cag	gtc	caa	atg	1920
Ala	Ser	Ser	His	Asp	His	Gly	Gly	Asp	Gly	Gly	Lys	Gln	Val	Gln	Met	
625					630				635						640	
ggc	tac	gac	tcc	tac	ctt	gtg	gga	gct	gac	gct	tac	ggc	gga	gga	gga	1968
Gly	Tyr	Asp	Ser	Tyr	Leu	Val	Gly	Ala	Asp	Ala	Tyr	Gly	Gly	Gly	Gly	
				645					650					655		
gct	ggg	cgc	atg	cct	agc	tgg	gcc	atg	acg	cct	gct	tct	gct	cct	gcg	2016
Ala	Gly	Arg	Met	Pro	Ser	Trp	Ala	Met	Thr	Pro	Ala	Ser	Ala	Pro	Ala	
			660					665					670			
gct	acg	agc	tcg	tcg	gat	atg	aca	gga	gtg	tgt	cat	ggc	gcc	caa	ctg	2064
Ala	Thr	Ser	Ser	Ser	Asp	Met	Thr	Gly	Val	Cys	His	Gly	Ala	Gln	Leu	
		675					680					685				
ttc	tcg	gtg	tgg	aat	gat	aca	tag									2088
Phe	Ser	Val	Trp	Asn	Asp	Thr										
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Met	Ala	Thr	Val	Asn	Asn	Trp	Leu	Ala	Phe	Ser	Leu	Ser	Pro	Gln	Glu	
1				5					10					15		
ctg	ccg	ccc	tcc	cag	acg	acg	gac	tcc	aca	ctc	atc	tcg	gcc	gcc	acc	96
Leu	Pro	Pro	Ser	Gln	Thr	Thr	Asp	Ser	Thr	Leu	Ile	Ser	Ala	Ala	Thr	
			20					25					30			
gcc	gac	cat	gtc	tcc	ggc	gat	gtc	tgc	ttc	aac	atc	ccc	caa	gat	tgg	144
Ala	Asp	His	Val	Ser	Gly	Asp	Val	Cys	Phe	Asn	Ile	Pro	Gln	Asp	Trp	
		35					40					45				
agc	atg	agg	gga	tca	gag	ctt	tcg	gcg	ctc	gtc	gcg	gag	ccg	aag	ctg	192
Ser	Met	Arg	Gly	Ser	Glu	Leu	Ser	Ala	Leu	Val	Ala	Glu	Pro	Lys	Leu	
	50					55					60					
gag	gac	ttc	ctc	ggc	ggc	atc	tcc	ttc	tcc	gag	cag	cat	cac	aag	gcc	240
Glu	Asp	Phe	Leu	Gly	Gly	Ile	Ser	Phe	Ser	Glu	Gln	His	His	Lys	Ala	
	65			70						75					80	
aac	tgc	aac	atg	ata	ccc	agc	act	agc	agc	aca	gtt	tgc	tac	gcg	agc	288
Asn	Cys	Asn	Met	Ile	Pro	Ser	Thr	Ser	Ser	Thr	Val	Cys	Tyr	Ala	Ser	
				85				90						95		
tca	ggg	gct	agc	acc	ggc	tac	cat	cac	cag	ctg	tac	cac	cag	ccc	acc	336
Ser	Gly	Ala	Ser	Thr	Gly	Tyr	His	His	Gln	Leu	Tyr	His	Gln	Pro	Thr	
			100				105						110			

Sequence Listing from Patent scope																
agc Ser	tca Ser	gcg Ala 115	ctc Leu	cac His	ttc Phe	gcg Ala 120	gac Asp	tcc Ser	gta Val	atg Met	gtg Val	gcc Ala 125	tcc Ser	tcg Ser	gcc Ala	384
ggt Gly	gtc Val 130	cac His	gac Asp	ggc Gly	ggt Gly	gcc Ala 135	atg Met	ctc Leu	agc Ser	gcg Ala	gcc Ala 140	gcc Ala	gct Ala	aac Asn	ggt Gly	432
gtc Val 145	gct Ala	ggc Gly	gct Ala	gcc Ala	agt Ser 150	gcc Ala	aac Asn	ggc Gly	ggc Gly	ggc Gly 155	atc Ile	ggg Gly	ctg Leu	tcc Ser	atg Met 160	480
att Ile	aag Lys	aac Asn	tgg Trp	ctg Leu 165	cgg Arg	agc Ser	caa Gln	ccg Pro	gcg Ala 170	ccc Pro	atg Met	cag Gln	ccg Pro	agg Arg 175	gtg Val	528
gcg Ala	gcg Ala	gct Ala	gag Glu 180	ggc Gly	gcg Ala	cag Gln	ggg Gly	ctc Leu 185	tct Ser	tig Leu	tcc Ser	atg Met	aac Asn 190	atg Met	gcg Ala	576
ggg Gly	acg Thr	acc Thr 195	caa Gln	ggc Gly	gct Ala	gct Ala	ggc Gly 200	atg Met	cca Pro	ctt Leu	ctc Leu	gct Ala 205	gga Gly	gag Glu	cgc Arg	624
gca Ala 210	cgg Arg	gcg Ala	ccc Pro	gag Glu	agt Ser	gta Val 215	tcg Ser	acg Thr	tca Ser	gca Ala	cag Gln 220	ggt Gly	gga Gly	gcc Ala	gtc Val	672
gtc Val 225	gtc Val	acg Thr	gcg Ala	ccg Pro	aag Lys 230	gag Glu	gat Asp	agc Ser	ggt Gly	ggc Gly 235	agc Ser	ggt Gly	gtt Val	gcc Ala	ggc Gly 240	720
gct Ala	cta Leu	gta Val	gcc Ala 245	gtg Val	agc Ser	acg Thr	gac Asp	acg Thr	ggt Gly 250	ggc Gly	agc Ser	ggc Gly	ggc Gly	gcg Ala 255	tcg Ser	768
gct Ala	gac Asp	aac Asn	acg Thr 260	gca Ala	agg Arg	aag Lys	acg Thr	gtg Val 265	gac Asp	acg Thr	ttc Phe	ggg Gly 270	cag Gln	cgc Arg	acg Thr	816
tcg Ser	att Ile	tac Tyr 275	cgt Arg	ggc Gly	gtg Val	aca Thr	agg Arg 280	cat His	aga Arg	tgg Trp	act Thr	ggg Gly 285	aga Arg	tat Tyr	gag Glu	864
gca Ala 290	cat His	ctt Leu	tgg Trp	gat Asp	aac Asn	agt Ser 295	tgc Cys	aga Arg	agg Arg	gaa Glu	ggg Gly 300	caa Gln	act Thr	cgt Arg	aag Lys	912
ggt Gly 305	cgt Arg	caa Gln	gtc Val	tat Tyr	tta Leu 310	ggt Gly	ggc Gly	tat Tyr	gat Asp	aaa Lys 315	gag Glu	gag Glu	aaa Lys	gct Ala	gct Ala 320	960
agg Arg	gct Ala	tat Tyr	gat Asp	ctt Leu 325	gct Ala	gct Ala	ctg Leu	aag Lys	tac Tyr 330	tgg Trp	ggt Gly	gcc Ala	aca Thr	aca Thr 335	aca Thr	1008
aca Thr	aat Asn	ttt Phe	cca Pro 340	gtg Val	agt Ser	aac Asn	tac Tyr	gaa Glu 345	aag Lys	gag Glu	ctc Leu	gag Glu	gac Asp 350	atg Met	aag Lys	1056
cac His	atg Met	aca Thr 355	agg Arg	cag Gln	gag Glu	ttt Phe	gta Val 360	gcg Ala	tct Ser	ctg Leu	aga Arg	agg Arg 365	aag Lys	agc Ser	agt Ser	1104

Sequence Listing from Patent scope

ggt G y	t t c Phe	t c c Ser	aga Arg	ggt G y	gca Al a	t c c Ser	att Ile	t ac Tyr	agg Arg	gga G y	gt g Val	act Thr	agg Arg	cat His	cac His	1152
caa G n	cat His	gga G y	aga Arg	tgg Trp	caa G n	gca Al a	cgg Arg	att Ile	gga G y	cga Arg	gt t Val	gca Al a	ggg G y	aac Asn	aag Lys	1200
gat Asp	ctt Leu	t ac Tyr	t t g Leu	ggc G y	acc Thr	t t c Phe	agc Ser	acc Thr	cag G n	gag G u	gag G u	gca Al a	gcg Al a	gag G u	gcg Al a	1248
t ac Tyr	gac Asp	at c Ile	gcg Al a	gcg Al a	at c Ile	aag Lys	t t c Phe	cgc Arg	ggc G y	ct c Leu	aac Asn	gcc Al a	gt c Val	acc Thr	aac Asn	1296
t t c Phe	gac Asp	at g Met	agc Ser	cgc Arg	t ac Tyr	gac Asp	gt g Val	aag Lys	agc Ser	at c Ile	ct g Leu	gac Asp	agc Ser	agc Ser	gcc Al a	1344
ct c Leu	ccc Pro	at c Ile	ggc G y	agc Ser	gcc Al a	gcc Al a	aag Lys	cgc Arg	ct c Leu	aag Lys	gag G u	gcc Al a	gag G u	gcc Al a	gca Al a	1392
gcg Al a	t c c Ser	gcg Al a	cag G n	cac His	cac His	cac His	gcc Al a	ggc G y	gt g Val	gt g Val	agc Ser	t ac Tyr	gac Asp	gt c Val	ggc G y	1440
cgc Arg	at c Ile	gcc Al a	t cg Ser	cag G n	ct c Leu	ggc G y	gac Asp	ggc G y	gga G y	gcc Al a	ct g Leu	gcg Al a	gcg Al a	gcg Al a	t ac Tyr	1488
ggc G y	gcg Al a	cac His	t ac Tyr	cac His	ggc G y	gcc Al a	gcc Al a	tgg Trp	ccg Pro	acc Thr	at c Ile	gcg Al a	t t c Phe	cag G n	ccg Pro	1536
ggc G y	gcc Al a	gcc Al a	agc Ser	aca Thr	ggc G y	ct g Leu	t ac Tyr	cac His	ccg Pro	t ac Tyr	gcg Al a	cag G n	cag G n	cca Pro	at g Met	1584
cgc Arg	ggc G y	ggc G y	ggg G y	tgg Trp	tgc Oys	aag Lys	cag G n	gag G u	cag G n	gac Asp	cac His	gcg Al a	gt g Val	at c Ile	gcg Al a	1632
gcc Al a	gcg Al a	cac His	agc Ser	ct g Leu	cag G n	gac Asp	ct c Leu	cac His	cac His	ct g Leu	aac Asn	ct g Leu	ggc G y	gcg Al a	gcc Al a	1680
ggc G y	gcg Al a	cac His	gac Asp	t t t Phe	t t c Phe	t cg Ser	gca Al a	ggg G y	cag G n	cag G n	gcc Al a	gcc Al a	gcc Al a	gct Al a	gcg Al a	1728
at g Met	cac His	ggc G y	ct g Leu	ggt G y	agc Ser	at c Ile	gac Asp	agt Ser	gcg Al a	t cg Ser	ct c Leu	gag G u	cac His	agc Ser	acc Thr	1776
ggc G y	t c c Ser	aac Asn	t c c Ser	gt c Val	gt c Val	t ac Tyr	aac Asn	ggc G y	ggg G y	gt c Val	ggc G y	gac Asp	agc Ser	aac Asn	ggc G y	1824
gcc Al a	agc Ser	gcc Al a	gt c Val	ggc G y	ggc G y	agt Ser	ggc G y	ggt G y	ggc G y	t ac Tyr	at g Met	at g Met	ccg Pro	at g Met	agc Ser	1872

Sequence Listing from Patent scope

610	615	620	
gct Ala 625	gcc Ala 630	gga Gly 635	gca Ala 640
acc Thr	act Thr	aca Thr	t cg Ser
gca Ala	at g Met	gt g Val	agc Ser
cac His	gag Glu	cag Gln	gt g Val
1920			
cat His	gca Ala	cgg Arg	gcc Ala
t ac Tyr 645	gac Asp	gaa Glu	gcc Ala
aag Lys	cag Gln	gct Ala	gct Ala
cag Gln	at g Met	ggg Gly	t ac Tyr
1968			
gag Glu	agc Ser	t ac Tyr	ct g Leu
gt g Val	aac Asn	gcg Ala	gag Glu
aac Asn	aat Asn	ggt Gly	ggc Gly
gga Gly	agg Arg	at g Met	t ct Ser
2016			
gca Ala	t gg Trp	ggg Gly	act Thr
gt c Val	gt g Val	t ct Ser	gca Ala
gcc Ala	gcg Ala	gcg Ala	gca Ala
gca Ala	gca Ala	gca Ala	agc Ser
agc Ser	2064		
aac Asn	gac Asp	aac Asn	at g Met
gcc Ala	gcc Ala	gac Asp	gt c Val
ggc Gly	cat His	ggc Gly	ggc Gly
gca Ala	cag Gln	ct c Leu	t t c Phe
2112			
agt Ser	gt c Val	t gg Trp	aac Asn
gac Asp	act Thr	t aa	2133

<210> 122
 <211> 710
 <212> PRT
 <213> Zea mays

<400> 122

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

Sequence Listing from Patent scope

Ala	Leu	Val	Ala	Val	Ser	Thr	Asp	Thr	Gly	Gly	Ser	Gly	Gly	Ala	Ser
				245					250					255	
Ala	Asp	Asn	Thr	Ala	Arg	Lys	Thr	Val	Asp	Thr	Phe	Gly	Gln	Arg	Thr
			260					265						270	
Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu
		275					280							285	
Ala	His	Leu	Trp	Asp	Asn	Ser	Oys	Arg	Arg	Glu	Gly	Gln	Thr	Arg	Lys
	290					295					300				
Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala
305					310					315					320
Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Ala	Thr	Thr	
				325					330					335	
Thr	Asn	Phe	Pro	Val	Ser	Asn	Tyr	Glu	Lys	Glu	Leu	Glu	Asp	Met	Lys
			340						345					350	
His	Met	Thr	Arg	Gln	Glu	Phe	Val	Ala	Ser	Leu	Arg	Arg	Lys	Ser	Ser
		355					360							365	
Gly	Phe	Ser	Arg	Gly	Ala	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His
	370					375					380				
Gln	His	Gly	Arg	Trp	Gln	Ala	Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys
385					390					395					400
Asp	Leu	Tyr	Leu	Gly	Thr	Phe	Ser	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala
				405					410					415	
Tyr	Asp	Ile	Ala	Ala	Ile	Lys	Phe	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn
			420					425						430	
Phe	Asp	Met	Ser	Arg	Tyr	Asp	Val	Lys	Ser	Ile	Leu	Asp	Ser	Ser	Ala
		435					440						445		
Leu	Pro	Ile	Gly	Ser	Ala	Ala	Lys	Arg	Leu	Lys	Glu	Ala	Glu	Ala	Ala
	450					455									
Ala	Ser	Ala	Gln	His	His	His	Ala	Gly	Val	Val	Ser	Tyr	Asp	Val	Gly
465					470					475					480
Arg	Ile	Ala	Ser	Gln	Leu	Gly	Asp	Gly	Gly	Ala	Leu	Ala	Ala	Ala	Tyr
				485					490					495	
Gly	Ala	His	Tyr	His	Gly	Ala	Ala	Trp	Pro	Thr	Ile	Ala	Phe	Gln	Pro
			500					505					510		
Gly	Ala	Ala	Ser	Thr	Gly	Leu	Tyr	His	Pro	Tyr	Ala	Gln	Gln	Pro	Met
		515					520					525			
Arg	Gly	Gly	Gly	Trp	Oys	Lys	Gln	Glu	Gln	Asp	His	Ala	Val	Ile	Ala
	530					535						540			
Ala	Ala	His	Ser	Leu	Gln	Asp	Leu	His	His	Leu	Asn	Leu	Gly	Ala	Ala
545					550					555					560
Gly	Ala	His	Asp	Phe	Phe	Ser	Ala	Gly	Gln	Gln	Ala	Ala	Ala	Ala	Ala
				565					570					575	
Met	His	Gly	Leu	Gly	Ser	Ile	Asp	Ser	Ala	Ser	Leu	Glu	His	Ser	Thr
			580					585					590		
Gly	Ser	Asn	Ser	Val	Val	Tyr	Asn	Gly	Gly	Val	Gly	Asp	Ser	Asn	Gly
		595					600					605			
Ala	Ser	Ala	Val	Gly	Gly	Ser	Gly	Gly	Gly	Tyr	Met	Met	Pro	Met	Ser
	610					615					620				
Ala	Ala	Gly	Ala	Thr	Thr	Thr	Ser	Ala	Met	Val	Ser	His	Glu	Gln	Val
625					630					635					640
His	Ala	Arg	Ala	Tyr	Asp	Glu	Ala	Lys	Gln	Ala	Ala	Gln	Met	Gly	Tyr
				645					650					655	
Glu	Ser	Tyr	Leu	Val	Asn	Ala	Glu	Asn	Asn	Gly	Gly	Gly	Arg	Met	Ser
			660					665					670		
Ala	Trp	Gly	Thr	Val	Val	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Ser
	675						680						685		
Asn	Asp	Asn	Met	Ala	Ala	Asp	Val	Gly	His	Gly	Gly	Ala	Gln	Leu	Phe
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Ser	Val	Trp	Asn	Asp	Thr										
705					710										

Sequence Listing from Patent scope

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<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid linker sequence

<400> 123
t cgaaggaga t agaaccgat ccacc 25

<210> 124
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid linker sequence

<400> 124
t gagct ag 8

<210> 125
<211> 508
<212> DNA
<213> Zea mays

<400> 125
ct at agt at t t t aaaaat t gc at t aacaaac at gt cct aat t ggt act cct gagat act at 60
accct cct gt t t t aaaaat ag t t ggcat t at cgaat t at ca t t t t act t t t t aat gt t t t c 120
t ct t ct t t t a at at at t t t a t gaat t t t aa t gt at t t t aa aat gt t at gc agt t cgct ct 180
ggact t t t ct cgt gcgcct a cact t gggg t t act gggcct aaat t cagcc t gaccgaccg 240
cct gcat t ga at aat ggat g agcaccgg t aaat ccgcgt acccaact t t cgagaagaac 300
cgagacgt gg cgggccgggc caccgacgca cggcaccagc gact gcacac gt cccgccgg 360
cgt acgt gt a cgt gct gt t c cct cact ggc cgcccaat cc act cat gcat gcccacgt ac 420
accct gccg t ggcgcgccc agat cct aat cct t t cgccg t t ct gcact t ct gct gcct a 480
t aaat ggcgg cat cgaccgt cacct gct 508

<210> 126
<211> 558
<212> DNA
<213> Zea mays

<400> 126
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t t aaaaat t gc at t aacaaac at gt cct aat t ggt act cct gagat act at accct cct gt 120
t t t aaaaat ag t t ggcat t at cgaat t at ca t t t t act t t t t aat gt t t t c t ct t ct t t t a 180
at at at t t t a t gaat t t t aa t gt at t t t aa aat gt t at gc agt t cgct ct ggact t t t ct 240
cgt gcgcct a cact t gggg t t act gggcct aaat t cagcc t gaccgaccg cct gcat t ga 300
at aat ggat g agcaccgg t aaat ccgcgt acccaact t t cgagaagaac cgagacgt gg 360
cgggccgggc caccgacgca cggcaccagc gact gcacac gt cccgccgg cgt acgt gt a 420
cgt gct gt t c cct cact ggc cgcccaat cc act cat gcat gcccacgt ac accct gccg 480
t ggcgcgccc agat cct aat cct t t cgccg t t ct gcact t ct gct gcct a t aaat ggcgg 540
cat cgaccgt cacct gct 558