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Recombinant polynucleotides and methods for modifying the phenotype of a plant are provided. In particular, the phenotype that is being modified is a plant's seed characteristics.



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SEED TRAIT GENES

RELATED APPLICATION INFORMATION

The present invention claims the benefit from US Provisional Patent Application Serial
5 Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and "Plant Trait
Modification III" filed August 22, 2000.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present
invention pertains to compositions and methods for phenotypically modifying a plant.

10 **BACKGROUND OF THE INVENTION**

Transcription factors can modulate gene expression, either increasing or
decreasing (inducing or repressing) the rate of transcription. This modulation results in
differential levels of gene expression at various developmental stages, in different tissues and cell
types, and in response to different exogenous (e.g., environmental) and endogenous stimuli
15 throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological
pathways, altering the expression levels of one or more transcription factors can change entire
biological pathways in an organism. For example, manipulation of the levels of selected
transcription factors may result in increased expression of economically useful proteins or
20 metabolic chemicals in plants or to improve other agriculturally relevant characteristics.
Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of
unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription
factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a
plant's traits.

25 The present invention provides novel transcription factors useful for modifying a
plant's phenotype in desirable ways, such as modifying the characteristics of a plant's seed.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide comprising
a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a
30 polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a
complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide
comprising a conservatively substituted variant of a polypeptide of (a); (c) a nucleotide sequence
comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a

complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's seed characteristics; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. Further, the invention may be a plant lacking a nucleotide sequence encoding a polypeptide described above. The plant may be a soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, or vegetable brassicas plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having
5 improved seed traits. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for modified seed traits.

In another aspect, the invention relates to a method of identifying a factor that is
10 modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional
15 protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or
20 polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a
25 polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant seed trait.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides
30 encoded by the polynucleotides. The method comprises providing a sequence database; and, querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant seed characteristics phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

5 Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number (GID), whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

10 Figure 2 provides a table of exemplary sequences that are homologous to other sequences provided in the Sequence Listing and that are derived from *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), identification of the homologous sequence, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

15 Figure 3 provides a table of exemplary sequences that are homologous to the sequences provided in Figures 1 and 2 and that are derived from plants other than *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), the unique GenBank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

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DETAILED DESCRIPTION

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants.

25 In particular, the polynucleotides or polypeptides are useful for modifying traits associated with a plant's seed characteristics when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered. Specifically, the polynucleotides and polypeptides are useful for modifying the nutritional content or composition of seeds: such as to modify the protein or oil content of seeds, to modify insoluble sugar content or composition, such as by altering the levels of arabinose, fucose, galactose, mannose, rhamnose
30 or xylose or the like; modify prenyl lipid content or composition, such as by altering the levels of lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-tocopherol or the like; modify fatty acid content or composition, such as by altering the levels of the fatty acids 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1

(oleic acid), 18:2 (linoleic acid), 20:0, 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2 and 22:1 (erucic acid); modify wax composition or content, such as by altering the levels of C29, C31, or C33 alkanes; modify sterol composition or content, such as by altering the levels of brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, or modify
 5 glucosinolate composition or content.

Other seed characteristics that may be modified include traits relating to a seed's germination characteristics; shelf-life; drydown characteristics; size; stress responses, such as to heat, cold, salt or osmotic shock; other nutritional content, such as vitamins, minerals, or flavonoids; seedling vigor; pest resistance, or seed coat quality, resistance to pathogens,
 10 germination rate, resistance to heavy metals and toxins. Yet another desirable phenotype is a change in the overall gene expression pattern of the seed.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one or more of the following transcription factor families: the AP2 (APETALA2) domain transcription
 15 factor family (Riechmann and Meyerowitz (1998) J. Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) J. Biol. Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the
 20 miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. 9: 597-604); the homeobox (HB) protein family (Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 1996 250:7-16);
 25 the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); and the golden protein
 30 (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression,

as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, of as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

DEFINITIONS

A “polynucleotide” is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5’ or 3’ untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A “recombinant polynucleotide” is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An “isolated polynucleotide” is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A “recombinant polypeptide” is a polypeptide produced by translation of a recombinant polynucleotide. An “isolated polypeptide,” whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or

more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term “fragment” or “domain,” with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, “a fragment” refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein.

The term “trait” refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by available biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

“Trait modification” refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like;

decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's seed characteristics.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the

manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

5 The polynucleotides of the invention were ectopically expressed in overexpressor or knockout plants and changes in the seed characteristics of the plants were observed. Therefore, the polynucleotides and polypeptides can be employed to improve the seed characteristics of plants.

Making polynucleotides

10 The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or
15 single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or
20 inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods
25 in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing
30 Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain

reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis).

5 Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR
10 expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically
15 ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors.
20 And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

HOMOLOGOUS SEQUENCES

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants
25 of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee,
30 cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype

can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such

5 pine, poplar and eucalyptus.

Transcription factors that are homologous to the listed sequences will typically share at least about 31% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences.

10 Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the

15 listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity.

20 Identifying Nucleic Acids by Hybridization
Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base

25 stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more

30 detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined

ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example
5 0.2 x SSC, 0.1% SDS at 65° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the
10 coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique
15 coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radio active label, or the like.

20 Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or
25 polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant
30 from which it is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acids			Codon							
Alanine	Ala	A	GCA	GCC	GCG	GCU				
Cysteine	Cys	C	TGC	TGT						
Aspartic acid	Asp	D	GAC	GAT						
Glutamic acid	Glu	E	GAA	GAG						
Phenylalanine	Phe	F	TTC	TTT						
Glycine	Gly	G	GGA	GGC	GGG	GGT				
Histidine	His	H	CAC	CAT						
Isoleucine	Ile	I	ATA	ATC	ATT					
Lysine	Lys	K	AAA	AAG						
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT		
Methionine	Met	M	ATG							
Asparagine	Asn	N	AAC	AAT						
Proline	Pro	P	CCA	CCC	CCG	CCT				
Glutamine	Gln	Q	CAA	CAG						
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT		
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT		
Threonine	Thr	T	ACA	ACC	ACG	ACT				
Valine	Val	V	GTA	GTC	GTG	GTT				
Tryptophan	Trp	W	TGG							
Tyrosine	Tyr	Y	TAC	TAT						

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed “silent” variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

25

30

Table 2

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

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/ FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence

5 Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences.

10 For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) *Nature* 370:389-391, and Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and
15 polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to
20 modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a
25 starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons
30 can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts which describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see*, e.g., Odel et al. (1985) Nature 313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the *dru 1* promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea *rbcS-3A* promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize *rbcS* promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant

genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences.

- 5 These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be
- 10 separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

- 15 The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e, nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic
- 20 acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acids, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the
- 25 references cited herein, including, Sambrook and Ausubel.

- The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al.,
- 30 (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium*

tumefaciens or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

5 The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

10 For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence
15 and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

Modified Amino Acids

20 Polypeptides of the invention may contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

25 Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the
30 literature.

IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of

interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired.

5 For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid
10 probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between
15 the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify
20 molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any
25 method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available
30 from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid

and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene.

Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

10 IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northernblots, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s)

appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

5 The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present
10 invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription
15 can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can
20 be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of
25 interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or
30 activity of a polynucleotide or polypeptide of the invention.

SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least

20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

5 Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization
10 protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain
15 reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the
20 polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

PRODUCTION OF TRANSGENIC PLANTS

Modification of Traits

The polynucleotides of the invention are favorably employed to produce
25 transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative
30 example of trait modification, improved seed characteristics, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997)

Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England.

In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a “knock-out”) of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous

mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of

the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated

transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

5 Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

10 Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

15 After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using
20 immunoblots or Western blots or gel shift assays.

INTEGRATED SYSTEMS—SEQUENCE IDENTITY

 Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify
25 sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such improved seed characteristics, with one or more identified sequence.

 For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package
30 Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized
5 implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A
10 description of the method is provided in Ausubel et al., *supra*.

A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for
15 performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This
20 algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them.
25 The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each
30 direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an

expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

5 In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur
10 by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using
15 progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings
20 with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed
25 computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

30 Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is

provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying
5 step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

10

EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known
15 transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription
20 factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60°C) and labeled with ^{32}P
25 dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO_4 pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60°C .

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA
30 library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the MarathonTM cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded

cDNA, blunting cDNA ends, followed by ligation of the MarathonTM Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

EXAMPLE III. TRANSFORMATION OF *AGROBACTERIUM* WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then

resuspended in 250 μ l chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 μ l chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 μ l and 750 μ l, respectively. Resuspended cells were then distributed into 40 μ l aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 μ l of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 μ F and 200 μ F using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 μ g/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

EXAMPLE IV. TRANSFORMATION OF *ARABIDOPSIS* PLANTS WITH *AGROBACTERIUM TUMEFACIENS* WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μ M benzylamino purine (Sigma), 200 μ l/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 μ E/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two
5 immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and
10 sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30%
15 (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l
20 kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T₁ generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

25 Primary transformants were crossed and progeny seeds (T₂) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

30

EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 pb to each others, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

EXAMPLE VII. IDENTIFICATION OF SEED CHARACTERISTICS PHENOTYPE IN OVEREXPRESSOR OR GENE KNOCKOUT PLANTS

Experiments were performed to identify those transformants or knockouts that exhibited an improved seed characteristics. For such studies, the transformants were observed by eye or biochemical assays were performed.

Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; prenol lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0, 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, glucosinolates, protein or oil levels

Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H₂SO₄ and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H₂SO₄ (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty

acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were analyzed with a Supelco SP-2330 column.

Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes, the extraction solvent is applied to a DEAE Sephadex column which had been previously
5 equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

For wax alkanes, samples were extracted using an identical method as fatty acids and extracts were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were
10 chromatographed on a J&W DB35 mass spectrometer (J&W Scientific).

To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol determination. For leaves, an aliquot was removed and diluted with methanol and
15 chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and
20 water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2%
25 methylene chloride in hexane and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 um phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al., Plant Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were separated from sugar polymers by
30 extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH₄, then were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times

of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 μ m x 0.2 μ m) using a temperature program beginning at 180° C for 2 minutes followed by an increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2 progeny plants were subjected to analysis by Near Infrared Reflectance (NIR) using a Foss NirSystems Model 6500 with a spinning cup transport system.

Table 3 shows the phenotypes observed for particular overexpressor or knockout plants and provides the SEQ ID No., the internal reference code (GID), whether a knockout or overexpressor plant was analyzed and the observed phenotype.

Table 3

GIDs	Knockout (KO) or overexpressor (OE)	Phenotype observed
G214	OE	Up to 111% increase in seed lutein
G226	OE	Up to 17% increase in seed protein content
G229	OE	Up to 11% increase in seed oil, 13% decrease in seed protein
G241	OE	Up to 13% decrease in seed oil
G464	OE	Up to 12% decrease in seed oil, 25% increase in seed protein
G663	OE	Up to 16% decrease in seed oil, 14% increase in seed protein
G776	OE	Up to 31% alteration in some seed fatty acids, including
G778	OE	Up to 32% increase in seed 18:1 fatty acid
G865	OE	Up to 39% increase seed protein; 23% increase in seed oil
G869	OE	Up to 25% alteration in some seed fatty acids
G883	OE	Up to 47% decrease in seed lutein
G938	OE	Up to 115% increase in some seed fatty acids
G1328	OE	Up to 43% decrease in seed lutein
G584	OE	Larger seeds
G668	OE	Reduced seed color

For a particular overexpressor that shows a less beneficial seed characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial seed characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

5 EXAMPLE VIII. IDENTIFICATION OF HOMOLOGOUS SEQUENCES

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the
10 BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified *Arabidopsis* homologous sequences are provided in Figure 2 and included in the Sequence Listing. The percent sequence identity among these sequences is as low as 47% sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences
15 from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs Nos. 1-54 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs
20 Nos. 1-54, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of $3.6e-40$ is 3.6×10^{-40} . For up to ten species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 3.

In addition to P-values, comparisons were also scored by percentage identity. Percentage
25 identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-Arabidopsis genes shown in Figure 3 and the Arabidopsis genes in the sequence listing are: SEQ ID No. 1: 38%-89%; SEQ ID No. 3: 50%-69%; SEQ ID No. 5: 68%-93%; SEQ ID No. 7: 69%-84%; SEQ ID No. 9: 34%-60%; SEQ ID No. 11: 52%-81%; SEQ ID No. 13: 48%-81%; SEQ ID No. 15: 37%-80%; SEQ ID No.
30 17: 48%-83%; SEQ ID No. 19: 31%-68%; SEQ ID No. 21: 47%-90%; SEQ ID No. 23: 57%-88%; SEQ ID No. 25: 39%-79%; SEQ ID No. 27: 35%-84%; SEQ ID No. 29: 54%-89%; SEQ ID No. 31: 42%-88%; SEQ ID No. 33: 41%-75%; SEQ ID No. 35: 34%-67%; SEQ ID No. 37: 72%-86%; SEQ ID No. 39: 39%-84%; SEQ ID No. 41: 40%-58%; SEQ ID No. 43: 44%-82%; SEQ ID

No. 45: 54%-68%; SEQ ID No. 47: 48%-64%; SEQ ID No. 49: 46%-88%; SEQ ID No. 51: 52%-92%; and SEQ ID No. 53: 48%-80%.

The polynucleotides and polypeptides in the Sequence Listing and the identified homologous sequences may be stored in a computer system and have associated or linked with
5 the sequences a function, such as that the polynucleotides and polypeptides are useful for modifying the seed characteristics of a plant.

All references, publications, patents and other documents herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with
10 reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.

MBI-17 Sequence Listing.ST25
SEQUENCE LISTING

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Creelman, Robert
Pilgrim, Marsha
Riechmann, Jose Luis
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1 5

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Cys Cys Glu Lys Val Gly Ile Lys Arg Gly Arg Trp Thr Ala Glu Glu
10 15 20

gac cag att ctc tcc aac tac att caa tcc aat ggt gaa ggt tct tgg 151
Asp Gln Ile Leu Ser Asn Tyr Ile Gln Ser Asn Gly Glu Gly Ser Trp
25 30 35

aga tct ctc ccc aaa aat gcc gga tta aaa agg tgt gga aag agc tgt 199
Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys
40 45 50

aga ttg aga tgg ata aac tat cta aga tca gac ctc aag cgt gga aac 247
Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp Leu Lys Arg Gly Asn
55 60 65

ata act cca gaa gaa gaa gaa ctc gtt gtt aaa ttg cat tcc act ttg 295
Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys Leu His Ser Thr Leu
70 75 80 85

gga aac agg tgg tca cta atc gcg ggt cat cta cca ggg aga aca gac 343
Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu Pro Gly Arg Thr Asp
90 95 100

aac gaa ata aaa aat tat tgg aac tct cat ctc agc cgt aaa ctc cac 391
Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys Leu His
105 110 115

aac ttc att agg aag cca tcc atc tct caa gac gtc tcc gcc gta atc 439
Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp Val Ser Ala Val Ile
120 125 130

atg gcg aac gct tct tca gcg cca ccg ccg ccg cag gca aaa cgc aga 487
Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro Gln Ala Lys Arg Arg
135 140 145

ctt ggg aga acg agt agg tcc gct atg aaa cca aaa atc cgc aga aca 535
Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro Lys Ile Arg Arg Thr
150 155 160 165

aaa act cgt aaa acg aag aaa acg tct gca cca ccg gag cct aac gcc 583
Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro Pro Glu Pro Asn Ala
170 175 180

gat gta gct ggg gct gat aaa gaa gca tta atg gtg gag tca agt gga 631
Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met Val Glu Ser Ser Gly
185 190 195

gcc gag gct gag cta gga cga cca tgt gac tac tat gga gat gat tgt 679
Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr Tyr Gly Asp Asp Cys
200 205 210

aac aaa aat ctc atg agc att aat ggc gat aat gga gtt tta acg ttt 727
Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn Gly Val Leu Thr Phe
215 220 225

gat gat gat atc atc gat ctt ttg ttg gac gag tca gat cct ggc cac 775
Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu Ser Asp Pro Gly His
230 235 240 245

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MBI-17 Sequence Listing.ST25

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ttg tac aca aac aca acg tgc ggt ggt ggt ggg gag ttg cat aac ata      823
Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly Glu Leu His Asn Ile
                250                      255                      260

aga gac tct gaa gga gcc aga ggg ttc tcg gat act tgg aac caa ggg      871
Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp Thr Trp Asn Gln Gly
                265                      270                      275

aat ctc gac tgt ctt ctt cag tct tgt cca tct gtg gag tcg ttt ctc      919
Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser Val Glu Ser Phe Leu
                280                      285                      290

aac tac gac cac caa gtt aac gac gcg tcg acg gat gag ttt atc gat      967
Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr Asp Glu Phe Ile Asp
                295                      300                      305

tgg gat tgt gtt tgg caa gaa ggt agt gat aat aat ctt tgg cat gag     1015
Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn Asn Leu Trp His Glu
310                      315                      320                      325

aaa gag aat ccc gac tca atg gtc tcg tgg ctt tta gac ggt gat gat     1063
Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu Leu Asp Gly Asp Asp
                330                      335                      340

gag gcc acg atc ggg aat agt aat tgt gag aac ttt gga gaa ccg tta     1111
Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn Phe Gly Glu Pro Leu
                345                      350                      355

gat cat gac gac gaa agc gct ttg gtc gct tgg ctt ctg tca tga         1156
Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp Leu Leu Ser
                360                      365                      370

tgatattgat tgatccgtta tgtaatcttt tttgtgcatt cacagtttga atc         1209

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<213> Arabidopsis thaliana

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<400> 6

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                20                25                30

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
                35                40                45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
                50                55                60

Leu Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys
65                70                75                80

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

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
                100                105                110

Ser Arg Lys Leu His Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp
                115                120                125

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MBI-17 Sequence Listing.ST25

Val Ser Ala Val Ile Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro
 130 135 140

Gln Ala Lys Arg Arg Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro
 145 150 155 160

Lys Ile Arg Arg Thr Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro
 165 170 175

Pro Glu Pro Asn Ala Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met
 180 185 190

Val Glu Ser Ser Gly Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr
 195 200 205

Tyr Gly Asp Asp Cys Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn
 210 215 220

Gly Val Leu Thr Phe Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu
 225 230 235 240

Ser Asp Pro Gly His Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly
 245 250 255

Glu Leu His Asn Ile Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp
 260 265 270

Thr Trp Asn Gln Gly Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser
 275 280 285

Val Glu Ser Phe Leu Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr
 290 295 300

Asp Glu Phe Ile Asp Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn
 305 310 315 320

Asn Leu Trp His Glu Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu
 325 330 335

Leu Asp Gly Asp Asp Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn
 340 345 350

Phe Gly Glu Pro Leu Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp
 355 360 365

Leu Leu Ser
 370

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MBI-17 Sequence Listing.ST25

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cca tgc tgt gag aag atg ggg ttg aag aga gga cca tgg aca cct gaa      105
Pro Cys Cys Glu Lys Met Gly Leu Lys Arg Gly Pro Trp Thr Pro Glu
5                               10                               15                               20

gaa gat caa atc ttg gtc tct ttt atc ctc aac cat gga cat agt aac      153
Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His Gly His Ser Asn
25                               30                               35

tgg cga gcc ctc cct aag caa gct ggt ctt ttg aga tgt gga aaa agc      201
Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys Gly Lys Ser
40                               45                               50

tgt aga ctt agg ttg atg aac tat tta aag cct gat att aaa cgt ggc      249
Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly
55                               60                               65

aat ttc acc aaa gaa gag gaa gat gct atc atc agc tta cac caa ata      297
Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser Leu His Gln Ile
70                               75                               80

ctt ggc aat aga ttg tca gcg att gca gca aaa ctg cct gga aga acc      345
Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu Pro Gly Arg Thr
85                               90                               95                               100

gat aac gag atc aag aac gta ttg cac act cac ttg aag aag aga ctc      393
Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu Lys Lys Arg Leu
105                               110                               115

gaa gat tat caa cca gct aaa cct aag acc agc aac aaa aag aag ggt      441
Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn Lys Lys Lys Gly
120                               125                               130

act aaa cca aaa tct gaa tcc gta ata acg agc tcg aac agt act aga      489
Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser Asn Ser Thr Arg
135                               140                               145

agc gaa tcg gag cta gca gat tca tca aac cct tct gga gaa agc tta      537
Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser Gly Glu Ser Leu
150                               155                               160

ttt tcg aca tcg cct tcg aca agt gag gtt tct tcg atg aca ctc ata      585
Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser Met Thr Leu Ile
165                               170                               175                               180

agc cac gac ggc tat agc aac gag att aat atg gat aac aaa ccg gga      633
Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp Asn Lys Pro Gly
185                               190                               195

gat atc agt act atc gat caa gaa tgt gtt tct ttc gaa act ttt ggt      681
Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe Glu Thr Phe Gly
200                               205                               210

gcg gat atc gat gaa agc ttc ttg aaa gag aca ctg tat agc caa gat      729
Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu Tyr Ser Gln Asp
215                               220                               225

gaa cac aac tac gta tcg aat gac cta gaa gtc gct ggt tta gtt gag      777
Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala Gly Leu Val Glu
230                               235                               240

ata caa caa gag ttt caa aac ttg ggc tcc gct aat aat gag atg att      825
Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn Asn Glu Met Ile
245                               250                               255                               260

ttt gac agt gag atg gaa ctt ctg gtt cga tgt att ggc tag      867
Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile Gly
265                               270

aaccggcggg gaacaagatc tcttagccgg gctctagtta acatgtttga ggagtaaagt      927

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MBI-17 Sequence Listing.ST25

gaaatggtgc aaattagtta aggctaagaa attcaaaagc ttttgtttac cgagaaaaaa 987

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 <212> PRT
 <213> Arabidopsis thaliana

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Trp Thr Pro Glu Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His
 20 25 30

Gly His Ser Asn Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp
 50 55 60

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

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

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu
 100 105 110

Lys Lys Arg Leu Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn
 115 120 125

Lys Lys Lys Gly Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser
 130 135 140

Asn Ser Thr Arg Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser
 145 150 155 160

Gly Glu Ser Leu Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser
 165 170 175

Met Thr Leu Ile Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp
 180 185 190

Asn Lys Pro Gly Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe
 195 200 205

Glu Thr Phe Gly Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu
 210 215 220

Tyr Ser Gln Asp Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala
 225 230 235 240

Gly Leu Val Glu Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn
 245 250 255

MBI-17 Sequence Listing.ST25

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 <223> G464

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 Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala Glu Ser Glu Leu Glu
 10 15 20

ttg gga tta ggg ctc agc ctc ggt ggt ggc gcg tgg aaa gag cgt ggg 151
 Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala Trp Lys Glu Arg Gly
 25 30 35

agg att ctt act gct aag gat ttt cct tcc gtt ggg tct aaa cgc tct 199
 Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ser
 40 45 50

gct gaa tct tcc tct cac caa gga gct tct cct cct cgt tca agt caa 247
 Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro Pro Arg Ser Ser Gln
 55 60 65

gtg gta gga tgg cca cca att ggg tta cac agg atg aac agt ttg gtt 295
 Val Val Gly Trp Pro Pro Ile Gly Leu His Arg Met Asn Ser Leu Val
 70 75 80 85

aat aac caa gct atg aag gca gca aga gcg gaa gaa gga gac ggg gag 343
 Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu Glu Gly Asp Gly Glu
 90 95 100

aag aaa gtt gtg aag aat ggt gag ctc aaa gat gtg tca atg aag gtg 391
 Lys Lys Val Val Lys Asn Gly Glu Leu Lys Asp Val Ser Met Lys Val
 105 110 115

aat ccg aaa gtt cag ggc tta ggg ttt gtt aag gtg aat atg gat gga 439
 Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys Val Asn Met Asp Gly
 120 125 130

gtt ggt ata ggc aga aaa gtg gat atg aga gct cat tcg tct tac gaa 487
 Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala His Ser Ser Tyr Glu
 135 140 145

aac ttg gct cag acg ctt gag gaa atg ttc ttt gga atg aca ggt act 535
 Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe Gly Met Thr Gly Thr
 150 155 160 165

act tgt cga gaa acg gtt aaa cct tta agg ctt tta gat gga tca tca 583
 Thr Cys Arg Glu Thr Val Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser
 170 175 180

gac ttt gta ctc act tat gaa gat aag ggg att gga tgc ttg ttg gag 631
 Asp Phe Val Leu Thr Tyr Glu Asp Lys Gly Ile Gly Cys Leu Leu Glu
 185 190 195

atg ttc cat gga gaa tgt tta tca act cgg tga aaaggcttcg gatcatggga 684
 Met Phe His Gly Glu Cys Leu Ser Thr Arg

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MBI-17 Sequence Listing.ST25

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205

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tttactcgat actttttgaa gaaagtattt tggagaatat ggataaaagc atgcagaagc 864
ttagatatga tttgaatccg gttttcggat atgggtttgc ttaggtcatt caattcgtag 924
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<213> Arabidopsis thaliana

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35 40 45

Gly Ser Lys Arg Ser Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro
50 55 60

Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Leu His Arg
65 70 75 80

Met Asn Ser Leu Val Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu
85 90 95

Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Gly Glu Leu Lys Asp
100 105 110

Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys
115 120 125

Val Asn Met Asp Gly Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala
130 135 140

His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe
145 150 155 160

Gly Met Thr Gly Thr Thr Cys Arg Glu Thr Val Lys Pro Leu Arg Leu
165 170 175

Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Gly Ile
180 185 190

Gly Cys Leu Leu Glu Met Phe His Gly Glu Cys Leu Ser Thr Arg
195 200 205

<210> 11

MBI-17 Sequence Listing.ST25

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 Gly Glu Thr Val Glu Leu Asp
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 tggcttttct ttcgtatattt agtaatgtat ttttctgtat gaagtaaaga atttcagcat 952
 tttaagaaaa atgggttatgt ttctacgtaa taaaaaaaaa cgttatttat aaaaaaaaaa 1012
 aaaaaaaaaa aaaaaaaaaa a 1033

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 <213> Arabidopsis thaliana

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

MBI-17 Sequence Listing.ST25

Glu His Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu
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Phe Asp Gly Glu Thr Val Glu Leu Asp
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 <223> G776

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 Met Gly Arg Glu Ser Val Ala Val Val Thr Ala Pro
 1 5 10
 ccc tcg gcg act gct ccg ggt act gct tcg gtg gcg acc tcg ctt gct 159
 Pro Ser Ala Thr Ala Pro Gly Thr Ala Ser Val Ala Thr Ser Leu Ala
 15 20 25
 cct ggc ttc cga ttt cat ccg act gat gag gaa ctc gtg agc tat tac 207
 Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr
 30 35 40
 ttg aag agg aag gtt ctg ggc caa cct gta cgc ttc gat gcg att gga 255
 Leu Lys Arg Lys Val Leu Gly Gln Pro Val Arg Phe Asp Ala Ile Gly
 45 50 55 60
 gag gtc gat ata tac aag cat gag ccc tgg gat tta gca gtg ttt tcg 303
 Glu Val Asp Ile Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser
 65 70 75
 aga ttg aag aca agg gac caa gaa tgg tac ttc tac agt gca tta gat 351
 Arg Leu Lys Thr Arg Asp Gln Glu Trp Tyr Phe Tyr Ser Ala Leu Asp
 80 85 90
 aag aag tat gga aac ggt gct agg atg aac cga gca act aac aga ggg 399
 Lys Lys Tyr Gly Asn Gly Ala Arg Met Asn Arg Ala Thr Asn Arg Gly
 95 100 105
 tac tgg aaa gct act gga aaa gac aga gaa atc cgc cgt gac att ctg 447
 Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile Arg Arg Asp Ile Leu
 110 115 120
 ctt ctc ggt atg aaa aag aca ctt gtt ttc cac agt ggg cgt gca cca 495
 Leu Leu Gly Met Lys Lys Thr Leu Val Phe His Ser Gly Arg Ala Pro
 125 130 135 140
 gac ggg ctt cgg act aat tgg gtt atg cat gag tat cgc ctt gtg gaa 543
 Asp Gly Leu Arg Thr Asn Trp Val Met His Glu Tyr Arg Leu Val Glu
 145 150 155
 tat gaa acc gag aaa aac gga aac ctg gtg caa gat gca tat gtg ttg 591
 Tyr Glu Thr Glu Lys Asn Gly Asn Leu Val Gln Asp Ala Tyr Val Leu
 160 165 170
 tgt aga gtc ttc cac aag aat aac att ggg cca cca agt ggg aac aga 639
 Cys Arg Val Phe His Lys Asn Asn Ile Gly Pro Pro Ser Gly Asn Arg
 175 180 185
 tat gct ccg ttc atg gaa gag gaa tgg gct gat gat gaa gga gct ctg 687
 Tyr Ala Pro Phe Met Glu Glu Glu Trp Ala Asp Asp Glu Gly Ala Leu
 190 195 200

MBI-17 Sequence Listing.ST25

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att cca gga ata gac gtt aag ctc agg cta gag ccg ccg cca gta gcc      735
Ile Pro Gly Ile Asp Val Lys Leu Arg Leu Glu Pro Pro Pro Val Ala
205                               210                               215                               220

aat gga aac gac cag atg gac cag gaa atc cag tca gcc agc aag agt      783
Asn Gly Asn Asp Gln Met Asp Gln Glu Ile Gln Ser Ala Ser Lys Ser
225                               230                               235

ctc atc aac atc aat gag cca ccg aga gag aca gct cca ctg gat atc      831
Leu Ile Asn Ile Asn Glu Pro Pro Arg Glu Thr Ala Pro Leu Asp Ile
240                               245                               250

gaa tcg gac caa cag aat cat cat gag aat gac ctc aag ccg gag gag      879
Glu Ser Asp Gln Gln Asn His His Glu Asn Asp Leu Lys Pro Glu Glu
255                               260                               265

cat aac aac aat aat aat tat gat gaa aac gag gaa aca ctc aaa cgc      927
His Asn Asn Asn Asn Asn Tyr Asp Glu Asn Glu Glu Thr Leu Lys Arg
270                               275                               280

gag cag atg gaa gaa gag gag cgt cct cct cga cct gta tgc gtt ctc      975
Glu Gln Met Glu Glu Glu Glu Arg Pro Pro Arg Pro Val Cys Val Leu
285                               290                               295                               300

aac aaa gaa gct cca tta cct ctt ctg caa tac aaa cgt aga cgc caa      1023
Asn Lys Glu Ala Pro Leu Pro Leu Leu Gln Tyr Lys Arg Arg Arg Gln
305                               310                               315

agc gag tcc aac aac aac tca agc agg aac aca cag gac cat tgt tcg      1071
Ser Glu Ser Asn Asn Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser
320                               325                               330

tcc aca aca aca act gtc gac aat aca acc act tta atc tca tca tct      1119
Ser Thr Thr Thr Thr Val Asp Asn Thr Thr Thr Leu Ile Ser Ser Ser
335                               340                               345

gcc gct gcc acc aac act gcc atc tct gca ttg ctt gag ttc tca ctc      1167
Ala Ala Ala Thr Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu
350                               355                               360

atg ggt atc tcc gac aag aaa gaa aag ccg cag caa ccg cta cgt cct      1215
Met Gly Ile Ser Asp Lys Lys Glu Lys Pro Gln Gln Pro Leu Arg Pro
365                               370                               375                               380

cac aag gaa cct ttg cct cct caa act cca ctt gca tct cct gaa gag      1263
His Lys Glu Pro Leu Pro Pro Gln Thr Pro Leu Ala Ser Pro Glu Glu
385                               390                               395

aag gtt aat gat ctc cag aag gag att cac cag atg tct gtt gaa aga      1311
Lys Val Asn Asp Leu Gln Lys Glu Ile His Gln Met Ser Val Glu Arg
400                               405                               410

gaa act ttc aag ctt gaa atg atg agt gca gaa gct atg atc agt att      1359
Glu Thr Phe Lys Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile
415                               420                               425

ctc cag tca agg atc gat gcg ctg cgt cag gag aac gag gaa ctc aag      1407
Leu Gln Ser Arg Ile Asp Ala Leu Arg Gln Glu Asn Glu Glu Leu Lys
430                               435                               440

aag aac aat gct aat gga caa taa aggctctaaa aacatctctc cagggtactt      1461
Lys Asn Asn Ala Asn Gly Gln
445                               450

cttattgccc ttcgcctttt atttagcttt aatctcccta atactatgac ccattctacat      1521

agctcctcta gacagattgc gaactgtgtg aatctctgtt gtaacatagg ataaaacgga      1581

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 <213> Arabidopsis thaliana

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<400> 14

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Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr Leu Lys Arg Lys
35 40 45

Val Leu Gly Gln Pro Val Arg Phe Asp Ala Ile Gly Glu Val Asp Ile
50 55 60

Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser Arg Leu Lys Thr
65 70 75 80

Arg Asp Gln Glu Trp Tyr Phe Tyr Ser Ala Leu Asp Lys Lys Tyr Gly
85 90 95

Asn Gly Ala Arg Met Asn Arg Ala Thr Asn Arg Gly Tyr Trp Lys Ala
100 105 110

Thr Gly Lys Asp Arg Glu Ile Arg Arg Asp Ile Leu Leu Leu Gly Met
115 120 125

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

Thr Asn Trp Val Met His Glu Tyr Arg Leu Val Glu Tyr Glu Thr Glu
145 150 155 160

Lys Asn Gly Asn Leu Val Gln Asp Ala Tyr Val Leu Cys Arg Val Phe
165 170 175

His Lys Asn Asn Ile Gly Pro Pro Ser Gly Asn Arg Tyr Ala Pro Phe
180 185 190

Met Glu Glu Glu Trp Ala Asp Asp Glu Gly Ala Leu Ile Pro Gly Ile
195 200 205

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

Gln Met Asp Gln Glu Ile Gln Ser Ala Ser Lys Ser Leu Ile Asn Ile
225 230 235 240

Asn Glu Pro Pro Arg Glu Thr Ala Pro Leu Asp Ile Glu Ser Asp Gln
245 250 255

Gln Asn His His Glu Asn Asp Leu Lys Pro Glu Glu His Asn Asn Asn
260 265 270

Asn Asn Tyr Asp Glu Asn Glu Glu Thr Leu Lys Arg Glu Gln Met Glu
275 280 285

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Glu Glu Glu Arg Pro Pro Arg Pro Val Cys Val Leu Asn Lys Glu Ala
 290 295 300

Pro Leu Pro Leu Leu Gln Tyr Lys Arg Arg Arg Gln Ser Glu Ser Asn
 305 310 315 320

Asn Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser Ser Thr Thr Thr
 325 330 335

Thr Val Asp Asn Thr Thr Thr Leu Ile Ser Ser Ser Ala Ala Ala Thr
 340 345 350

Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu Met Gly Ile Ser
 355 360 365

Asp Lys Lys Glu Lys Pro Gln Gln Pro Leu Arg Pro His Lys Glu Pro
 370 375 380

Leu Pro Pro Gln Thr Pro Leu Ala Ser Pro Glu Glu Lys Val Asn Asp
 385 390 395 400

Leu Gln Lys Glu Ile His Gln Met Ser Val Glu Arg Glu Thr Phe Lys
 405 410 415

Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile Leu Gln Ser Arg
 420 425 430

Ile Asp Ala Leu Arg Gln Glu Asn Glu Glu Leu Lys Lys Asn Asn Ala
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Asn Gly Gln
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 Cys Val Pro Asn Cys His Ile Asp Asp Thr Pro Ala Ala Ala Thr Thr
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acc gtc cgc tcc acc aca gcc gca gac atc ccc ata tta gac tac gag 154
 Thr Val Arg Ser Thr Thr Ala Ala Asp Ile Pro Ile Leu Asp Tyr Glu
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gta gcc gag ctg acg tgg gag aac ggg caa cta ggc ttg cac ggc tta 202
 Val Ala Glu Leu Thr Trp Glu Asn Gly Gln Leu Gly Leu His Gly Leu
 40 45 50

ggc cca ccg cga gtg acg gct tcg tcg acc aag tac tcc aca ggc gcc 250
 Gly Pro Pro Arg Val Thr Ala Ser Ser Thr Lys Tyr Ser Thr Gly Ala
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Gly Gly Thr Leu Glu Ser Ile Val Asp Gln Ala Thr Arg Leu Pro Asn	
70 75 80	
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Pro Lys Pro Thr Asp Glu Leu Val Pro Trp Phe His His Arg Ser Ser	
85 90 95	
agg gcc gcg atg gca atg gac gcg ctt gtc cct tgc tcc aac cta gta	394
Arg Ala Ala Met Ala Met Asp Ala Leu Val Pro Cys Ser Asn Leu Val	
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cac gag cag cag agc aag cct ggt ggc gtt ggc tcc acc cgg gtg ggg	442
His Glu Gln Gln Ser Lys Pro Gly Gly Val Gly Ser Thr Arg Val Gly	
120 125 130	
tca tgt agc gat ggt cgt acc atg ggc ggt gga aaa cga gca aga gtg	490
Ser Cys Ser Asp Gly Arg Thr Met Gly Gly Gly Lys Arg Ala Arg Val	
135 140 145	
gca ccg gag tgg agc ggc ggc ggg agt cag cgg ctg acc atg gac act	538
Ala Pro Glu Trp Ser Gly Gly Gly Ser Gln Arg Leu Thr Met Asp Thr	
150 155 160	
tac gac gta ggt ttc acc tca aca tca atg ggc tcg cac gat aac aca	586
Tyr Asp Val Gly Phe Thr Ser Thr Ser Met Gly Ser His Asp Asn Thr	
165 170 175	
atc gac gat cat gac tcc gtc tgc cac agc cgc cca cag atg gag gac	634
Ile Asp Asp His Asp Ser Val Cys His Ser Arg Pro Gln Met Glu Asp	
180 185 190 195	
gaa gaa gag aag aaa gcc gga gga aaa tca tca gtt tca acc aag aga	682
Glu Glu Glu Lys Lys Ala Gly Gly Lys Ser Ser Val Ser Thr Lys Arg	
200 205 210	
agc aga gct gct gct att cat aac caa tcc gaa cgt aag agg aga gat	730
Ser Arg Ala Ala Ala Ile His Asn Gln Ser Glu Arg Lys Arg Arg Asp	
215 220 225	
aaa atc aat caa agg atg aag act ttg caa aaa ctg gtt ccc aat tcc	778
Lys Ile Asn Gln Arg Met Lys Thr Leu Gln Lys Leu Val Pro Asn Ser	
230 235 240	
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Ser Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Val Ile Glu Tyr Leu	
245 250 255	
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Lys Gln Leu Gln Ala Gln Val Ser Met Met Ser Arg Met Asn Met Pro	
260 265 270 275	
tct atg atg ctt cct atg gcc atg cag caa caa caa cta caa atg	922
Ser Met Met Leu Pro Met Ala Met Gln Gln Gln Gln Leu Gln Met	
280 285 290	
tct ctc atg tcc aat ccc atg ggt tta ggg atg ggc atg ggg atg ccc	970
Ser Leu Met Ser Asn Pro Met Gly Leu Gly Met Gly Met Gly Met Pro	
295 300 305	
ggt ctc ggt ctc ctc gac ctt aat tct atg aac cga gct gct gca agc	1018
Gly Leu Gly Leu Leu Asp Leu Asn Ser Met Asn Arg Ala Ala Ala Ser	
310 315 320	
gct cct aat atc cat gcc aac atg atg cca aac cca ttt ttg ccc atg	1066
Ala Pro Asn Ile His Ala Asn Met Met Pro Asn Pro Phe Leu Pro Met	
325 330 335	
aat tgt cca tcg tgg gat gct tct tcc aat gac tct cga ttt cag tct	1114
Asn Cys Pro Ser Trp Asp Ala Ser Ser Asn Asp Ser Arg Phe Gln Ser	
340 345 350 355	
cct ctc atc ccc gat cct atg tct gcc ttt ctt gca tgc tct act cag	1162
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MBI-17 Sequence Listing.ST25

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Pro Thr Thr Met Glu Ala Tyr Ser Arg Met Ala Thr Leu Tyr Gln Gln
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atg caa caa caa ctt cct cct cct tcg aat cca aaa tga ttattactca 1259
Met Gln Gln Gln Leu Pro Pro Pro Ser Asn Pro Lys
          390          395

aacacctcta tatagtttac gtctatatat gtgtagtca catacataca tatatatatt 1319

ccatcataat tattttattta tatgtatagg cttctcatga attatgatat tatacgtatt 1379

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          35          40          45

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

Leu Pro Asn Pro Lys Pro Thr Asp Glu Leu Val Pro Trp Phe His His
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Arg Ser Ser Arg Ala Ala Met Ala Met Asp Ala Leu Val Pro Cys Ser
          100          105          110

Asn Leu Val His Glu Gln Gln Ser Lys Pro Gly Gly Val Gly Ser Thr
          115          120          125

Arg Val Gly Ser Cys Ser Asp Gly Arg Thr Met Gly Gly Gly Lys Arg
          130          135          140

Ala Arg Val Ala Pro Glu Trp Ser Gly Gly Gly Ser Gln Arg Leu Thr
145          150          155          160

Met Asp Thr Tyr Asp Val Gly Phe Thr Ser Thr Ser Met Gly Ser His
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Asp Asn Thr Ile Asp Asp His Asp Ser Val Cys His Ser Arg Pro Gln
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MBI-17 Sequence Listing.ST25

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Arg Arg Asp Lys Ile Asn Gln Arg Met Lys Thr Leu Gln Lys Leu Val
 225 230 235 240

Pro Asn Ser Ser Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Val Ile
 245 250 255

Glu Tyr Leu Lys Gln Leu Gln Ala Gln Val Ser Met Met Ser Arg Met
 260 265 270

Asn Met Pro Ser Met Met Leu Pro Met Ala Met Gln Gln Gln Gln Gln
 275 280 285

Leu Gln Met Ser Leu Met Ser Asn Pro Met Gly Leu Gly Met Gly Met
 290 295 300

Gly Met Pro Gly Leu Gly Leu Leu Asp Leu Asn Ser Met Asn Arg Ala
 305 310 315 320

Ala Ala Ser Ala Pro Asn Ile His Ala Asn Met Met Pro Asn Pro Phe
 325 330 335

Leu Pro Met Asn Cys Pro Ser Trp Asp Ala Ser Ser Asn Asp Ser Arg
 340 345 350

Phe Gln Ser Pro Leu Ile Pro Asp Pro Met Ser Ala Phe Leu Ala Cys
 355 360 365

Ser Thr Gln Pro Thr Thr Met Glu Ala Tyr Ser Arg Met Ala Thr Leu
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 385 390 395

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 Met Val Ser Ala Leu
 1 5
 agc cgt gtc ata gag aat ccg aca gac ccg ccg gtc aaa caa gag ctt 344
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MBI-17 Sequence Listing.ST25

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atc cgc gat cca aag aaa gca gcc cgt gtc tgg ctc ggg act ttc gag	488		
Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu			
55 60 65			
acg gca gag gaa gct gct tta gcc tat gac cga gct gcc ctc aaa ttc	536		
Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg Ala Ala Leu Lys Phe			
70 75 80 85			
aaa ggc acc aag gct aaa ctg aac ttc cct gaa cgg gtc caa ggc cct	584		
Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu Arg Val Gln Gly Pro			
90 95 100			
act acc acc aca acc att tct cat gca cca aga gga gtt agt gaa tcc	632		
Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg Gly Val Ser Glu Ser			
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Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu Gln Tyr Ala Gln Leu			
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Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr Tyr Thr Ser Thr Leu			
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Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser Ser Ser Ser Ser Gln			
170 175 180			
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185 190 195			
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Val Lys Gln Glu Leu Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp
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Gln Pro Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly

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 Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg
 65 70 75 80
 Ala Ala Leu Lys Phe Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu
 85 90 95
 Arg Val Gln Gly Pro Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg
 100 105 110
 Gly Val Ser Glu Ser Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro
 115 120 125
 Ser Thr Thr Thr Thr Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu
 130 135 140
 Gln Tyr Ala Gln Leu Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr
 145 150 155 160
 Tyr Thr Ser Thr Leu Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser
 165 170 175
 Ser Ser Ser Ser Gln Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln
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 Tyr Pro Arg Glu
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MBI-17 Sequence Listing.ST25																
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caa	gaa	acc	caa	cct	ttg	agg	aaa	gtc	cgt	att	att	gtg	aat	gat	cct	565
Gln	Glu	Thr	Gln	Pro	Leu	Arg	Lys	Val	Arg	Ile	Ile	Val	Asn	Asp	Pro	
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tat	gct	act	gat	gat	tcc	tct	agt	gat	gag	gaa	gag	ctt	aag	gtt	cct	613
Tyr	Ala	Thr	Asp	Asp	Ser	Ser	Ser	Asp	Glu	Glu	Glu	Leu	Lys	Val	Pro	
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Lys	Pro	Arg	Lys	Met	Lys	Arg	Ile	Val	Arg	Glu	Ile	Asn	Phe	Pro	Ser	
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Met	Glu	Val	Ser	Glu	Gln	Pro	Ser	Glu	Ser	Ser	Ser	Gln	Asp	Ser	Thr	
	80					85					90					
aaa	act	gat	ggc	aag	ata	gct	gtg	tca	gct	tct	cct	gct	gtt	cct	agg	757
Lys	Thr	Asp	Gly	Lys	Ile	Ala	Val	Ser	Ala	Ser	Pro	Ala	Val	Pro	Arg	
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Lys	Lys	Pro	Val	Gly	Val	Arg	Gln	Arg	Lys	Trp	Gly	Lys	Trp	Ala	Ala	
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gag	att	aga	gat	cct	att	aag	aaa	act	agg	act	tgg	ttg	ggc	act	ttt	853
Glu	Ile	Arg	Asp	Pro	Ile	Lys	Lys	Thr	Arg	Thr	Trp	Leu	Gly	Thr	Phe	
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Asp	Thr	Leu	Glu	Glu	Ala	Ala	Lys	Ala	Tyr	Asp	Ala	Lys	Lys	Leu	Glu	
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Phe	Asp	Ala	Ile	Val	Ala	Gly	Asn	Val	Ser	Thr	Thr	Lys	Arg	Asp	Val	
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Ser	Ser	Ser	Glu	Thr	Ser	Gln	Cys	Ser	Arg	Ser	Ser	Pro	Val	Val	Pro	
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Val	Glu	Gln	Asp	Asp	Thr	Ser	Ala	Ser	Ala	Leu	Thr	Cys	Val	Asn	Asn	
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cct	gat	gac	gtc	tcg	acc	gtt	gct	cca	act	gct	cca	act	cca	aat	gtt	1093
Pro	Asp	Asp	Val	Ser	Thr	Val	Ala	Pro	Thr	Ala	Pro	Thr	Pro	Asn	Val	
			210					215					220			
cct	gct	ggc	gga	aac	aag	gaa	acg	ttg	ttc	gat	ttc	gac	ttt	act	aat	1141
Pro	Ala	Gly	Gly	Asn	Lys	Glu	Thr	Leu	Phe	Asp	Phe	Asp	Phe	Thr	Asn	
		225					230					235				
cta	cag	atc	cct	gat	ttt	ggc	ttc	ttg	gca	gag	gag	caa	caa	gac	cta	1189
Leu	Gln	Ile	Pro	Asp	Phe	Gly	Phe	Leu	Ala	Glu	Glu	Gln	Gln	Asp	Leu	
	240					245					250					
gac	ttc	gat	tgt	ttc	ctc	gcg	gat	gat	cag	ttt	gat	gat	ttc	ggc	ttg	1237
Asp	Phe	Asp	Cys	Phe	Leu	Ala	Asp	Asp	Gln	Phe	Asp	Asp	Phe	Gly	Leu	
255					260					265					270	
ctt	gat	gac	att	caa	gga	ttc	gaa	gat	aac	ggc	cca	agt	gcg	tta	cca	1285
Leu	Asp	Asp	Ile	Gln	Gly	Phe	Glu	Asp	Asn	Gly	Pro	Ser	Ala	Leu	Pro	
				275					280					285		
gat	ttc	gac	ttt	gcg	gat	gtt	gaa	gat	ctt	cag	cta	gct	gac	tct	agt	1333
Asp	Phe	Asp	Phe	Ala	Asp	Val	Glu	Asp	Leu	Gln	Leu	Ala	Asp	Ser	Ser	
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 Lys Ser Phe Ala Ala Ser
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gtgttttgtt ttttcgttta tgcttttagta atttaagaca tacaaaagtg tgtgttccgg 1492
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 aagtttttagt ttatgtttg 1571

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Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro Tyr Ala
 35 40 45

Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro Lys Pro
 50 55 60

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

Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr Lys Thr
 85 90 95

Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg Lys Lys
 100 105 110

Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala Glu Ile
 115 120 125

Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe Asp Thr
 130 135 140

Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu Phe Asp
 145 150 155 160

Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val Ser Ser
 165 170 175

Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro Val Glu
 180 185 190

Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn Pro Asp
 195 200 205

Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val Pro Ala
 210 215 220

MBI-17 Sequence Listing.ST25

Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn Leu Gln
225 230 235 240

Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu Asp Phe
245 250 255

Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu Leu Asp
260 265 270

Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro Asp Phe
275 280 285

Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser Phe Gly
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Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu Lys Ser
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Phe Ala Ala Ser

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Met Ala Val Asp Leu Met Arg Phe Pro Lys Ile Asp Asp Gln
1 5 10
acg gct att cag gaa gct gca tcg caa ggt tta caa agt atg gaa cat 156
Thr Ala Ile Gln Glu Ala Ala Ser Gln Gly Leu Gln Ser Met Glu His
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ctg atc cgt gtc ctc tct aac cgt ccc gaa caa caa cac aac gtt gac 204
Leu Ile Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp
35 40 45
tgc tcc gag atc act gac ttc acc gtt tct aaa ttc aaa acc gtc att 252
Cys Ser Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile
50 55 60
tct ctc ctt aac cgt act ggt cac gct cgg ttc aga cgc gga ccg gtt 300
Ser Leu Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val
65 70 75
cac tcc act tcc tct gcc gca tct cag aaa cta cag agt cag atc gtt 348
His Ser Thr Ser Ser Ala Ala Ser Gln Lys Leu Gln Ser Gln Ile Val
80 85 90
aaa aat act caa cct gag gct ccg ata gtg aga aca act acg aat cac 396
Lys Asn Thr Gln Pro Glu Ala Pro Ile Val Arg Thr Thr Thr Asn His
95 100 105 110
cct caa atc gtt cct cca ccg tct agt gta aca ctc gat ttc tct aaa 444
Pro Gln Ile Val Pro Pro Pro Ser Ser Val Thr Leu Asp Phe Ser Lys
115 120 125

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cca agc atc ttc ggc acc aaa gct aag agc gcc gag ctg gaa ttc tcc      492
Pro Ser Ile Phe Gly Thr Lys Ala Lys Ser Ala Glu Leu Glu Phe Ser
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Lys Glu Asn Phe Ser Val Ser Leu Asn Ser Ser Phe Met Ser Ser Ala
      145      150      155

ata acc gga gac ggc agc gtc tcc aat gga aaa atc ttc ctt gct tct      588
Ile Thr Gly Asp Gly Ser Val Ser Asn Gly Lys Ile Phe Leu Ala Ser
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gct ccg tcg cag cct gtt aac tct tcc gga aaa cca ccg ttg gct ggt      636
Ala Pro Ser Gln Pro Val Asn Ser Ser Gly Lys Pro Pro Leu Ala Gly
      175      180      185

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His Pro Tyr Arg Lys Arg Cys Leu Glu His Glu His Ser Glu Ser Phe
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Ser Gly Lys Val Ser Gly Ser Ala Tyr Gly Lys Cys His Cys Lys Lys
      210      215      220

agg aaa aat cgg atg aag aga acc gtg aga gta ccg gcg ata agt gca      780
Arg Lys Asn Arg Met Lys Arg Thr Val Arg Val Pro Ala Ile Ser Ala
      225      230      235

aag atc gcc gat att cca ccg gac gaa tat tcg tgg agg aag tac gga      828
Lys Ile Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly
      240      245      250

caa aaa ccg atc aag ggc tca cca cac cca cgt ggt tac tac aag tgc      876
Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys
      255      260      265

agt aca ttc aga gga tgt cca gcg agg aaa cac gtg gaa cga gca tta      924
Ser Thr Phe Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu
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gat gat cca gcg atg ctt att gtg aca tac gaa gga gag cac cgt cat      972
Asp Asp Pro Ala Met Leu Ile Val Thr Tyr Glu Gly Glu His Arg His
      290      295      300

aac caa tcc gcg atg cag gag aat att tct tct tca ggc att aat gat      1020
Asn Gln Ser Ala Met Gln Glu Asn Ile Ser Ser Ser Gly Ile Asn Asp
      305      310      315

tta gtg ttt gcc tcg gct tga cttttttttg tactatttgt tttttgattt      1071
Leu Val Phe Ala Ser Ala
      320

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aaaa

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Glu	Ile	Thr	Asp	Phe	Thr	Val	Ser	Lys	Phe	Lys	Thr	Val	Ile	Ser	Leu
	50					55					60				
Leu	Asn	Arg	Thr	Gly	His	Ala	Arg	Phe	Arg	Arg	Gly	Pro	Val	His	Ser
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Thr	Ser	Ser	Ala	Ala	Ser	Gln	Lys	Leu	Gln	Ser	Gln	Ile	Val	Lys	Asn
				85					90					95	
Thr	Gln	Pro	Glu	Ala	Pro	Ile	Val	Arg	Thr	Thr	Thr	Asn	His	Pro	Gln
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Ile	Val	Pro	Pro	Pro	Ser	Ser	Val	Thr	Leu	Asp	Phe	Ser	Lys	Pro	Ser
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Ile	Phe	Gly	Thr	Lys	Ala	Lys	Ser	Ala	Glu	Leu	Glu	Phe	Ser	Lys	Glu
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Asn	Phe	Ser	Val	Ser	Leu	Asn	Ser	Ser	Phe	Met	Ser	Ser	Ala	Ile	Thr
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Gly	Asp	Gly	Ser	Val	Ser	Asn	Gly	Lys	Ile	Phe	Leu	Ala	Ser	Ala	Pro
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Ser	Gln	Pro	Val	Asn	Ser	Ser	Gly	Lys	Pro	Pro	Leu	Ala	Gly	His	Pro
			180					185					190		
Tyr	Arg	Lys	Arg	Cys	Leu	Glu	His	Glu	His	Ser	Glu	Ser	Phe	Ser	Gly
		195					200					205			
Lys	Val	Ser	Gly	Ser	Ala	Tyr	Gly	Lys	Cys	His	Cys	Lys	Lys	Arg	Lys
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Asn	Arg	Met	Lys	Arg	Thr	Val	Arg	Val	Pro	Ala	Ile	Ser	Ala	Lys	Ile
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Ala	Asp	Ile	Pro	Pro	Asp	Glu	Tyr	Ser	Trp	Arg	Lys	Tyr	Gly	Gln	Lys
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Pro	Ile	Lys	Gly	Ser	Pro	His	Pro	Arg	Gly	Tyr	Tyr	Lys	Cys	Ser	Thr
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Phe	Arg	Gly	Cys	Pro	Ala	Arg	Lys	His	Val	Glu	Arg	Ala	Leu	Asp	Asp
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Pro	Ala	Met	Leu	Ile	Val	Thr	Tyr	Glu	Gly	Glu	His	Arg	His	Asn	Gln
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 gaa cct gta gtt gaa gat gtc gac tac acc gat gat gag atg gat gtg 144
 Glu Pro Val Val Glu Asp Val Asp Tyr Thr Asp Asp Glu Met Asp Val
 35 40 45
 gat gag ctt gag aag agg atg tgg aga gac aaa atg cgt ttg aaa cgt 192
 Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
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 Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
 65 70 75 80
 cag agg cag tcg caa gag caa gct agg agg aag aaa atg tct aga gcc 288
 Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
 85 90 95
 caa gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa 336
 Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
 100 105 110
 gct caa ggc ttt gtt tat ggt att att cct gag aag ggt aag cct gtg 384
 Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
 115 120 125
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 Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
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 Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
 145 150 155 160
 aat att tct gga ggg agt aat gat tgt aac agc ttg gtt ggt cca aca 528
 Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
 165 170 175
 ccg cat acg ctt cag gag ctt cag gac acg act ctt ggt tcg ctt tta 576
 Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
 180 185 190
 tcg gct ttg atg caa cat tgt gat cca ccg cag aga cgg ttt cct ttg 624
 Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
 195 200 205
 gag aaa gga gtt tct cca cct tgg tgg cct aat ggg aat gaa gag tgg 672
 Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
 210 215 220
 tgg cct cag ctt ggt tta cca aat gag caa ggt cct cct cct tat aag 720
 Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys
 225 230 235 240
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			260					265					270			
agg	caa	tca	aaa	tgc	ttg	cag	gat	aag	atg	acg	gcg	aaa	gag	agt	gct	864
Arg	Gln	Ser	Lys	Cys	Leu	Gln	Asp	Lys	Met	Thr	Ala	Lys	Glu	Ser	Ala	
		275					280					285				
act	tgg	ctt	gcc	att	att	aac	caa	gaa	gag	gtt	gtg	gct	cgg	gag	ctt	912
Thr	Trp	Leu	Ala	Ile	Ile	Asn	Gln	Glu	Glu	Val	Val	Ala	Arg	Glu	Leu	
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tat	ccc	gag	tca	tgc	cct	cct	ctt	tct	tct	tct	tca	tca	tta	gga	agc	960
Tyr	Pro	Glu	Ser	Cys	Pro	Pro	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Gly	Ser	
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Gly	Ser	Leu	Leu	Ile	Asn	Asp	Cys	Ser	Glu	Tyr	Asp	Val	Glu	Gly	Phe	
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Glu	Lys	Glu	Gln	His	Gly	Phe	Asp	Val	Glu	Glu	Arg	Lys	Pro	Glu	Ile	
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Val	Met	Met	His	Pro	Leu	Ala	Ser	Phe	Gly	Val	Ala	Lys	Met	Gln	His	
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Phe	Pro	Ile	Lys	Glu	Glu	Val	Ala	Thr	Thr	Val	Asn	Leu	Glu	Phe	Thr	
	370					375					380					
aga	aag	agg	aag	cag	aac	aat	gat	atg	aat	gtt	atg	gta	atg	gac	aga	1200
Arg	Lys	Arg	Lys	Gln	Asn	Asn	Asp	Met	Asn	Val	Met	Val	Met	Asp	Arg	
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tca	gca	ggt	tac	act	tgt	gag	aat	ggt	cag	tgt	cct	cac	agc	aaa	atg	1248
Ser	Ala	Gly	Tyr	Thr	Cys	Glu	Asn	Gly	Gln	Cys	Pro	His	Ser	Lys	Met	
			405					410						415		
aat	ctt	gga	ttt	caa	gac	agg	agt	tca	agg	gac	aac	cac	cag	atg	gtt	1296
Asn	Leu	Gly	Phe	Gln	Asp	Arg	Ser	Ser	Arg	Asp	Asn	His	Gln	Met	Val	
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tgt	cca	tat	aga	gac	aat	cgt	tta	gcg	tat	gga	gca	tcc	aag	ttt	cat	1344
Cys	Pro	Tyr	Arg	Asp	Asn	Arg	Leu	Ala	Tyr	Gly	Ala	Ser	Lys	Phe	His	
		435					440					445				
atg	ggt	gga	atg	aaa	cta	gta	gtt	cct	cag	caa	cca	gtc	caa	ccg	atc	1392
Met	Gly	Gly	Met	Lys	Leu	Val	Val	Pro	Gln	Gln	Pro	Val	Gln	Pro	Ile	
	450					455					460					
gac	cta	tcg	ggc	gtt	gga	gtt	ccg	gaa	aac	ggg	cag	aag	atg	atc	acc	1440
Asp	Leu	Ser	Gly	Val	Gly	Val	Pro	Glu	Asn	Gly	Gln	Lys	Met	Ile	Thr	
465					470					475					480	
gag	ctt	atg	gcc	atg	tac	gac	aga	aat	gtc	caa	agc	aac	caa	acg	cct	1488
Glu	Leu	Met	Ala	Met	Tyr	Asp	Arg	Asn	Val	Gln	Ser	Asn	Gln	Thr	Pro	
			485						490					495		
cct	act	ttg	atg	gaa	aac	caa	agc	atg	gtc	att	gat	gca	aaa	gca	gct	1536
Pro	Thr	Leu	Met	Glu	Asn	Gln	Ser	Met	Val	Ile	Asp	Ala	Lys	Ala	Ala	
		500						505					510			
cag	aat	cag	cag	ctg	aat	ttc	aac	agt	ggc	aat	caa	atg	ttt	atg	caa	1584
Gln	Asn	Gln	Gln	Leu	Asn	Phe	Asn	Ser	Gly	Asn	Gln	Met	Phe	Met	Gln	
		515					520					525				
caa	ggg	acg	aac	aac	ggg	gtt	aac	aat	cgg	ttc	cag	atg	gtg	ttt	gat	1632
Gln	Gly	Thr	Asn	Asn	Gly	Val	Asn	Asn	Arg	Phe	Gln	Met	Val	Phe	Asp	
	530					535					540					
tcg	aca	cca	ttc	gat	atg	gca	gca	ttc	gat	tac	aga	gat	gat	tgg	caa	1680

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Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
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 Thr Gly Ala Met Glu Gly Met Gly Lys Gln Gln Gln Gln Gln Gln
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 Gln Gln Asp Val Ser Ile Trp Phe
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Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
 50 55 60

Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
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Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
 85 90 95

Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
 100 105 110

Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
 115 120 125

Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
 130 135 140

Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
 145 150 155 160

Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
 165 170 175

Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
 180 185 190

Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
 195 200 205

Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
 210 215 220

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MBI-17 Sequence Listing.ST25

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				245					250					255	
Val	Ile	Lys	His	Met	Ser	Pro	Asp	Ile	Ala	Lys	Ile	Arg	Lys	Leu	Val
			260					265					270		
Arg	Gln	Ser	Lys	Cys	Leu	Gln	Asp	Lys	Met	Thr	Ala	Lys	Glu	Ser	Ala
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Thr	Trp	Leu	Ala	Ile	Ile	Asn	Gln	Glu	Glu	Val	Val	Ala	Arg	Glu	Leu
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Tyr	Pro	Glu	Ser	Cys	Pro	Pro	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Gly	Ser
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Gly	Ser	Leu	Leu	Ile	Asn	Asp	Cys	Ser	Glu	Tyr	Asp	Val	Glu	Gly	Phe
				325					330					335	
Glu	Lys	Glu	Gln	His	Gly	Phe	Asp	Val	Glu	Glu	Arg	Lys	Pro	Glu	Ile
			340					345					350		
Val	Met	Met	His	Pro	Leu	Ala	Ser	Phe	Gly	Val	Ala	Lys	Met	Gln	His
		355					360					365			
Phe	Pro	Ile	Lys	Glu	Glu	Val	Ala	Thr	Thr	Val	Asn	Leu	Glu	Phe	Thr
	370					375					380				
Arg	Lys	Arg	Lys	Gln	Asn	Asn	Asp	Met	Asn	Val	Met	Val	Met	Asp	Arg
385					390					395					400
Ser	Ala	Gly	Tyr	Thr	Cys	Glu	Asn	Gly	Gln	Cys	Pro	His	Ser	Lys	Met
				405					410					415	
Asn	Leu	Gly	Phe	Gln	Asp	Arg	Ser	Ser	Arg	Asp	Asn	His	Gln	Met	Val
			420					425					430		
Cys	Pro	Tyr	Arg	Asp	Asn	Arg	Leu	Ala	Tyr	Gly	Ala	Ser	Lys	Phe	His
		435					440					445			
Met	Gly	Gly	Met	Lys	Leu	Val	Val	Pro	Gln	Gln	Pro	Val	Gln	Pro	Ile
	450					455					460				
Asp	Leu	Ser	Gly	Val	Gly	Val	Pro	Glu	Asn	Gly	Gln	Lys	Met	Ile	Thr
465					470					475				480	
Glu	Leu	Met	Ala	Met	Tyr	Asp	Arg	Asn	Val	Gln	Ser	Asn	Gln	Thr	Pro
				485					490					495	
Pro	Thr	Leu	Met	Glu	Asn	Gln	Ser	Met	Val	Ile	Asp	Ala	Lys	Ala	Ala
			500					505					510		
Gln	Asn	Gln	Gln	Leu	Asn	Phe	Asn	Ser	Gly	Asn	Gln	Met	Phe	Met	Gln
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MBI-17 Sequence Listing.ST25

Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
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Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
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Gln Gln Asp Val Ser Ile Trp Phe
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Met Gly Arg Ser Pro Cys Cys Glu Lys Lys Asn Gly Leu Lys
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Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile
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Asn Ile His Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly
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Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu
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cga cca gat att aag cgt gga aga ttc tct ttt gaa gaa gaa gaa acc 300
Arg Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr
65 70 75
att att caa ctt cac agc atc atg gga aac aag tgg tct gcg att gcg 348
Ile Ile Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala
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gct cgt ttg cct gga aga aca gac aac gag atc aaa aac tat tgg aac 396
Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn
95 100 105 110
act cac atc aga aaa aga ctt cta aag atg gga atc gac ccg gtt aca 444
Thr His Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr
115 120 125
cac act cca cgt ctt gat ctt ctc gat atc tcc tcc att ctc agc tca 492
His Thr Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser
130 135 140
tct atc tac aac tct tcg cat cat cat cat cat cat cat caa caa cat 540
Ser Ile Tyr Asn Ser Ser His His His His His His His Gln Gln His
145 150 155
atg aac atg tcg agg ctc atg atg agt gat ggt aat cat caa cca ttg 588
Met Asn Met Ser Arg Leu Met Met Ser Asp Gly Asn His Gln Pro Leu
160 165 170

MBI-17 Sequence Listing.ST25

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gtt aac ccc gag ata ctc aaa ctc gca acc tct ctc ttt tca aac caa      636
Val Asn Pro Glu Ile Leu Lys Leu Ala Thr Ser Leu Phe Ser Asn Gln
175                      180                      185                      190

aac cac ccc aac aac aca cac gag aac aac acg gtt aac caa acc gaa      684
Asn His Pro Asn Asn Thr His Glu Asn Asn Thr Val Asn Gln Thr Glu
                      195                      200                      205

gta aac caa tac caa acc ggt tac aac atg cct ggt aat gaa gaa tta      732
Val Asn Gln Tyr Gln Thr Gly Tyr Asn Met Pro Gly Asn Glu Glu Leu
                      210                      215                      220

caa tct tgg ttc cct atc atg gat caa ttc acg aat ttc caa gac ctc      780
Gln Ser Trp Phe Pro Ile Met Asp Gln Phe Thr Asn Phe Gln Asp Leu
                      225                      230                      235

atg cca atg aag acg acg gtc caa aat tca ttg tca tac gat gat gat      828
Met Pro Met Lys Thr Thr Val Gln Asn Ser Leu Ser Tyr Asp Asp Asp
                      240                      245                      250

tgt tcg aag tcc aat ttt gta tta gaa cct tat tac tcc gac ttt gct      876
Cys Ser Lys Ser Asn Phe Val Leu Glu Pro Tyr Tyr Ser Asp Phe Ala
255                      260                      265                      270

tca gtc ttg acc aca cct tct tca agc ccg act ccg tta aac tca agt      924
Ser Val Leu Thr Thr Pro Ser Ser Ser Pro Thr Pro Leu Asn Ser Ser
                      275                      280                      285

tcc tca act tac atc aat agt agc act tgc agc acc gag gat gaa aaa      972
Ser Ser Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys
                      290                      295                      300

gag agt tat tac agt gat aat atc act aat tat tcg ttt gat gtt aat      1020
Glu Ser Tyr Tyr Ser Asp Asn Ile Thr Asn Tyr Ser Phe Asp Val Asn
                      305                      310                      315

ggt ttt ctc caa ttc caa taa acaaaacgcc attggaatag agttatgtaa      1071
Gly Phe Leu Gln Phe Gln
                      320

acatgcaatc attgtatttg ttatatagat ttgtttacat atccaaaatc caaaatacta      1131

tagtttttaaa ataataaaaaa aaaaaaaaaaa      1161

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<210> 26
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<213> Arabidopsis thaliana

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<400> 26

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Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile Asn Ile
                      20                      25                      30

His Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly Leu Gln
                      35                      40                      45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro
                      50                      55                      60

Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr Ile Ile
65                      70                      75                      80

Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg
                      85                      90                      95

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MBI-17 Sequence Listing.ST25

Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
 100 105 110

Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr His Thr
 115 120 125

Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser Ser Ile
 130 135 140

Tyr Asn Ser Ser His His His His His His His Gln Gln His Met Asn
 145 150 155 160

Met Ser Arg Leu Met Met Ser Asp Gly Asn His Gln Pro Leu Val Asn
 165 170 175

Pro Glu Ile Leu Lys Leu Ala Thr Ser Leu Phe Ser Asn Gln Asn His
 180 185 190

Pro Asn Asn Thr His Glu Asn Asn Thr Val Asn Gln Thr Glu Val Asn
 195 200 205

Gln Tyr Gln Thr Gly Tyr Asn Met Pro Gly Asn Glu Glu Leu Gln Ser
 210 215 220

Trp Phe Pro Ile Met Asp Gln Phe Thr Asn Phe Gln Asp Leu Met Pro
 225 230 235 240

Met Lys Thr Thr Val Gln Asn Ser Leu Ser Tyr Asp Asp Asp Cys Ser
 245 250 255

Lys Ser Asn Phe Val Leu Glu Pro Tyr Tyr Ser Asp Phe Ala Ser Val
 260 265 270

Leu Thr Thr Pro Ser Ser Ser Pro Thr Pro Leu Asn Ser Ser Ser Ser
 275 280 285

Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys Glu Ser
 290 295 300

Tyr Tyr Ser Asp Asn Ile Thr Asn Tyr Ser Phe Asp Val Asn Gly Phe
 305 310 315 320

Leu Gln Phe Gln

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 <212> DNA
 <213> Arabidopsis thaliana

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 <223> G584

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 Met Ser Pro Thr Asn

MBI-17 Sequence Listing.ST25

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Val	Gln	Val	Thr	Asp	Tyr	His	Leu	Asn	Gln	Ser	Lys	Thr	Asp	Thr	Thr	
				10					15					20		
aat	ctc	tgg	tca	acc	gac	gac	gat	gca	tcg	gta	atg	gaa	gct	ttc	atc	150
Asn	Leu	Trp	Ser	Thr	Asp	Asp	Asp	Ala	Ser	Val	Met	Glu	Ala	Phe	Ile	
			25					30					35			
ggc	ggc	ggc	tcc	gat	cat	tct	tct	ctt	ttt	cct	cca	ctt	cct	cct	cct	198
Gly	Gly	Gly	Ser	Asp	His	Ser	Ser	Leu	Phe	Pro	Pro	Leu	Pro	Pro	Pro	
		40					45					50				
cct	ctt	cct	caa	gtc	aac	gaa	gat	aat	ctc	cag	caa	cgt	ctc	caa	gct	246
Pro	Leu	Pro	Gln	Val	Asn	Glu	Asp	Asn	Leu	Gln	Gln	Arg	Leu	Gln	Ala	
	55					60					65					
tta	atc	gaa	gga	gca	aac	gag	aac	tgg	act	tac	gcc	gtg	ttc	tgg	caa	294
Leu	Ile	Glu	Gly	Ala	Asn	Glu	Asn	Trp	Thr	Tyr	Ala	Val	Phe	Trp	Gln	
70					75				80						85	
tca	tct	cac	ggt	ttc	gcc	gga	gaa	gac	aac	aac	aac	aac	aac	aca	gtg	342
Ser	Ser	His	Gly	Phe	Ala	Gly	Glu	Asp	Asn	Asn	Asn	Asn	Asn	Thr	Val	
				90					95					100		
ttg	tta	ggt	tgg	gga	gat	ggt	tat	tac	aaa	gga	gaa	gaa	gag	aag	tct	390
Leu	Leu	Gly	Trp	Gly	Asp	Gly	Tyr	Tyr	Lys	Gly	Glu	Glu	Glu	Lys	Ser	
			105					110					115			
aga	aag	aag	aaa	tca	aat	cca	gct	agt	gca	gct	gaa	caa	gag	cat	cgt	438
Arg	Lys	Lys	Lys	Ser	Asn	Pro	Ala	Ser	Ala	Ala	Glu	Gln	Glu	His	Arg	
			120				125					130				
aag	aga	gtg	att	aga	gag	ctc	aac	tct	tta	atc	tcc	ggt	ggt	gta	gga	486
Lys	Arg	Val	Ile	Arg	Glu	Leu	Asn	Ser	Leu	Ile	Ser	Gly	Gly	Val	Gly	
	135					140					145					
gga	gga	gat	gaa	gct	gga	gat	gaa	gaa	gtt	aca	gat	act	gaa	tgg	ttc	534
Gly	Gly	Asp	Glu	Ala	Gly	Asp	Glu	Glu	Val	Thr	Asp	Thr	Glu	Trp	Phe	
150					155					160					165	
ttc	tta	gtt	tca	atg	aca	cag	agc	ttt	gtc	aag	ggt	act	ggt	tta	cct	582
Phe	Leu	Val	Ser	Met	Thr	Gln	Ser	Phe	Val	Lys	Gly	Thr	Gly	Leu	Pro	
				170					175					180		
ggt	caa	gct	ttc	tca	aat	tca	gac	acg	att	tgg	tta	tct	ggt	tct	aat	630
Gly	Gln	Ala	Phe	Ser	Asn	Ser	Asp	Thr	Ile	Trp	Leu	Ser	Gly	Ser	Asn	
			185					190					195			
gct	tta	gct	gga	tca	agt	tgt	gag	aga	gct	cgt	caa	ggt	cag	att	tat	678
Ala	Leu	Ala	Gly	Ser	Ser	Cys	Glu	Arg	Ala	Arg	Gln	Gly	Gln	Ile	Tyr	
		200					205					210				
ggg	tta	caa	aca	atg	gtg	tgt	gta	gcg	aca	gag	aat	ggt	gtc	gtt	gag	726
Gly	Leu	Gln	Thr	Met	Val	Cys	Val	Ala	Thr	Glu	Asn	Gly	Val	Val	Glu	
	215					220					225					
ctt	ggt	tcg	tcg	gag	att	att	cat	caa	agt	tca	gat	ctt	gtt	gat	aaa	774
Leu	Gly	Ser	Ser	Glu	Ile	Ile	His	Gln	Ser	Ser	Asp	Leu	Val	Asp	Lys	
230					235					240					245	
gtt	gac	acc	ttt	ttc	aat	ttt	aac	aat	ggt	ggt	ggt	gaa	ttt	ggt	tct	822
Val	Asp	Thr	Phe	Phe	Asn	Phe	Asn	Asn	Gly	Gly	Gly	Glu	Phe	Gly	Ser	
				250					255					260		
tgg	gcg	ttt	aat	ttg	aat	cca	gat	caa	gga	gag	aat	gat	cca	ggt	ttg	870
Trp	Ala	Phe	Asn	Leu	Asn	Pro	Asp	Gln	Gly	Glu	Asn	Asp	Pro	Gly	Leu	
			265					270					275			
tgg	att	agt	gaa	cct	aat	ggt	gtt	gac	tct	ggt	ctt	gta	gct	gct	ccg	918
Trp	Ile	Ser	Glu	Pro	Asn	Gly	Val	Asp	Ser	Gly	Leu	Val	Ala	Ala	Pro	
		280					285					290				
gtg	atg	aat	aat	ggt	gga	aat	gac	tca	act	tct	aat	tct	gat	tct	caa	966

MBI-17 Sequence Listing.ST25																
Val	Met	Asn	Asn	Gly	Gly	Asn	Asp	Ser	Thr	Ser	Asn	Ser	Asp	Ser	Gln	
295						300					305					
cca	att	tct	aag	ctt	tgt	aat	gga	agc	tct	gtt	gaa	aac	cct	aac	cct	1014
Pro	Ile	Ser	Lys	Leu	Cys	Asn	Gly	Ser	Ser	Val	Glu	Asn	Pro	Asn	Pro	
310					315					320					325	
aaa	gtt	ctg	aaa	tct	tgt	gaa	atg	gtg	aat	ttc	aag	aat	ggg	att	gag	1062
Lys	Val	Leu	Lys	Ser	Cys	Glu	Met	Val	Asn	Phe	Lys	Asn	Gly	Ile	Glu	
				330					335					340		
aat	ggg	caa	gaa	gaa	gat	agt	agt	aat	aag	aag	aga	tca	ccg	gtt	tcg	1110
Asn	Gly	Gln	Glu	Glu	Asp	Ser	Ser	Asn	Lys	Lys	Arg	Ser	Pro	Val	Ser	
			345					350					355			
aat	aat	gaa	gaa	ggg	atg	ctt	tct	ttt	acc	tct	gtt	ctt	cca	tgt	gac	1158
Asn	Asn	Glu	Glu	Gly	Met	Leu	Ser	Phe	Thr	Ser	Val	Leu	Pro	Cys	Asp	
		360				365						370				
tcg	aat	cac	tct	gat	ctt	gaa	gct	tca	gtg	gct	aaa	gaa	gct	gag	agt	1206
Ser	Asn	His	Ser	Asp	Leu	Glu	Ala	Ser	Val	Ala	Lys	Glu	Ala	Glu	Ser	
	375				380						385					
aac	aga	gtt	gtg	gtt	gaa	ccg	gag	aag	aaa	ccg	agg	aaa	cga	ggg	aga	1254
Asn	Arg	Val	Val	Val	Glu	Pro	Glu	Lys	Lys	Pro	Arg	Lys	Arg	Gly	Arg	
390					395					400				405		
aaa	ccg	gcg	aat	gga	aga	gaa	gag	cct	ttg	aat	cat	gta	gag	gca	gag	1302
Lys	Pro	Ala	Asn	Gly	Arg	Glu	Glu	Pro	Leu	Asn	His	Val	Glu	Ala	Glu	
				410					415				420			
aga	cag	aga	aga	gag	aag	ttg	aat	cag	aga	ttc	tat	tct	tta	aga	gct	1350
Arg	Gln	Arg	Arg	Glu	Lys	Leu	Asn	Gln	Arg	Phe	Tyr	Ser	Leu	Arg	Ala	
			425					430					435			
gtg	gtt	cct	aat	gtg	tct	aag	atg	gat	aaa	gct	tct	cta	tta	gga	gat	1398
Val	Val	Pro	Asn	Val	Ser	Lys	Met	Asp	Lys	Ala	Ser	Leu	Leu	Gly	Asp	
		440				445						450				
gct	att	tcg	tat	atc	agt	gag	ctt	aag	tct	aag	ttg	caa	aag	gct	gaa	1446
Ala	Ile	Ser	Tyr	Ile	Ser	Glu	Leu	Lys	Ser	Lys	Leu	Gln	Lys	Ala	Glu	
	455					460					465					
tct	gat	aaa	gaa	gag	ttg	cag	aag	cag	att	gat	gtg	atg	aat	aaa	gaa	1494
Ser	Asp	Lys	Glu	Glu	Leu	Gln	Lys	Gln	Ile	Asp	Val	Met	Asn	Lys	Glu	
470					475					480				485		
gcg	gga	aat	gcg	aaa	agt	tcg	gta	aaa	gat	cga	aaa	tgt	ttg	aat	caa	1542
Ala	Gly	Asn	Ala	Lys	Ser	Ser	Val	Lys	Asp	Arg	Lys	Cys	Leu	Asn	Gln	
				490					495				500			
gaa	tcg	agt	gtg	ttg	ata	gag	atg	gag	gtt	gat	gtg	aag	att	att	ggg	1590
Glu	Ser	Ser	Val	Leu	Ile	Glu	Met	Glu	Val	Asp	Val	Lys	Ile	Ile	Gly	
			505					510					515			
tgg	gat	gca	atg	ata	agg	att	caa	tgt	agt	aag	agg	aat	cat	cct	ggg	1638
Trp	Asp	Ala	Met	Ile	Arg	Ile	Gln	Cys	Ser	Lys	Arg	Asn	His	Pro	Gly	
		520				525						530				
gct	aag	ttc	atg	gaa	gca	ctt	aag	gag	ttg	gat	ttg	gaa	gtg	aat	cat	1686
Ala	Lys	Phe	Met	Glu	Ala	Leu	Lys	Glu	Leu	Asp	Leu	Glu	Val	Asn	His	
	535					540				545						
gcg	agt	tta	tcg	gta	gtg	aat	gat	ctt	atg	atc	caa	caa	gcg	act	gtg	1734
Ala	Ser	Leu	Ser	Val	Val	Asn	Asp	Leu	Met	Ile	Gln	Gln	Ala	Thr	Val	
550					555					560					565	
aaa	atg	ggg	aat	cag	ttt	ttc	acg	caa	gat	caa	ctc	aag	gtt	gct	cta	1782
Lys	Met	Gly	Asn	Gln	Phe	Phe	Thr	Gln	Asp	Gln	Leu	Lys	Val	Ala	Leu	
				570					575					580		
acg	gag	aaa	gtt	gga	gaa	tgt	cca	tga	attgaagtca	gcac	cttttag					1829
Thr	Glu	Lys	Val	Gly	Glu	Cys	Pro									
			585													

MBI-17 Sequence Listing.ST25

ggctaataca ccggagaata ctgcgaaaag tcgaaaacaa cgatcatagt ataagccgcg 1889
 gtaaaaagtg ttaaacccttt cacacaagtt tctctagtga atgtagttgt aaactctatt 1949
 gtgtaagggt aattttgtag taccacttg ttgctattga atgcttggtta gagaggattc 2009
 ttagtgtagt atatgattag gttgggggttt gttgtttcat gagataaata aatgtgtttg 2069
 atcaatgggt aagtctttgg tttgttggtg tatgtatgta aataaggctt ttgttagaaa 2129
 taagacaaat gggactgaag ttggagttaa aaa 2162

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<400> 28

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Met Glu Ala Phe Ile Gly Gly Gly Ser Asp His Ser Ser Leu Phe Pro
35 40 45

Pro Leu Pro Pro Pro Pro Leu Pro Gln Val Asn Glu Asp Asn Leu Gln
50 55 60

Gln Arg Leu Gln Ala Leu Ile Glu Gly Ala Asn Glu Asn Trp Thr Tyr
65 70 75 80

Ala Val Phe Trp Gln Ser Ser His Gly Phe Ala Gly Glu Asp Asn Asn
85 90 95

Asn Asn Asn Thr Val Leu Leu Gly Trp Gly Asp Gly Tyr Tyr Lys Gly
100 105 110

Glu Glu Glu Lys Ser Arg Lys Lys Lys Ser Asn Pro Ala Ser Ala Ala
115 120 125

Glu Gln Glu His Arg Lys Arg Val Ile Arg Glu Leu Asn Ser Leu Ile
130 135 140

Ser Gly Gly Val Gly Gly Gly Asp Glu Ala Gly Asp Glu Glu Val Thr
145 150 155 160

Asp Thr Glu Trp Phe Phe Leu Val Ser Met Thr Gln Ser Phe Val Lys
165 170 175

Gly Thr Gly Leu Pro Gly Gln Ala Phe Ser Asn Ser Asp Thr Ile Trp
180 185 190

Leu Ser Gly Ser Asn Ala Leu Ala Gly Ser Ser Cys Glu Arg Ala Arg
195 200 205

Gln Gly Gln Ile Tyr Gly Leu Gln Thr Met Val Cys Val Ala Thr Glu
210 215 220

MBI-17 Sequence Listing.ST25

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Asn Gly Val Val Glu Leu Gly Ser Ser Glu Ile Ile His Gln Ser Ser
225                230                235                240

Asp Leu Val Asp Lys Val Asp Thr Phe Phe Asn Phe Asn Asn Gly Gly
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Gly Glu Phe Gly Ser Trp Ala Phe Asn Leu Asn Pro Asp Gln Gly Glu
                260                265                270

Asn Asp Pro Gly Leu Trp Ile Ser Glu Pro Asn Gly Val Asp Ser Gly
                275                280                285

Leu Val Ala Ala Pro Val Met Asn Asn Gly Gly Asn Asp Ser Thr Ser
                290                295                300

Asn Ser Asp Ser Gln Pro Ile Ser Lys Leu Cys Asn Gly Ser Ser Val
305                310                315                320

Glu Asn Pro Asn Pro Lys Val Leu Lys Ser Cys Glu Met Val Asn Phe
                325                330                335

Lys Asn Gly Ile Glu Asn Gly Gln Glu Glu Asp Ser Ser Asn Lys Lys
                340                345                350

Arg Ser Pro Val Ser Asn Asn Glu Glu Gly Met Leu Ser Phe Thr Ser
                355                360                365

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

Lys Glu Ala Glu Ser Asn Arg Val Val Val Glu Pro Glu Lys Lys Pro
385                390                395                400

Arg Lys Arg Gly Arg Lys Pro Ala Asn Gly Arg Glu Glu Pro Leu Asn
                405                410                415

His Val Glu Ala Glu Arg Gln Arg Arg Glu Lys Leu Asn Gln Arg Phe
                420                425                430

Tyr Ser Leu Arg Ala Val Val Pro Asn Val Ser Lys Met Asp Lys Ala
                435                440                445

Ser Leu Leu Gly Asp Ala Ile Ser Tyr Ile Ser Glu Leu Lys Ser Lys
                450                455                460

Leu Gln Lys Ala Glu Ser Asp Lys Glu Glu Leu Gln Lys Gln Ile Asp
465                470                475                480

Val Met Asn Lys Glu Ala Gly Asn Ala Lys Ser Ser Val Lys Asp Arg
                485                490                495

Lys Cys Leu Asn Gln Glu Ser Ser Val Leu Ile Glu Met Glu Val Asp
                500                505                510

Val Lys Ile Ile Gly Trp Asp Ala Met Ile Arg Ile Gln Cys Ser Lys
                515                520                525

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MBI-17 Sequence Listing.ST25

Arg Asn His Pro Gly Ala Lys Phe Met Glu Ala Leu Lys Glu Leu Asp
530 535 540

Leu Glu Val Asn His Ala Ser Leu Ser Val Val Asn Asp Leu Met Ile
545 550 555 560

Gln Gln Ala Thr Val Lys Met Gly Asn Gln Phe Phe Thr Gln Asp Gln
565 570 575

Leu Lys Val Ala Leu Thr Glu Lys Val Gly Glu Cys Pro
580 585

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<212> DNA
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<223> G668

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

WO 01/35727

PCT/US00/31457

MBI-17 Sequence Listing.ST25

Ser	Ser	Ser	Ser	Ser	Leu	Pro	Thr	Pro	Val	Ile	Thr	Gln	Gln	Asn	Ile		
			180					185					190				
cgt	aac	ttc	tca	tca	gct	ttg	ctt	gac	cgt	tgt	tat	gat	cca	tcc	tct	624	
Arg	Asn	Phe	Ser	Ser	Ala	Leu	Leu	Asp	Arg	Cys	Tyr	Asp	Pro	Ser	Ser		
		195					200					205					
tct	tct	tca	tct	acc	aca	acc	acc	act	aca	agc	aac	act	act	aat	cca	672	
Ser	Ser	Ser	Ser	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Asn	Thr	Thr	Asn	Pro		
	210					215					220						
tac	cca	tca	ggg	gta	tat	gcg	tca	agt	gct	gag	aac	atc	gcc	cgg	ttg	720	
Tyr	Pro	Ser	Gly	Val	Tyr	Ala	Ser	Ser	Ala	Glu	Asn	Ile	Ala	Arg	Leu		
225					230				235						240		
ctt	caa	gat	ttc	atg	aaa	gac	aca	ccc	aag	gct	tta	act	tta	tca	tct	768	
Leu	Gln	Asp	Phe	Met	Lys	Asp	Thr	Pro	Lys	Ala	Leu	Thr	Leu	Ser	Ser		
				245					250					255			
tca	tct	ccg	gtt	tca	gag	act	gga	cca	ctc	act	gct	gca	gtc	tcg	gaa	816	
Ser	Ser	Pro	Val	Ser	Glu	Thr	Gly	Pro	Leu	Thr	Ala	Ala	Val	Ser	Glu		
			260					265					270				
gaa	ggt	gga	gaa	ggg	ttt	gaa	caa	tct	ttc	ttc	agc	ttc	aat	tca	atg	864	
Glu	Gly	Gly	Glu	Gly	Phe	Glu	Gln	Ser	Phe	Phe	Ser	Phe	Asn	Ser	Met		
		275					280					285					
gac	gaa	act	caa	aac	ttg	act	cag	gag	aca	agc	ttc	ttc	cat	gat	caa	912	
Asp	Glu	Thr	Gln	Asn	Leu	Thr	Gln	Glu	Thr	Ser	Phe	Phe	His	Asp	Gln		
	290					295					300						
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Val	Ile	Lys	Pro	Glu	Ile	Thr	Met	Asp	Gln	Asp	His	Gly	Leu	Ile	Ser		
305					310				315						320		
caa	ggg	tct	ctg	tct	ttg	ttt	gag	aaa	tgg	tta	ttt	gat	gag	caa	agc	1008	
Gln	Gly	Ser	Leu	Ser	Leu	Phe	Glu	Lys	Trp	Leu	Phe	Asp	Glu	Gln	Ser		
				325				330						335			
cac	gag	atg	gtt	ggg	atg	gca	cta	gca	gga	caa	gaa	ggg	atg	ttc	tag	1056	
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Gln	Ala	Leu	Leu	Gly	Asn	Arg	Trp	Ala	Ala	Ile	Ala	Ser	Tyr	Leu	Pro
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 145 150 155 160
 Gln Ala Leu Cys Glu Ala Leu Ser Leu Asp Lys Pro Ser Ser Thr Leu
 165 170 175
 Ser Ser Ser Ser Ser Leu Pro Thr Pro Val Ile Thr Gln Gln Asn Ile
 180 185 190
 Arg Asn Phe Ser Ser Ala Leu Leu Asp Arg Cys Tyr Asp Pro Ser Ser
 195 200 205
 Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Ser Asn Thr Thr Asn Pro
 210 215 220
 Tyr Pro Ser Gly Val Tyr Ala Ser Ser Ala Glu Asn Ile Ala Arg Leu
 225 230 235 240
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 245 250 255
 Ser Ser Pro Val Ser Glu Thr Gly Pro Leu Thr Ala Ala Val Ser Glu
 260 265 270
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 Val Ile Lys Pro Glu Ile Thr Met Asp Gln Asp His Gly Leu Ile Ser
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MBI-17 Sequence Listing.ST25

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Thr Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe Phe Thr
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aag ttg gag aaa gag gct gaa gtt aaa ggc atc cct gtt tgc caa gct      595
Lys Leu Glu Lys Glu Ala Glu Val Lys Gly Ile Pro Val Cys Gln Ala
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ttg gac ata gaa att ccg cct cct cgt cct aaa cga aaa ccc aat act      643
Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro Lys Arg Lys Pro Asn Thr
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Ser Ser Ala Lys Asp Ala Lys Leu Val Ser Ser Ala Ser Ser Ser Gln
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Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu Asn Cys Ser Gly Val Ser
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act gtg aac aag tat ccc tta cca acg aaa cag gta agt ggc gac att      883
Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys Gln Val Ser Gly Asp Ile
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gaa aca agt aag acc tca act gtg gac aac gcg gtt caa gat gtt ccc      931
Glu Thr Ser Lys Thr Ser Thr Val Asp Asn Ala Val Gln Asp Val Pro
185                               190                               195

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atg caa aac tac cct tgg cat ttc cac gca gat att gtg aac ggg aat      1027
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215                               220                               225                               230

ata gca aaa tgc cct caa aat cat ccc tca ggt atg gta tct caa gac      1075
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MBI-17 Sequence Listing.ST25

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Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr Ala Ser His Gln Ala Phe	
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cca gct tgt cat tca cag gat gat tac cgt tcg ttt ctc cag ata tca	1219
Pro Ala Cys His Ser Gln Asp Asp Tyr Arg Ser Phe Leu Gln Ile Ser	
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Ser Ile Thr Ala Ile Ala Ala Ala Thr Val Ala Ala Ala Thr Ala Trp	
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Trp Ala Ser His Gly Leu Leu Pro Val Cys Ala Pro Ala Pro Ile Thr	
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Cys Val Pro Phe Ser Thr Val Ala Val Pro Thr Pro Ala Met Thr Glu	
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Met Asp Thr Val Glu Asn Thr Gln Pro Phe Glu Lys Gln Asn Thr Ala	
395 400 405	
ctg caa gat caa acc ttg gct tcg aaa tct cca gct tca tca tct gat	1603
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Asp Ser Asp Glu Thr Gly Val Thr Lys Leu Asn Ala Asp Ser Lys Thr	
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aat gat gat aaa att gag gag gtt gtt gtt act gcc gct gtg cat gac	1699
Asn Asp Asp Lys Ile Glu Glu Val Val Val Thr Ala Ala Val His Asp	
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Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu Thr Asp Ala Leu Asp Lys	
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490 495 500	
gat gtt att gag tta aat aac cgt aag att aaa atg aga gac aac aac	1891
Asp Val Ile Glu Leu Asn Asn Arg Lys Ile Lys Met Arg Asp Asn Asn	
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Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp Lys Glu Val Ser Glu Glu	
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Ala Ala Asp Gln Glu Gly Val Val Met Ile Gly Val Gly Thr Cys Lys
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agt ctt aaa acg aga cag aca gga ttt aag cca tac aag aga tgt tca      2179
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MBI-17 Sequence Listing.ST25

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Ala	Val	Gln	Asp	Val	Pro	Lys	Lys	Asn	Lys	Asp	Lys	Asp	Gly	Asn	Asp
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Asp	Ile	Val	Asn	Gly	Asn	Ile	Ala	Lys	Cys	Pro	Gln	Asn	His	Pro	Ser
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His	Gly	His	Ala	Asn	Leu	Gln	Ala	Thr	Thr	Ala	Ser	Ala	Thr	Thr	Thr
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Ala	Ser	His	Gln	Ala	Phe	Pro	Ala	Cys	His	Ser	Gln	Asp	Asp	Tyr	Arg
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Val	Trp	Pro	Tyr	Ala	Ser	Val	Gly	Asn	Ser	Gly	Asp	Ser	Ser	Thr	Pro
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Met	Ser	Ser	Ser	Pro	Pro	Ser	Ile	Thr	Ala	Ile	Ala	Ala	Ala	Thr	Val
			340					345					350		
Ala	Ala	Ala	Thr	Ala	Trp	Trp	Ala	Ser	His	Gly	Leu	Leu	Pro	Val	Cys
		355					360					365			
Ala	Pro	Ala	Pro	Ile	Thr	Cys	Val	Pro	Phe	Ser	Thr	Val	Ala	Val	Pro
	370					375					380				
Thr	Pro	Ala	Met	Thr	Glu	Met	Asp	Thr	Val	Glu	Asn	Thr	Gln	Pro	Phe
385					390					395					400
Glu	Lys	Gln	Asn	Thr	Ala	Leu	Gln	Asp	Gln	Thr	Leu	Ala	Ser	Lys	Ser
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Pro	Ala	Ser	Ser	Ser	Asp	Asp	Ser	Asp	Glu	Thr	Gly	Val	Thr	Lys	Leu
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MBI-17 Sequence Listing.ST25

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 Thr Asp Ala Leu Asp Lys Met Glu Lys Asp Lys Glu Asp Val Lys Glu
 485 490 495

 Thr Asp Glu Asn Gln Pro Asp Val Ile Glu Leu Asn Asn Arg Lys Ile
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 Lys Met Arg Asp Asn Asn Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp
 515 520 525

 Lys Glu Val Ser Glu Glu Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala
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 Arg Glu Arg Leu Pro Gln Ser Phe Ser Pro Pro Gln Val Ala Glu Asn
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 Val Asn Arg Lys Gln Ser Asp Thr Ser Met Pro Leu Ala Pro Asn Phe
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 Lys Ser Gln Asp Ser Cys Ala Ala Asp Gln Glu Gly Val Val Met Ile
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 Gly Val Gly Thr Cys Lys Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys
 595 600 605

 Pro Tyr Lys Arg Cys Ser Met Glu Val Lys Glu Ser Gln Val Gly Asn
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MBI-17 Sequence Listing.ST25

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gga gaa att gag agg ttt tgg gtc atg aaa aat tga	228		
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Met Phe Arg Ser Asp Lys	
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gcg gaa aaa atg gat aaa cga cga cgg aga cag agc aaa gcc aag gct	222
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Ser Cys Ser Glu Glu Val Ser Ser Ile Glu Trp Glu Ala Val Lys Met	
25 30 35	

tca gaa gaa gaa gaa gat ctc att tct cgg atg tat aaa ctc gtt ggc	318
Ser Glu Glu Glu Glu Asp Leu Ile Ser Arg Met Tyr Lys Leu Val Gly	
40 45 50	

gac agg tgg gag ttg atc gcc gga agg atc ccg gga cgg acg ccg gag	366
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MBI-17 Sequence Listing.ST25

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 Arg Arg Arg Asp Phe Phe Arg Lys
 90
 agaaaatttt cctctcctta attcacaaga caagaaaaaa aggaaatgta cctgtccttg 521
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 35 40 45

Met Tyr Lys Leu Val Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile
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 5 10 15 20

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 Glu Asp Arg Thr Leu Ser Asp Tyr Ile Gln Ser Asn Gly Glu Gly Ser
 25 30 35

MBI-17 Sequence Listing.ST25																
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Cys	Arg	Leu	Arg	Trp	Ile	Asn	Tyr	Leu	Arg	Ser	Asp	Ile	Lys	Arg	Gly	
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Asn	Ile	Thr	Pro	Glu	Glu	Glu	Asp	Val	Ile	Val	Lys	Leu	His	Ser	Thr	
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Leu	Gly	Thr	Arg	Trp	Ser	Thr	Ile	Ala	Ser	Asn	Leu	Pro	Gly	Arg	Thr	
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Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Asn	Ser	His	Leu	Ser	Arg	Lys	Leu	
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cac	ggt	tac	ttc	aga	aaa	cca	act	gtc	gcc	aat	acc	gtc	gag	aat	gcg	499
His	Gly	Tyr	Phe	Arg	Lys	Pro	Thr	Val	Ala	Asn	Thr	Val	Glu	Asn	Ala	
			120					125					130			
cct	ccg	cct	cct	aag	cgt	aga	cct	gga	aga	acc	agc	aga	tcc	gcc	atg	547
Pro	Pro	Pro	Pro	Lys	Arg	Arg	Pro	Gly	Arg	Thr	Ser	Arg	Ser	Ala	Met	
			135				140						145			
aaa	ccc	aaa	ttt	atc	cta	aac	cct	aaa	aac	cac	aaa	acc	cct	aat	tct	595
Lys	Pro	Lys	Phe	Ile	Leu	Asn	Pro	Lys	Asn	His	Lys	Thr	Pro	Asn	Ser	
	150					155					160					
ttt	aaa	gca	aac	aaa	agt	gac	atc	gtt	ttg	cca	act	acg	aca	ata	gag	643
Phe	Lys	Ala	Asn	Lys	Ser	Asp	Ile	Val	Leu	Pro	Thr	Thr	Thr	Ile	Glu	
165					170					175					180	
aat	gga	gag	gga	gac	aaa	gaa	gac	gca	tta	atg	gtg	ttg	tca	agt	agt	691
Asn	Gly	Glu	Gly	Asp	Lys	Glu	Asp	Ala	Leu	Met	Val	Leu	Ser	Ser	Ser	
				185					190					195		
agc	tta	agt	gga	gca	gag	gaa	ccc	ggt	tta	gga	cca	tgt	ggt	tat	gga	739
Ser	Leu	Ser	Gly	Ala	Glu	Glu	Pro	Gly	Leu	Gly	Pro	Cys	Gly	Tyr	Gly	
			200					205					210			
gac	gat	ggc	gat	tgt	aac	cca	agc	att	aat	ggc	gac	gat	gga	gct	ttg	787
Asp	Asp	Gly	Asp	Cys	Asn	Pro	Ser	Ile	Asn	Gly	Asp	Asp	Gly	Ala	Leu	
		215					220					225				
tgt	ctc	aat	gac	gac	att	ttc	gat	tct	tgt	ttt	cta	ttg	gac	gac	tct	835
Cys	Leu	Asn	Asp	Asp	Ile	Phe	Asp	Ser	Cys	Phe	Leu	Leu	Asp	Asp	Ser	
	230					235					240					
cat	gct	gtc	cac	gtg	tcc	tca	tgt	gag	tcg	aac	aac	gta	aaa	aac	tct	883
His	Ala	Val	His	Val	Ser	Ser	Cys	Glu	Ser	Asn	Asn	Val	Lys	Asn	Ser	
	245				250					255					260	
gag	cca	tat	gga	ggg	atg	tca	gtt	ggg	cac	aaa	aat	atc	gaa	acg	atg	931
Glu	Pro	Tyr	Gly	Gly	Met	Ser	Val	Gly	His	Lys	Asn	Ile	Glu	Thr	Met	
				265				270						275		
gct	gat	gat	ttc	gtt	gac	tgg	gac	ttt	gta	tgg	aga	gaa	ggt	caa	acc	979
Ala	Asp	Asp	Phe	Val	Asp	Trp	Asp	Phe	Val	Trp	Arg	Glu	Gly	Gln	Thr	
			280					285					290			
ctt	tgg	gac	gaa	aaa	gag	gat	ctt	gat	tcg	gtt	ttg	tcg	agg	ctg	tta	1027
Leu	Trp	Asp	Glu	Lys	Glu	Asp	Leu	Asp	Ser	Val	Leu	Ser	Arg	Leu	Leu	
		295					300					305				
gat	gga	gag	gaa	atg	gaa	tct	gag	atc	aga	caa	agg	gac	tcc	aac	gac	1075
Asp	Gly	Glu	Glu	Met	Glu	Ser	Glu	Ile	Arg	Gln	Arg	Asp	Ser	Asn	Asp	
	310					315					320					
ttt	gga	gaa	ccg	ttg	gat	att	gac	gaa	gaa	aac	aag	atg	gct	gct	tgg	1123
Phe	Gly	Glu	Pro	Leu	Asp	Ile	Asp	Glu	Glu	Asn	Lys	Met	Ala	Ala	Trp	
325					330					335					340	

MBI-17 Sequence Listing.ST25

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ctt ttt tcc tta aaa att tta ccc cct tcc ttt tcc ctt ttc ccc ctt 1171
Leu Phe Ser Leu Lys Ile Leu Pro Pro Ser Phe Ser Leu Phe Pro Leu
      345              350              355

taa tttttaccaa aacccccct tgccagatcc tgtccgtttt tccattaaac 1224

ctttttctcc ccctaccttc ctttttttat ttttaatttt ttttttttcc ttttttttc 1284

ctttcctttt ttaattccga tttttggcgg gttgccaatt aaccaaatta aatccatcct 1344

taaaaaaaaaa aaaaaaaaaa aaaaa 1369

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<210> 38
<211> 356
<212> PRT
<213> Arabidopsis thaliana

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<400> 38

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Met Gly Arg Ala Pro Cys Cys Glu Lys Val Gly Ile Lys Lys Gly Arg,
1          5          10          15

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Trp Thr Ala Glu Glu Asp Arg Thr Leu Ser Asp Tyr Ile Gln Ser Asn
      20          25          30

```

```

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
      35          40          45

```

```

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
      50          55          60

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```

Ile Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Asp Val Ile Val Lys
65          70          75          80

```

```

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

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```

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
      100          105          110

```

```

Ser Arg Lys Leu His Gly Tyr Phe Arg Lys Pro Thr Val Ala Asn Thr
      115          120          125

```

```

Val Glu Asn Ala Pro Pro Pro Pro Lys Arg Arg Pro Gly Arg Thr Ser
      130          135          140

```

```

Arg Ser Ala Met Lys Pro Lys Phe Ile Leu Asn Pro Lys Asn His Lys
145          150          155          160

```

```

Thr Pro Asn Ser Phe Lys Ala Asn Lys Ser Asp Ile Val Leu Pro Thr
      165          170          175

```

```

Thr Thr Ile Glu Asn Gly Glu Gly Asp Lys Glu Asp Ala Leu Met Val
      180          185          190

```

```

Leu Ser Ser Ser Ser Leu Ser Gly Ala Glu Glu Pro Gly Leu Gly Pro
      195          200          205

```

```

Cys Gly Tyr Gly Asp Asp Gly Asp Cys Asn Pro Ser Ile Asn Gly Asp
      210          215          220

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MBI-17 Sequence Listing.ST25

Asp Gly Ala Leu Cys Leu Asn Asp Asp Ile Phe Asp Ser Cys Phe Leu
225 230 235 240

Leu Asp Asp Ser His Ala Val His Val Ser Ser Cys Glu Ser Asn Asn
245 250 255

Val Lys Asn Ser Glu Pro Tyr Gly Gly Met Ser Val Gly His Lys Asn
260 265 270

Ile Glu Thr Met Ala Asp Asp Phe Val Asp Trp Asp Phe Val Trp Arg
275 280 285

Glu Gly Gln Thr Leu Trp Asp Glu Lys Glu Asp Leu Asp Ser Val Leu
290 295 300

Ser Arg Leu Leu Asp Gly Glu Glu Met Glu Ser Glu Ile Arg Gln Arg
305 310 315 320

Asp Ser Asn Asp Phe Gly Glu Pro Leu Asp Ile Asp Glu Glu Asn Lys
325 330 335

Met Ala Ala Trp Leu Phe Ser Leu Lys Ile Leu Pro Pro Ser Phe Ser
340 345 350

Leu Phe Pro Leu
355

<210> 39
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<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (46)..(867)
<223> G233

<400> 39
gaaaaacatt tcaacttctt ttatcagcaa tcacaaatca aagag atg gga aga gct 57
Met Gly Arg Ala
1

cca tgc tgt gag aag atg ggg ttg aag aga gga cca tgg aca cct gaa 105
Pro Cys Cys Glu Lys Met Gly Leu Lys Arg Gly Pro Trp Thr Pro Glu
5 10 15 20

gaa gat caa atc ttg gtc tct ttt atc ctc aac cat gga cat agt aac 153
Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His Gly His Ser Asn
25 30 35

tgg cga gcc ctc cct aag caa gct ggt ctt ttg aga tgt gga aaa agc 201
Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys Gly Lys Ser
40 45 50

tgt aga ctt agg tgg atg aac tat tta aag cct gat att aaa cgt ggc 249
Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly
55 60 65

aat ttc acc aaa gaa gag gaa gat gct atc atc agc tta cac caa ata 297
Asn Phe Thr Lys Glu Glu Asp Ala Ile Ile Ser Leu His Gln Ile
70 75 80

ctt ggc aat aga tgg tca gcg att gca gca aaa ctg cct gga aga acc 345

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Leu	Gly	Asn	Arg	Trp	Ser	Ala	Ile	Ala	Ala	Lys	Leu	Pro	Gly	Arg	Thr	
85					90					95					100	
gat	aac	gag	atc	aag	aac	gta	tgg	cac	act	cac	ttg	aag	aag	aga	ctc	393
Asp	Asn	Glu	Ile	Lys	Asn	Val	Trp	His	Thr	His	Leu	Lys	Lys	Arg	Leu	
				105					110					115		
gaa	gat	tat	caa	cca	gct	aaa	cct	aag	acc	agc	aac	aaa	aag	aag	ggt	441
Glu	Asp	Tyr	Gln	Pro	Ala	Lys	Pro	Lys	Thr	Ser	Asn	Lys	Lys	Lys	Gly	
			120					125					130			
act	aaa	cca	aaa	tct	gaa	tcc	gta	ata	acg	agc	tcg	aac	agt	act	aga	489
Thr	Lys	Pro	Lys	Ser	Glu	Ser	Val	Ile	Thr	Ser	Ser	Asn	Ser	Thr	Arg	
		135					140					145				
agc	gaa	tcg	gag	cta	gca	gat	tca	tca	aac	cct	tct	gga	gaa	agc	tta	537
Ser	Glu	Ser	Glu	Leu	Ala	Asp	Ser	Ser	Asn	Pro	Ser	Gly	Glu	Ser	Leu	
	150					155					160					
ttt	tcg	aca	tcg	cct	tcg	aca	agt	gag	gtt	tct	tcg	atg	aca	ctc	ata	585
Phe	Ser	Thr	Ser	Pro	Ser	Thr	Ser	Glu	Val	Ser	Ser	Met	Thr	Leu	Ile	
165					170				175						180	
agc	cac	gac	ggc	tat	agc	aac	gag	att	aat	atg	gat	aac	aaa	ccg	gga	633
Ser	His	Asp	Gly	Tyr	Ser	Asn	Glu	Ile	Asn	Met	Asp	Asn	Lys	Pro	Gly	
				185					190					195		
gat	atc	agt	act	atc	gat	caa	gaa	tgt	gtt	tct	ttc	gaa	act	ttt	ggt	681
Asp	Ile	Ser	Thr	Ile	Asp	Gln	Glu	Cys	Val	Ser	Phe	Glu	Thr	Phe	Gly	
			200					205					210			
gcg	gat	atc	gat	gaa	agc	ttc	tgg	aaa	gag	aca	ctg	tat	agc	caa	gat	729
Ala	Asp	Ile	Asp	Glu	Ser	Phe	Trp	Lys	Glu	Thr	Leu	Tyr	Ser	Gln	Asp	
		215					220					225				
gaa	cac	aac	tac	gta	tcg	aat	gac	cta	gaa	gtc	gct	ggt	tta	gtt	gag	777
Glu	His	Asn	Tyr	Val	Ser	Asn	Asp	Leu	Glu	Val	Ala	Gly	Leu	Val	Glu	
	230					235					240					
ata	caa	caa	gag	ttt	caa	aac	ttg	ggc	tcc	gct	aat	aat	gag	atg	att	825
Ile	Gln	Gln	Glu	Phe	Gln	Asn	Leu	Gly	Ser	Ala	Asn	Asn	Glu	Met	Ile	
245					250				255					260		
ttt	gac	agt	gag	atg	gaa	ctt	ctg	gtt	cga	tgt	att	ggc	tag			867
Phe	Asp	Ser	Glu	Met	Glu	Leu	Leu	Val	Arg	Cys	Ile	Gly				
				265				270								
aaccggcggg	gaacaagatc	tcttagccgg	gctctagtta	acatgtttga	ggagtaaagt											927
gaaatggtgc	aaattagtta	aggctaagaa	attcaaaagc	ttttgtttac	cgagaaaaaa											987
acacactcta	actcttgatg	tgatgtagtt	agtgtattaa	ttagaggctg	cgttttcaa											1046

<210> 40
 <211> 273
 <212> PRT
 <213> Arabidopsis thaliana

<400> 40

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

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

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

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu
100 105 110

Lys Lys Arg Leu Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn
115 120 125

Lys Lys Lys Gly Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser
130 135 140

Asn Ser Thr Arg Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser
145 150 155 160

Gly Glu Ser Leu Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser
165 170 175

Met Thr Leu Ile Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp
180 185 190

Asn Lys Pro Gly Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe
195 200 205

Glu Thr Phe Gly Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu
210 215 220

Tyr Ser Gln Asp Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala
225 230 235 240

Gly Leu Val Glu Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn
245 250 255

Asn Glu Met Ile Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile
260 265 270

Gly

<210> 41
<211> 1262
<212> DNA
<213> Arabidopsis thaliana

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<222> (217)..(957)
<223> G463

<400> 41
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tctttctttc tttgtcttcc tttcccaggt tgtttttttt tgctctctct gccttcttga 120
ctttcaaaag actctttctt tcttttggat tgattttgga ttctagggct ctctttcttt 180

MBI-17 Sequence Listing.ST25

tagtggggttt ttgtttgttgt tgttgtgggtc tctctg atg att act gaa ctt gag	234
Met Ile Thr Glu Leu Glu	
1 5	
atg ggg aaa ggt gag agt gag ctt gag ctt ggt cta ggg ctg agt ctt	282
Met Gly Lys Gly Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu	
10 15 20	
ggc ggt gga acg gcg gcc aag att ggt aaa tca ggt ggt ggt ggc gcg	330
Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys Ser Gly Gly Gly Gly Ala	
25 30 35	
tgg gga gag cgt gga agg ctt ttg acg gct aag gat ttt cct tct gtt	378
Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala Lys Asp Phe Pro Ser Val	
40 45 50	
ggt tct aaa cgt gct gct gat tct gct tct cat gct ggt tca tct cct	426
Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser His Ala Gly Ser Ser Pro	
55 60 65 70	
cct cgt tca agt caa gtt gtt gga tgg cct cct ata ggg tca cac agg	474
Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Ser His Arg	
75 80 85	
atg aac agt ttg gtt aat aac caa gct aca aag tca gca aga gaa gaa	522
Met Asn Ser Leu Val Asn Asn Gln Ala Thr Lys Ser Ala Arg Glu Glu	
90 95 100	
gaa gaa gct ggt aag aag aaa gtg aaa gat gat gaa cct aaa gat gtg	570
Glu Glu Ala Gly Lys Lys Lys Val Lys Asp Asp Glu Pro Lys Asp Val	
105 110 115	
aca aag aaa gtg aat ggg aaa gta caa gtt gga ttt att aag gtg aac	618
Thr Lys Lys Val Asn Gly Lys Val Gln Val Gly Phe Ile Lys Val Asn	
120 125 130	
atg gat gga gtt gct ata gga aga aaa gtg gat ttg aat gct cat tct	666
Met Asp Gly Val Ala Ile Gly Arg Lys Val Asp Leu Asn Ala His Ser	
135 140 145 150	
tct tac gag aat ttg gcg caa aca ttg gaa gat atg ttc ttt cgc act	714
Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Asp Met Phe Phe Arg Thr	
155 160 165	
aat ccg ggt act gtc ggg tta acc agt cag ttc act aaa ccg ttg agg	762
Asn Pro Gly Thr Val Gly Leu Thr Ser Gln Phe Thr Lys Pro Leu Arg	
170 175 180	
ctt tta gat gga tcg tct gag ttt gta ctt act tat gaa gat aag gaa	810
Leu Leu Asp Gly Ser Ser Glu Phe Val Leu Thr Tyr Glu Asp Lys Glu	
185 190 195	
gga gat tgg atg ctt gtt ggt gat gtt cca tgg aga atg ttc atc aac	858
Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn	
200 205 210	
tcg gtg aaa agg cta cgt gtg atg aaa acc tct gaa gct aat gga ctc	906
Ser Val Lys Arg Leu Arg Val Met Lys Thr Ser Glu Ala Asn Gly Leu	
215 220 225 230	
gct gca cga aat caa gaa cca aac gag aga cag cga aag cag ccg gtt	954
Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg Gln Arg Lys Gln Pro Val	
235 240 245	
tag atctcttttc gacgttacgg tgttacaggt tttatatattt ggggttttgc	1007
aagtctgaga tacttctgaa gcaagcataa gctagattga tcttatatcc agttttgtgta	1067
ttttcttggt tcttataatg gtttttactg gttttcttta gttttttttt ttgctgtctt	1127
ttaatttttcg gttgcgattt cactatatac tatggatgga agagaatgct ctttatatct	1187
tttactacac tgtaaatatt tgaagcttat ctaatatcgt ttttaagggt taaaaaaccc	1247

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MBI-17 Sequence Listing.ST25

tgacgtagcc tcgag

1262

<210> 42
 <211> 246
 <212> PRT
 <213> Arabidopsis thaliana

<400> 42

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 1 5 10 15

Gly Leu Gly Leu Ser Leu Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys
 20 25 30

Ser Gly Gly Gly Gly Ala Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala
 35 40 45

Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser
 50 55 60

His Ala Gly Ser Ser Pro Pro Arg Ser Ser Gln Val Val Gly Trp Pro
 65 70 75 80

Pro Ile Gly Ser His Arg Met Asn Ser Leu Val Asn Asn Gln Ala Thr
 85 90 95

Lys Ser Ala Arg Glu Glu Glu Glu Ala Gly Lys Lys Lys Val Lys Asp
 100 105 110

Asp Glu Pro Lys Asp Val Thr Lys Lys Val Asn Gly Lys Val Gln Val
 115 120 125

Gly Phe Ile Lys Val Asn Met Asp Gly Val Ala Ile Gly Arg Lys Val
 130 135 140

Asp Leu Asn Ala His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu
 145 150 155 160

Asp Met Phe Phe Arg Thr Asn Pro Gly Thr Val Gly Leu Thr Ser Gln
 165 170 175

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

Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val Gly Asp Val Pro
 195 200 205

Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg Val Met Lys Thr
 210 215 220

Ser Glu Ala Asn Gly Leu Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg
 225 230 235 240

Gln Arg Lys Gln Pro Val
 245

<210> 43

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MBI-17 Sequence Listing.ST25

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<211> 741
<212> DNA
<213> Arabidopsis thaliana

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<222> (1)..(741)
<223> G2422

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1                               5                               10                               15

gaa gat att ctc ttg agg caa tgc att gat aag tat gga gaa ggc aaa      96
Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
20                               25                               30

tgg cat cga gtt cct tta aga act ggt ctc aat cgg tgc cga aag agt     144
Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
35                               40                               45

tgt aga ctt aga tgg ttg aat tat ttg aag cca agt att aag aga gga     192
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50                               55                               60

aaa ctc tgc tcc gat gaa gtt gat ctt gtt ctt cgc ctt cat aaa ctt     240
Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65                               70                               75                               80

cta gga aat agg tgg tcc ttg atc gct ggt aga ttg cct ggt cgg act     288
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85                               90                               95

gct aat gat gtc aag aat tac tgg aac act cat ttg agt aag aag cac     336
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100                              105                              110

gat gaa cga tgc tgt aag acg aag atg ata aac aaa aac att act tct     384
Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
115                              120                              125

cat cct act tca tcg gcc caa aaa atc gat gtt tta aag cct cgg cct     432
His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
130                              135                              140

cga tcc ttc tcc gat aaa aat agt tgc aac gat gtc aat atc ttg cca     480
Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145                              150                              155                              160

aaa gtt gac gtt gtt cct tta cat ctt gga ctc aac aac aat tat gtt     528
Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
165                              170                              175

tgt gaa agt agt att aca tgt aac aaa gat gag caa aaa gat aag ctt     576
Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
180                              185                              190

att aat att aat cta ttg gat gga gat aat atg tgg tgg gaa agt tta     624
Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
195                              200                              205

ctg gag gca gat gtg ttg ggt cca gaa gct acg gaa aca gca aag ggt     672
Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
210                              215                              220

gtg acc tta ccg ctt gac ttt gag caa att tgg gct cgg ttt gat gaa     720
Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225                              230                              235                              240

gag act tta gaa ctg aat tag                                           741
Glu Thr Leu Glu Leu Asn
245

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MBI-17 Sequence Listing.ST25

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<210> 44
<211> 246
<212> PRT
<213> Arabidopsis thaliana

<400> 44
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Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
20          25          30
Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
35          40          45
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50          55          60
Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65          70          75          80
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85          90          95
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100         105         110
Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
115        120        125
His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
130        135        140
Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145        150        155        160
Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
165        170        175
Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
180        185        190
Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
195        200        205
Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
210        215        220
Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225        230        235        240
Glu Thr Leu Glu Leu Asn
245

<210> 45
<211> 762
<212> DNA

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MBI-17 Sequence Listing.ST25

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(630)

<223> G2421

<400> 45

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Met	Glu	Gly	Ser	Ser	Lys	Gly	Leu	Arg	Lys	Gly	Ala	Trp	Thr	Ala	Glu	
1				5					10					15		

gaa	gat	agt	ctc	ttg	agg	cag	tgt	att	ggt	aag	tat	gga	gaa	ggc	aaa	96
Glu	Asp	Ser	Leu	Leu	Arg	Gln	Cys	Ile	Gly	Lys	Tyr	Gly	Glu	Gly	Lys	
			20				25						30			

tgg	cat	caa	ggt	cct	tta	aga	gct	ggg	cta	aat	cgg	tgc	agg	aaa	agt	144
Trp	His	Gln	Val	Pro	Leu	Arg	Ala	Gly	Leu	Asn	Arg	Cys	Arg	Lys	Ser	
		35					40					45				

tgt	aga	cta	aga	tgg	tta	aac	tat	ttg	aag	cca	agt	atc	aag	aga	gga	192
Cys	Arg	Leu	Arg	Trp	Leu	Asn	Tyr	Leu	Lys	Pro	Ser	Ile	Lys	Arg	Gly	
	50					55					60					

aaa	ttt	agt	tct	gat	gaa	ggt	gat	ctt	ctt	ctt	cgt	ctt	cat	aag	ctt	240
Lys	Phe	Ser	Ser	Asp	Glu	Val	Asp	Leu	Leu	Leu	Arg	Leu	His	Lys	Leu	
65					70					75					80	

cta	gga	aat	agg	tgg	tcc	ttg	att	gct	ggt	cga	tta	cct	ggt	cgg	acc	288
Leu	Gly	Asn	Arg	Trp	Ser	Leu	Ile	Ala	Gly	Arg	Leu	Pro	Gly	Arg	Thr	
			85						90					95		

gct	aat	gat	gtc	aag	aac	tac	tgg	aac	acc	cat	ctg	agt	aag	aag	cat	336
Ala	Asn	Asp	Val	Lys	Asn	Tyr	Trp	Asn	Thr	His	Leu	Ser	Lys	Lys	His	
			100					105						110		

gaa	ccg	tgt	tgt	aaa	act	aag	ata	aaa	agg	ata	aat	att	ata	acc	cct	384
Glu	Pro	Cys	Cys	Lys	Thr	Lys	Ile	Lys	Arg	Ile	Asn	Ile	Ile	Thr	Pro	
		115					120					125				

cct	aat	aca	ccg	gcc	caa	aaa	ggt	tgt	gaa	aat	agt	atc	aca	tgt	aac	432
Pro	Asn	Thr	Pro	Ala	Gln	Lys	Val	Cys	Glu	Asn	Ser	Ile	Thr	Cys	Asn	
		130				135						140				

aaa	gat	gat	gag	aaa	gat	gat	ttt	gtg	gat	aat	ttt	atg	ggt	gga	gat	480
Lys	Asp	Asp	Glu	Lys	Asp	Asp	Phe	Val	Asp	Asn	Phe	Met	Val	Gly	Asp	
145					150					155					160	

aat	ata	tgg	ttg	gag	cgt	ttg	cta	gac	gag	ggc	caa	gag	gta	gat	gtg	528
Asn	Ile	Trp	Leu	Glu	Arg	Leu	Leu	Asp	Glu	Gly	Gln	Glu	Val	Asp	Val	
				165					170					175		

ctg	ggt	aca	gaa	gcg	gcg	gca	aca	gaa	aag	gag	ggc	act	ttg	gcg	ttt	576
Leu	Val	Thr	Glu	Ala	Ala	Ala	Thr	Glu	Lys	Glu	Gly	Thr	Leu	Ala	Phe	
			180					185					190			

gac	ggt	gag	caa	ctt	tgg	aat	ttg	ttc	gat	gga	gag	act	gtg	atc	ttt	624
Asp	Val	Glu	Gln	Leu	Trp	Asn	Leu	Phe	Asp	Gly	Glu	Thr	Val	Ile	Phe	
		195					200					205				

gat	tag	tgtttataaaa	cgtttgtggt	ctcttgtttg	tgaggtttct	ctattttaatt	680
Asp							

tagtatctat	tttctaaatt	aactaatatc	ttatagtatt	ttaggcaaac	cttatgtttc	740
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cgtttctgtg	cggccgctct	ag	762
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<211> 209

<212> PRT

<213> Arabidopsis thaliana

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<400> 46

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Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65 70 75 80

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

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
115 120 125

Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
130 135 140

Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
145 150 155 160

Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
165 170 175

Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
180 185 190

Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
195 200 205

Asp

<210> 47

<211> 1665

<212> DNA

<213> Arabidopsis thaliana

<220>

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<223> G772

<400> 47

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Met Gly Arg Glu Ser Leu Ala
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gtt gtg tcc tcg ccg cca tcg gcg act gcg ccc agt act gct gtg tcg 101

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MBI-17 Sequence Listing.ST25															
Val	Val	Ser	Ser	Pro	Pro	Ser	Ala	Thr	Ala	Pro	Ser	Thr	Ala	Val	Ser
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gct	acc	tcg	ctt	gct	cct	ggc	ttt	cga	ttt	cat	ccg	act	gat	gag	gaa
Ala	Thr	Ser	Leu	Ala	Pro	Gly	Phe	Arg	Phe	His	Pro	Thr	Asp	Glu	Glu
	25					30					35				
ctc	gtg	agc	tat	tac	ttg	aag	agg	aag	gtt	ctg	ggc	aaa	cct	gta	cgc
Leu	Val	Ser	Tyr	Tyr	Leu	Lys	Arg	Lys	Val	Leu	Gly	Lys	Pro	Val	Arg
40					45					50					55
ttc	gat	gcg	att	gga	gag	gta	gat	atc	tac	aag	cat	gag	ccc	tgg	gat
Phe	Asp	Ala	Ile	Gly	Glu	Val	Asp	Ile	Tyr	Lys	His	Glu	Pro	Trp	Asp
				60				65						70	
tta	gca	gtg	ttt	tcg	aag	ttg	aaa	act	cgg	gac	caa	gaa	tgg	tac	ttc
Leu	Ala	Val	Phe	Ser	Lys	Leu	Lys	Thr	Arg	Asp	Gln	Glu	Trp	Tyr	Phe
			75					80					85		
ttc	agt	gcg	tta	gat	aag	aag	tac	ggc	aat	ggc	gct	agg	atg	aat	cga
Phe	Ser	Ala	Leu	Asp	Lys	Lys	Tyr	Gly	Asn	Gly	Ala	Arg	Met	Asn	Arg
		90					95					100			
gca	act	aac	aaa	ggg	tac	tgg	aaa	gca	act	gga	aaa	gac	aga	gaa	atc
Ala	Thr	Asn	Lys	Gly	Tyr	Trp	Lys	Ala	Thr	Gly	Lys	Asp	Arg	Glu	Ile
	105					110					115				
cgc	cgg	gat	att	cag	ttg	ctc	ggc	atg	aaa	aag	acg	ctt	gtt	ttc	cac
Arg	Arg	Asp	Ile	Gln	Leu	Leu	Gly	Met	Lys	Lys	Thr	Leu	Val	Phe	His
120					125					130					135
agc	ggg	cgt	gct	cca	gac	ggc	ctt	cgg	act	aat	tgg	gtc	atg	cac	gag
Ser	Gly	Arg	Ala	Pro	Asp	Gly	Leu	Arg	Thr	Asn	Trp	Val	Met	His	Glu
				140					145					150	
tat	cgc	ctt	gtg	gaa	tat	gaa	act	gaa	act	aac	gga	agc	ctg	ctg	cag
Tyr	Arg	Leu	Val	Glu	Tyr	Glu	Thr	Glu	Thr	Asn	Gly	Ser	Leu	Leu	Gln
			155					160					165		
gat	gca	tat	gtg	ttg	tgc	aga	gtg	ttt	cac	aag	aat	aac	att	ggg	cca
Asp	Ala	Tyr	Val	Leu	Cys	Arg	Val	Phe	His	Lys	Asn	Asn	Ile	Gly	Pro
		170					175					180			
cca	agt	ggg	aac	aga	tat	gcg	cca	ttc	atg	gaa	gaa	gaa	tgg	gct	gat
Pro	Ser	Gly	Asn	Arg	Tyr	Ala	Pro	Phe	Met	Glu	Glu	Glu	Trp	Ala	Asp
	185					190					195				
ggc	gga	gga	gct	ctg	att	cca	gga	ata	gac	gtt	agg	gtc	agg	gta	gag
Gly	Gly	Gly	Ala	Leu	Ile	Pro	Gly	Ile	Asp	Val	Arg	Val	Arg	Val	Glu
200					205					210					215
gct	cta	cca	caa	gcc	aat	gga	aac	aac	cag	atg	gac	cag	gaa	atg	cat
Ala	Leu	Pro	Gln	Ala	Asn	Gly	Asn	Asn	Gln	Met	Asp	Gln	Glu	Met	His
				220					225					230	
tca	gca	agc	aag	gat	ctc	att	aac	atc	aac	gag	cta	ccg	aga	gat	gct
Ser	Ala	Ser	Lys	Asp	Leu	Ile	Asn	Ile	Asn	Glu	Leu	Pro	Arg	Asp	Ala
			235					240					245		
act	cca	atg	gac	atc	gaa	cct	aac	caa	cag	aat	cat	cat	gag	agt	gcc
Thr	Pro	Met	Asp	Ile	Glu	Pro	Asn	Gln	Gln	Asn	His	His	Glu	Ser	Ala
		250					255					260			
ttc	aag	cca	cag	gag	agt	aac	aac	cat	agt	ggc	tat	gaa	gaa	gat	gag
Phe	Lys	Pro	Gln	Glu	Ser	Asn	Asn	His	Ser	Gly	Tyr	Glu	Glu	Asp	Glu
	265					270					275				
gac	aca	ctc	aaa	cgc	gag	cac	gca	gaa	gaa	gat	gag	cgt	cct	cct	tct
Asp	Thr	Leu	Lys	Arg	Glu	His	Ala	Glu	Glu	Asp	Glu	Arg	Pro	Pro	Ser
280					285					290					295
cta	tgc	att	ctc	aac	aaa	gaa	gct	cca	cta	cct	ctc	ctg	caa	tac	aaa
Leu	Cys	Ile	Leu	Asn	Lys	Glu	Ala	Pro	Leu	Pro	Leu	Leu	Gln	Tyr	Lys
				300					305					310	

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cgt aga cgc caa aac gag tcc aac aac aac tca agc agg aac aca cag	1013
Arg Arg Arg Gln Asn Glu Ser Asn Asn Asn Ser Ser Arg Asn Thr Gln	
315 320 325	
gac cat tgt tcg tcc aca ata aca acc gtc gac aat aca acc acc tta	1061
Asp His Cys Ser Ser Thr Ile Thr Thr Val Asp Asn Thr Thr Thr Leu	
330 335 340	
atc tca tca tct gct gct gct gct acc aac act gcc atc tct gca ttg	1109
Ile Ser Ser Ser Ala Ala Ala Ala Thr Asn Thr Ala Ile Ser Ala Leu	
345 350 355	
ctt gag ttc tca ctt atg ggt atc tcc gac aag aaa gaa aac cag cag	1157
Leu Glu Phe Ser Leu Met Gly Ile Ser Asp Lys Lys Glu Asn Gln Gln	
360 365 370 375	
aaa gag gaa act tct cct cct agt cca att gca tct cct gaa gag aag	1205
Lys Glu Glu Thr Ser Pro Pro Ser Pro Ile Ala Ser Pro Glu Glu Lys	
380 385 390	
gtt aat gat ctc cag aag gag gtt cac cag atg tct gtt gaa aga gaa	1253
Val Asn Asp Leu Gln Lys Glu Val His Gln Met Ser Val Glu Arg Glu	
395 400 405	
act ttc aag ctt gag atg atg agt gca gag gct atg atc agc att ctc	1301
Thr Phe Lys Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile Leu	
410 415 420	
cag tca aga atc gat gcg ctg cgt cag gag aac gag gaa ctt aag aag	1349
Gln Ser Arg Ile Asp Ala Leu Arg Gln Glu Asn Glu Glu Leu Lys Lys	
425 430 435	
aag aac gcc agt gga caa gct agt taa accaccgcaa catctctcca	1396
Lys Asn Ala Ser Gly Gln Ala Ser	
440 445	
gggtgtcttct tcttcttctt cttcttcttt gcctcttagc tgtaatcttc ttaatagtat	1456
gagctatgga ttagcttct tcagacggat cagaaacctt atgaatctct gttgtaaaat	1516
taggataaaa cggaacggag ccaaccaact aggtcttttt attttatcct tttttacttt	1576
ggatgtttct gcatcttttg ggaacatttt caggctgac cattgtcgta tattatcatc	1636
tatctatcta gtcttttcag acaaaaaaa	1665

<210> 48
 <211> 447
 <212> PRT
 <213> Arabidopsis thaliana

<400> 48

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

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

Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr Leu Lys Arg Lys
 35 40 45

Val Leu Gly Lys Pro Val Arg Phe Asp Ala Ile Gly Glu Val Asp Ile
 50 55 60

Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser Lys Leu Lys Thr
 65 70 75 80

Arg Asp Gln Glu Trp Tyr Phe Phe Ser Ala Leu Asp Lys Lys Tyr Gly

MBI-17 Sequence Listing.ST25

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

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MBI-17 Sequence Listing.ST25

Ile Ala Ser Pro Glu Glu Lys Val Asn Asp Leu Gln Lys Glu Val His
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Gln Met Ser Val Glu Arg Glu Thr Phe Lys Leu Glu Met Met Ser Ala
405 410 415

Glu Ala Met Ile Ser Ile Leu Gln Ser Arg Ile Asp Ala Leu Arg Gln
420 425 430

Glu Asn Glu Glu Leu Lys Lys Lys Asn Ala Ser Gly Gln Ala Ser
435 440 445

<210> 49
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<223> G866

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Thr Val Asp Ile Met Arg Leu Pro Lys Met Glu Asp Gln Thr Ala Ile
5 10 15

caa gaa gct gca tca caa ggc tta aaa agc atg gaa cac ttg att cgt 154
Gln Glu Ala Ala Ser Gln Gly Leu Lys Ser Met Glu His Leu Ile Arg
20 25 30

gtc ctc tct aac cgt ccc gaa gaa cgt aac gtt gat tgc tct gag atc 202
Val Leu Ser Asn Arg Pro Glu Glu Arg Asn Val Asp Cys Ser Glu Ile
35 40 45

act gat ttc aca gtt tct aag ttc aag aaa gtt atc tct ctt ctt aac 250
Thr Asp Phe Thr Val Ser Lys Phe Lys Lys Val Ile Ser Leu Leu Asn
50 55 60 65

cgt tcc ggt cac gcc cgg ttt aga cgt ggt ccg gtt cat tcc cct cct 298
Arg Ser Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser Pro Pro
70 75 80

tcc tcc tcc gtt cct cca ccg gtg aaa gtg aca act ccg gct ccc act 346
Ser Ser Ser Val Pro Pro Pro Val Lys Val Thr Thr Pro Ala Pro Thr
85 90 95

cag atc tct gct cca gca ccg gtt agc ttc gtt cag gca aat caa caa 394
Gln Ile Ser Ala Pro Ala Pro Val Ser Phe Val Gln Ala Asn Gln Gln
100 105 110

agc gtg acg tta gat ttc act aga ccg agc gtt ttt ggc gct aaa acc 442
Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys Thr
115 120 125

aag agc tcg gag gtt gtt gag ttt gct aaa gag agc ttt agc gta tct 490
Lys Ser Ser Glu Val Val Glu Phe Ala Lys Glu Ser Phe Ser Val Ser
130 135 140 145

tct aac tct tct ttc atg tct tct gcg atc acc ggt gat gga agt gtc 538
Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser Val
150 155 160

tct aaa ggc tct tcg atc ttt ctt gct ccg gct cca gcg gtg cca gtg 586
Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro Val
165 170 175

MBI-17 Sequence Listing.ST25

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act tcc tcc ggg aaa ccg ccg ctt tct ggt ctt cct tac agg aag aga      634
Thr Ser Ser Gly Lys Pro Pro Leu Ser Gly Leu Pro Tyr Arg Lys Arg
      180      185      190

tgc ttt gaa cat gac cac tct gaa ggc ttt tcc ggc aag atc tct ggc      682
Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser Gly
      195      200      205

tcc ggc aac ggc aag tgc cat tgc aag aaa agc cga aaa aat cgg atg      730
Ser Gly Asn Gly Lys Cys His Cys Lys Lys Ser Arg Lys Asn Arg Met
      210      215      220      225

aag aga acc gtg aga gta ccg gcg gta agt gca aag atc gcc gat ata      778
Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp Ile
      230      235      240

cca cca gac gaa tat tca tgg aga aag tat gga caa aaa ccg atc aaa      826
Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys
      245      250      255

ggc tca cca cat cca cgg ggt tat tac aag tgt agt aca ttt aga gga      874
Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr Phe Arg Gly
      260      265      270

tgt cca gcg agg aaa cac gtg gaa aga gct ttg gat gat tca acg atg      922
Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr Met
      275      280      285

ttg att gtg acg tac gaa gga gag cac cgt cat cac cag tcc acg atg      970
Leu Ile Val Thr Tyr Glu Gly Glu His Arg His His Gln Ser Thr Met
      290      295      300      305

cag gag cat gta act cct agc gtg agt ggt ttg gtg ttt ggt tcg gct      1018
Gln Glu His Val Thr Pro Ser Val Ser Gly Leu Val Phe Gly Ser Ala
      310      315      320

tga agaattaatt agtttggttag ttttgtaata ttttgagaaa tagagggggtt      1071

gggttttgtaa ttttttttct ataacaaaat tagtttttaga ttttttttta gtagtctttt      1131

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aaaaaaaaa      1198

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<213> Arabidopsis thaliana

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      20      25      30

Arg Val Leu Ser Asn Arg Pro Glu Glu Arg Asn Val Asp Cys Ser Glu
      35      40      45

Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Lys Val Ile Ser Leu Leu
      50      55      60

Asn Arg Ser Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser Pro
65      70      75      80

Pro Ser Ser Ser Val Pro Pro Pro Val Lys Val Thr Thr Pro Ala Pro
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MBI-17 Sequence Listing.ST25

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Gln Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys
      115                      120                      125

Thr Lys Ser Ser Glu Val Val Glu Phe Ala Lys Glu Ser Phe Ser Val
      130                      135                      140

Ser Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser
      145                      150                      155                      160

Val Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro
      165                      170                      175

Val Thr Ser Ser Gly Lys Pro Pro Leu Ser Gly Leu Pro Tyr Arg Lys
      180                      185                      190

Arg Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser
      195                      200                      205

Gly Ser Gly Asn Gly Lys Cys His Cys Lys Lys Ser Arg Lys Asn Arg
      210                      215                      220

Met Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp
      225                      230                      235                      240

Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile
      245                      250                      255

Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr Phe Arg
      260                      265                      270

Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr
      275                      280                      285

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MBI-17 Sequence Listing.ST25

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 Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu
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 cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt 322
 Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
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 Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
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 Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
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 cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc 946
 His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
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 aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa 994
 Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
 260 265 270
 tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg 1042
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MBI-17 Sequence Listing.ST25																	
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gag	tca	tgt	cca	cct	ctt	tct	ctg	tct	ggg	gga	agt	tgc	tcg	ctt	ctg	1138	
Glu	Ser	Cys	Pro	Pro	Leu	Ser	Leu	Ser	Gly	Gly	Ser	Cys	Ser	Leu	Leu		
305						310					315					320	
atg	aat	gat	tgc	agt	caa	tac	gat	gtt	gaa	ggg	ttc	gag	aag	gag	tct	1186	
Met	Asn	Asp	Cys	Ser	Gln	Tyr	Asp	Val	Glu	Gly	Phe	Glu	Lys	Glu	Ser		
						325					330					335	
cac	tat	gaa	gtg	gaa	gag	ctc	aag	cca	gaa	aaa	gtt	atg	aat	tct	tca	1234	
His	Tyr	Glu	Val	Glu	Glu	Leu	Lys	Pro	Glu	Lys	Val	Met	Asn	Ser	Ser		
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Asn	Phe	Gly	Met	Val	Ala	Lys	Met	His	Asp	Phe	Pro	Val	Lys	Glu	Glu		
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gtc	cca	gca	gga	aac	tcg	gaa	ttc	atg	aga	aag	aga	aag	cca	aac	aga	1330	
Val	Pro	Ala	Gly	Asn	Ser	Glu	Phe	Met	Arg	Lys	Arg	Lys	Pro	Asn	Arg		
						370					375					380	
gat	ctg	aac	act	att	atg	gac	aga	acc	gtt	ttc	acc	tgc	gag	aat	ctt	1378	
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Gly	Cys	Ala	His	Ser	Glu	Ile	Ser	Arg	Gly	Phe	Leu	Asp	Arg	Asn	Ser		
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aga	gac	aac	cat	caa	ctg	gca	tgt	cca	cat	cga	gac	agt	cgc	tta	ccg	1474	
Arg	Asp	Asn	His	Gln	Leu	Ala	Cys	Pro	His	Arg	Asp	Ser	Arg	Leu	Pro		
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tat	gga	gca	gca	cca	tcc	agg	ttt	cat	gtc	aat	gaa	gtt	aag	cct	gta	1522	
Tyr	Gly	Ala	Ala	Pro	Ser	Arg	Phe	His	Val	Asn	Glu	Val	Lys	Pro	Val		
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Val	Gly	Phe	Pro	Gln	Pro	Arg	Pro	Val	Asn	Ser	Val	Ala	Gln	Pro	Ile		
						450					455					460	
gac	tta	acg	ggg	ata	gtt	cct	gaa	gat	gga	cag	aag	atg	atc	tca	gag	1618	
Asp	Leu	Thr	Gly	Ile	Val	Pro	Glu	Asp	Gly	Gln	Lys	Met	Ile	Ser	Glu		
						470					475					480	
ctc	atg	tcc	atg	tac	gac	aga	aat	gtc	cag	agc	aac	caa	acc	tct	atg	1666	
Leu	Met	Ser	Met	Tyr	Asp	Arg	Asn	Val	Gln	Ser	Asn	Gln	Thr	Ser	Met		
						485					490					495	
gtc	atg	gaa	aat	caa	agc	gtg	tca	ctg	ctt	caa	ccc	aca	gtc	cat	aac	1714	
Val	Met	Glu	Asn	Gln	Ser	Val	Ser	Leu	Leu	Gln	Pro	Thr	Val	His	Asn		
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cat	caa	gaa	cat	ctc	cag	ttc	cca	gga	aac	atg	gtg	gaa	gga	agt	ttc	1762	
His	Gln	Glu	His	Leu	Gln	Phe	Pro	Gly	Asn	Met	Val	Glu	Gly	Ser	Phe		
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Phe	Glu	Asp	Leu	Asn	Ile	Pro	Asn	Arg	Ala	Asn	Asn	Asn	Asn	Ser	Ser		
						530					535					540	
aac	aat	caa	acg	ttt	ttt	caa	ggg	aac	aac	aac	aac	aac	aat	gtg	ttt	1858	
Asn	Asn	Gln	Thr	Phe	Phe	Gln	Gly	Asn	Asn	Asn	Asn	Asn	Asn	Val	Phe		
						545					550					555	
aag	ttc	gac	act	gca	gat	cac	aac	aac	ttt	gaa	gct	gca	cat	aac	aac	1906	
Lys	Phe	Asp	Thr	Ala	Asp	His	Asn	Asn	Phe	Glu	Ala	Ala	His	Asn	Asn		
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 Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val
 610 615 620
 tcc ata tgg ttc taa agtcttggtgta gtagatttca tcttctctta tttttatctt 2105
 Ser Ile Trp Phe
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 35 40 45
 Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
 50 55 60
 Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
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 Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
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 Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
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 Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
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MBI-17 Sequence Listing.ST25

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Gly	Val	Pro	Pro	Pro	Trp	Trp	Pro	Asn	Gly	Lys	Glu	Asp	Trp	Trp	Pro
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Glu	Ser	Cys	Pro	Pro	Leu	Ser	Leu	Ser	Gly	Gly	Ser	Cys	Ser	Leu	Leu
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Met	Asn	Asp	Cys	Ser	Gln	Tyr	Asp	Val	Glu	Gly	Phe	Glu	Lys	Glu	Ser
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His	Tyr	Glu	Val	Glu	Glu	Leu	Lys	Pro	Glu	Lys	Val	Met	Asn	Ser	Ser
			340					345					350		
Asn	Phe	Gly	Met	Val	Ala	Lys	Met	His	Asp	Phe	Pro	Val	Lys	Glu	Glu
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Val	Pro	Ala	Gly	Asn	Ser	Glu	Phe	Met	Arg	Lys	Arg	Lys	Pro	Asn	Arg
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Gly	Cys	Ala	His	Ser	Glu	Ile	Ser	Arg	Gly	Phe	Leu	Asp	Arg	Asn	Ser
				405					410					415	
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			420					425					430		
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		435					440					445			
Val	Gly	Phe	Pro	Gln	Pro	Arg	Pro	Val	Asn	Ser	Val	Ala	Gln	Pro	Ile
	450					455					460				
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MBI-17 Sequence Listing.ST25

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 Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe
 545 550 555 560
 Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
 565 570 575
 Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
 580 585 590
 Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
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 Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly Thr Cys Leu
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 caa aga tgt ggc aaa agt tgt agg tta agg tgg act aat tat ctc cga 192
 Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg
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 cca gat ata aaa cga gga aga ttc tct ttt gag gaa gaa gaa gcc att 240
 Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Ala Ile
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 att cag ctt cat agc ttc tta gga aac aag tgg tct gcg att gcg gcg 288
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MBI-17 Sequence Listing.ST25

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115	120	125	
agt cca cga ctc gat ctc ctc gat atc tca tcc atc tta gct tca tct	Ser Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ala Ser Ser	432	
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165	170	175	
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225	230	235	240
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260	265	270	
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275	280	285	
tca agt tca aat ttt gtc tta gat cat tct tat tcg gat cag agc ttc	Ser Ser Ser Asn Phe Val Leu Asp His Ser Tyr Ser Asp Gln Ser Phe	912	
290	295	300	
aac ttc gca aat tcg gtc tta aac acg cca tcc tcg agc ccg agc ccg	Asn Phe Ala Asn Ser Val Leu Asn Thr Pro Ser Ser Ser Pro Ser Pro	960	
305	310	315	320
act acg tta aac tcg agt tac atc aat agt agc agt tgc agc act gag	Thr Thr Leu Asn Ser Ser Tyr Ile Asn Ser Ser Ser Cys Ser Thr Glu	1008	
325	330	335	
gat gaa ata gaa agc tat tgc agt aat ctc atg aag ttt gat att ccc	Asp Glu Ile Glu Ser Tyr Cys Ser Asn Leu Met Lys Phe Asp Ile Pro	1056	
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MBI-17 Sequence Listing.ST25

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Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg
 50 55 60

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

Ile Gln Leu His Ser Phe Leu Gly Asn Lys Trp Ser Ala Ile Ala Ala
 85 90 95

Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Asn Thr
 100 105 110

His Ile Arg Lys Lys Leu Leu Arg Met Gly Ile Asp Pro Val Thr His
 115 120 125

Ser Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ala Ser Ser
 130 135 140

Leu Tyr Asn Ser Ser Ser His His Met Asn Met Ser Arg Leu Met Met
 145 150 155 160

Asp Thr Asn Arg Arg His Gln Gln Gln His Pro Leu Val Asn Pro Glu
 165 170 175

Ile Leu Lys Leu Ala Thr Ser Ile Phe Ser Gln Asn Gln Asn Gln Asn
 180 185 190

His Asn Gln Asn Gln Asn Gln Asn Gln Asn Leu Val Val Asp His Glu
 195 200 205

Lys Gln Thr Val Tyr His His His Asp Val Asn Gln Thr Gly Val Asn
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Gln Tyr Gln Thr Asp Gln Tyr Phe Glu Asn Ala Ile Thr Gln Glu Leu
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Gln Ser Ser Met Pro Pro Phe Pro Asn Glu Ala His Gln Phe Asn Asp
 245 250 255

Met Asp His His Phe Asn Gly Phe Gly Glu Gln Asn Leu Val Ser Thr
 260 265 270

Ser Thr Thr Ser Val Gln Asp Cys Tyr Asn Pro Ser Phe Asn Asp Tyr
 275 280 285

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MBI-17 Sequence Listing.ST25

Ser	Ser	Ser	Asn	Phe	Val	Leu	Asp	His	Ser	Tyr	Ser	Asp	Gln	Ser	Phe
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Asn	Phe	Ala	Asn	Ser	Val	Leu	Asn	Thr	Pro	Ser	Ser	Ser	Pro	Ser	Pro
305					310					315					320
Thr	Thr	Leu	Asn	Ser	Ser	Tyr	Ile	Asn	Ser	Ser	Ser	Cys	Ser	Thr	Glu
			325					330						335	
Asp	Glu	Ile	Glu	Ser	Tyr	Cys	Ser	Asn	Leu	Met	Lys	Phe	Asp	Ile	Pro
			340					345					350		
Asp	Phe	Leu	Asp	Val	Asn	Gly	Phe	Ile	Ile						
		355					360								

What is claimed is:

1. A transgenic plant with modified seed characteristics, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - 5 (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof;
 - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
 - (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-10 1, where N=1-27, or a complementary nucleotide sequence thereof;
 - (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
 - (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
 - (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of 15 any of (a)-(e);
 - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's seed characteristics;
 - (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence 20 of any of (a)-(g);
 - (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
 - (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27;
 - 25 (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and
 - (l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27.
- 30 2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to said nucleotide sequence.
3. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf,

banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, and vegetable brassicas.

5

4. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof;
- 10 (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a complementary nucleotide sequence thereof;
- (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
- 15 (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which
- 20 subsequence or fragment encodes a polypeptide that modifies a plant's seed characteristics;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide
- 25 sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27;
- (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and
- 30 (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27.

5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence.
6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.
7. A cell comprising the cloning or expression vector of claim 6.
8. A transgenic plant comprising the isolated or recombinant polynucleotide of claim 4.
9. A composition produced by one or more of:
- (a) incubating one or more polynucleotide of claim 4 with a nuclease;
 - (b) incubating one or more polynucleotide of claim 4 with a restriction enzyme;
 - (c) incubating one or more polynucleotide of claim 4 with a polymerase;
 - (d) incubating one or more polynucleotide of claim 4 with a polymerase and a primer;
 - (e) incubating one or more polynucleotide of claim 4 with a cloning vector, or
 - (f) incubating one or more polynucleotide of claim 4 with a cell.
10. A composition comprising two or more different polynucleotides of claim 4.
11. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.
12. A plant ectopically expressing an isolated polypeptide of claim 11.
13. A method for producing a plant having a modified seed characteristics, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 11 in a plant, thereby producing a modified plant, and selecting the modified plant for improved seed characteristics thereby providing the modified plant with a modified seed characteristics.
14. The method of claim 13, wherein the polynucleotide is a polynucleotide of claim 4.

15. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:

- (a) expressing a polypeptide encoded by the polynucleotide in a plant; and
- (b) identifying at least one factor that is modulated by or interacts with the polypeptide.

5

16. The method of claim 15, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.

10 17. The method of claim 15, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

18. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:

- 15 (a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and,
- (b) monitoring one or more of:
 - (i) expression level of the polynucleotide in the plant;
 - (ii) expression level of the polypeptide in the plant;
 - 20 (iii) modulation of an activity of the polypeptide in the plant; or
 - (iv) modulation of an activity of the polynucleotide in the plant.

19. An integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of claim 4, or to a polypeptide encoded by the polynucleotide.

25

20. The integrated system, computer or computer readable medium of claim 19, further comprising a link between said one or more sequence strings to a modified plant seed characteristics phenotype.

30

21. A method of identifying a sequence similar or homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:

- (a) providing a sequence database; and,

(b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

5

22. The method of claim 21, wherein the querying comprises aligning one or more of the target sequences with one or more of the one or more sequence members in the sequence database.

10

23. The method of claim 21, wherein the querying comprises identifying one or more of the one or more sequence members of the database that meet a user-selected identity criteria with one or more of the target sequences.

15

24. The method of claim 21, further comprising linking the one or more of the polynucleotides of claim 4, or encoded polypeptides, to a modified plant seed characteristics phenotype.

25. A plant comprising altered expression levels of an isolated or recombinant polynucleotide of claim 4.

20

26. A plant comprising altered expression levels or the activity of an isolated or recombinant polypeptide of claim 11.

27. A plant lacking a nucleotide sequence encoding a polypeptide of claim 11.

25

Figure 1

SEQ ID No.	GID	cDNA or protein	conserved domain
1	G214	cDNA	
2	G214	protein	22-71
3	G226	cDNA	
4	G226	protein	28-78
5	G229	cDNA	
6	G229	protein	14-120
7	G241	cDNA	
8	G241	protein	14-114
9	G464	cDNA	
10	G464	protein	7-15,70-80,125-158,183-219
11	G663	cDNA	
12	G663	protein	9-111
13	G776	cDNA	
14	G776	protein	27-175
15	G778	cDNA	
16	G778	protein	220-267
17	G865	cDNA	
18	G865	protein	36-103
19	G869	cDNA	
20	G869	protein	109-177
21	G883	cDNA	
22	G883	protein	245-302
23	G938	cDNA	
24	G938	protein	96-104
25	G1328	cDNA	
26	G1328	protein	14-119
27	G584	cDNA	
28	G584	protein	401-494
29	G668	cDNA	
30	G668	protein	13-113

Figure 2

SEQ ID No.	GID	homolog	cDNA or protein	conserved domain
31	G680	homolog of G214	cDNA	
32	G680	homolog of G214	protein	24-70
33	G682	homolog of G226	cDNA	
34	G682	homolog of G226	protein	22-53
35	G225	homolog of G226	cDNA	
36	G225	homolog of G226	protein	39-76
37	G678	homolog of G229	cDNA	
38	G678	homolog of G229	protein	14-115
39	G233	homolog of G241	cDNA	
40	G233	homolog of G241	protein	14-114
41	G463	homolog of G464	cDNA	
42	G463	homolog of G464	protein	14-23, 77-88, 130-146, 194-227
43	G2422	homolog of G663	cDNA	
44	G2422	homolog of G663	protein	9-110
45	G2421	homolog of G663	cDNA	
46	G2421	homolog of G663	protein	9-110
47	G772	homolog of G776	cDNA	
48	G772	homolog of G776	protein	27-176
49	G866	homolog of G883	cDNA	
50	G866	homolog of G883	protein	43-300
51	G941	homolog of G938	cDNA	
52	G941	homolog of G938	protein	95-103
53	G198	homolog of G1328	cDNA	
54	G198	homolog of G1328	protein	14-117

Figure 3A

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
1	G214	8170933	8.80E-35	Lycopersicon esculentum
1	G214	9205339	1.20E-27	Glycine max
1	G214	8577344	1.80E-23	Zea mays
1	G214	9119112	2.40E-18	Medicago truncatula
1	G214	7660673	4.80E-15	Sorghum bicolor
1	G214	8213273	4.40E-14	Oryza sativa
1	G214	3325786	4.70E-10	Gossypium hirsutum
1	G214	9435251	1.50E-09	Hordeum vulgare
1	G214	9411569	6.80E-09	Triticum aestivum
1	G214	7614730	3.00E-07	Lotus japonicus
3	G226	4396287	5.10E-15	Glycine max
3	G226	9410205	1.50E-05	Triticum aestivum
3	G226	3857004	0.11	Populus tremula x Populus tremuloides
3	G226	2428139	0.35	Oryza sativa
5	G229	7337390	5.20E-51	Lycopersicon esculentum
5	G229	7244424	3.90E-50	Mentha x piperita
5	G229	7776053	1.30E-49	Lotus japonicus
5	G229	2921335	4.60E-48	Gossypium hirsutum
5	G229	1491932	3.60E-47	Zea mays
5	G229	6455590	2.20E-44	Glycine max
5	G229	6020191	1.60E-41	Pinus taeda
5	G229	7765706	4.10E-41	Medicago truncatula
5	G229	7629167	3.20E-40	Gossypium arboreum
5	G229	6850206	4.30E-40	Oryza sativa
7	G241	6552360	2.60E-54	Nicotiana tabacum
7	G241	6782745	2.20E-53	Oryza sativa
7	G241	8097368	5.70E-53	Hordeum vulgare
7	G241	20560	1.80E-52	Petunia x hybrida
7	G241	7217727	2.70E-52	Sorghum bicolor
7	G241	5891408	4.60E-52	Lycopersicon esculentum
7	G241	5139803	7.40E-52	Glycine max
7	G241	7560175	4.10E-50	Medicago truncatula
7	G241	8381332	1.40E-44	Gossypium arboreum
7	G241	4886263	1.20E-42	Antirrhinum majus
9	G464	6527230	3.60E-31	Lycopersicon esculentum
9	G464	9305572	1.10E-22	Sorghum bicolor
9	G464	6604917	6.70E-22	Medicago truncatula
9	G464	5058123	2.30E-21	Glycine max
9	G464	3760881	1.20E-19	Oryza sativa
9	G464	5044476	1.20E-17	Gossypium hirsutum
9	G464	9412603	6.40E-15	Triticum aestivum
9	G464	7777277	3.20E-13	Lotus japonicus
9	G464	9410371	1.70E-11	Hordeum vulgare
9	G464	7624108	2.10E-10	Gossypium arboreum
11	G663	7673087	4.10E-43	Petunia integrifolia
11	G663	7673091	2.60E-41	Petunia x hybrida
11	G663	7339148	1.30E-39	Lycopersicon esculentum
11	G663	7673097	1.90E-36	Petunia axillaris
11	G663	5048991	9.90E-34	Gossypium hirsutum
11	G663	6455590	2.00E-31	Glycine max
11	G663	7560175	1.50E-27	Medicago truncatula
11	G663	7244424	3.20E-26	Mentha x piperita
11	G663	6020191	2.90E-25	Pinus taeda

Figure 3B

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
11	G663	4138298	3.40E-25	Oryza sativa subsp. indica
13	G776	8578423	5.80E-57	Mesembryanthemum crystallinum
13	G776	7411573	2.40E-52	Lycopersicon esculentum
13	G776	9253340	5.80E-43	Solanum tuberosum
13	G776	8383411	6.00E-43	Euphorbia esula
13	G776	7565426	1.50E-39	Medicago truncatula
13	G776	6666629	2.50E-33	Glycine max
13	G776	6732155	3.60E-33	Triticum monococcum
13	G776	7502501	3.00E-32	Gossypium arboreum
13	G776	8708684	3.80E-32	Hordeum vulgare
13	G776	9307772	2.10E-31	Sorghum bicolor
15	G778	9258500	3.10E-36	Glycine max
15	G778	9211293	9.40E-21	Oryza sativa
15	G778	4380303	7.60E-08	Lycopersicon esculentum
15	G778	7718953	4.10E-07	Medicago truncatula
15	G778	7720768	6.80E-07	Lotus japonicus
15	G778	6536575	8.70E-07	Zea mays
15	G778	1668906	0.82	Citrus sinensis
17	G865	9417297	1.70E-32	Triticum aestivum
17	G865	7206394	4.90E-29	Medicago truncatula
17	G865	7796858	5.70E-27	Glycine max
17	G865	4387560	9.20E-25	Lycopersicon esculentum
17	G865	569065	1.50E-23	Oryza sativa
17	G865	7788764	4.10E-23	Lotus japonicus
17	G865	790362	8.40E-22	Nicotiana tabacum
17	G865	7528275	5.90E-21	Mesembryanthemum crystallinum
17	G865	3264766	8.80E-20	Prunus armeniaca
17	G865	8098026	2.00E-19	Hordeum vulgare
19	G869	2213784	1.30E-19	Lycopersicon esculentum
19	G869	3065894	7.30E-19	Nicotiana tabacum
19	G869	8570080	4.20E-18	Oryza sativa
19	G869	7560260	1.50E-17	Medicago truncatula
19	G869	7534890	5.20E-14	Sorghum bicolor
19	G869	6455322	1.10E-13	Glycine max
19	G869	9362061	2.70E-13	Triticum aestivum
19	G869	7788764	5.70E-13	Lotus japonicus
19	G869	7624302	2.50E-12	Gossypium arboreum
19	G869	3858036	2.80E-12	Populus balsamifera subsp. trichocarpa
21	G883	4760595	2.40E-84	Nicotiana tabacum
21	G883	4894962	3.50E-45	Avena sativa
21	G883	6719425	1.70E-36	Glycine max
21	G883	5273248	2.80E-35	Lycopersicon esculentum
21	G883	9302479	3.00E-34	Sorghum bicolor
21	G883	6799932	1.40E-31	Medicago truncatula
21	G883	5456433	4.30E-31	Zea mays
21	G883	8706346	1.40E-30	Hordeum vulgare
21	G883	8404566	2.70E-30	Oryza sativa
21	G883	1432055	2.00E-27	Petroselinum crispum
23	G938	4239844	3.10E-180	Nicotiana tabacum
23	G938	7739794	2.30E-145	Dianthus caryophyllus
23	G938	7567728	9.60E-98	Medicago truncatula
23	G938	8894549	2.70E-93	Cicer arietinum
23	G938	8104209	9.60E-90	Lycopersicon esculentum

Figure 3C

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
23	G938	6462339	4.60E-79	Gossypium hirsutum
23	G938	9204568	1.20E-78	Glycine max
23	G938	7720839	1.10E-69	Lotus japonicus
23	G938	7324903	1.60E-52	Lycopersicon pennellii
23	G938	2427923	4.20E-47	Oryza sativa
25	G1328	4383290	5.10E-65	Lycopersicon esculentum
25	G1328	1946266	1.30E-58	Oryza sativa
25	G1328	9264503	1.40E-53	Glycine max
25	G1328	8381332	1.10E-52	Gossypium arboreum
25	G1328	9363004	3.30E-49	Triticum aestivum
25	G1328	7765706	1.90E-47	Medicago truncatula
25	G1328	20562	3.90E-47	Petunia x hybrida
25	G1328	5050757	4.10E-46	Gossypium hirsutum
25	G1328	5860031	7.80E-45	Pinus taeda
25	G1328	4886263	5.30E-44	Antirrhinum majus
27	G584	1142618	2.30E-153	Phaseolus vulgaris
27	G584	4321761	2.40E-128	Zea mays
27	G584	9280727	9.70E-122	Oryza sativa
27	G584	6175251	4.80E-78	Lycopersicon esculentum
27	G584	9193975	2.20E-59	Medicago truncatula
27	G584	9364538	1.40E-53	Triticum aestivum
27	G584	6847033	1.70E-49	Glycine max
27	G584	5049283	8.90E-46	Gossypium hirsutum
27	G584	7781217	1.00E-43	Lotus japonicus
27	G584	4519200	1.20E-27	Perilla frutescens
29	G668	8172976	9.70E-73	Medicago truncatula
29	G668	9252441	1.10E-70	Solanum tuberosum
29	G668	5897694	1.90E-66	Lycopersicon esculentum
29	G668	8380712	7.00E-65	Gossypium arboreum
29	G668	7685936	2.20E-58	Glycine max
29	G668	1945280	4.60E-48	Oryza sativa
29	G668	20562	1.10E-40	Petunia x hybrida
29	G668	7217727	8.20E-37	Sorghum bicolor
29	G668	6552360	1.90E-36	Nicotiana tabacum
29	G668	4886263	5.80E-36	Antirrhinum majus
31	G680	9258166	5.70E-36	Glycine max
31	G680	9255178	3.00E-29	Zea mays
31	G680	5274804	1.20E-27	Lycopersicon esculentum
31	G680	4974199	3.00E-22	Oryza sativa
31	G680	3325786	2.10E-21	Gossypium hirsutum
31	G680	9119112	1.30E-18	Medicago truncatula
31	G680	7660673	3.20E-17	Sorghum bicolor
31	G680	7243970	6.10E-16	Mentha x piperita
31	G680	3858093	2.10E-10	Populus balsamifera subsp. trichocarpa
31	G680	8845091	3.70E-10	Triticum aestivum
33	G682	309571	4.40E-08	Zea mays
33	G682	4396287	1.10E-05	Glycine max
33	G682	3857004	0.00051	Populus tremula x Populus tremuloides
33	G682	9410205	0.00085	Triticum aestivum
33	G682	8382118	0.0079	Gossypium arboreum
33	G682	2428139	0.017	Oryza sativa
33	G682	7339148	0.13	Lycopersicon esculentum
33	G682	9302672	0.32	Sorghum bicolor

Figure 3D

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
33	G682	5048991	0.39	Gossypium hirsutum
33	G682	6555777	0.46	Pinus taeda
35	G225	4396287	4.40E-16	Glycine max
35	G225	309571	0.00029	Zea mays
35	G225	3857004	0.001	Populus tremula x Populus tremuloides
35	G225	9410205	0.019	Triticum aestivum
35	G225	9426190	0.025	Triticum turgidum subsp. durum
35	G225	8382118	0.046	Gossypium arboreum
35	G225	6782756	0.27	Oryza sativa
35	G225	7721017	0.4	Lotus japonicus
35	G225	6020136	0.47	Pinus taeda
35	G225	2921331	0.48	Gossypium hirsutum
37	G678	7244424	8.70E-50	Mentha x piperita
37	G678	7776053	2.70E-46	Lotus japonicus
37	G678	7337390	2.90E-46	Lycopersicon esculentum
37	G678	2921335	2.30E-43	Gossypium hirsutum
37	G678	6455590	8.30E-43	Glycine max
37	G678	1491932	1.60E-42	Zea mays
37	G678	5860031	4.80E-40	Pinus taeda
37	G678	7765706	3.20E-38	Medicago truncatula
37	G678	6850206	8.20E-38	Oryza sativa
37	G678	7217727	2.00E-37	Sorghum bicolor
39	G233	6552360	6.50E-66	Nicotiana tabacum
39	G233	20560	7.60E-65	Petunia x hybrida
39	G233	5139813	1.70E-58	Glycine max
39	G233	5891103	3.80E-58	Lycopersicon esculentum
39	G233	6782745	1.80E-52	Oryza sativa
39	G233	7560175	1.80E-51	Medicago truncatula
39	G233	7217727	8.30E-51	Sorghum bicolor
39	G233	8097368	5.80E-49	Hordeum vulgare
39	G233	8381332	4.60E-43	Gossypium arboreum
39	G233	5048991	3.50E-41	Gossypium hirsutum
41	G463	6527230	4.90E-36	Lycopersicon esculentum
41	G463	9305572	5.50E-36	Sorghum bicolor
41	G463	3760881	1.20E-31	Oryza sativa
41	G463	6604917	1.30E-23	Medicago truncatula
41	G463	5058123	2.50E-21	Glycine max
41	G463	5044476	1.10E-19	Gossypium hirsutum
41	G463	9412603	1.70E-17	Triticum aestivum
41	G463	9419394	6.00E-17	Hordeum vulgare
41	G463	7624108	6.20E-17	Gossypium arboreum
41	G463	8547152	3.20E-16	Nicotiana tabacum
43	G2422	7673087	9.60E-45	Petunia integrifolia
43	G2422	7339148	6.30E-43	Lycopersicon esculentum
43	G2422	7673083	7.20E-43	Petunia x hybrida
43	G2422	7673097	3.30E-40	Petunia axillaris
43	G2422	5048991	3.30E-36	Gossypium hirsutum
43	G2422	6455590	3.00E-33	Glycine max
43	G2422	6020191	3.20E-32	Pinus taeda
43	G2422	309571	3.60E-30	Zea mays
43	G2422	7560832	9.00E-30	Medicago truncatula
43	G2422	9363004	1.30E-29	Triticum aestivum
45	G2421	7673087	1.10E-46	Petunia integrifolia

Figure 3E

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
45	G2421	5048991	1.30E-35	Gossypium hirsutum
45	G2421	7673091	1.50E-31	Petunia x hybrida
45	G2421	8380196	7.30E-31	Gossypium arboreum
45	G2421	7673095	1.90E-30	Petunia axillaris
45	G2421	7339148	2.80E-30	Lycopersicon esculentum
45	G2421	8747182	9.00E-30	Medicago truncatula
45	G2421	7217727	1.30E-27	Sorghum bicolor
45	G2421	6073050	5.50E-27	Glycine max
45	G2421	1101769	7.40E-27	Picea mariana
47	G772	8578423	4.80E-58	Mesembryanthemum crystallinum
47	G772	7570276	3.00E-52	Medicago truncatula
47	G772	7411573	1.30E-44	Lycopersicon esculentum
47	G772	6341483	6.30E-33	Glycine max
47	G772	1279639	2.00E-32	Petunia x hybrida
47	G772	7722907	3.50E-32	Lotus japonicus
47	G772	8405571	4.70E-32	Hordeum vulgare
47	G772	6730945	6.40E-32	Oryza sativa
47	G772	9302206	2.50E-31	Sorghum bicolor
47	G772	5047907	1.10E-30	Gossypium hirsutum
49	G866	4760595	3.50E-85	Nicotiana tabacum
49	G866	4894962	1.70E-38	Avena sativa
49	G866	6719425	6.60E-35	Glycine max
49	G866	5273248	1.10E-33	Lycopersicon esculentum
49	G866	9302479	7.40E-33	Sorghum bicolor
49	G866	6799932	3.60E-31	Medicago truncatula
49	G866	4886128	4.50E-31	Zea mays
49	G866	8404566	1.40E-29	Oryza sativa
49	G866	8706346	1.10E-28	Hordeum vulgare
49	G866	1432055	3.50E-26	Petroselinum crispum
51	G941	4239844	3.80E-198	Nicotiana tabacum
51	G941	7739794	1.20E-141	Dianthus caryophyllus
51	G941	7567728	7.10E-102	Medicago truncatula
51	G941	8104209	3.70E-97	Lycopersicon esculentum
51	G941	8894549	2.10E-95	Cicer arietinum
51	G941	5606033	1.60E-79	Glycine max
51	G941	6462339	4.60E-79	Gossypium hirsutum
51	G941	7720839	6.60E-70	Lotus japonicus
51	G941	7324903	1.00E-55	Lycopersicon pennellii
51	G941	2427923	6.90E-47	Oryza sativa
53	G198	4383290	3.50E-64	Lycopersicon esculentum
53	G198	1946266	1.10E-58	Oryza sativa
53	G198	9363004	5.40E-51	Triticum aestivum
53	G198	8381332	6.40E-51	Gossypium arboreum
53	G198	9264503	1.30E-50	Glycine max
53	G198	5050757	4.10E-46	Gossypium hirsutum
53	G198	20562	9.30E-46	Petunia x hybrida
53	G198	7765706	2.70E-45	Medicago truncatula
53	G198	5860031	5.40E-45	Pinus taeda
53	G198	4886263	7.30E-45	Antirrhinum majus