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(54) Title: ISOLATED POLYNUCLEOTIDES EXPRESSING OR MODULATING MICRORNAs OR TARGETS OF SAME, TRANSGENIC PLANTS COMPRISING SAME AND USES THEREOF IN IMPROVING NITROGEN USE EFFICIENCY, ABIOTIC STRESS TOLERANCE, BIOMASS, VIGOR OR YIELD OF A PLANT

FIG. 2A

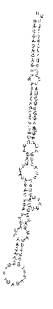


FIG. 2B

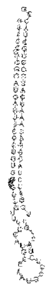


FIG. 2C

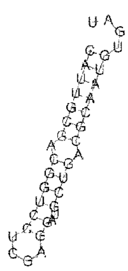


FIG. 2D

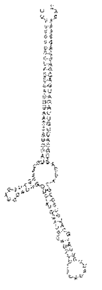


FIG. 2E

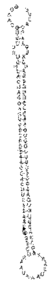


FIG. 2F

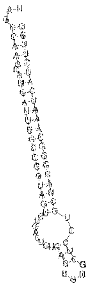


FIG. 2G

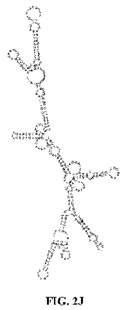


FIG. 2H

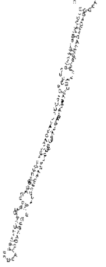


FIG. 2I

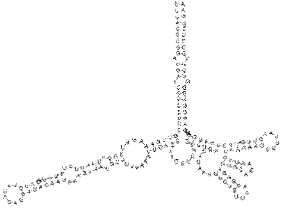
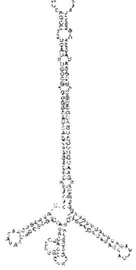


FIG. 2J



(57) **Abstract**: Isolated polynucleotides expressing or modulating microRNAs or targets of same are provided. Also provided are transgenic plants comprising same and uses thereof in improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

ISOLATED POLYNUCLEOTIDES EXPRESSING OR MODULATING microRNAs OR TARGETS OF SAME, TRANSGENIC PLANTS COMPRISING SAME AND USES THEREOF IN IMPROVING NITROGEN USE EFFICIENCY, ABIOTIC STRESS TOLERANCE, BIOMASS, VIGOR OR YIELD OF A PLANT

RELATED APPLICATION/S

This Application claims priority from U.S. Provisional Patent Application No. 61/406,184 filed on October 25, 2010, the contents of which are hereby incorporated by reference in its entirety.

FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to isolated polynucleotides expressing or modulating microRNAs or targets of same, transgenic plants comprising same and uses thereof in improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant.

Plant growth is reliant on a number of basic factors: light, air, water, nutrients, and physical support. All these factors, with the exception of light, are controlled by soil to some extent, which integrates non-living substances (minerals, organic matter, gases and liquids) and living organisms (bacteria, fungi, insects, worms, etc.). The soil's volume is almost equally divided between solids and water/gases. An adequate nutrition in the form of natural as well as synthetic fertilizers, may affect crop yield and quality, and its response to stress factors such as disease and adverse weather. The great importance of fertilizers can best be appreciated when considering the direct increase in crop yields over the last 40 years, and the fact that they account for most of the overhead expense in agriculture. Sixteen natural nutrients are essential for plant growth, three of which, carbon, hydrogen and oxygen, are retrieved from air and water. The soil provides the remaining 13 nutrients.

Nutrients are naturally recycled within a self-sufficient environment, such as a rainforest. However, when grown in a commercial situation, plants consume nutrients for their growth and these nutrients need to be replenished in the system. Several nutrients are consumed by plants in large quantities and are referred to as macronutrients. Three macronutrients are considered the basic building blocks of plant growth, and are provided as main fertilizers; Nitrogen (N), Phosphate (P) and Potassium (K). Yet, only nitrogen needs to be replenished every year since plants only absorb approximately half of the nitrogen fertilizer applied. A proper balance of nutrients is crucial; when too much of an essential nutrient is available, it may become toxic to plant growth. Utilization efficiencies of macronutrients directly correlate with yield and general plant tolerance, and increasing them will benefit the plants themselves and the environment by decreasing seepage to ground water.

Nitrogen is responsible for biosynthesis of amino and nucleic acids, prosthetic groups, plant hormones, plant chemical defenses, etc, and thus is utterly essential for the plant. For this reason, plants store nitrogen throughout their developmental stages, in the specific case of corn during the period of grain germination, mostly in the leaves and stalk. However, due to the low nitrogen use efficiency (NUE) of the main crops (e.g., in the range of only 30-70 %), nitrogen supply needs to be replenished at least twice during the growing season. This requirement for fertilizer refill may become the rate-limiting element in plant growth and increase fertilizer expenses for the farmer. Limited land resources combined with rapid population growth will inevitably lead to added increase in fertilizer use. In light of this prediction, advanced, biotechnology-based solutions to allow stable high yields with an added potential to reduce fertilizer costs are highly desirable. Subsequently, developing plants with increased NUE will lower fertilizer input in crop cultivation, and allow growth on lower-quality soils.

The major agricultural crops (corn, rice, wheat, canola and soybean) account for over half of total human caloric intake, giving their yield and quality vast importance. They can be consumed either directly (eating their seeds which are also used as a source of sugars, oils and metabolites), or indirectly (eating meat products raised on processed seeds or forage). Various factors may influence a crop's yield, including but not limited to, quantity and size of the plant organs, plant architecture , vigor (e.g. seedling), growth rate, root development, utilization of water and nutrients (e.g., nitrogen), and stress tolerance. Plant yield may be amplified through multiple approaches; (1) enhancement of innate traits (e.g., dry matter accumulation rate, cellulose/lignin composition), (2) improvement of structural features (e.g., stalk strength, meristem size, plant branching pattern), and (3) amplification of seed yield and quality (e.g., fertilization efficiency, seed development, seed filling or content of oil, starch or protein). Increasing plant yield through any of the above methods would ultimately have many applications in agriculture and additional fields such as in the biotechnology industry.

Two main adverse environmental conditions, malnutrition (nutrient deficiency) and drought, elicit a response in the plant that mainly affects root architecture (Jiang and Huang (2001), *Crop Sci* 41:1168-1173; Lopez-Bucio et al. (2003), *Curr Opin Plant Biol*, 6:280-287; Morgan and Condon (1986), *Aust J Plant Physiol* 13:523-532), causing activation of plant metabolic pathways to maximize water assimilation. Improvement of root architecture, i.e. making branched and longer roots, allows the plant to reach water and nutrient/fertilizer deposits located deeper in the soil by an increase in soil coverage. Root morphogenesis has already shown to increase tolerance to low phosphorus availability in soybean (Miller et al., (2003), *Funct Plant Biol* 30:973-985) and maize (Zhu and Lynch (2004), *Funct Plant Biol* 31:949-958). Thus, genes governing enhancement of root architecture may be used to improve NUE and drought tolerance. An example for a gene associated with root developmental changes is ANR1, a putative transcription factor with a role in nitrate ($NO3^-$) signaling. When expression of ANR1 is down-regulated, the resulting transgenic lines are defective in their root response to localized supplies of nitrate (Zhang and Forde (1998), *Science* 270:407). Enhanced root system and/or increased storage capabilities, which are seen in responses to different environmental stresses, are strongly favorable at normal or optimal growing conditions as well.

Abiotic stress refers to a range of suboptimal conditions as water deficit or drought, extreme temperatures and salt levels, and high or low light levels. High or low nutrient level also falls into the category of abiotic stress. The response to any stress may involve both stress specific and common stress pathways (Pastori and Foyer (2002), *Plant Physiol*, 129: 460-468), and drains energy from the plant, eventually resulting in lowered yield. Thus, distinguishing between the genes activated in each pathway and subsequent manipulation of only specific relevant genes could lead to a partial stress response without the parallel loss in yield. Contrary to the complex polygenic nature of plant traits responsible for adaptations to adverse environmental stresses, information on miRNAs involved in these responses is very limited. The most common approach for crop and horticultural improvements is through cross breeding, which is relatively slow, inefficient, and limited in the degree of variability achieved because it can only manipulate the naturally existing genetic diversity. Taken together with the limited genetic resources (i.e., compatible plant species) for crop improvement, conventional breeding is evidently unfavorable. By creating a pool of genetically modified plants, one broadens the possibilities for producing crops with improved economic or horticultural traits.

SUMMARY OF THE INVENTION

According to an aspect of some embodiments of the present invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 10, 6-9, 21, 22, 23-37, 38-52, 1209, 1211, 1212, wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing a polynucleotide having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 10, 6-9, 23-37, wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of the plant.

According to some embodiments of the invention, said exogenous polynucleotide encodes a precursor of said nucleic acid sequence.

According to some embodiments of the invention, said precursor of said nucleic acid sequence is at least 60 % identical to SEQ ID NO: 21, 22, 38-52, 1209, 1211, 1212.

According to some embodiments of the invention, said exogenous polynucleotide encodes a miRNA or a precursor thereof.

According to some embodiments of the invention, said exogenous polynucleotide encodes a siRNA or a precursor thereof.

According to some embodiments of the invention, said exogenous polynucleotide is selected from the group consisting of SEQ ID NO: 10, 6-9, 21, 22, 23-37, 38-52, 1209, 1211, 1212.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide having a nucleic acid sequence at least 90 % identical to SEQ ID NO: 6, 7 and 9, wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of a plant.

According to some embodiments of the invention, said nucleic acid sequence is selected from the group consisting of SEQ ID NO: 6, 7 and 9.

According to some embodiments of the invention, said polynucleotide encodes a precursor of said nucleic acid sequence.

According to some embodiments of the invention, said polynucleotide encodes a miRNA or a precursor thereof.

According to some embodiments of the invention, said polynucleotide encodes a siRNA or a precursor thereof.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising the isolated polynucleotide above under the regulation of a cis-acting regulatory element.

According to some embodiments of the invention, said cis-acting regulatory element comprises a promoter.

According to some embodiments of the invention, said promoter comprises a tissue-specific promoter.

According to some embodiments of the invention, said tissue-specific promoter comprises a root specific promoter.

According to an aspect of some embodiments of the present invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a gene encoding an RNAi molecule having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a gene encoding an RNAi molecule having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide which downregulates an activity or expression of a gene encoding an RNAi molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209.

According to some embodiments of the invention, said polynucleotide encodes a miRNA-Resistant Target as set forth in SEQ ID NO1104-1124.

According to some embodiments of the invention, said isolated polynucleotide encodes a target mimic as set forth in SEQ ID NO: 18 or 19.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising the isolated polynucleotide above under the regulation of a cis-acting regulatory element.

According to some embodiments of the invention, said cis-acting regulatory element comprises a promoter.

According to some embodiments of the invention, said promoter comprises a tissue-specific promoter.

According to some embodiments of the invention, said tissue-specific promoter comprises a root specific promoter.

According to some embodiments of the invention, the method further comprises growing the plant under limiting nitrogen conditions.

According to some embodiments of the invention, the method further comprises growing the plant under abiotic stress.

According to some embodiments of the invention, said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

According to some embodiments of the invention, the plant is a monocotyledon.

According to some embodiments of the invention, the plant is a dicotyledon.

According to an aspect of some embodiments of the present invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 927-1021, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing a polynucleotide encoding a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 927-1021, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising a polynucleotide encoding a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 927-1021, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, and wherein said polynucleotide is under a transcriptional control of a cis-acting regulatory element.

According to some embodiments of the invention, said polynucleotide is selected from the group consisting of SEQ ID NO: 1022-1090.

According to some embodiments of the invention, said polypeptide is selected from the group consisting of SEQ ID NO: 927-1021.

According to some embodiments of the invention, said cis-acting regulatory element comprises a promoter.

According to some embodiments of the invention, said promoter comprises a tissue-specific promoter.

According to some embodiments of the invention, said tissue-specific promoter comprises a root specific promoter.

According to some embodiments of the invention, the method further comprises growing the plant under limiting nitrogen conditions.

According to some embodiments of the invention, the method further comprises growing the plant under abiotic stress.

According to some embodiments of the invention, said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

According to some embodiments of the invention, the plant is a monocotyledon.

According to some embodiments of the invention, the plant is a dicotyledon.

According to an aspect of some embodiments of the present invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 854-894, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 854-894, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 854-894, wherein said polypeptide is capable of regulating nitrogen use efficiency of a plant, said nucleic acid sequence being under the regulation of a cis-acting regulatory element.

According to some embodiments of the invention, said polynucleotide acts by a mechanism selected from the group consisting of sense suppression, antisense suppresion, ribozyme inhibition, gene disruption.

According to some embodiments of the invention, said cis-acting regulatory element comprises a promoter.

According to some embodiments of the invention, said promoter comprises a tissue-specific promoter.

According to some embodiments of the invention, said tissue-specific promoter comprises a root specific promoter.

Unless otherwise defined, all technical and/or scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of the invention, exemplary methods and/or materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be necessarily limiting.

BRIEF DESCRIPTION OF THE DRAWINGS

Some embodiments of the invention are herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of embodiments of the invention. In this regard, the description taken with the drawings makes apparent to those skilled in the art how embodiments of the invention may be practiced.

In the drawings:

FIG. 1 is a scheme of a binary vector that can be used according to some embodiments of the invention;

FIGs. 2A-J are schematic illustrations of some of the miRNA sequences which may be used in accordance with the present invention.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

The present invention, in some embodiments thereof, relates to isolated polynucleotides expressing or modulating microRNAs or targets of same, transgenic plants comprising same and uses thereof in improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant.

Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not necessarily limited in its application to the details set forth in the following description or exemplified by the Examples. The invention is capable of other embodiments or of being practiced or carried out in various ways.

The doubling of agricultural food production worldwide over the past four decades has been associated with a 7-fold increase in the use of nitrogen (N) fertilizers.

As a consequence, both the recent and future intensification of the use of nitrogen fertilizers in agriculture already has and will continue to have major detrimental impacts on the diversity and functioning of the non-agricultural neighbouring bacterial, animal, and plant ecosystems. The most typical examples of such an impact are the eutrophication of freshwater and marine ecosystems as a result of leaching when high rates of nitrogen fertilizers are applied to agricultural fields. In addition, there can be gaseous emission of nitrogen oxides reacting with the stratospheric ozone and the emission of toxic ammonia into the atmosphere. Furthermore, farmers are facing increasing economic pressures with the rising fossil fuels costs required for production of nitrogen fertilizers.

It is therefore of major importance to identify the critical steps controlling plant nitrogen use efficiency (NUE). Such studies can be harnessed towards generating new energy crop species that have a larger capacity to produce biomass with the minimal amount of nitrogen fertilizer.

While reducing the present invention to practice, the present inventors have uncovered microRNA (miRNA) sequences that are differentially expressed in maize plants grown under nitrogen limiting conditions versus maize plants grown under conditions wherein nitrogen is a non-limiting factor. Following extensive experimentation and screening the present inventors have identified miRNA sequences that are upregulated or downregulated in roots and leaves, and suggest using same or sequences controlling same in the generation of transgenic plants having improved nitrogen use efficiency. While further reducing the present invention to practice, the present inventors have analyzed the level of expression of the identified miRNA sequences under optima, and nitrogen deficient conditions by quantitiative RT-PCR and validated the correlation between miRNA expression nitrogen availability. These findings support the use of the miRNA sequences or sequences controlling same or targets thereof in the generation of transgenic plants characterized by improved nitrogen use efficiency and abiotic stress tolerance.

According to some embodiments, the newly uncovered miRNA sequences relay their effect by affecting at least one of:

root architecture so as to increase nutrient uptake;

activation of plant metabolic pathways so as to maximize nitrogen absorption or localization; or alternatively or additionally

modulating plant surface permeability.

Each of the above mechanisms may affect water uptake as well as salt absorption and therefore embodiments of the invention further relate to enhancement of abiotic stress tolerance, biomass, vigor or yield of the plant.

Thus, according to an aspect of the invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide having a nucleic acid sequence at least 80 %, 85 %, 90 % or 95 % identical to SEQ ID NOs: 10, 6-9 and 23-37 wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

According to a specific embodiment the exogenous polynucleotide has a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 10, 6-9, 23-37.

According to a specific embodiment the exogenous polynucleotide has a nucleic acid sequence at least 95 % identical to SEQ ID NOs: 10, 6-9, 23-37.

According to a specific embodiment the exogenous polynucleotide has a nucleic acid sequence as set forth in SEQ ID NOs: 10, 6-9, 23-37.

As used herein the phrase "nitrogen use efficiency (NUE)" refers to a measure of crop production per unit of nitrogen fertilizer input. Fertilizer use efficiency (FUE) is a measure of NUE. Crop production can be measured by biomass, vigor or yield. The plant's nitrogen use efficiency is typically a result of an alteration in at least one of the uptake, spread, absorbance, accumulation, relocation (within the plant) and use of nitrogen absorbed by the plant. Improved NUE is with respect to that of a non-transgenic plant (i.e., lacking the transgene of the transgenic plant) of the same species and of the same developmental stage and grown under the same conditions.

As used herein the phrase “nitrogen-limiting conditions” refers to growth conditions which include a level (e.g., concentration) of nitrogen (e.g., ammonium or nitrate) applied which is below the level needed for optimal plant metabolism, growth, reproduction and/or viability.

The phrase "abiotic stress" as used herein refers to any adverse effect on metabolism, growth, viability and/or reproduction of a plant. Abiotic stress can be induced by any of suboptimal environmental growth conditions such as, for example, water deficit or drought, flooding, freezing, low or high temperature, strong winds, heavy metal toxicity, anaerobiosis, high or low nutrient levels (e.g. nutrient deficiency), high or low salt levels (e.g. salinity), atmospheric pollution, high or low light intensities (e.g. insufficient light) or UV irradiation. Abiotic stress may be a short term effect (e.g. acute effect, e.g. lasting for about a week) or alternatively may be persistent (e.g. chronic effect, e.g. lasting for example 10 days or more). The present invention contemplates situations in which there is a single abiotic stress condition or alternatively situations in which two or more abiotic stresses occur.

According to an exemplary embodiment the abiotic stress refers to salinity.

According to another exemplary embodiment the abiotic stress refers to drought.

As used herein the phrase "abiotic stress tolerance" refers to the ability of a plant to endure an abiotic stress without exhibiting substantial physiological or physical damage (e.g. alteration in metabolism, growth, viability and/or reproductivity of the plant).

As used herein the term/phrase "biomass", "biomass of a plant" or "plant biomass" refers to the amount (e.g., measured in grams of air-dry tissue) of a tissue produced from the plant in a growing season. An increase in plant biomass can be in the whole plant or in parts thereof such as aboveground (e.g. harvestable) parts, vegetative biomass, roots and/or seeds.

As used herein the term/phrase "vigor", "vigor of a plant" or "plant vigor" refers to the amount (e.g., measured by weight) of tissue produced by the plant in a given time. Increased vigor could determine or affect the plant yield or the yield per growing time or growing area. In addition, early vigor (e.g. seed and/or seedling) results in improved field stand.

As used herein the term/phrase "yield", "yield of a plant" or "plant yield" refers to the amount (e.g., as determined by weight or size) or quantity (e.g., numbers) of tissues or organs produced per plant or per growing season. Increased yield of a plant can affect the economic benefit one can obtain from the plant in a certain growing area and/or growing time.

According to an exemplary embodiment the yield is measured by cellulose content.

According to another exemplary embodiment the yield is measured by oil content.

According to another exemplary embodiment the yield is measured by protein content.

According to another exemplary embodiment, the yield is measured by seed number per plant or part thereof (e.g., kernel).

A plant yield can be affected by various parameters including, but not limited to, plant biomass; plant vigor; plant growth rate; seed yield; seed or grain quantity; seed or grain quality; oil yield; content of oil, starch and/or protein in harvested organs (e.g., seeds or vegetative parts of the plant); number of flowers (e.g. florets) per panicle (e.g. expressed as a ratio of number of filled seeds over number of primary panicles); harvest index; number of plants grown per area; number and size of harvested organs per plant and per area; number of plants per growing area (e.g. density); number of harvested organs in field; total leaf area; carbon assimilation and carbon partitioning (e.g. the distribution/allocation of carbon within the plant); resistance to shade; number of harvestable organs (e.g. seeds), seeds per pod, weight per seed; and modified architecture [such as increase stalk diameter, thickness or improvement of physical properties (e.g. elasticity)] .

As used herein the term "improving" or "increasing" refers to at least about 2 %, at least about 3 %, at least about 4 %, at least about 5 %, at least about 10 %, at least about 15 %, at least about 20 %, at least about 25 %, at least about 30 %, at least about 35 %, at least about 40 %, at least about 45 %, at least about 50 %, at least about 60 %, at least about 70 %, at least about 80 %, at least about 90 % or greater increase in NUE, in tolerance to abiotic stress, in yield, in biomass or in vigor of a plant, as compared to a native or wild-type plants [i.e., plants not genetically modified to express the biomolecules (polynucleotides) of the invention, e.g., a non-transformed plant of the same species and of the same developmental stage which is grown under the same growth conditions as the transformed plant].

Improved plant NUE is translated in the field into either harvesting similar quantities of yield, while implementing less fertilizers, or increased yields gained by implementing the same levels of fertilizers. Thus, improved NUE or FUE has a direct effect on plant yield in the field.

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, roots (including tubers), and isolated plant cells, tissues and organs. The plant may be in any form including suspension cultures, embryos, meristematic regions, callus tissue, leaves, gametophytes, sporophytes, pollen, and microspores.

As used herein the phrase “plant cell” refers to plant cells which are derived and isolated from disintegrated plant cell tissue or plant cell cultures.

As used herein the phrase "plant cell culture" refers to any type of native (naturally occurring) plant cells, plant cell lines and genetically modified plant cells, which are not assembled to form a complete plant, such that at least one biological structure of a plant is not present. Optionally, the plant cell culture of this aspect of the present invention may comprise a particular type of a plant cell or a plurality of different types of plant cells. It should be noted that optionally plant cultures featuring a particular type of plant cell may be originally derived from a plurality of different types of such plant cells.

Any commercially or scientifically valuable plant is envisaged in accordance with these embodiments of the invention. Plants that are particularly useful in the methods of the invention include all plants which belong to the super family Viridiplantae, in particular monocotyledonous and dicotyledonous plants including a fodder or forage legume, ornamental plant, food crop, tree, or shrub selected from the list comprising Acacia spp., Acer spp., Actinidia spp., Aesculus spp., Agathis australis, Albizia amara, Alsophila tricolor, Andropogon spp., Arachis spp, Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula spp., Brassica spp., Bruguiera gymnorrhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra spp, Camellia sinensis, Canna indica, Capsicum spp., Cassia spp., Centroema pubescens, Chacoomeles spp., Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coronillia varia, Cotoneaster serotina, Crataegus spp., Cucumis spp., Cupressus spp., Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon spp., Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium spp., Dicksonia squarosa, Dibeteropogon amplectens, Dioclea spp, Dolichos spp., Dorycnium rectum, Echinochloa pyramidalis, Ehraffia spp., Eleusine coracana, Eragrestis spp., Erythrina spp., Eucalyptus spp., Euclea schimperi, Eulalia vi/losa, Pagopyrum spp., Feijoa sellowlana, Fragaria spp., Flemingia spp, Freycinetia banksli, Geranium thunbergii, GinAgo biloba, Glycine javanica, Gliricidia spp, Gossypium hirsutum, Grevillea spp., Guibourtia coleosperma, Hedysarum spp., Hemaffhia altissima, Heteropogon contoffus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hypeffhelia dissolute, Indigo incamata, Iris spp., Leptarrhena pyrolifolia, Lespediza spp., Lettuca spp., Leucaena leucocephala, Loudetia simplex, Lotonus bainesli, Lotus spp., Macrotyloma axillare, Malus spp., Manihot esculenta, Medicago saliva, Metasequoia glyptostroboides, Musa sapientum, Nicotianum spp., Onobrychis spp., Ornithopus spp., Oryza spp., Peltophorum africanum, Pennisetum spp., Persea gratissima, Petunia spp., Phaseolus spp., Phoenix canariensis, Phormium cookianum, Photinia spp., Picea glauca, Pinus spp., Pisum sativam, Podocarpus totara, Pogonarthria fleckii, Pogonaffhria squarrosa, Populus spp., Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus spp., Rhaphiolepsis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes spp., Robinia pseudoacacia, Rosa spp., Rubus spp., Salix spp., Schyzachyrium sanguineum, Sciadopitys vefficillata, Sequoia sempervirens, Sequoiadendron giganteum, Sorghum bicolor, Spinacia spp., Sporobolus fimbriatus, Stiburus alopecuroides, Stylosanthos humilis, Tadehagi spp, Taxodium distichum, Themeda triandra, Trifolium spp., Triticum spp., Tsuga heterophylla, Vaccinium spp., Vicia spp., Vitis vinifera, Watsonia pyramidata, Zantedeschia aethiopica, Zea mays, amaranth, artichoke, asparagus, broccoli, Brussels sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugar beet, sugar cane, sunflower, tomato, squash tea, maize, wheat, barely, rye, oat, peanut, pea, lentil and alfalfa, cotton, rapeseed, canola, pepper, sunflower, tobacco, eggplant, eucalyptus, a tree, an ornamental plant, a perennial grass and a forage crop. Alternatively algae and other non-Viridiplantae can be used for the methods of the present invention.

According to some embodiments of the invention, the plant used by the method of the invention is a crop plant including, but not limited to, cotton, Brassica vegetables, oilseed rape, sesame, olive tree, palm oil, banana, wheat, corn or maize, barley, alfalfa, peanuts, sunflowers, rice, oats, sugarcane, soybean, turf grasses, barley, rye, sorghum, sugar cane, chicory, lettuce, tomato, zucchini, bell pepper, eggplant, cucumber, melon, watermelon, beans, hibiscus, okra, apple, rose, strawberry, chile, garlic, pea, lentil , canola, mums, arabidopsis, broccoli, cabbage, beet, quinoa, spinach, squash, onion, leek, tobacco, potato, sugarbeet, papaya, pineapple, mango, Arabidopsis thaliana, and also plants used in horticulture, floriculture or forestry, such as, but not limited to, poplar, fir, eucalyptus, pine, an ornamental plant, a perennial grass and a forage crop, coniferous plants, moss, algae, as well as other plants listed in World Wide Web (dot) nationmaster (dot) com/encyclopedia/Plantae.

According to a specific embodiment of the present invention, the plant comprises corn.

According to a specific embodiment of the present invention, the plant comprises sorghum.

As used herein, the phrase "exogenous polynucleotide" refers to a heterologous nucleic acid sequence which may not be naturally expressed within the plant or which overexpression in the plant is desired. The exogenous polynucleotide may be introduced into the plant in a stable or transient manner, so as to produce a ribonucleic acid (RNA) molecule. It should be noted that the exogenous polynucleotide may comprise a nucleic acid sequence which is identical or partially homologous to an endogenous nucleic acid sequence of the plant.

As mentioned the present teachings are based on the identification of miRNA sequences which modulate nitrogen use efficiency of plants.

According to some embodiments the exogenous polynucleotide encodes a miRNA or a precursor thereof.

As used herein, the phrase "microRNA (also referred to herein interchangeably as "miRNA" or "miR") or a precursor thereof" refers to a microRNA (miRNA) molecule acting as a post-transcriptional regulator. Typically, the miRNA molecules are RNA molecules of about 20 to 22 nucleotides in length which can be loaded into a RISC complex and which direct the cleavage of another RNA molecule, wherein the other RNA molecule comprises a nucleotide sequence essentially complementary to the nucleotide sequence of the miRNA molecule.

Typically, a miRNA molecule is processed from a “pre-miRNA” or as used herein a precursor of a pre-miRNA molecule by proteins, such as DCL proteins, present in any plant cell and loaded onto a RISC complex where it can guide the cleavage of the target RNA molecules.

Pre-microRNA molecules are typically processed from pri-microRNA molecules (primary transcripts). The single stranded RNA segments flanking the pre-microRNA are important for processing of the pri-miRNA into the pre-miRNA. The cleavage site appears to be determined by the distance from the stem-ssRNA junction (Han et al. 2006, Cell 125, 887-901, 887-901).

As used herein, a “pre-miRNA” molecule is an RNA molecule of about 100 to about 200 nucleotides, preferably about 100 to about 130 nucleotides which can adopt a secondary structure comprising a double stranded RNA stem and a single stranded RNA loop (also referred to as "hairpin") and further comprising the nucleotide sequence of the miRNA (and its complement sequence) in the double stranded RNA stem. According to a specific embodiment, the miRNA and its complement are located about 10 to about 20 nucleotides from the free ends of the miRNA double stranded RNA stem. The length and sequence of the single stranded loop region are not critical and may vary considerably, e.g. between 30 and 50 nt in length. The complementarity between the miRNA and its complement need not be perfect and about 1 to 3 bulges of unpaired nucleotides can be tolerated. The secondary structure adopted by an RNA molecule can be predicted by computer algorithms conventional in the art such as mFOLD. The particular strand of the double stranded RNA stem from the pre-miRNA which is released by DCL activity and loaded onto the RISC complex is determined by the degree of complementarity at the 5′ end, whereby the strand which at its 5′ end is the least involved in hydrogen bounding between the nucleotides of the different strands of the cleaved dsRNA stem is loaded onto the RISC complex and will determine the sequence specificity of the target RNA molecule degradation. However, if empirically the miRNA molecule from a particular synthetic pre-miRNA molecule is not functional (because the “wrong” strand is loaded on the RISC complex), it will be immediately evident that this problem can be solved by exchanging the position of the miRNA molecule and its complement on the respective strands of the dsRNA stem of the pre-miRNA molecule. As is known in the art, binding between A and U involving two hydrogen bounds, or G and U involving two hydrogen bounds is less strong that between G and C involving three hydrogen bounds. Exemplary hairpin sequences are provided in Tables 1, 3 and 4, below.

Naturally occurring miRNA molecules may be comprised within their naturally occurring pre-miRNA molecules but they can also be introduced into existing pre-miRNA molecule scaffolds by exchanging the nucleotide sequence of the miRNA molecule normally processed from such existing pre-miRNA molecule for the nucleotide sequence of another miRNA of interest. The scaffold of the pre-miRNA can also be completely synthetic. Likewise, synthetic miRNA molecules may be comprised within, and processed from, existing pre-miRNA molecule scaffolds or synthetic pre-miRNA scaffolds. Some pre-miRNA scaffolds may be preferred over others for their efficiency to be correctly processed into the designed microRNAs, particularly when expressed as a chimeric gene wherein other DNA regions, such as untranslated leader sequences or transcription termination and polyadenylation regions are incorporated in the primary transcript in addition to the pre-microRNA.

According to the present teachings, the miRNA molecules may be naturally occurring or synthetic.

Thus, the present teachings contemplate expressing an exogenous polynucleotide having a nucleic acid sequence at least 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 % 99 % or 100 % identical to SEQ ID NOs1-10, 23-37, 57-449, provided that they regulate nitrogen use efficiency.

Alternatively or additionally, the present teachings contemplate expressing an exogenous polynucleotide having a nucleic acid sequence at least 65%, 50 %, 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 % 99 % or 100 % identical to SEQ ID NOs. 1-10, 21 and 22 (mature and precursors Tables 1 and 3, and Figures 2A-H representing the core maize genes), provided that they regulate nitrogen use efficiency.

Tables 1 and 3 below illustrates exemplary miRNA sequences and precursors thereof which over expression are associated with modulation of nitrogen use efficiency.

The present invention envisages the use of homologous and orthologous sequences of the above miRNA molecules. At the precursor level use of homologous sequences can be done to a much broader extend. Thus, in such precursor sequences the degree of homology may be lower in all those sequences not including the mature miRNA segment therein.

As used herein, the phrase "stem-loop precursor" refers to stem loop precursor RNA structure from which the miRNA can be processed.

Pre-microRNA molecules are typically processed from pri-microRNA molecules (primary transcripts). The single stranded RNA segments flanking the pre-microRNA are important for processing of the pri-miRNA into the pre-miRNA. The cleavage site appears to be determined by the distance from the stem-ssRNA junction (Han et al. 2006, Cell 125, 887-901, 887-901).

As used herein, a “pre-miRNA” molecule is an RNA molecule of about 100 to about 200 nucleotides, preferably about 100 to about 130 nucleotides which can adopt a secondary structure comprising a double stranded RNA stem and a single stranded RNA loop (also referred to as "hairpin") and further comprising the nucleotide sequence of the miRNA (and its complement sequence) in the double stranded RNA stem. According to a specific embodiment, the miRNA and its complement are located about 10 to about 20 nucleotides from the free ends of the miRNA double stranded RNA stem. The length and sequence of the single stranded loop region are not critical and may vary considerably, e.g. between 30 and 50 nt in length. The complementarity between the miRNA and its complement need not be perfect and about 1 to 3 bulges of unpaired nucleotides can be tolerated. The secondary structure adopted by an RNA molecule can be predicted by computer algorithms conventional in the art such as mFOLD. The particular strand of the double stranded RNA stem from the pre-miRNA which is released by DCL activity and loaded onto the RISC complex is determined by the degree of complementarity at the 5′ end, whereby the strand which at its 5′ end is the least involved in hydrogen bounding between the nucleotides of the different strands of the cleaved dsRNA stem is loaded onto the RISC complex and will determine the sequence specificity of the target RNA molecule degradation. However, if empirically the miRNA molecule from a particular synthetic pre-miRNA molecule is not functional (because the “wrong” strand is loaded on the RISC complex), it will be immediately evident that this problem can be solved by exchanging the position of the miRNA molecule and its complement on the respective strands of the dsRNA stem of the pre-miRNA molecule. As is known in the art, binding between A and U involving two hydrogen bounds, or G and U involving two hydrogen bounds is less strong that between G and C involving three hydrogen bounds.

Thus, according to a specific embodiment, the exogenous polynucleotide encodes a stem-loop precursor of the nucleic acid sequence. Such a stem-loop precursor can be at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 85 %, at least about 90 %, at least about 95 % or more identical to SEQ ID NOs: 21-22, 38-52, 1209, 1211, 1212, 454-846, 53-56, 1209 (homologs precursor Tables 1 and 3 and Figures 2A-H), provided that it regulates nitrogen use efficiency.

Identity (e.g., percent identity) can be determined using any homology comparison software, including for example, the BlastN software of the National Center of Biotechnology Information (NCBI) such as by using default parameters.

Homology (e.g., percent homology, identity + similarity) can be determined using any homology comparison software, including for example, the TBLASTN software of the National Center of Biotechnology Information (NCBI) such as by using default parameters.

According to some embodiments of the invention, the term “homology” or “homologous” refers to identity of two or more nucleic acid sequences; or identity of two or more amino acid sequences.

Homologous sequences include both orthologous and paralogous sequences. The term “paralogous” relates to gene-duplications within the genome of a species leading to paralogous genes. The term “orthologous” relates to homologous genes in different organisms due to ancestral relationship.

One option to identify orthologues in monocot plant species is by performing a reciprocal blast search. This may be done by a first blast involving blasting the sequence-of-interest against any sequence database, such as the publicly available NCBI database which may be found at: Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov. The blast results may be filtered. The full-length sequences of either the filtered results or the non-filtered results are then blasted back (second blast) against the sequences of the organism from which the sequence-of-interest is derived. The results of the first and second blasts are then compared. An orthologue is identified when the sequence resulting in the highest score (best hit) in the first blast identifies in the second blast the query sequence (the original sequence-of-interest) as the best hit. Using the same rational a paralogue (homolog to a gene in the same organism) is found. In case of large sequence families, the ClustalW program may be used [Hypertext Transfer Protocol://World Wide Web (dot) ebi (dot) ac (dot) uk/Tools/clustalw2/index (dot) html], followed by a neighbor-joining tree (Hypertext Transfer Protocol://en (dot) wikipedia (dot) org/wiki/Neighbor-joining) which helps visualizing the clustering.

Interestingly, while screening for RNAi regulatory sequences, the present inventors have identified a number of miRNA sequences which have never been described before.

Thus, according to an aspect of the invention there is provided an isolated polynucleotide having a nucleic acid sequence at least 80 %, 85 % or preferably 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 % 99 % or 100 % identical to SEQ ID NO: 6, 7, 9, 1209, 1210, 1211, 1212 (Table 1 predicted both upregulated and downregulated), wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of a plant.

According to a specific embodiment, the isolated polynucleotide encodes a stem-loop precursor of the nucleic acid sequence.

According to a specific embodiment, the stem-loop precursor is at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 85 %, at least about 90 %, at least about 95 % or more identical to the precursor sequence of SEQ ID NOs: 21, 22, 38-52, 1209, 1211, 1212, 454-846 and 53-56, 1209 (predicted stem and loop), provided that it regulates nitrogen use efficiency.

As mentioned, the present inventors have also identified RNAi sequences which are down regulated under nitrogen limiting conditions.

Thus, according to an aspect of the invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a gene encoding a miRNA molecule having a nucleic acid sequence at least 80 %, 85 % or preferably 90 %, 95 % or even 100 % identical to the sequence selected from the group consisting of SEQ ID NOs: 4, 1-3, 5, 53-56, 1209, 57-449, 454-846 (Tables 1 and 4 down-regulated), thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant

There are various approaches to down regulate miRNA sequences.

As used herein the term "down-regulation" refers to reduced activity or expression of the miRNA (at least 10 %, 20 %, 30 %, 50 %, 60 %, 70 %, 80 %, 90 % or 100 % reduction in activity or expression) as compared to its activity or expression in a plant of the same species and the same developmental stage not expressing the exogenous polynucleotide.

Nucleic acid agents that down-regulate miR activity include, but are not limited to, a target mimic, a micro-RNA resistant gene and a miRNA inhibitor.

The target mimic or micro-RNA resistant target is essentially complementary to the microRNA provided that one or more of following mismatches are allowed:

(a) a mismatch between the nucleotide at the 5' end of the microRNA and the corresponding nucleotide sequence in the target mimic or micro-RNA resistant target;

(b) a mismatch between any one of the nucleotides in position 1 to position 9 of the microRNA and the corresponding nucleotide sequence in the target mimic or micro-RNA resistant target; or

(c) three mismatches between any one of the nucleotides in position 12 to position 21 of the microRNA and the corresponding nucleotide sequence in the target mimic or micro-RNA resistant target provided that there are no more than two consecutive mismatches.

The target mimic RNA is essentially similar to the target RNA modified to render it resistant to miRNA induced cleavage, e.g. by modifying the sequence thereof such that a variation is introduced in the nucleotide of the target sequence complementary to the nucleotides 10 or 11 of the miRNA resulting in a mismatch.

Alternatively, a microRNA-resistant target may be implemented. Thus, a silent mutation may be introduced in the microRNA binding site of the target gene so that the DNA and resulting RNA sequences are changed in a way that prevents microRNA binding, but the amino acid sequence of the protein is unchanged. Thus, a new sequence can be synthesized instead of the existing binding site, in which the DNA sequence is changed, resulting in lack of miRNA binding to its target.

Tables 10 and 11 below provide non-limiting examples of target mimics and target resistant sequences that can be used to down-regulate the activity of the miRs of the invention.

According to a specific embodiment, the target mimic or micro-RNA resistant target is linked to the promoter naturally associated with the pre-miRNA recognizing the target gene and introduced into the plant cell. In this way, the miRNA target mimic or micro-RNA resistant target RNA will be expressed under the same circumstances as the miRNA and the target mimic or micro-RNA resistant target RNA will substitute for the non-target mimic/micro-RNA resistant target RNA degraded by the miRNA induced cleavage.

Non-functional miRNA alleles or miRNA resistant target genes may also be introduced by homologous recombination to substitute the miRNA encoding alleles or miRNA sensitive target genes.

Recombinant expression is effected by cloning the nucleic acid of interest (e.g., miRNA, target gene, silencing agent etc) into a nucleic acid expression construct under the expression of a plant promoter, as further described hereinbelow.

In other embodiments of the invention, synthetic single stranded nucleic acids are used as miRNA inhibitors. A miRNA inhibitor is typically between about 17 to 25 nucleotides in length and comprises a 5' to 3' sequence that is at least 90 % complementary to the 5' to 3' sequence of a mature miRNA. In certain embodiments, a miRNA inhibitor molecule is 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length, or any range derivable therein. Moreover, a miRNA inhibitor has a sequence (from 5' to 3') that is or is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.1, 99.2, 99.3, 99.4, 99.5, 99.6, 99.7, 99.8, 99.9 or 100 % complementary, or any range derivable therein, to the 5' to 3' sequence of a mature miRNA, particularly a mature, naturally occurring miRNA.

While further reducing the present invention to practice, the present inventors have identified gene targets for the differentially expressed miRNA molecules. It is therefore contemplated, that gene targets of those miRNAs that are down regulated during stress should be overexpressed in order to confer tolerance, while gene targets of those miRNAs that are up regulated during stress should be downregulated in the plant in order to confer tolerance.

Thus, according to an aspect of the invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide having an amino acid sequence at least 80 %, 82 %, 84 %, 85 %, 86 %, 88 %, 90 %, 92 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or 100 % homologous to SEQ ID NOs: 927-1021 (gene targets of down regulated miRNAs, see Table 6), wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

Nucleic acid sequences (also referred to herein as polynucleotides) of the polypeptides of some embodiments of the invention may be optimized for expression in a specific plant host. Examples of such sequence modifications include, but are not limited to, an altered G/C content to more closely approach that typically found in the plant species of interest, and the removal of codons atypically found in the plant species commonly referred to as codon optimization.

The phrase "codon optimization" refers to the selection of appropriate DNA nucleotides for use within a structural gene or fragment thereof that approaches codon usage within the plant of interest. Therefore, an optimized gene or nucleic acid sequence refers to a gene in which the nucleotide sequence of a native or naturally occurring gene has been modified in order to utilize statistically-preferred or statistically-favored codons within the plant. The nucleotide sequence typically is examined at the DNA level and the coding region optimized for expression in the plant species determined using any suitable procedure, for example as described in Sardana *et al.* (1996, Plant Cell Reports 15:677-681). In this method, the standard deviation of codon usage, a measure of codon usage bias, may be calculated by first finding the squared proportional deviation of usage of each codon of the native gene relative to that of highly expressed plant genes, followed by a calculation of the average squared deviation. The formula used is: 1 SDCU = n = 1 N [(Xn - Yn) / Yn] 2 / N, where Xn refers to the frequency of usage of codon n in highly expressed plant genes, where Yn to the frequency of usage of codon n in the gene of interest and N refers to the total number of codons in the gene of interest. A table of codon usage from highly expressed genes of dicotyledonous plants is compiled using the data of Murray *et al.* (1989, Nuc Acids Res. 17:477-498).

One method of optimizing the nucleic acid sequence in accordance with the preferred codon usage for a particular plant cell type is based on the direct use, without performing any extra statistical calculations, of codon optimization tables such as those provided on-line at the Codon Usage Database through the NIAS (National Institute of Agrobiological Sciences) DNA bank in Japan (www.kazusa.or.jp/codon/). The Codon Usage Database contains codon usage tables for a number of different species, with each codon usage table having been statistically determined based on the data present in Genbank.

By using the above tables to determine the most preferred or most favored codons for each amino acid in a particular species (for example, rice), a naturally-occurring nucleotide sequence encoding a protein of interest can be codon optimized for that particular plant species. This is effected by replacing codons that may have a low statistical incidence in the particular species genome with corresponding codons, in regard to an amino acid, that are statistically more favored. However, one or more less-favored codons may be selected to delete existing restriction sites, to create new ones at potentially useful junctions (5' and 3' ends to add signal peptide or termination cassettes, internal sites that might be used to cut and splice segments together to produce a correct full-length sequence), or to eliminate nucleotide sequences that may negatively effect mRNA stability or expression.

The naturally-occurring encoding nucleotide sequence may already, in advance of any modification, contain a number of codons that correspond to a statistically-favored codon in a particular plant species. Therefore, codon optimization of the native nucleotide sequence may comprise determining which codons, within the native nucleotide sequence, are not statistically-favored with regards to a particular plant, and modifying these codons in accordance with a codon usage table of the particular plant to produce a codon optimized derivative. A modified nucleotide sequence may be fully or partially optimized for plant codon usage provided that the protein encoded by the modified nucleotide sequence is produced at a level higher than the protein encoded by the corresponding naturally occurring or native gene. Construction of synthetic genes by altering the codon usage is described in for example PCT Patent Application 93/07278.

Target genes which are contemplated according to the present teachings are provided in the polynucleotide sequences which comprise nucleic acid sequences as set forth in the maize polynucleotides listed in Tables 5 and 6). However the present teachings also relate to orthologs or homologs at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 85 %, at least about 90 %, or at least about 95 % or more identical or similar to SEQ ID NO: 895-926 or 1022-1090 (polynucleotides listed in Tables 5 and 6). Parameters for determining the level of identity are provided hereinbelow.

Alternatively or additionally, target genes which are contemplated according to the present teachings are provided in the polypeptide sequences which comprise amino acid sequences as set forth the maize polypeptides of Tables 5 and 6). However the present teachings also relate to of orthologs or homologs at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 85 %, at least about 90 %, or at least about 95 % or more identical or similar to SEQ ID NO: 854-894 or 927-1021 (Tables 5 and 6).

Homology (e.g., percent homology, identity + similarity) can be determined using any homology comparison software, including for example, the TBLASTN software of the National Center of Biotechnology Information (NCBI) such as by using default parameters, when starting from a polypeptide sequence; or the tBLASTX algorithm (available via the NCBI) such as by using default parameters, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database.

According to some embodiments of the invention, the term "homology" or "homologous" refers to identity of two or more nucleic acid sequences; or identity of two or more amino acid sequences.

Homologous sequences include both orthologous and paralogous sequences. The term "paralogous" relates to gene-duplications within the genome of a species leading to paralogous genes. The term "orthologous" relates to homologous genes in different organisms due to ancestral relationship.

One option to identify orthologues in monocot plant species is by performing a reciprocal blast search. This may be done by a first blast involving blasting the sequence-of-interest against any sequence database, such as the publicly available NCBI database which may be found at: Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov. The blast results may be filtered. The full-length sequences of either the filtered results or the non-filtered results are then blasted back (second blast) against the sequences of the organism from which the sequence-of-interest is derived. The results of the first and second blasts are then compared. An orthologue is identified when the sequence resulting in the highest score (best hit) in the first blast identifies in the second blast the query sequence (the original sequence-of-interest) as the best hit. Using the same rational a paralogue (homolog to a gene in the same organism) is found. In case of large sequence families, the ClustalW program may be used [Hypertext Transfer Protocol://World Wide Web (dot) ebi (dot) ac (dot) uk/Tools/clustalw2/index (dot) html], followed by a neighbor-joining tree (Hypertext Transfer Protocol://en (dot) wikipedia (dot) org/wiki/Neighbor-joining) which helps visualizing the clustering.

As mentioned the present inventors have also identified genes which down-regulation may be done in order to improve their NUE, biomass, vigor, yield and abiotic stress tolerance.

Thus, according to an aspect of the invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 %, 85 %, 90 %, 95 %, or 100 % homologous to SEQ ID NOs: 854-894 (polypeptides of Table 5), wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

Down regulation of activity or expression is by at least 10 %, 20 %, 30 %, 40 %, 50 %, 60 %, 70 %, 80 %, 90 % or even complete (100 %) loss of activity or expression. Assays for measuring gene expression can be effected at the protein level (e.g,. Western blot, ELISA) or at the mRNA level such as by RT-PCR.

According to a specific embodiment the amino acid sequence of the target gene is as set forth in SEQ ID NOs: 854-894 of Table 5.

Alternatively or additionally, the amino acid sequence of the target gene is encoded by a polynucleotide sequence as set forth in SEQ ID NOs: 895-926 of Table 5.

Examples of polynucleotide downregulating agents that inhibit (also referred to herein as inhibitors or nucleic acid agents) the expression of a target gene are given below.

1. Polynucleotide-Based Inhibition of Gene Expression.

It will be appreciated, that any of these methods when specifically referring to downregulating expression/activity of the target genes can be used, at least in part, to downregulate expression or activity of endogenous RNA molecules.

i. Sense Suppression/Cosuppression

In some embodiments of the invention, inhibition of the expression of target gene may be obtained by sense suppression or cosuppression. For cosuppression, an expression cassette is designed to express an RNA molecule corresponding to all or part of a messenger RNA encoding a target gene in the "sense" orientation. Over-expression of the RNA molecule can result in reduced expression of the native gene. Accordingly, multiple plant lines transformed with the cosuppression expression cassette are screened to identify those that show the greatest inhibition of target gene expression.

The polynucleotide used for cosuppression may correspond to all or part of the sequence encoding the target gene, all or part of the 5' and/or 3' untranslated region of a target transcript, or all or part of both the coding sequence and the untranslated regions of a transcript encoding the target gene. In some embodiments where the polynucleotide comprises all or part of the coding region for the target gene, the expression cassette is designed to eliminate the start codon of the polynucleotide so that no protein product will be transcribed.

Cosuppression may be used to inhibit the expression of plant genes to produce plants having undetectable protein levels for the proteins encoded by these genes. See, for example, Broin, et al., (2002) Plant Cell 15:1517-1532. Cosuppression may also be used to inhibit the expression of multiple proteins in the same plant. Methods for using cosuppression to inhibit the expression of endogenous genes in plants are described in Flavell, et al., (1995) Proc. Natl. Acad. Sci. USA 91:3590-3596; Jorgensen, et al.,

(1996) Plant Mol. Biol. 31:957-973; Johansen and Carrington, (2001) Plant Physiol. 126:930-938; Broin, et al., (2002) Plant Cell 15:1517-1532; Stoutjesdijk, et al., (2002) Plant Physiol. 129:1723-1731; Yu, et al., (2003) Phytochemistry 63:753-763; and U.S. Pat. Nos. 5,035,323, 5,283,185 and 5,952,657; each of which is herein incorporated by reference. The efficiency of cosuppression may be increased by including a poly-dt region in the expression cassette at a position 3' to the sense sequence and 5' of the polyadenylation signal. See, US Patent Publication Number 20020058815, herein incorporated by reference. Typically, such a nucleotide sequence has substantial sequence identity to the sequence of the transcript of the endogenous gene, optimally greater than about 65 % sequence identity, more optimally greater than about 85 % sequence identity, most optimally greater than about 95 % sequence identity. See, U.S. Pat. Nos. 5,283,185 and 5,035,323; herein incorporated by reference.

Transcriptional gene silencing (TGS) may be accomplished through use of hpRNA constructs wherein the inverted repeat of the hairpin shares sequence identity with the promoter region of a gene to be silenced. Processing of the hpRNA into short RNAs which can interact with the homologous promoter region may trigger degradation or methylation to result in silencing. (Aufsatz, et al., (2002) PNAS 99(4):16499-16506; Mette, et al., (2000) EMBO J. 19(19):5194-5201)

ii. Antisense Suppression

In some embodiments of the invention, inhibition of the expression of the target gene may be obtained by antisense suppression. For antisense suppression, the expression cassette is designed to express an RNA molecule complementary to all or part of a messenger RNA encoding the target gene. Over-expression of the antisense RNA molecule can result in reduced expression of the native gene. Accordingly, multiple plant lines transformed with the antisense suppression expression cassette are screened to identify those that show the greatest inhibition of target gene expression.

The polynucleotide for use in antisense suppression may correspond to all or part of the complement of the sequence encoding the target gene, all or part of the complement of the 5' and/or 3' untranslated region of the target gene transcript, or all or part of the complement of both the coding sequence and the untranslated regions of a transcript encoding the target gene. In addition, the antisense polynucleotide may be fully complementary (i.e., 100% identical to the complement of the target sequence) or partially complementary (i.e., less than 100% identical to the complement of the target sequence) to the target sequence. Antisense suppression may be used to inhibit the expression of multiple proteins in the same plant. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides, 100 nucleotides, 200 nucleotides, 300, 500, 550, 500, 550 or greater may be used. Methods for using antisense suppression to inhibit the expression of endogenous genes in plants are described, for example, in Liu, et al., (2002) Plant Physiol. 129:1732-1753 and U.S. Pat. No. 5,759,829, which is herein incorporated by reference. Efficiency of antisense suppression may be increased by including a poly-dt region in the expression cassette at a position 3' to the antisense sequence and 5' of the polyadenylation signal. See, US Patent Publication Number 20020058815.

iii. Double-Stranded RNA Interference

In some embodiments of the invention, inhibition of the expression of a target gene may be obtained by double-stranded RNA (dsRNA) interference. For dsRNA interference, a sense RNA molecule like that described above for cosuppression and an antisense RNA molecule that is fully or partially complementary to the sense RNA molecule are expressed in the same cell, resulting in inhibition of the expression of the corresponding endogenous messenger RNA.

Expression of the sense and antisense molecules can be accomplished by designing the expression cassette to comprise both a sense sequence and an antisense sequence. Alternatively, separate expression cassettes may be used for the sense and antisense sequences. Multiple plant lines transformed with the dsRNA interference expression cassette or expression cassettes are then screened to identify plant lines that show the greatest inhibition of target gene expression. Methods for using dsRNA interference to inhibit the expression of endogenous plant genes are described in Waterhouse, et al., (1998) Proc. Natl. Acad. Sci. USA 95:13959-13965, Liu, et al., (2002) Plant Physiol. 129:1732-1753, and WO 99/59029, WO 99/53050, WO 99/61631, and WO 00/59035;

iv. Hairpin RNA Interference and Intron-Containing Hairpin RNA Interference

In some embodiments of the invention, inhibition of the expression of one or more target gene may be obtained by hairpin RNA (hpRNA) interference or intron-containing hairpin RNA (ihpRNA) interference. These methods are highly efficient at downregulating the expression of endogenous genes. See, Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38 and the references cited therein.

For hpRNA interference, the expression cassette is designed to express an RNA molecule that hybridizes with itself to form a hairpin structure that comprises a single-stranded loop region and a base-paired stem. The base-paired stem region comprises a sense sequence corresponding to all or part of the endogenous messenger RNA encoding the gene whose expression is to be inhibited, and an antisense sequence that is fully or partially complementary to the sense sequence. Thus, the base-paired stem region of the molecule generally determines the specificity of the RNA interference. hpRNA molecules are highly efficient at inhibiting the expression of endogenous genes, and the RNA interference they induce is inherited by subsequent generations of plants. See, for example, Chuang and Meyerowitz, (2000) Proc. Natl. Acad. Sci. USA 97:5985-5990; Stoutjesdijk, et al., (2002) Plant Physiol. 129:1723-1731; and Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38. Methods for using hpRNA interference to inhibit or silence the expression of genes are described, for example, in Chuang and Meyerowitz, (2000) Proc. Natl. Acad. Sci. USA 97:5985-5990; Stoutjesdijk, et al., (2002) Plant Physiol. 129:1723-1731; Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38; Pandolfini, et al., BMC Biotechnology 3:7, and US Patent Publication Number 20030175965; each of which is herein incorporated by reference. A transient assay for the efficiency of hpRNA constructs to silence gene expression in vivo has been described by Panstruga, et al., (2003) Mol. Biol. Rep. 30:135-150, herein incorporated by reference.

For ihpRNA, the interfering molecules have the same general structure as for hpRNA, but the RNA molecule additionally comprises an intron that is capable of being spliced in the cell in which the ihpRNA is expressed. The use of an intron minimizes the size of the loop in the hairpin RNA molecule following splicing, and this increases the efficiency of interference. See, for example, Smith, et al., (2000) Nature 507:319-320. In fact, Smith, et al., show 100 % suppression of endogenous gene expression using ihpRNA-mediated interference. Methods for using ihpRNA interference to inhibit the expression of endogenous plant genes are described, for example, in Smith, et al., (2000) Nature 507:319-320; Wesley, et al., (2001) Plant J. 27:584, 1-3, 590; Wang and

Waterhouse, (2001) Curr. Opin. Plant Biol. 5:156-150; Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38; Helliwell and Waterhouse, (2003) Methods 30:289-295, and US Patent Publication Number 20030180955, each of which is herein incorporated by reference.

The expression cassette for hpRNA interference may also be designed such that the sense sequence and the antisense sequence do not correspond to an endogenous RNA. In this embodiment, the sense and antisense sequence flank a loop sequence that comprises a nucleotide sequence corresponding to all or part of the endogenous messenger RNA of the target gene. Thus, it is the loop region that determines the specificity of the RNA interference. See, for example, WO 02/00905, herein incorporated by reference.

v. Amplicon-Mediated Interference

Amplicon expression cassettes comprise a plant virus-derived sequence that contains all or part of the target gene but generally not all of the genes of the native virus. The viral sequences present in the transcription product of the expression cassette allow the transcription product to direct its own replication. The transcripts produced by the amplicon may be either sense or antisense relative to the target sequence (i.e., the messenger RNA for target gene). Methods of using amplicons to inhibit the expression of endogenous plant genes are described, for example, in Angell and Baulcombe, (1997) EMBO J. 16:3675-3685, Angell and Baulcombe, (1999) Plant J. 20:357-362, and U.S. Pat. No. 6,656,805, each of which is herein incorporated by reference.

vi. Ribozymes

In some embodiments, the polynucleotide expressed by the expression cassette of the invention is catalytic RNA or has ribozyme activity specific for the messenger RNA of target gene. Thus, the polynucleotide causes the degradation of the endogenous messenger RNA, resulting in reduced expression of the target gene. This method is described, for example, in U.S. Pat. No. 5,987,071, herein incorporated by reference.

2. Gene Disruption

In some embodiments of the present invention, the activity of a miRNA or a target gene is reduced or eliminated by disrupting the gene encoding the target polypeptide. The gene encoding the target polypeptide may be disrupted by any method known in the art. For example, in one embodiment, the gene is disrupted by transposon tagging. In another embodiment, the gene is disrupted by mutagenizing plants using random or targeted mutagenesis, and selecting for plants that have reduced response regulator activity.

Any of the nucleic acid agents described herein (for overexpression or downregulation of either the target gene of the miRNA) can be provided to the plant as naked RNA or expressed from a nucleic acid expression construct, where it is operaly linked to a regulatory sequence.

According to a specific embodiment of the invention, there is provided a nucleic acid construct comprising a nucleic acid sequence encoding a the nucleic acid agent (e.g., miRNA or a precursor thereof as described herein, gene targetm or silencing agent), said nucleic acid sequence being under a transcriptional control of a regulatory sequence such as a tissue specific promoter.

An exemplary nucleic acid construct which can be used for plant transformation include, the pORE E2 binary vector (Figure 1) in which the relevant nucleic acid sequence is ligated under the transcriptional control of a promoter.

A coding nucleic acid sequence is "operably linked" or "transcriptionally linked to a regulatory sequence (e.g., promoter)" if the regulatory sequence is capable of exerting a regulatory effect on the coding sequence linked thereto. Thus, the regulatory sequence controls the transcription of the miRNA or precursor thereof, gene target or silencing agent.

The term “regulatory sequence”, as used herein, means any DNA, that is involved in driving transcription and controlling (i.e., regulating) the timing and level of transcription of a given DNA sequence, such as a DNA coding for a miRNA, precursor or inhibitor of same. For example, a 5′ regulatory region (or “promoter region”) is a DNA sequence located upstream (i.e., 5′) of a coding sequence and which comprises the promoter and the 5′-untranslated leader sequence. A 3′ regulatory region is a DNA sequence located downstream (i.e., 3′) of the coding sequence and which comprises suitable transcription termination (and/or regulation) signals, including one or more polyadenylation signals.

For the purpose of the invention, the promoter is a plant-expressible promoter. As used herein, the term “plant-expressible promoter” means a DNA sequence which is capable of controlling (initiating) transcription in a plant cell. This includes any promoter of plant origin, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell, i.e., certain promoters of viral or bacterial origin Thus, any suitable promoter sequence can be used by the nucleic acid construct of the present invention. According to some embodiments of the invention, the promoter is a constitutive promoter, a tissue-specific promoter or an inducible promoter (e.g. an abiotic stress-inducible promoter).

Suitable constitutive promoters include, for example, hydroperoxide lyase (HPL) promoter, CaMV 35S promoter (Odell et al, Nature 313:810-812, 1985); Arabidopsis At6669 promoter (see PCT Publication No. WO04081173A2); Arabidopsis new At6669 promoter; maize Ubi 1 (Christensen et al., Plant Sol. Biol. 18:675-689, 1992); rice actin (McElroy et al., Plant Cell 2:163-171, 1990); pEMU (Last et al, Theor. Appl. Genet. 81 :584, 1-3, 588, 1991); CaMV 19S (Nilsson et al, Physiol. Plant 100:456-462, 1997); GOS2 (de Pater et al, Plant J Nov;2(6):837-44, 1992); ubiquitin (Christensen et al, Plant Mol. Biol. 18: 675-689, 1992); Rice cyclophilin (Bucholz et al, Plant Mol Biol. 25(5):837-43, 1994); Maize H3 histone (Lepetit et al, Mol. Gen. Genet. 231 : 276-285, 1992); Actin 2 (An et al, Plant J. 10(l);107-121, 1996) and Synthetic Super MAS (Ni et al., The Plant Journal 7: 661-76, 1995). Other constitutive promoters include those in U.S. Pat. Nos. 5,659,026, 5,608,149; 5.608,144; 5,604,121; 5.569,597: 5.466,785; 5,399,680; 5,268,463; and 5,608,142.

Suitable tissue-specific promoters include, but not limited to, leaf-specific promoters [such as described, for example, by Yamamoto et al., Plant J. 12:255-265, 1997; Kwon et al., Plant Physiol. 105:357-67, 1994; Yamamoto et al., Plant Cell Physiol. 35:773-778, 1994; Gotor et al., Plant J. 3:509-18, 1993; Orozco et al., Plant Mol. Biol. 23:1129-1138, 1993; and Matsuoka et al., Proc. Natl. Acad. Sci. USA 90:9586-9590, 1993], seed-preferred promoters [e.g., from seed specific genes (Simon, et al., Plant Mol. Biol. 5. 191, 1985; Scofield, et al., J. Biol. Chem. 262: 12202, 1987; Baszczynski, et al., Plant Mol. Biol. 14: 633, 1990), Brazil Nut albumin (Pearson' et al., Plant Mol. Biol. 18: 235- 245, 1992), legumin (Ellis, et al. Plant Mol. Biol. 10: 203-214, 1988), Glutelin (rice) (Takaiwa, et al., Mol. Gen. Genet. 208: 15-22, 1986; Takaiwa, et al., FEBS Letts. 221 : 43-47, 1987), Zein (Matzke et al., Plant Mol Biol, 143)323-32 1990), napA (Stalberg, et al., Planta 199: 515-519, 1996), Wheat SPA (Albanietal, Plant Cell, 9: 171- 184, 1997), sunflower oleosin (Cummins, etal, Plant

Mol. Biol. 19: 873- 876, 1992)], endosperm specific promoters [e.g., wheat LMW and HMW, glutenin-1 (Mol Gen Genet 216:81-90, 1989; NAR 17:461-2), wheat a, b and g gliadins (EMBO3: 1409-15, 1984), Barley ltrl promoter, barley Bl, C, D hordein (Theor Appl Gen 98:1253-62, 1999; Plant J 4:343-55, 1993; Mol Gen Genet 250:750- 60, 1996), Barley DOF (Mena et al., The Plant Journal, 116(1): 53- 62, 1998), Biz2 (EP99106056.7), Synthetic promoter (Vicente-Carbajosa et al., Plant J. 13: 629-640, 1998), rice prolamin NRP33, rice -globulin Glb-I (Wu et al., Plant Cell Physiology 39(8) 885- 889, 1998), rice alpha-globulin REB/OHP-1 (Nakase et al. Plant Mol. Biol. 33: 513-S22, 1997), rice ADP-glucose PP (Trans Res 6:157-68, 1997), maize ESR gene family (Plant J 12:235-46, 1997), sorghum gamma- kafirin (PMB 32:1029-35, 1996); e.g., the Napin promoter], embryo specific promoters [e.g., rice OSHl (Sato et al, Proc. Natl. Acad. Sci. USA, 93: 8117-8122), KNOX (Postma-Haarsma et al, Plant Mol. Biol. 39:257-71, 1999), rice oleosin (Wu et at, J. Biochem., 123:386, 1998)], and flower-specific promoters [e.g., AtPRP4, chalene synthase (chsA) (Van der Meer, et al., Plant Mol. Biol. 15, 95-109, 1990), LAT52 (Twell et al., Mol. Gen Genet. 217:240-245; 1989), apetala- 3]. Also contemplated are root-specific promoters such as the ROOTP promoter described in Vissenberg K, et al. Plant Cell Physiol. 2005 January; 46(1):192-200.

The nucleic acid construct of some embodiments of the invention can further include an appropriate selectable marker and/or an origin of replication.

The nucleic acid construct of some embodiments of the invention can be utilized to stably or transiently transform plant cells. In stable transformation, the exogenous polynucleotide is integrated into the plant genome and as such it represents a stable and inherited trait. In transient transformation, the exogenous polynucleotide is expressed by the cell transformed but it is not integrated into the genome and as such it represents a transient trait.

When naked RNA or DNA is introduced into a cell, the polynucleotides may be synthesized using any method known in the art, including either enzymatic syntheses or solid-phase syntheses. These are especially useful in the case of short polynucleotide sequences with or without modifications as explained above. Equipment and reagents for executing solid-phase synthesis are commercially available from, for example, Applied Biosystems. Any other means for such synthesis may also be employed; the actual synthesis of the oligonucleotides is well within the capabilities of one skilled in the art and can be accomplished via established methodologies as detailed in, for example: Sambrook, J. and Russell, D. W. (2001), "Molecular Cloning: A Laboratory Manual"; Ausubel, R. M. et al., eds. (1994, 1989), "Current Protocols in Molecular Biology," Volumes I-III, John Wiley & Sons, Baltimore, Maryland; Perbal, B. (1988), "A Practical Guide to Molecular Cloning," John Wiley & Sons, New York; and Gait, M. J., ed. (1984), "Oligonucleotide Synthesis"; utilizing solid-phase chemistry, e.g. cyanoethyl phosphoramidite followed by deprotection, desalting, and purification by, for example, an automated trityl-on method or HPLC.

There are various methods of introducing foreign genes into both monocotyledonous and dicotyledonous plants (Potrykus, L, Annu. Rev. Plant. Physiol, Plant. Mol. Biol. (1991) 42:205-225; Shimamoto et al., Nature (1989) 338:274-276).

The principle methods of causing stable integration of exogenous DNA into plant genomic DNA include two main approaches:

(i) Agrobacterium-mediated gene transfer (e.g., T-DNA using Agrobacterium tumefaciens or Agrobacterium rhizogenes); see for example, Klee et al. (1987) Annu. Rev. Plant Physiol. 38:467-486; Klee and Rogers in Cell Culture and Somatic Cell Genetics of Plants, Vol. 6, Molecular Biology of Plant Nuclear Genes, eds. Schell, J., and Vasil, L. K., Academic Publishers, San Diego, Calif. (1989) p. 2- 25; Gatenby, in Plant Biotechnology, eds. Kung, S, and Arntzen, C. J., Butterworth Publishers, Boston, Mass. (1989) p. 93-112.

(ii) Direct DNA uptake: Paszkowski et al., in Cell Culture and Somatic Cell Genetics of Plants, Vol. 6, Molecular Biology of Plant Nuclear Genes eds. Schell, J., and Vasil, L. K., Academic Publishers, San Diego, Calif. (1989) p. 52-68; including methods for direct uptake of DNA into protoplasts, Toriyama, K. et al. (1988) Bio/Technology 6:1072-1074. DNA uptake induced by brief electric shock of plant cells: Zhang et al. Plant Cell Rep. (1988) 7:379-384. Fromm et al. Nature (1986) 319:791-793. DNA injection into plant cells or tissues by particle bombardment, Klein et al. Bio/Technology (1988) 6:559-563; McCabe et al. Bio/Technology (1988) 6:923-926; Sanford, Physiol. Plant. (1990) 79:206-209; by the use of micropipette systems: Neuhaus et al., Theor. Appl. Genet. (1987) 75:30-36; Neuhaus and Spangenberg, Physiol. Plant. (1990) 79:213-217; glass fibers or silicon carbide whisker transformation of cell cultures, embryos or callus tissue, U.S. Pat. No. 5,464,765 or by the direct incubation of DNA with germinating pollen, DeWet et al. in Experimental Manipulation of Ovule Tissue, eds. Chapman, G. P. and Mantell, S. H. and Daniels, W. Longman, London, (1985) p. 197-209; and Ohta, Proc. Natl. Acad. Sci. USA (1986) 83:715-719.

The Agrobacterium system includes the use of plasmid vectors that contain defined DNA segments that integrate into the plant genomic DNA. Methods of inoculation of the plant tissue vary depending upon the plant species and the Agrobacterium delivery system. A widely used approach is the leaf disc procedure which can be performed with any tissue explant that provides a good source for initiation of whole plant differentiation. See, e.g., Horsch et al. in Plant Molecular Biology Manual A5, Kluwer Academic Publishers, Dordrecht (1988) p. 1-9. A supplementary approach employs the Agrobacterium delivery system in combination with vacuum infiltration. The Agrobacterium system is especially viable in the creation of transgenic dicotyledonous plants.

According to a specific embodiment of the present invention, the exogenous polynucleotide is introduced into the plant by infecting the plant with a bacteria, such as using a floral dip transformation method (as described in further detail in Example 5, of the Examples section which follows).

There are various methods of direct DNA transfer into plant cells. In electroporation, the protoplasts are briefly exposed to a strong electric field. In microinjection, the DNA is mechanically injected directly into the cells using very small micropipettes. In microparticle bombardment, the DNA is adsorbed on microprojectiles such as magnesium sulfate crystals or tungsten particles, and the microprojectiles are physically accelerated into cells or plant tissues.

Following stable transformation plant propagation is exercised. The most common method of plant propagation is by seed. Regeneration by seed propagation, however, has the deficiency that due to heterozygosity there is a lack of uniformity in the crop, since seeds are produced by plants according to the genetic variances governed by Mendelian rules. Basically, each seed is genetically different and each will grow with its own specific traits. Therefore, it is preferred that the transformed plant be produced such that the regenerated plant has the identical traits and characteristics of the parent transgenic plant. For this reason it is preferred that the transformed plant be regenerated by micropropagation which provides a rapid, consistent reproduction of the transformed plants.

Micropropagation is a process of growing new generation plants from a single piece of tissue that has been excised from a selected parent plant or cultivar. The new generation plants which are produced are genetically identical to, and have all of the characteristics of, the original plant. Micropropagation allows mass production of quality plant material in a short period of time and offers a rapid multiplication of selected cultivars in the preservation of the characteristics of the original transgenic or transformed plant. The advantages of cloning plants are the speed of plant multiplication and the quality and uniformity of plants produced.

Micropropagation is a multi-stage procedure that requires alteration of culture medium or growth conditions between stages. Thus, the micropropagation process involves four basic stages: Stage one, initial tissue culturing; stage two, tissue culture multiplication; stage three, differentiation and plant formation; and stage four, greenhouse culturing and hardening. During stage one, initial tissue culturing, the tissue culture is established and certified contaminant- free. During stage two, the initial tissue culture is multiplied until a sufficient number of tissue samples are produced to meet production goals. During stage three, the tissue samples grown in stage two are divided and grown into individual plantlets. At stage four, the transformed plantlets are transferred to a greenhouse for hardening where the plants' tolerance to light is gradually increased so that it can be grown in the natural environment.

Although stable transformation is presently preferred, transient transformation of leaf cells, meristematic cells or the whole plant is also envisaged by the present invention.

Transient transformation can be effected by any of the direct DNA transfer methods described above or by viral infection using modified plant viruses.

Viruses that have been shown to be useful for the transformation of plant hosts include CaMV, Tobacco mosaic virus (TMV), brome mosaic virus (BMV) and Bean Common Mosaic Virus (BV or BCMV). Transformation of plants using plant viruses is described in U.S. Pat. No. 4,855,237 (bean golden mosaic virus; BGV), EP-A 67,553 (TMV), Japanese Published Application No. 63-14693 (TMV), EPA 194,809 (BV), EPA 278,667 (BV); and Gluzman, Y. et al., Communications in Molecular Biology:

Viral Vectors, Cold Spring Harbor Laboratory, New York, pp. 172-189 (1988). Pseudovirus particles for use in expressing foreign DNA in many hosts, including plants are described in WO 87/06261. According to some embodiments of the invention, the virus used for transient transformations is avirulent and thus is incapable of causing severe symptoms such as reduced growth rate, mosaic, ring spots, leaf roll, yellowing, streaking, pox formation, tumor formation and pitting. A suitable avirulent virus may be a naturally occurring avirulent virus or an artificially attenuated virus. Virus attenuation may be effected by using methods well known in the art including, but not limited to, sub-lethal heating, chemical treatment or by directed mutagenesis techniques such as described, for example, by Kurihara and Watanabe (Molecular Plant Pathology 4:259-269, 2003), Galon et al. (1992), Atreya et al. (1992) and Huet et al. (1994).

Suitable virus strains can be obtained from available sources such as, for example, the American Type culture Collection (ATCC) or by isolation from infected plants. Isolation of viruses from infected plant tissues can be effected by techniques well known in the art such as described, for example by Foster and Tatlor, Eds. "Plant Virology Protocols: From Virus Isolation to Transgenic Resistance (Methods in Molecular Biology (Humana Pr), Vol 81)", Humana Press, 1998. Briefly, tissues of an infected plant believed to contain a high concentration of a suitable virus, preferably young leaves and flower petals, are ground in a buffer solution (e.g., phosphate buffer solution) to produce a virus infected sap which can be used in subsequent inoculations.

Construction of plant RNA viruses for the introduction and expression of non-viral exogenous polynucleotide sequences in plants is demonstrated by the above references as well as by Dawson, W. O. et al, Virology (1989) 172:285-292; Takamatsu et al. EMBO J. (1987) 6:307-311; French et al. Science (1986) 231 :1294-1297; Takamatsu et al. FEBS Letters (1990) 269:73-76; and U.S. Pat. No. 5,316,931.

When the virus is a DNA virus, suitable modifications can be made to the virus itself. Alternatively, the virus can first be cloned into a bacterial plasmid for ease of constructing the desired viral vector with the foreign DNA. The virus can then be excised from the plasmid. If the virus is a DNA virus, a bacterial origin of replication can be attached to the viral DNA, which is then replicated by the bacteria. Transcription and translation of this DNA will produce the coat proteins which will encapsidate the viral DNA. If the virus is an RNA virus, the virus is generally cloned as a cDNA and inserted into a plasmid. The plasmid is then used to make all of the constructions. The RNA virus is then produced by transcribing the viral sequence of the plasmid and translation of the viral genes to produce the coat protein(s) which encapsidate the viral RNA.

In one embodiment, a plant viral nucleic acid is provided in which the native coat protein coding sequence has been deleted from a viral nucleic acid, a non-native plant viral coat protein coding sequence and a non-native promoter, preferably the subgenomic promoter of the non-native coat protein coding sequence, capable of expression in the plant host, packaging of the recombinant plant viral nucleic acid, and ensuring a systemic infection of the host by the recombinant plant viral nucleic acid, has been inserted. Alternatively, the coat protein gene may be inactivated by insertion of the non-native nucleic acid sequence within it, such that a protein is produced. The recombinant plant viral nucleic acid may contain one or more additional non-native subgenomic promoters. Each non-native subgenomic promoter is capable of transcribing or expressing adjacent genes or nucleic acid sequences in the plant host and incapable of recombination with each other and with native subgenomic promoters. Non-native (foreign) nucleic acid sequences may be inserted adjacent the native plant viral subgenomic promoter or the native and a non-native plant viral subgenomic promoters if more than one nucleic acid sequence is included. The non-native nucleic acid sequences are transcribed or expressed in the host plant under control of the subgenomic promoter to produce the desired products.

In a second embodiment, a recombinant plant viral nucleic acid is provided as in the first embodiment except that the native coat protein coding sequence is placed adjacent one of the non-native coat protein subgenomic promoters instead of a non-native coat protein coding sequence.

In a third embodiment, a recombinant plant viral nucleic acid is provided in which the native coat protein gene is adjacent its subgenomic promoter and one or more non-native subgenomic promoters have been inserted into the viral nucleic acid. The inserted non-native subgenomic promoters are capable of transcribing or expressing adjacent genes in a plant host and are incapable of recombination with each other and with native subgenomic promoters. Non-native nucleic acid sequences may be inserted adjacent the non-native subgenomic plant viral promoters such that the sequences are transcribed or expressed in the host plant under control of the subgenomic promoters to produce the desired product.

In a fourth embodiment, a recombinant plant viral nucleic acid is provided as in the third embodiment except that the native coat protein coding sequence is replaced by a non-native coat protein coding sequence.

The viral vectors are encapsidated by the coat proteins encoded by the recombinant plant viral nucleic acid to produce a recombinant plant virus. The recombinant plant viral nucleic acid or recombinant plant virus is used to infect appropriate host plants. The recombinant plant viral nucleic acid is capable of replication in the host, systemic spread in the host, and transcription or expression of foreign gene(s) (isolated nucleic acid) in the host to produce the desired sequence.

In addition to the above, the nucleic acid molecule of the present invention can also be introduced into a chloroplast genome thereby enabling chloroplast expression.

A technique for introducing exogenous nucleic acid sequences to the genome of the chloroplasts is known. This technique involves the following procedures. First, plant cells are chemically treated so as to reduce the number of chloroplasts per cell to about one. Then, the exogenous nucleic acid is introduced via particle bombardment into the cells with the aim of introducing at least one exogenous nucleic acid molecule into the chloroplasts. The exogenous nucleic acid is selected such that it is integratable into the chloroplast's genome via homologous recombination which is readily effected by enzymes inherent to the chloroplast. To this end, the exogenous nucleic acid includes, in addition to a gene of interest, at least one nucleic acid stretch which is derived from the chloroplast's genome. In addition, the exogenous nucleic acid includes a selectable marker, which serves by sequential selection procedures to ascertain that all or substantially all of the copies of the chloroplast genomes following such selection will include the exogenous nucleic acid. Further details relating to this technique are found in U.S. Pat. Nos. 4,945,050; and 5,693,507 which are incorporated herein by reference.

Regardless of the method of transformation, propagation or regeneration, the present invention also contemplates a transgenic plant exogenously expressing the polynucleotide/nucleic acid agent of the invention.

According to a specific embodiment, the transgenic plant exogenously expresses a polynucleotide having a nucleic acid sequence at least , 80 %, 85 %, 90 %, 95 % or even 100 % identical to SEQ ID NOs: 2-20, 23-37, 57-449, 21-22, 38-52, 1209, 1211, 1212, 454-846 and 53-56, 1209 (Tables 1, 3 and 4), wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of the plant.

According to further embodiments, the exogenous polynucleotide encodes a precursor of said nucleic acid sequence.

According to yet further embodiments, the stem-loop precursor is at least 60 %, 65 % , 70 %, 75 %, 80 %, 85 %, 90 %, 95 % or even 100 % identical to SEQ ID NOs: 21-22, 38-52, 1209, 1211, 1212, 454-846, 53-56, 1209 (Tables 1, 3 and 4) identical to SEQ ID NO: 21-22, 38-52, 1209, 1211, 1212, 54-846 and 53-56, 1209 (precursor sequences of Tables 1, 3 and 4). More specifically the exogenous polynucleotide is selected from the group consisting of SEQ ID NO: 21-22 and 38-52, 1209, 1211, 1212 (precursor and mature sequences of upregulated Tables 1 and 3).

Alternatively, there is provided a transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a gene encoding a miRNA molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209 (downregulated Tables 1 and 4) or homologs thereof which are at least at least 80 %, 85 %, 90 % or 95 % identical to SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209 (downregulated Tables 1 and 4).

More specifically, the transgenic plant expresses the nucleic acid agent of Tables 8-11.

More specifically, the transgenic plant expresses the nucleic acid agent of Tables 8 and 11.

Alternatively or additionally there is provided a transgenic plant exogenously expressing a polynucleotide encoding a polypeptide having an amino acid sequence at least 80 %, 85 %, 90 %, 95 % or even 100 % homologous to SEQ ID NOs: 854-894 (polypeptides of Table 5), wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

Alternatively or additionally there is provided a transgenic plant exogenously expressing a polynucleotide encoding a polypeptide having an amino acid sequence at least 80 %, 85 %, 90 %, 95 % or even 100 % homologous to SEQ ID NOs: 927-1021 (polypeptides of Table 6), wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

Alternatively or additionally there is provided a transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 %, 85 %, 90 %, 95 % or even 100 % homologous to SEQ ID NOs: 854-894, 927-1021 (targets of Tables 5 and 6), wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

Also contemplated are hybrids of the above described transgenic plants. A "hybrid plant" refers to a plant or a part thereof resulting from a cross between two parent plants, wherein one parent is a genetically engineered plant of the invention (transgenic plant expressing an exogenous miRNA sequence or a precursor thereof). Such a cross can occur naturally by, for example, sexual reproduction, or artificially by, for example, in vitro nuclear fusion. Methods of plant breeding are well-known and within the level of one of ordinary skill in the art of plant biology.

Since nitrogen use efficiency, abiotic stress tolerance as well as yield, vigor or biomass of the plant can involve multiple genes acting additively or in synergy (see, for example, in Quesda et al., Plant Physiol. 130:951-063, 2002), the invention also envisages expressing a plurality of exogenous polynucleotides in a single host plant to thereby achieve superior effect on the efficiency of nitrogen use, yield, vigor and biomass of the plant.

Expressing a plurality of exogenous polynucleotides in a single host plant can be effected by co-introducing multiple nucleic acid constructs, each including a different exogenous polynucleotide, into a single plant cell. The transformed cell can then be regenerated into a mature plant using the methods described hereinabove. Alternatively, expressing a plurality of exogenous polynucleotides in a single host plant can be effected by co-introducing into a single plant-cell a single nucleic-acid construct including a plurality of different exogenous polynucleotides. Such a construct can be designed with a single promoter sequence which can transcribe a polycistronic messenger RNA including all the different exogenous polynucleotide sequences. Alternatively, the construct can include several promoter sequences each linked to a different exogenous polynucleotide sequence.

The plant cell transformed with the construct including a plurality of different exogenous polynucleotides can be regenerated into a mature plant, using the methods described hereinabove.

Alternatively, expressing a plurality of exogenous polynucleotides can be effected by introducing different nucleic acid constructs, including different exogenous polynucleotides, into a plurality of plants. The regenerated transformed plants can then be cross-bred and resultant progeny selected for superior yield or tolerance traits as described above, using conventional plant breeding techniques.

Expression of the miRNAs of the present invention or precursors thereof can be qualified using methods which are well known in the art such as those involving gene amplification e.g., PCR or RT-PCR or Northern blot or in-situ hybrdization.

According to some embodiments of the invention, the plant expressing the exogenous polynucleotide(s) is grown under stress (nitrogen or abiotic) or normal conditions (e.g., biotic conditions and/or conditions with sufficient water, nutrients such as nitrogen and fertilizer). Such conditions, which depend on the plant being grown, are known to those skilled in the art of agriculture, and are further, described above.

According to some embodiments of the invention, the method further comprises growing the plant expressing the exogenous polynucleotide(s) under abiotic stress or nitrogen limiting conditions. Non-limiting examples of abiotic stress conditions include, water deprivation, drought, excess of water (e.g., flood, waterlogging), freezing, low temperature, high temperature, strong winds, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, salinity, atmospheric pollution, intense light, insufficient light, or UV irradiation, etiolation and atmospheric pollution.

Thus, the invention encompasses plants exogenously expressing the polynucleotide(s), the nucleic acid constructs of the invention.

Methods of determining the level in the plant of the RNA transcribed from the exogenous polynucleotide are well known in the art and include, for example, Northern blot analysis, reverse transcription polymerase chain reaction (RT-PCR) analysis (including quantitative, semi-quantitative or real-time RT-PCR) and RNA-m situ hybridization.

The sequence information and annotations uncovered by the present teachings can be harnessed in favor of classical breeding. Thus, sub-sequence data of those polynucleotides described above, can be used as markers for marker assisted selection (MAS), in which a marker is used for indirect selection of a genetic determinant or determinants of a trait of interest (e.g., tolerance to abiotic stress). Nucleic acid data of the present teachings (DNA or RNA sequence) may contain or be linked to polymorphic sites or genetic markers on the genome such as restriction fragment length polymorphism (RFLP), microsatellites and single nucleotide polymorphism (SNP), DNA fingerprinting (DFP), amplified fragment length polymorphism (AFLP), expression level polymorphism, and any other polymorphism at the DNA or RNA sequence.

Examples of marker assisted selections include, but are not limited to, selection for a morphological trait (e.g., a gene that affects form, coloration, male sterility or resistance such as the presence or absence of awn, leaf sheath coloration, height, grain color, aroma of rice); selection for a biochemical trait (e.g., a gene that encodes a protein that can be extracted and observed; for example, isozymes and storage proteins); selection for a biological trait (e.g., pathogen races or insect biotypes based on host pathogen or host parasite interaction can be used as a marker since the genetic constitution of an organism can affect its susceptibility to pathogens or parasites).

The polynucleotides described hereinabove can be used in a wide range of economical plants, in a safe and cost effective manner.

Plant lines exogenously expressing the polynucleotide of the invention can be screened to identify those that show the greatest increase of the desired plant trait.

Thus, according to an additional embodiment of the present invention, there is provided a method of evaluating a trait of a plant, the method comprising: (a) expressing in a plant or a portion thereof the nucleic acid construct; and (b) evaluating a trait of a plant as compared to a wild type plant of the same type; thereby evaluating the trait of the plant.

Thus, the effect of the transgene (the exogenous polynucleotide) on different plant characteristics may be determined any method known to one of ordinary skill in the art.

Thus, for example, tolerance to limiting nitrogen conditions may be compared in transformed plants {i.e., expressing the transgene) compared to non-transformed (wild type) plants exposed to the same stress conditions (other stress conditions are contemplated as well, e.g. water deprivation, salt stress e.g. salinity, suboptimal temperatureosmotic stress, and the like), using the following assays.

Methods of qualifying plants as being tolerant or having improved tolerance to abiotic stress or limiting nitrogen levels are well known in the art and are further described hereinbelow.

Fertilizer use efficiency - To analyze whether the transgenic plants are more responsive to fertilizers, plants are grown in agar plates or pots with a limited amount of fertilizer, as described, for example, in Yanagisawa et al (Proc Natl Acad Sci U S A. 2004; 101:7833-8). The plants are analyzed for their overall size, time to flowering, yield, protein content of shoot and/or grain. The parameters checked are the overall size of the mature plant, its wet and dry weight, the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Other parameters that may be tested are: the chlorophyll content of leaves (as nitrogen plant status and the degree of leaf verdure is highly correlated), amino acid and the total protein content of the seeds or other plant parts such as leaves or shoots, oil content, etc. Similarly, instead of providing nitrogen at limiting amounts, phosphate or potassium can be added at increasing concentrations. Again, the same parameters measured are the same as listed above. In this way, nitrogen use efficiency (NUE), phosphate use efficiency (PUE) and potassium use efficiency (KUE) are assessed, checking the ability of the transgenic plants to thrive under nutrient restraining conditions.

Nitrogen use efficiency – To analyze whether the transgenic plants (e.g., Arabidopsis plants) are more responsive to nitrogen, plant are grown in 0.75-3 millimolar (mM, nitrogen deficient conditions) or 10, 6-9 mM (optimal nitrogen concentration). Plants are allowed to grow for additional 25 days or until seed production. The plants are then analyzed for their overall size, time to flowering, yield, protein content of shoot and/or grain/ seed production. The parameters checked can be the overall size of the plant, wet and dry weight, the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Other parameters that may be tested are: the chlorophyll content of leaves (as nitrogen plant status and the degree of leaf greenness is highly correlated), amino acid and the total protein content of the seeds or other plant parts such as leaves or shoots and oil content. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher measured parameters levels than wild-type plants, are identified as nitrogen use efficient plants.

Nitrogen Use efficiency assay using plantlets – The assay is done according to Yanagisawa-S. et al. with minor modifications ("Metabolic engineering with Dof1 transcription factor in plants: Improved nitrogen assimilation and growth under low-nitrogen conditions" *Proc. Natl. Acad. Sci. USA* 101, 7833-7838). Briefly, transgenic plants which are grown for 7-10 days in 0.5 x MS [Murashige-Skoog] supplemented with a selection agent are transferred to two nitrogen-limiting conditions: MS media in which the combined nitrogen concentration (NH_4NO_3 and KNO_3) was 0.75 mM (nitrogen deficient conditions) or 6-15 mM (optimal nitrogen concentration). Plants are allowed to grow for additional 30-40 days and then photographed, individually removed from the Agar (the shoot without the roots) and immediately weighed (fresh weight) for later statistical analysis. Constructs for which only T1 seeds are available are sown on selective media and at least 20 seedlings (each one representing an independent transformation event) are carefully transferred to the nitrogen-limiting media. For constructs for which T2 seeds are available, different transformation events are analyzed. Usually, 20 randomly selected plants from each event are transferred to the nitrogen-limiting media allowed to grow for 3-4 additional weeks and individually weighed at the end of that period. Transgenic plants are compared to control plants grown in parallel under the same conditions. Mock- transgenic plants expressing the uidA reporter gene (GUS) under the same promoter or transgenic plants carrying the same promoter but lacking a reporter gene are used as control.

Nitrogen determination – The procedure for N (nitrogen) concentration determination in the structural parts of the plants involves the potassium persulfate digestion method to convert organic N to NO_3^- (Purcell and King 1996 Argon. J. 88:111-113, the modified Cd^- mediated reduction of NO_3^- to NO_2^- (Vodovotz 1996 Biotechniques 20:390-394) and the measurement of nitrite by the Griess assay (Vodovotz 1996, supra). The absorbance values are measured at 550 nm against a standard curve of $NaNO_2$. The procedure is described in details in Samonte et al. 2006 Agron. J. 98:168-176.

Tolerance to abiotic stress (e.g. tolerance to drought or salinity) can be evaluated by determining the differences in physiological and/or physical condition, including but not limited to, vigor, growth, size, or root length, or specifically, leaf color or leaf area size of the transgenic plant compared to a non-modified plant of the same species grown under the same conditions. Other techniques for evaluating tolerance to abiotic stress include, but are not limited to, measuring chlorophyll fluorescence, photosynthetic rates and gas exchange rates. Further assays for evaluating tolerance to abiotic stress are provided hereinbelow and in the Examples section which follows.

Drought tolerance assay - Soil-based drought screens are performed with plants overexpressing the polynucleotides detailed above. Seeds from control Arabidopsis plants, or other transgenic plants overexpressing nucleic acid of the invention are germinated and transferred to pots. Drought stress is obtained after irrigation is ceased. Transgenic and control plants are compared to each other when the majority of the control plants develop severe wilting. Plants are re-watered after obtaining a significant fraction of the control plants displaying a severe wilting. Plants are ranked comparing to controls for each of two criteria: tolerance to the drought conditions and recovery (survival) following re-watering.

Quantitative parameters of tolerance measured include, but are not limited to, the average wet and dry weight, growth rate, leaf size, leaf coverage (overall leaf area), the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher biomass than wild-type plants, are identified as drought stress tolerant plants

Salinity tolerance assay - Transgenic plants with tolerance to high salt concentrations are expected to exhibit better germination, seedling vigor or growth in high salt. Salt stress can be effected in many ways such as, for example, by irrigating the plants with a hyperosmotic solution, by cultivating the plants hydroponically in a hyperosmotic growth solution (e.g., Hoagland solution with added salt), or by culturing the plants in a hyperosmotic growth medium [e.g., 50 % Murashige-Skoog medium (MS medium) with added salt]. Since different plants vary considerably in their tolerance to salinity, the salt concentration in the irrigation water, growth solution, or growth medium can be adjusted according to the specific characteristics of the specific plant cultivar or variety, so as to inflict a mild or moderate effect on the physiology and/or morphology of the plants (for guidelines as to appropriate concentration see, Bernstein and Kafkafi, Root Growth Under Salinity Stress In: Plant Roots, The Hidden Half 3rd ed. Waisel Y, Eshel A and Kafkafi U. (editors) Marcel Dekker Inc., New York, 2002, and reference therein).

For example, a salinity tolerance test can be performed by irrigating plants at different developmental stages with increasing concentrations of sodium chloride (for example 50 mM, 150 mM, 300 mM NaCl) applied from the bottom and from above to ensure even dispersal of salt. Following exposure to the stress condition the plants are frequently monitored until substantial physiological and/or morphological effects appear in wild type plants. Thus, the external phenotypic appearance, degree of chlorosis and overall success to reach maturity and yield progeny are compared between control and transgenic plants. Quantitative parameters of tolerance measured include, but are not limited to, the average wet and dry weight, growth rate, leaf size, leaf coverage (overall leaf area), the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher biomass than wild-type plants, are identified as abiotic stress tolerant plants.

Osmotic tolerance test - Osmotic stress assays (including sodium chloride and PEG assays) are conducted to determine if an osmotic stress phenotype was sodium chloride-specific or if it was a general osmotic stress related phenotype. Plants which are tolerant to osmotic stress may have more tolerance to drought and/or freezing. For salt and osmotic stress experiments, the medium is supplemented for example with 50 mM, 100 mM, 200 mM NaCl or 15 %, 20 % or 25 % PEG.

Cold stress tolerance - One way to analyze cold stress is as follows. Mature (25 day old) plants are transferred to 4 °C chambers for 1 or 2 weeks, with constitutive light. Later on plants are moved back to greenhouse. Two weeks later damages from chilling period, resulting in growth retardation and other phenotypes, are compared between control and transgenic plants, by measuring plant weight (wet and dry), and by comparing growth rates measured as time to flowering, plant size, yield, and the like.

Heat stress tolerance - One way to measure heat stress tolerance is by exposing the plants to temperatures above 34 °C for a certain period. Plant tolerance is examined after transferring the plants back to 22 °C for recovery and evaluation after 5 days relative to internal controls (non-transgenic plants) or plants not exposed to neither cold or heat stress.

The biomass, vigor and yield of the plant can also be evaluated using any method known to one of ordinary skill in the art. Thus, for example, plant vigor can be calculated by the increase in growth parameters such as leaf area, fiber length, rosette diameter, plant fresh weight, oil content, seed yield and the like per time.

As mentioned, the increase of plant yield can be determined by various parameters. For example, increased yield of rice may be manifested by an increase in one or more of the following: number of plants per growing area, number of panicles per plant, number of spikelets per panicle, number of flowers per panicle, increase in the seed filling rate, increase in thousand kernel weight (1000-weight), increase oil content per seed, increase starch content per seed, among others. An increase in yield may also result in modified architecture, or may occur because of modified architecture. Similarly, increased yield of soybean may be manifested by an increase in one or more of the following: number of plants per growing area, number of pods per plant, number of seeds per pod, increase in the seed filling rate, increase in thousand seed weight (1000-weight), reduce pod shattering, increase oil content per seed, increase protein content per seed, among others. An increase in yield may also result in modified architecture, or may occur because of modified architecture.

Thus, the present invention is of high agricultural value for increasing tolerance of plants to nitrogen deficiency or abiotic stress as well as promoting the yield, biomass and vigor of commercially desired crops.

According to another embodiment of the present invention, there is provided a food or feed comprising the plants or a portion thereof of the present invention.

In a further aspect the invention, the transgenic plants of the present invention or parts thereof are comprised in a food or feed product (e.g., dry, liquid, paste). A food or feed product is any ingestible preparation containing the transgenic plants, or parts thereof, of the present invention, or preparations made from these plants. Thus, the plants or preparations are suitable for human (or animal) consumption, i.e. the transgenic plants or parts thereof are more readily digested. Feed products of the present invention further include a oil or a beverage adapted for animal consumption.

It will be appreciated that the transgenic plants, or parts thereof, of the present invention may be used directly as feed products or alternatively may be incorporated or mixed with feed products for consumption. Furthermore, the food or feed products may be processed or used as is. Exemplary feed products comprising the transgenic plants, or parts thereof, include, but are not limited to, grains, cereals, such as oats, e.g. black oats, barley, wheat, rye, sorghum, corn, vegetables, leguminous plants, especially soybeans, root vegetables and cabbage, or green forage, such as grass or hay.

It is expected that during the life of a patent maturing from this application many relevant homolog/ortholog sequences will be developed and the scope of the term polynucleotide/nucleic acid agent is intended to include all such new technologies *a priori*.

As used herein the term “about” refers to ± 10 %.

The terms "comprises", "comprising", "includes", "including", “having” and their conjugates mean "including but not limited to".

The term “consisting of means “including and limited to”.

The term "consisting essentially of" means that the composition, method or structure may include additional ingredients, steps and/or parts, but only if the additional ingredients, steps and/or parts do not materially alter the basic and novel characteristics of the claimed composition, method or structure.

As used herein, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a compound" or "at least one compound" may include a plurality of compounds, including mixtures thereof.

Throughout this application, various embodiments of this invention may be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

Whenever a numerical range is indicated herein, it is meant to include any cited numeral (fractional or integral) within the indicated range. The phrases “ranging/ranges between” a first indicate number and a second indicate number and “ranging/ranges from” a first indicate number “to” a second indicate number are used herein interchangeably and are meant to include the first and second indicated numbers and all the fractional and integral numerals therebetween.

As used herein the term "method" refers to manners, means, techniques and procedures for accomplishing a given task including, but not limited to, those manners, means, techniques and procedures either known to, or readily developed from known manners, means, techniques and procedures by practitioners of the chemical, pharmacological, biological, biochemical and medical arts.

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination or as suitable in any other described embodiment of the invention. Certain features described in the context of various embodiments are not to be considered essential features of those embodiments, unless the embodiment is inoperative without those elements.

Various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below find experimental support in the following examples.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions illustrate some embodiments of the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); “Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., Eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

EXAMPLE 1

Differential Expression of miRNAs in Maize Plant under Optimal Versus limited Nitrogen

Experimental Procedures

Plant Material

Corn seeds were obtained from Galil seeds (Israel). Corn variety 5605 was used in all experiments. Plants were grown at 28 °C under a 16 hr light:8 hr dark regime.

Stress Induction

Corn seeds were germinated and grown on defined growth media containing either sufficient (100% N_2) or insufficient nitrogen levels (1 % or 10 % N_2). Seedlings aged one or two weeks were used for tissue samples for RNA analysis, as described below.

Total RNA extraction

Total RNA of leaf or root samples from four to eight biological repeats were extracted using the mirVana^{TM} kit (Ambion, Austin, TX) by pooling 3-4 plants to one biological repeat.

Microarray design

Custom microarrays were manufactured by Agilent Technologies by *in situ* synthesis. The first generation microarray consisted of a total of 13619 non-redundant DNA probes, the majority of which arose from deep sequencing data and includes different small RNA molecules (i.e. miRNAs, siRNA and predicted small RNA sequences), with each probe being printed once. An in-depth analysis of the first generation microarray, which included hybridization experiments as well as structure and orientation verifications on all its small RNAs, resulted in the formation of an improved, second generation, microarray. The second generation microarray consisted of a total 4721 non-redundant DNA 45-nucleotide long probes for all known plant small RNAs, with 912 sequences (19.32 %) from Sanger version 15 and the rest (3809), encompassing miRNAs (968=20.5%), siRNAs (1626=34.44%) and predicted small RNA sequences (1215=25.74%), from deep sequencing data accumulated by the inventors, with each probe being printed in triplicate.

Results

Wild type maize plants were allowed to grow at standard, optimal conditions or nitrogen deficient conditions for one or two weeks, at the end of which they were evaluated for NUE. Three to four plants from each group were used for reproducibility. Four to eight repeats were obtained for each group, and RNA was extracted from leaf or root tissue. The expression level of the maize miRNAs was analyzed by high throughput microarray to identify miRNAs that were differentially expressed between the experimental groups.

Tables 1-2 below presents sequences that were found to be differentially expressed in corn grown in various nitrogen levels. To clarify, the sequence of an up-regulated miRNA is induced under nitrogen limiting conditions and the sequence of a down-regulated miRNA is repressed under nitrogen limiting conditions compared to optimal conditions.

Table 1: Differentially Expressed miRNAs in Leaf of Plants Growing under Nitrogen Deficient Versus Optimal Conditions.

P value - Leaf	Fold Change - Leaf	Sequence/SEQ ID NO:	Up/Down regulated	Small RNA name
3.90E-03	1.66	AGAAGAGAGAGAGTACAGCCT/1	Down	Zma-miR529
3.30E-06	3.35	TAGCCAGGGATGATTTGCCTG/2	Down	Zma-miR1691
ND	ND	GGAATCTTGATGATGCTGCAT/3	Down	Zma-miR172e
ND	ND	GTGAAGTGTTTGGGGGAACTC/4	Down	Zma-miR395b
2.20E-07	2.51	TAGCCAAGCATGATTTGCCCG/5	Down	Predicted zma mir 50601
ND	ND	AGGATGTGAGGCTATTGGGGAC/6	Up	Predicted zma mir 48492
ND	ND	CCAAGTCGAGGGCAGACCAGGC/7	Up	Predicted zma mir 48879
ND	ND	ATTCACGGGGACGAACCTCCT/8	Up	Mtr-miR2647a
1.80E-02	1.72	AGGATGCTGACGCAATGGGAT/9	Up	Predicted zma mir 48486
9.80E-03	1.61	TTAGATGACCATCAGCAAACA/10	Up	Zma-miR827

Table 2: Differentially Expressed miRNAs in Roots of Plants Growing under Nitrogen Deficient Versus Optimal Conditions.

P value - Root	Fold Change - Root	Sequence/SEQ ID NO:	Up/Down regulated	Small RNA name
ND	ND	AGAAGAGAGAGAGTACAGCCT/1	Down	Zma-miR529
1.40E-05	2.56	TAGCCAGGGATGATTTGCCTG/2	Down	Zma-miR1691
5.40E-05	2.08	GTGAAGTGTTTGGGGGAACTC/4	Down	Zma-miR395b
2.30E-04	1.66	TAGCCAAGCATGATTTGCCCG/5	Down	Predicted zma mir 50601
4.50E-02	1.75	GGAATCTTGATGATGCTGCAT/3	Down	Zma-miR172e
1.60E-02	1.8	AGGATGCTGACGCAATGGGAT/9	Up	Predicted zma mir 48486
ND	ND	TTAGATGACCATCAGCAAACA/10	Up	Zma-miR827
1.30E-04	2.75	AGGATGTGAGGCTATTGGGGAC/6	Up	Predicted zma mir 48492
5.60E-04	1.95	CCAAGTCGAGGGCAGACCAGGC/7	Up	Predicted zma mir 48879
3.90E-02	1.79	ATTCACGGGGACGAACCTCCT/8	Up	Mtr-miR2647a

EXAMPLE 2

Identification of Homologous and Orthologous Sequences of Differential Small RNAs Associated with Increased NUE

The small RNA sequences of the invention that were either down- or upregulated under nitrogen limiting conditions were examined for homologous and orthologous sequences using the miRBase database (wwwdotmirbasedotorg/) and the Plant MicroRNA Database (PMRD, wwwdotbioinformaticsdotcaudotedudotcn/PMRD). The mature miRNA sequences that are homologous or orthologous to the miRNAs of the invention (listed in Table 1) are found using miRNA public databases, having at least 90% identity of the entire small RNA length, and are summarized in Table 3 below. Of note, if homologs of only 90 % are uncovered, they are subject for family members search and are listed with a cutoff of 80 % identity to the homolog sequence, not to the original maize miR.

Table 3: Summary of Homologs/Orthologs to NUE small RNA Probes (upregulated)

Homolog Stem-loop seq id no:	% Identity	Homolog length	sequence	Homolog names	Stem-loop seq id no:	MiR length	Mature sequence	MiR Name
38	1	21	ATTCACGGGGACGAACCTCCT/23	mtr-miR2647b	21	21	ATTCACGGGGACGAACCTCCT/8	mtr-miR2647a
39	1	21	ATTCACGGGGACGAACCTCCT/24	mtr-miR2647c				
40	0.9	21	TTAGATGACCATCAACAAACG/25	aly-miR827	22	21	TTAGATGACCATCAGCAAACA/10	zma-miR827
41	0.9	21	TTAGATGACCATCAACAAACT/26	ath-miR827				
42	1	21	TTAGATGACCATCAGCAAACA/27	bdi-miR827				
43	0.95	21	TTAGATGACCATCAACAAACA/28	csi-miR827				
44	0.95	21	TTAGATGACCATCAACAAACA/29	ghr-miR827a				
45	0.95	21	TTAGATGACCATCAACAAACA/30	ghr-miR827b				
46	0.95	21	TTAGATGACCATCAACAAACA/31	ghr-miR827c				
47	0.86	21	TAAGATGACCATCAGCGAAAA/32	osa-miR827				
48	1	21	TTAGATGACCATCAGCAAACA/33	osa-miR827a				
49	1	21	TTAGATGACCATCAGCAAACA/34	osa-miR827b				
50	0.86	21	TTAGATGACCATCAACGAAAA/35	ptc-miR827				

51	1	21	TTAGATGACCATCAGCAAACA/36	ssp-miR827				
52	0.95	21	TTAGATGACCATCAACAAACA/37	tcc-miR827				

Table 4: Summary of Homologs/Orthologs to NUE small RNA Probes (Downregulated)

Homolog Stem-loop seq id no:	**% Identity**	**Homolog length**	**sequence**	**Homolog names**	**Stem-loop seq id no:**	**MiR length**	**Mature sequence**	**MiR Name**
454	0.81	21	CAGCCAAGGATGACTTGCCGG/57	aly-miR169b	53	21	TAGCCAGGGATGATTTGCCTG/2	zma-miR169l
455	0.81	21	CAGCCAAGGATGACTTGCCGG/58	aly-miR169c				
456	0.9	21	TAGCCAAGGATGACTTGCCTG/59	aly-miR169h				
457	0.9	21	TAGCCAAGGATGACTTGCCTG/60	aly-miR169i				
458	0.9	21	TAGCCAAGGATGACTTGCCTG/61	aly-miR169j				
459	0.9	21	TAGCCAAGGATGACTTGCCTG/62	aly-miR169k				
460	0.9	21	TAGCCAAGGATGACTTGCCTG/63	aly-miR169l				
461	0.9	21	TAGCCAAGGATGACTTGCCTG/64	aly-miR169m				
462	0.86	21	TAGCCAAAGATGACTTGCCTG/65	aly-miR169n				
463	0.86	21	TAGCCAAGGATGACTTGCCTA/66	aqc-miR169a				
464	0.9	21	TAGCCAAGGATGACTTGCCTG/67	aqc-miR169b				
465	0.81	21	CAGCCAAG	aqc-				

			GATGACTTGCCGG/68	miR169c				
466	0.86	21	TAGCCAAGGATGAATTGCCAG/69	ata-miR169				
467	0.81	21	CAGCCAAGGATGACTTGCCGG/70	ath-miR169b				
468	0.81	21	CAGCCAAGGATGACTTGCCGG/71	ath-miR169c				
469	0.9	21	TAGCCAAGGATGACTTGCCTG/72	ath-miR169h				
470	0.9	21	TAGCCAAGGATGACTTGCCTG/73	ath-miR169i				
471	0.9	21	TAGCCAAGGATGACTTGCCTG/74	ath-miR169j				
472	0.9	21	TAGCCAAGGATGACTTGCCTG/75	ath-miR169k				
473	0.9	21	TAGCCAAGGATGACTTGCCTG/76	ath-miR169l				
474	0.9	21	TAGCCAAGGATGACTTGCCTG/77	ath-miR169m				
475	0.9	21	TAGCCAAGGATGACTTGCCTG/78	ath-miR169n				
476	0.86	21	TAGCCAAGGATGACTTGCCGG/79	bdi-miR169b				
477	0.81	21	CAGCCAAGGATGACTTGCCGG/80	bdi-miR169c				
478	0.81	21	TAGCCAAGAATGACTTGCCTA/81	bdi-miR169d				
479	0.9	21	TAGCCAAGGATGACTTGCCTG/82	bdi-miR169e				
480	0.81	21	CAGCCAAGGATGACTTGCCGG/83	bdi-miR169f				
481	0.9	21	TAGCCAAGGATGACTTGCCTG/84	bdi-miR169g				
482	0.86	21	TAGCCAAGGATGACTTGCCTA/85	bdi-miR169h				
483	0.81	21	TAGCCAGGAATGGCTTGCCTA/86	bdi-miR169j				

484	0.95	22	TAGCCAAGGATGATTTGCCTGT/87	bdi-miR169k				
485	0.86	21	TAGCCAAGGATGACTTGCCTA/88	bna-miR169c				
486	0.86	21	TAGCCAAGGATGACTTGCCTA/89	bna-miR169d				
487	0.86	21	TAGCCAAGGATGACTTGCCTA/90	bna-miR169e				
488	0.86	21	TAGCCAAGGATGACTTGCCTA/91	bna-miR169f				
489	0.9	22	TAGCCAAGGATGACTTGCCTGC/92	bna-miR169g				
490	0.9	22	TAGCCAAGGATGACTTGCCTGC/93	bna-miR169h				
491	0.9	22	TAGCCAAGGATGACTTGCCTGC/94	bna-miR169i				
492	0.9	22	TAGCCAAGGATGACTTGCCTGC/95	bna-miR169j				
493	0.9	22	TAGCCAAGGATGACTTGCCTGC/96	bna-miR169k				
494	0.9	22	TAGCCAAGGATGACTTGCCTGC/97	bna-miR169l				
495	0.86	21	TAGCCAAGGATGACTTGCCTA/98	far-miR169				
496	0.9	21	TAGCCAAGGATGACTTGCCTG/99	ghb-miR169a				
497	0.81	21	CAGCCAAGGATGACTTGCCGG/100	gma-miR169a				
498	0.81	23	TGAGCCAAGGATGACTTGCCGGT/101	gma-miR169d				
499	0.81	20	AGCCAAGGATGACTTGCCGG/102	gma-miR169e				
500	0.86	21	AAGCCAAGGATGAGTTGCCTG/103	hvu-miR169				
501	0.81	21	CAGCCAAGGGTGATTTGCCGG/104	mtr-miR169c				
502	0.81	21	AAGCCAAG	mtr-				

			GATGACTTGCCGG/105	miR169d				
503	0.81	21	AAGCCAAGGATGACTTGCCTA/106	mtr-miR169f				
504	0.81	21	CAGCCAAGGATGACTTGCCGG/107	mtr-miR169g				
505	0.81	21	CAGCCAAGGATGACTTGCCGG/108	mtr-miR169j				
506	0.81	21	CAGCCAAGGGTGATTTGCCGG/109	mtr-miR169k				
507	0.81	21	AAGCCAAGGATGACTTGCCGG/110	mtr-miR169l				
508	0.81	21	GAGCCAAGGATGACTTGCCGG/111	mtr-miR169m				
509	0.81	21	CAGCCAAGGATGACTTGCCGG/112	osa-miR169b				
510	0.81	21	CAGCCAAGGATGACTTGCCGG/113	osa-miR169c				
511	0.86	21	TAGCCAAGGATGAATTGCCGG/114	osa-miR169d				
512	0.86	21	TAGCCAAGGATGACTTGCCGG/115	osa-miR169e				
513	0.86	21	TAGCCAAGGATGACTTGCCTA/116	osa-miR169f				
514	0.86	21	TAGCCAAGGATGACTTGCCTA/117	osa-miR169g				
515	0.9	21	TAGCCAAGGATGACTTGCCTG/118	osa-miR169h				
516	0.9	21	TAGCCAAGGATGACTTGCCTG/119	osa-miR169i				
517	0.9	21	TAGCCAAGGATGACTTGCCTG/120	osa-miR169j				
518	0.9	21	TAGCCAAGGATGACTTGCCTG/121	osa-miR169k				
519	0.9	21	TAGCCAAGGATGACTTGCCTG/122	osa-miR169l				
520	0.9	21	TAGCCAAGGATGACTTGCCTG/123	osa-miR169m				

521	0.81	21	TAGCCAAGAATGACTTGCCTA/124	osa-miR169n				
522	0.81	21	TAGCCAAGAATGACTTGCCTA/125	osa-miR169o				
523	0.81	21	CAGCCAAGGATGACTTGCCGG/126	ptc-miR169d				
524	0.81	21	CAGCCAAGGATGACTTGCCGG/127	ptc-miR169e				
525	0.81	21	CAGCCAAGGATGACTTGCCGG/128	ptc-miR169f				
526	0.81	21	CAGCCAAGGATGACTTGCCGG/129	ptc-miR169g				
527	0.81	21	CAGCCAAGGATGACTTGCCGG/130	ptc-miR169h				
528	0.9	21	TAGCCAAGGATGACTTGCCTG/131	ptc-miR169i				
529	0.9	21	TAGCCAAGGATGACTTGCCTG/132	ptc-miR169j				
530	0.9	21	TAGCCAAGGATGACTTGCCTG/133	ptc-miR169k				
531	0.9	21	TAGCCAAGGATGACTTGCCTG/134	ptc-miR169l				
532	0.9	21	TAGCCAAGGATGACTTGCCTG/135	ptc-miR169m				
533	0.86	21	AAGCCAAGGATGACTTGCCTG/136	ptc-miR169o				
534	0.86	21	AAGCCAAGGATGACTTGCCTG/137	ptc-miR169p				
535	0.86	21	TAGCCAAGGACGACTTGCCTG/138	ptc-miR169q				
536	0.86	21	TAGCCAAGGATGACTTGCCTA/139	ptc-miR169r				
537	0.81	21	TAGCCAAGGACGACTTGCCTA/140	ptc-miR169u				
538	0.81	21	TAGCCAAGGATGACTTGCCCA/141	ptc-miR169v				
539	0.81	21	TAGCCAAGGATGACTT	ptc-miR169w				

			GCCCA/142					
540	0.81	21	TAGCCAAGGATGACTTGCTCG/143	ptc-miR169x				
541	0.9	21	TAGCCATGGATGAATTGCCTG/144	ptc-miR169y				
542	0.81	21	CAGCCAAGAATGATTTGCCGG/145	ptc-miR169z				
543	0.81	21	CAGCCAAGGATGACTTGCCGG/146	rco-miR169a				
544	0.81	21	CAGCCAAGGATGACTTGCCGG/147	rco-miR169b				
545	0.81	21	CAGCCAAGGATGACTTGCCGG/148	sbi-miR169b				
546	0.86	21	TAGCCAAGGATGACTTGCCTA/149	sbi-miR169c				
547	0.86	21	TAGCCAAGGATGACTTGCCTA/150	sbi-miR169d				
548	0.86	21	TAGCCAAGGATGACTTGCCGG/151	sbi-miR169e				
549	0.9	21	TAGCCAAGGATGACTTGCCTG/152	sbi-miR169f				
550	0.9	21	TAGCCAAGGATGACTTGCCTG/153	sbi-miR169g				
551	0.86	21	TAGCCAAGGATGACTTGCCTA/154	sbi-miR169h				
552	0.81	21	TAGCCAAGAATGACTTGCCTA/155	sbi-miR169i				
553	0.86	21	TAGCCAAGGATGACTTGCCGG/156	sbi-miR169j				
554	0.81	21	CAGCCAAGGATGACTTGCCGG/157	sbi-miR169k				
555	0.9	21	TAGCCAAGGATGACTTGCCTG/158	sbi-miR169l				
556	0.86	21	TAGCCAAGGATGACTTGCCTA/159	sbi-miR169m				
557	0.86	21	TAGCCAAGGATGACTTGCCTA/160	sbi-miR169n				
558	0.95	21	TAGCCAAG	sbi-				

			GATGATTTGCCTG/161	miR169o				
559	0.81	21	CAGCCAAGGATGACTTGCCGG/162	sly-miR169a				
560	0.9	21	TAGCCAAGGATGACTTGCCTG/163	sly-miR169b				
561	0.86	21	TAGCCAAGGATGACTTGCCTA/164	sly-miR169d				
562	0.86	21	TAGCCAAGGATGACTTGCCGG/165	ssp-miR169				
563	0.81	21	CAGCCAAGGATGACTTGCCGG/166	tcc-miR169b				
564	0.86	21	TAGCCAAGGATGACTTGCCTA/167	tcc-miR169d				
565	0.81	21	AAGCCAAGAATGACTTGCCTG/168	tcc-miR169f				
566	0.9	21	TAGCCAGGGATGACTTGCCTA/169	tcc-miR169g				
567	0.9	21	TAGCCAAGGATGACTTGCCTG/170	tcc-miR169h				
568	0.9	21	TAGCCAAGGATGAGTTGCCTG/171	tcc-miR169i				
569	0.9	21	TAGCCAAGGATGACTTGCCTG/172	tcc-miR169j				
570	0.81	21	CAGCCAAGGATGACTTGCCGG/173	tcc-miR169k				
571	0.81	21	CAGCCAAGGATGACTTGCCGG/174	tcc-miR169l				
572	0.81	21	CAGCCAAGGATGACTTGCCGG/175	vvi-miR169a				
573	0.81	21	CAGCCAAGGATGACTTGCCGG/176	vvi-miR169c				
574	0.81	21	CAGCCAAGAATGATTTGCCGG/177	vvi-miR169d				
575	0.9	22	TAGCCAAGGATGACTTGCCTGC/178	vvi-miR169e				
576	0.81	21	CAGCCAAGGATGACTTGCCGG/179	vvi-miR169j				

577	0.81	21	CAGCCAAGGATGACTTGCCGG/180	vvi-miR169k				
578	0.81	21	GAGCCAAGGATGACTTGCCGG/181	vvi-miR169m				
579	0.81	21	GAGCCAAGGATGACTTGCCGG/182	vvi-miR169n				
580	0.81	21	GAGCCAAGGATGACTTGCCGG/183	vvi-miR169p				
581	0.81	21	GAGCCAAGGATGACTTGCCGG/184	vvi-miR169q				
582	0.81	21	CAGCCAAGGATGACTTGCCGG/185	vvi-miR169s				
583	0.81	21	AAGCCAAGGATGAATTGCCGG/186	vvi-miR169v				
584	0.81	21	CAGCCAAGGATGACTTGCCGG/187	vvi-miR169w				
585	0.86	21	TAGCCAAGGATGACTTGCCTA/188	vvi-miR169x				
586	0.81	21	TAGCGAAGGATGACTTGCCTA/189	vvi-miR169y				
587	0.81	21	CAGCCAAGGATGACTTGCCGG/190	zma-miR169c				
588	0.86	21	TAGCCAAGGATGACTTGCCTA/191	zma-miR169f				
589	0.86	21	TAGCCAAGGATGACTTGCCTA/192	zma-miR169g				
590	0.86	21	TAGCCAAGGATGACTTGCCTA/193	zma-miR169h				
591	0.9	21	TAGCCAAGGATGACTTGCCTG/194	zma-miR169i				
592	0.9	21	TAGCCAAGGATGACTTGCCTG/195	zma-miR169j				
593	0.9	21	TAGCCAAGGATGACTTGCCTG/196	zma-miR169k				
594	0.81	21	TAGCCAAGAATGACTTGCCTA/197	zma-miR169o				
595	0.86	21	TAGCCAAGGATGACTT	zma-miR169p				

			GCCGG/198					
596	0.81	21	CAGCCAAGGATGACTTGCCGG/199	zma-miR169r				
597	0.95	21	AGAATCTTGATGATGCTGCAT/200	aly-miR172a	54	21	GGAATCTTGATGATGCTGCAT/3	zma-miR172e
598	0.95	21	AGAATCTTGATGATGCTGCAT/201	aly-miR172b				
599	0.9	21	AGAATCTTGATGATGCTGCAG/202	aly-miR172c				
600	0.9	21	AGAATCTTGATGATGCTGCAG/203	aly-miR172d				
601	0.95	20	GAATCTTGATGATGCTGCAT/204	aly-miR172e				
602	0.95	21	AGAATCTTGATGATGCTGCAT/205	aqc-miR172a				
603	1	21	GGAATCTTGATGATGCTGCAT/206	aqc-miR172b				
604	0.86	21	AGGATCTTGATGATGCTGCAG/207	asp-miR172				
605	0.95	23	TGAGAATCTTGATGATGCTGCAT/208	ata-miR172				
606	0.95	21	AGAATCTTGATGATGCTGCAT/209	ath-miR172a				
607	0.95	21	AGAATCTTGATGATGCTGCAT/210	ath-miR172b				
608	0.9	21	AGAATCTTGATGATGCTGCAG/211	ath-miR172c				
609	0.9	21	AGAATCTTGATGATGCTGCAG/212	ath-miR172d				
610	1	21	GGAATCTTGATGATGCTGCAT/213	ath-miR172e				
611	0.86	21	AGAATCCTGATGATGCTGCAG/214	ath-miR172m				
612	0.95	21	AGAATCTTGATGATGCTGCAT/215	bdi-miR172a				
613	1	21	GGAATCTTGATGATGC	bdi-miR172b				

			TGCAT/216					
614	0.86	21	AGAATCCTGATGATGCTGCAG/217	bdi-miR172d				
615	0.95	21	AGAATCTTGATGATGCTGCAT/218	bol-miR172a				
616	0.95	21	AGAATCTTGATGATGCTGCAT/219	bol-miR172b				
617	0.95	21	AGAATCTTGATGATGCTGCAT/220	bra-miR172a				
618	0.95	21	AGAATCTTGATGATGCTGCAT/221	bra-miR172b				
619	0.9	20	AGAATCTTGATGATGCTGCA/222	csi-miR172				
620	0.9	20	AGAATCTTGATGATGCTGCA/223	csi-miR172a				
621	0.86	21	AGAATCTTGATGATGCGGCAA/224	csi-miR172b				
622	0.95	22	TGGAATCTTGATGATGCTGCAG/225	csi-miR172c				
623	0.86	21	AGAATCCTGATGATGCTGCAG/226	ghr-miR172				
624	0.95	21	AGAATCTTGATGATGCTGCAT/227	gma-miR172a				
625	0.95	21	AGAATCTTGATGATGCTGCAT/228	gma-miR172b				
626	0.95	21	GGAATCTTGATGATGCTGCAG/229	gma-miR172c				
627	0.95	24	GGAATCTTGATGATGCTGCAGCAG/230	gma-miR172d				
628	0.95	24	GGAATCTTGATGATGCTGCAGCAG/231	gma-miR172e				
629	0.9	20	AGAATCTTGATGATGCTGCA/232	gma-miR172f				
630	0.95	21	AGAATCTTGATGATGCTGCAT/233	gra-miR172a				
631	0.9	21	AAAATCTTGATGATGC	gra-miR172b				

			TGCAT/234					
632	0.86	21	AGAATCCTGATGATGCTGCAG/235	hvv-miR172a				
633	0.86	21	AGAATCCTGATGATGCTGCAG/236	hvv-miR172b				
634	0.86	21	AGAATCCTGATGATGCTGCAG/237	hvv-miR172c				
635	0.86	21	AGAATCCTGATGATGCTGCAG/238	hvv-miR172d				
636	0.95	21	AGAATCTTGATGATGCTGCAT/239	mes-miR172				
637	0.86	21	AGAATCCTGATGATGCTGCAG/240	mtr-miR172				
638	0.9	21	GGAATCTTGATGATTCTGCAC/241	mtr-miR172a				
639	0.95	21	AGAATCTTGATGATGCTGCAT/242	osa-miR172a				
640	1	21	GGAATCTTGATGATGCTGCAT/243	osa-miR172b				
641	0.9	21	TGAATCTTGATGATGCTGCAC/244	osa-miR172c				
642	0.95	21	AGAATCTTGATGATGCTGCAT/245	osa-miR172d				
643	0.86	21	AGAATCCTGATGATGCTGCAG/246	osa-miR172m				
644	0.86	21	AGAATCCTGATGATGCTGCAG/247	osa-miR172n				
645	0.86	21	AGAATCCTGATGATGCTGCAG/248	osa-miR172o				
646	0.86	21	AGAATCCTGATGATGCTGCAG/249	osa-miR172p				
647	0.86	21	AGAATCCTGATGATGCTGCAC/250	pga-miR172				
648	0.95	21	AGAATCTTGATGATGCTGCAT/251	ppd-miR172a				
649	0.86	21	TGAATCTTGATGATGCTCCAC/252	ppd-miR172b				
650	0.86	21	AGAATCCT	psi-				

			GATGATGCTGCAC/253	miR172				
651	0.95	21	AGAATCTTGATGATGCTGCAT/254	ptc-miR172a				
652	0.95	21	AGAATCTTGATGATGCTGCAT/255	ptc-miR172b				
653	0.95	21	AGAATCTTGATGATGCTGCAT/256	ptc-miR172c				
654	1	21	GGAATCTTGATGATGCTGCAT/257	ptc-miR172d				
655	1	21	GGAATCTTGATGATGCTGCAT/258	ptc-miR172e				
656	0.95	21	AGAATCTTGATGATGCTGCAT/259	ptc-miR172f				
657	0.95	21	GGAATCTTGATGATGCTGCAG/260	ptc-miR172g				
658	0.95	21	GGAATCTTGATGATGCTGCAG/261	ptc-miR172h				
659	0.86	21	AGAATCCTGATGATGCTGCAA/262	ptc-miR172i				
660	0.95	21	GGAATCTTGATGATGCTGCAG/263	rco-miR172				
661	0.9	20	AGAATCTTGATGATGCTGCA/264	sbi-miR172a				
662	0.95	20	GGAATCTTGATGATGCTGCA/265	sbi-miR172b				
663	0.9	20	AGAATCTTGATGATGCTGCA/266	sbi-miR172c				
664/847	0.9	20	AGAATCTTGATGATGCTGCA/267	sbi-miR172d				
665	0.9	21	TGAATCTTGATGATGCTGCAC/268	sbi-miR172e				
666	0.86	21	AGAATCCTGATGATGCTGCAC/269	sbi-miR172f				
667	0.95	21	AGAATCTTGATGATGCTGCAT/270	sly-miR172a				
668	0.95	21	AGAATCTTGATGATGCTGCAT/271	sly-miR172b				

669	0.86	21	AGAATCCTGATGATGCTGCAG/272	sof-miR172a				
670	0.95	21	AGAATCTTGATGATGCTGCAT/273	stu-miR172				
671	0.86	21	AGAATCCTGATGATGCTGCAG/274	tae-miR172a				
672	0.86	21	AGAATCCTGATGATGCTGCAG/275	tae-miR172b				
673	0.86	21	AGGATCTTGATGATGCTGCAG/276	tae-miR172c				
674	0.86	21	AGAATCCTGATGATGCTGCAG/277	tca-miR172				
675	0.95	20	GGAATCTTGATGATGCTGCA/278	tcc-miR172a				
676	0.95	21	AGAATCTTGATGATGCTGCAT/279	tcc-miR172b				
677	1	21	GGAATCTTGATGATGCTGCAT/280	tcc-miR172c				
678	0.9	21	AGAATCCTGATGATGCTGCAT/281	tcc-miR172d				
679	0.95	21	AGAATCTTGATGATGCTGCAT/282	tcc-miR172e				
680	0.9	21	TGAATCTTGATGATGCTACAT/283	vvi-miR172a				
681	0.86	21	TGAATCTTGATGATGCTACAC/284	vvi-miR172b				
682	0.95	21	GGAATCTTGATGATGCTGCAG/285	vvi-miR172c				
683	0.95	23/21	TGAGAATCTTGATGATGCTGCAT/286/AGAATCTTGATGATGCTGCAT/450	vvi-miR172d				
684/848	0.9	20	AGAATCTTGATGATGCTGCA/287	zma-miR172a				
685	0.9	20	AGAATCTTGATGATGCTGCA/288	zma-miR172b				
686	0.9	20	AGAATCTTGATGATGC	zma-miR172c				

			TGCA/289					
687	0.9	20	AGAATCTTGATGATGCTGCA/290	zma-miR172d				
688	1	21	GGAATCTTGATGATGCTGCAT/291	zma-miR172f				
689	0.86	21	AGAATCCTGATGATGCTGCAG/292	zma-miR172m				
690	0.9	21	AGAATCCTGATGATGCTGCAT/293	zma-miR172n				
691	0.9	21	CTGAAGTGTTTGGGGGGACTC/294	aly-miR395b	55	21	GTGAAGTGTTTGGGGGAACTC/4	zma-miR395b
692	0.86	21	CTGAAGTGTTTGGGGGGACTT/295	aly-miR395c				
693	0.95	21	CTGAAGTGTTTGGGGGAACTC/296	aly-miR395d				
694	0.95	21	CTGAAGTGTTTGGGGGAACTC/297	aly-miR395e				
695	0.9	21	CTGAAGTGTTTGGGGGGACTC/298	aly-miR395f				
696	0.95	21	CTGAAGTGTTTGGGGGAACTC/299	aly-miR395g				
697	0.9	21	CTGAAGTGTTTGGGGGGACTC/300	aly-miR395h				
698	0.9	21	CTGAAGTGTTTGGAGGAACTC/301	aly-miR395i				
699	0.86	21	CTGAAGGGTTTGGAGGAACTC/302	aqc-miR395a				
700	0.86	21	CTGAAGGGTTTGGAGGAACTC/303	aqc-miR395b				
701	0.95	21	CTGAAGTGTTTGGGGGAACTC/304	ath-miR395a				
702	0.9	21	CTGAAGTGTTTGGGGGGACTC/305	ath-miR395b				
703	0.9	21	CTGAAGTGTTTGGGGGGACTC/306	ath-miR395c				
704	0.95	21	CTGAAGTGTTTGGGGGAACTC/307	ath-miR395d				

705	0.95	21	CTGAAGTGTTTGGGGGAACTC/308	ath-miR395e				
706	0.9	21	CTGAAGTGTTTGGGGGGACTC/309	ath-miR395f				
707	0.95	20	TGAAGTGTTTGGGGGAACTC/310	bdi-miR395a				
708	0.95	20	TGAAGTGTTTGGGGGAACTC/311	bdi-miR395b				
709	0.95	20	TGAAGTGTTTGGGGGAACTC/312	bdi-miR395c				
710	0.81	21	AAGTGTTTGGGGAACTCTAGG/313	bdi-miR395d				
711	0.95	20	TGAAGTGTTTGGGGGAACTC/314	bdi-miR395e				
712	0.95	20	TGAAGTGTTTGGGGGAACTC/315	bdi-miR395f				
713	0.95	20	TGAAGTGTTTGGGGGAACTC/316	bdi-miR395g				
714	0.95	20	TGAAGTGTTTGGGGGAACTC/317	bdi-miR395h				
715	0.95	20	TGAAGTGTTTGGGGGAACTC/318	bdi-miR395i				
716	0.95	20	TGAAGTGTTTGGGGGAACTC/319	bdi-miR395j				
717	0.95	20	TGAAGTGTTTGGGGGAACTC/320	bdi-miR395k				
718	0.95	20	TGAAGTGTTTGGGGGAACTC/321	bdi-miR395l				
719	0.95	20	TGAAGTGTTTGGGGGAACTC/322	bdi-miR395m				
720	0.95	20	TGAAGTGTTTGGGGGAACTC/323	bdi-miR395n				
721	0.95	21	CTGAAGTGTTTGGGGGAACTC/324	csi-miR395				
722	0.9	21	TTGAAGTGTTTGGGGGAACTT/325	ghr-miR395a				
723	0.86	21	CTAAAGTGTTTAGGGG	ghr-miR395c				

			AACTC/326					
724	0.95	21	CTGAAGTGTTTGGGGGAACTC/327	ghr-miR395d				
725	0.95	21	ATGAAGTGTTTGGGGGAACTC/328	gma-miR395				
726	0.95	21	ATGAAGTGTTTGGGGGAACTC/329	mtr-miR395a				
727	0.9	21	ATGAAGTATTTGGGGGAACTC/330	mtr-miR395b				
728	0.95	21	ATGAAGTGTTTGGGGGAACTC/331	mtr-miR395c				
729	0.95	21	ATGAAGTGTTTGGGGGAACTC/332	mtr-miR395d				
730	0.95	21	ATGAAGTGTTTGGGGGAACTC/333	mtr-miR395e				
731	0.95	21	ATGAAGTGTTTGGGGGAACTC/334	mtr-miR395f				
732	0.95	21	TTGAAGTGTTTGGGGGAACTC/335	mtr-miR395g				
733	0.9	21	ATGAAGTGTTTGGGGGAACTT/336	mtr-miR395h				
734	0.95	21	ATGAAGTGTTTGGGGGAACTC/337	mtr-miR395i				
735	0.95	21	ATGAAGTGTTTGGGGGAACTC/338	mtr-miR395j				
736	0.95	21	ATGAAGTGTTTGGGGGAACTC/339	mtr-miR395k				
737	0.95	21	ATGAAGTGTTTGGGGGAACTC/340	mtr-miR395l				
738	0.95	21	ATGAAGTGTTTGGGGGAACTC/341	mtr-miR395m				
739	0.95	21	ATGAAGTGTTTGGGGGAACTC/342	mtr-miR395n				
740	0.95	21	ATGAAGTGTTTGGGGGAACTC/343	mtr-miR395o				
741	0.9	21	TTGAAGCGTTTGGGGGAACTC/344	mtr-miR395p				
742	0.95	21	ATGAAGTG	mtr-				

			TTTGGGGGAACTC/345	miR395q				
743	0.95	21	ATGAAGTGTTTGGGGGAACTC/346	mtr-miR395r				
744	0.95	21	GTGAAGTGCTTGGGGGAACTC/347	osa-miR395a				
745	0.9	20	TGAAGTGCTTGGGGGAACTC/348	osa-miR395a.2				
746	1	21	GTGAAGTGTTTGGGGGAACTC/349	osa-miR395b				
747	0.95	21	GTGAAGTGTTTGGAGGAACTC/350	osa-miR395c				
748	1	21	GTGAAGTGTTTGGGGGAACTC/351	osa-miR395d				
749	1	21	GTGAAGTGTTTGGGGGAACTC/352	osa-miR395e				
750	0.95	21	GTGAATTGTTTGGGGGAACTC/353	osa-miR395f				
751	1	21	GTGAAGTGTTTGGGGGAACTC/354	osa-miR395g				
752	1	21	GTGAAGTGTTTGGGGGAACTC/355	osa-miR395h				
753	1	21	GTGAAGTGTTTGGGGGAACTC/356	osa-miR395i				
754	1	21	GTGAAGTGTTTGGGGGAACTC/357	osa-miR395j				
755	1	21	GTGAAGTGTTTGGGGGAACTC/358	osa-miR395k				
756	1	21	GTGAAGTGTTTGGGGGAACTC/359	osa-miR395l				
757	1	21	GTGAAGTGTTTGGGGGAACTC/360	osa-miR395m				
758	1	21	GTGAAGTGTTTGGGGGAACTC/361	osa-miR395n				
759	0.9	21	ATGAAGTGTTTGGAGGAACTC/362	osa-miR395o				
760	1	21	GTGAAGTGTTTGGGGGAACTC/363	osa-miR395p				

761	1	21	GTGAAGTGTTTGGGGGAACTC/364	osa-miR395q				
762	1	21	GTGAAGTGTTTGGGGGAACTC/365	osa-miR395r				
763	1	21	GTGAAGTGTTTGGGGGAACTC/366	osa-miR395s				
764	0.95	21	GTGAAGTGTTTGGGGAAACTC/367	osa-miR395t				
765	0.9	21	GTGAAGCGTTTGGGGGAAATC/368	osa-miR395u				
766	0.9	21	GTGAAGTATTTGGCGGAACTC/369	osa-miR395v				
767	0.81	22	GTGAAGTGTTTGGGGGATTCTC/370	osa-miR395w				
768	0.86	21	GTGAAGTGTTTGGAGTAGCTC/371	osa-miR395x				
769	1	21	GTGAAGTGTTTGGGGGAACTC/372	osa-miR395y				
770	0.86	21	CTGAAGTGTTTGGAGGAACTT/373	pab-miR395				
771	0.86	21	CTGAAGGGTTTGGAGGAACTC/374	ptc-miR395a				
772	0.95	21	CTGAAGTGTTTGGGGGAACTC/375	ptc-miR395b				
773	0.95	21	CTGAAGTGTTTGGGGGAACTC/376	ptc-miR395c				
774	0.95	21	CTGAAGTGTTTGGGGGAACTC/377	ptc-miR395d				
775	0.95	21	CTGAAGTGTTTGGGGGAACTC/378	ptc-miR395e				
776	0.95	21	CTGAAGTGTTTGGGGGAACTC/379	ptc-miR395f				
777	0.95	21	CTGAAGTGTTTGGGGGAACTC/380	ptc-miR395g				
778	0.95	21	CTGAAGTGTTTGGGGGAACTC/381	ptc-miR395h				
779	0.95	21	CTGAAGTGTTTGGGGG	ptc-miR395i				

			AACTC/382					
780	0.95	21	CTGAAGTGTTTGGGGGAACTC/383	ptc-miR395j				
781	0.95	21	CTGAAGTGTTTGGGGGAACTC/384	rco-miR395a				
782	0.95	21	CTGAAGTGTTTGGGGGAACTC/385	rco-miR395b				
783	0.95	21	CTGAAGTGTTTGGGGGAACTC/386	rco-miR395c				
784	0.95	21	CTGAAGTGTTTGGGGGAACTC/387	rco-miR395d				
785	0.95	21	CTGAAGTGTTTGGGGGAACTC/388	rco-miR395e				
786	1	21	GTGAAGTGTTTGGGGGAACTC/389	sbi-miR395a				
787	1	21	GTGAAGTGTTTGGGGGAACTC/390	sbi-miR395b				
788/849	1	21	GTGAAGTGTTTGGGGGAACTC/391	sbi-miR395c				
789/850	1	21	GTGAAGTGTTTGGGGGAACTC/392	sbi-miR395d				
790	1	21	GTGAAGTGTTTGGGGGAACTC/393	sbi-miR395e				
791	0.95	21	ATGAAGTGTTTGGGGGAACTC/394	sbi-miR395f				
792	1	21	GTGAAGTGTTTGGGGGAACTC/395	sbi-miR395g				
793	1	21	GTGAAGTGTTTGGGGGAACTC/396	sbi-miR395h				
794	1	21	GTGAAGTGTTTGGGGGAACTC/397	sbi-miR395i				
795	1	21	GTGAAGTGTTTGGGGGAACTC/398	sbi-miR395j				
796	0.95	21	GTGAAGTGTTTGGAGGAACTC/399	sbi-miR395k				
797	0.95	21	GTGAAGTGCTTGGGGGAACTC/400	sbi-miR395l				
798	0.95	21	CTGAAGTG	sde-				

			TTTGGGGGAACTC/401	miR395				
799	0.95	22	CTGAAGTGTTTGGGGGAACTCC/402	sly-miR395a				
800	0.95	22	CTGAAGTGTTTGGGGGAACTCC/403	sly-miR395b				
801	1	21	GTGAAGTGTTTGGGGGAACTC/404	tae-miR395a				
802	0.95	20	TGAAGTGTTTGGGGGAACTC/405	tac-miR395b				
803	0.95	21	CTGAAGTGTTTGGGGGAACTC/406	tcc-miR395a				
804	0.95	21	CTGAAGTGTTTGGGGGAACTC/407	tcc-miR395b				
805	0.95	21	CTGAAGTGTTTGGGGGAACTC/408	vvi-miR395a				
806	0.95	21	CTGAAGTGTTTGGGGGAACTC/409	vvi-miR395b				
807	0.95	21	CTGAAGTGTTTGGGGGAACTC/410	vvi-miR395c				
808	0.95	21	CTGAAGTGTTTGGGGGAACTC/411	vvi-miR395d				
809	0.95	21	CTGAAGTGTTTGGGGGAACTC/412	vvi-miR395e				
810	0.95	21	CTGAAGTGTTTGGGGGAACTC/413	vvi-miR395f				
811	0.95	21	CTGAAGTGTTTGGGGGAACTC/414	vvi-miR395g				
812	0.95	21	CTGAAGTGTTTGGGGGAACTC/415	vvi-miR395h				
813	0.95	21	CTGAAGTGTTTGGGGGAACTC/416	vvi-miR395i				
814	0.95	21	CTGAAGTGTTTGGGGGAACTC/417	vvi-miR395j				
815	0.95	21	CTGAAGTGTTTGGGGGAACTC/418	vvi-miR395k				
816	0.95	21	CTGAAGTGTTTGGGGGAACTC/419	vvi-miR395l				

817	0.95	21	CTGAAGTGTTTGGGGGAACTC/420	vvi-miR395m				
818	0.81	21	CTGAAGAGTCTGGAGGAACTC/421	vvi-miR395n				
819	1	21	GTGAAGTGTTTGGGGGAACTC/422	zma-miR395a				
820	0.95	21	GTGAAGTGTTTGGAGGAACTC/423	zma-miR395c				
821/851	1.00/0.90	21/20	GTGAAGTGTTTGGGGGAACTC/424/GTGAAGTGTTTGGAGGAACT/451	zma-miR395d				
822/852	1.00/0.95	21	GTGAAGTGTTTGGGGGAACTC/425/GTGAAGTGTTTGGAGGAACTC/452	zma-miR395e				
823/853	1.00/0.90	21	GTGAAGTGTTTGGGGGAACTC/426/GTGAAGTGTTTGAGGAAACTC/453	zma-miR395f				
824	1	21	GTGAAGTGTTTGGGGGAACTC/427	zma-miR395g				
825	1	21	GTGAAGTGTTTGGGGGAACTC/428	zma-miR395h				
826	1	21	GTGAAGTGTTTGGGGGAACTC/429	zma-miR395i				
827	1	21	GTGAAGTGTTTGGGGGAACTC/430	zma-miR395j				
828	0.9	21	GTGAAGTGTTTGAGGAAACTC/431	zma-miR395k				
829	0.95	21	GTGAAGTGTTTGGAGGAACTC/432	zma-miR395l				
830	0.95	21	GTGAAGTGTTTGGAGGAACTC/433	zma-miR395m				
831	1	21	GTGAAGTGTTTGGGGGAACTC/434	zma-miR395n				
832	0.95	21	GTGAAGTGTTTGGGTG	zma-miR395o				

			AACTC/435					
833	1	21	GTGAAGTG TTTGGGGG AACTC/436	zma-miR395p				
834	0.86	21	AGAAGAGA GAGAGCAC AACCC/437	aqc-miR529	56	21	AGAAGA GAGAGA GTACAG CCT/1	zma-miR529
835	1	21	AGAAGAGA GAGAGTAC AGCCT/438	bdi-miR529				
836	0.9	21	AGAAGAGA GAGAGCAC AGCTT/439	far-miR529				
837	0.95	21	AGAAGAGA GAGAGTAC AGCTT/440	osa-miR529b				
838	0.86	21	CGAAGAGA GAGAGCAC AGCCC/441	ppt-miR529a				
839	0.86	21	CGAAGAGA GAGAGCAC AGCCC/442	ppt-miR529b				
840	0.86	21	CGAAGAGA GAGAGCAC AGCCC/443	ppt-miR529c				
841	0.9	21	AGAAGAGA GAGAGCAC AGCCC/444	ppt-miR529d				
842	0.95	21	AGAAGAGA GAGAGTAC AGCCC/445	ppt-miR529e				
843	0.95	21	AGAAGAGA GAGAGTAC AGCCC/446	ppt-miR529f				
844	0.81	21	CGAAGAGA GAGAGCAC AGTCC/447	ppt-miR529g				
845	0.9	22	TAGCCAAG GATGATTT GCCTGT/448	bdi-miR169k		21	TAGCCA AGCATG ATTTGCC CG/5	Predicted zma mir 50601
846	0.9	21	TAGCCAAG GATGATTT GCCTG/449	sbi-miR169o				

EXAMPLE 3

Identification of miRNAs Associated with Increased NUE and Target Prediction Using Bioinformatics Tools

miRNAs that are associated with improved NUE and/or abiotic or biotic stress tolerance were identified by computational algorithms that analyze RNA expression profiles alongside publicly available gene and protein databases. A high throughput screening was performed on microarrays loaded with miRNAs that were found to be differentially expressed under multiple stress and optimal environmental conditions and in different plant tissues. The initial trait-associated miRNAs were later validated by quantitative Real Time PCR (qRT-PCR).

Target prediction – orthologous genes to the genes of interest in maize and/or Arabidopsis were found through a bioinformatic tool that analyzes publicly available genomic as well as expression and gene annotation databases from multiple plant species. Homologous as well as orthologous protein and nucleotide sequences of target genes of the small RNA sequences of the invention, were found using BLAST having at least 70 % identity on at least 60 % of the entire master (maize) gene length, and are summarized in Tables 5-6 below.

Table 5: Target Genes of Small RNA Molecules that are upregulated during NUE.

Nucleotide Sequence seq id no:	**Protein Sequence seq id no:**	**Organism**	**% Identity**	**Anotation**	**Nucleotide NCBI GI number**	**Homolog NCBI Accession**	**miR Binding Position**	**miR sequence**	**miR name**
895	854	Zea mays	1	hypothetical protein LOC100384547 [Zea mays] >gi|238005886|gb|ACR33978.1| unknown [Zea mays]	293331460	NP_001170533	105-125	AGGATGCTGACGCAATGGGAT/9	Predicted zma mir 48486
	855	Zea mays	1	putative gag-pol polyprotein [Zea mays]	23928433	AAN40030	33-54	AGGATGTGAGGCTATTGGGGAC/6	Predicted zma mir 48492
896	856	Eulaliopsis binata	1	embryonic flower 1 protein [Eulaliopsis binata]	315493433	ADU32889	1977-1997	TTAGATGACCATCAGCAAACA/10	zma-miR827
897	857	Zea mays	0.923445	EMF-like [Zea mays]	85062576	ABC69154			

<table>
<tr><td>898</td><td>858</td><td>Zea mays</td><td>0.9346093</td><td>VEF family protein [Zea mays] >gi|29569111|gb|AAO84022.1| VEF family protein [Zea mays] >gi|60687422|gb|AAX35735.1| embryonic flower 2 [Zea mays]</td><td>162461707</td><td>NP_001105530</td><td></td><td></td><td></td></tr>
<tr><td>899</td><td>859</td><td>Dendrocalamus latiflorus</td><td>0.8054226</td><td>EMF2 [Dendrocalamus latiflorus]</td><td>82469918</td><td>ABB77210</td><td></td><td></td><td></td></tr>
<tr><td>900</td><td>860</td><td>Triticum aestivum</td><td>0.7974482</td><td>embryonic flower 2 [Triticum aestivum]</td><td>62275660</td><td>AAX78232</td><td></td><td></td><td></td></tr>
<tr><td>901</td><td>861</td><td>Oryza sativa Japonica Group</td><td>0.7575758</td><td>Os09g0306800 [Oryza sativa Japonica Group] >gi|255678755|dbj|BAF24739.2| Os09g0306800 [Oryza sativa Japonica Group]</td><td>115478459</td><td>NP_001062825</td><td></td><td></td><td></td></tr>
<tr><td></td><td>862</td><td>Oryza sativa Japonica Group</td><td>0.7575758</td><td>putative VEF family protein [Oryza sativa Japonica Group]</td><td>51091694</td><td>BAD36510</td><td></td><td></td><td></td></tr>
<tr><td>902</td><td>863</td><td>Eulaliopsis binata</td><td>0.7575758</td><td>embryonic flower 2 protein [Eulaliopsis binata]</td><td>315493435</td><td>ADU32890</td><td></td><td></td><td></td></tr>
<tr><td>903</td><td>864</td><td>Hordeum vulgare subsp. vulgare</td><td>0.76874</td><td>predicted protein [Hordeum vulgare subsp. vulgare]</td><td>326503299</td><td>BAJ99275</td><td></td><td></td><td></td></tr>
<tr><td>904</td><td>865</td><td>Hordeum vulgare</td><td>0.7703349</td><td>HvEMF2b [Hordeum vulgare]</td><td>66796110</td><td>BAD99131</td><td></td><td></td><td></td></tr>
</table>

905	866	Zea mays	1	VEF family protein [Zea mays] >gi|29569111|gb|AAO84022.1| VEF family protein [Zea mays] >gi|60687422|gb|AAX35735.1| embryonic flower 2 [Zea mays]	162461707	NP_001105530	1748-1768		
906	867	Zea mays	0.9792332	EMF-like [Zea mays]	85062576	ABC69154			
907	868	Eulaliopsis binata	0.9361022	embryonic flower 1 protein [Eulaliopsis binata]	315493433	ADU32889			
908	869	Dendrocalamus latiflorus	0.8083067	EMF2 [Dendrocalamus latiflorus]	82469918	ABB77210			
909	870	Triticum aestivum	0.8019169	embryonic flower 2 [Triticum aestivum]	62275660	AAX78232			
910	871	Oryza sativa Japonica Group	0.7571885	Os09g0306800 [Oryza sativa Japonica Group] >gi|255678755|dbj|BAF24739.2| Os09g0306800 [Oryza sativa Japonica Group]	115478459	NP_001062825			
	872	Oryza sativa Japonica Group	0.7555911	putative VEF family protein [Oryza sativa Japonica Group]	51091694	BAD36510			
911	873	Eulaliopsis binata	0.7635783	embryonic flower 2 protein [Eulaliopsis binata]	315493435	ADU32890			
912	874	Hordeum vulgare subsp.	0.7747604	predicted protein [Hordeum	326503299	BAJ99275			

		vulgare		vulgare subsp. vulgare]					
913	875	Hordeum vulgare	0.7763578	HvEMF2b [Hordeum vulgare]	66796110	BAD99131			
	876	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_04g031920 [Sorghum bicolor] >gi|241934313|gb|EES07458.1| hypothetical protein SORBIDRAFT_04g031920 [Sorghum bicolor]	255761094	XP_002454482	580-600		
914	877	Zea mays	0.9425287	unknown [Zea mays]	223972968	ACN30672			
915	878	Zea mays	0.941092	hypothetical protein LOC100501893 [Zea mays] >gi|238011698|gb|ACR36884.1| unknown [Zea mays]	308044322	NP_001183461			

	879	Oryza sativa Japonica Group	0.8706897	RecName: Full=SPX domain-containing membrane protein Os02g45520 >gi|306756291|sp|A2X8A7.2|SPXM1_ORYSI RecName: Full=SPX domain-containing membrane protein OsI_08463 >gi|50252990|dbj|BAD29241.1| SPX (SYG1/Pho81/XPR1) domain-containing protein-like [Oryza sativa Japonica Group] >gi|50253121|dbj|BAD29367.1| SPX (SYG1/Pho81/XPR1) domain-containing protein-like [Oryza sativa Japonica Group]		Q6EPQ3			
916	880	Hordeum vulgare subsp. vulgare	0.8347701	predicted protein [Hordeum vulgare subsp. vulgare]	326502341	BAJ95234			
	881	Oryza sativa Japonica Group	0.808908	OSJNBa0019K04.6 [Oryza sativa Japonica Group] >gi|125591348|gb|EAZ31698.1| hypothetical protein	38605939	CAD41659			

				OsJ_15847 [Oryza sativa Japonica Group]					
917	882	Oryza sativa Japonica Group	0.808908	Os04g0573000 [Oryza sativa Japonica Group] >gi|306756012|sp|B8AT51.1|SPXM2_ORYSI RecName: Full=SPX domain-containing membrane protein OsI_17046 >gi|306756288|sp|Q0JAW2.2|SPXM2_ORYSJ RecName: Full=SPX domain-containing membrane protein Os04g0573000 >gi|215694614|dbj|BAG89805.1| unnamed protein product [Oryza sativa Japonica Group] >gi|218195403|gb|EEC77830.1| hypothetical protein OsI_17046 [Oryza sativa Indica Group] >gi|255675707|dbj|BAF15525.2|	115460021	NP_001053611			

				Os04g0573000 [Oryza sativa Japonica Group]					
918	883	Oryza sativa Indica Group	0.8060345	OSIGBa0147H17.5 [Oryza sativa Indica Group]	116309919	CAH66957			
	884	Sorghum bicolor	0.7844828	hypothetical protein SORBIDRAFT_06g025950 [Sorghum bicolor] >gi|241938147|gb|EES11292.1| hypothetical protein SORBIDRAFT_06g025950 [Sorghum bicolor]	255761094	XP_002446964			
919	885	Vitis vinifera	0.7212644	PREDICTED: hypothetical protein [Vitis vinifera] >gi|297742609|emb|CB	225426756	XP_002282540			

				I34758.3| unnamed protein product [Vitis vinifcra]					
	886	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_02g027920 [Sorghum bicolor] >gi|241925925|gb|EER99069.1| hypothetical protein SORBIDRAFT_02g027920 [Sorghum bicolor]	255761094	XP_002462548	965-985		
920	887	Zea mays	0.8819188	hypothetical protein LOC100279277 [Zea mays] >gi|219884365|gb|ACL52557.1| unknown [Zea mays]	226498793	NP_001145770			
921	888	Zea mays	0.8523985	unknown [Zea mays]	224030802	ACN34477			
922	889	Zea mays	0.8523985	hypothetical protein LOC100278416 [Zea mays] >gi|195652339|gb|ACG45637.1| hypothetical protein [Zea mays]	226530255	NP_001145176			
923	890	Zea mays	1	hypothetical protein LOC100191388 [Zea mays] >gi|194688768|gb|ACF78468.1| unknown [Zea mays]	212274814	NP_001130294	1075-1095		

924	891	Oryza sativa Japonica Group	0.7869822	Os09g0135400 [Oryza sativa Japonica Group] >gi|47848428|dbj|BAD22285.1| putative octicosapeptide/Phox/Bem1p (PB1) domain-containing protein [Oryza sativa Japonica Group] >gi|113630871|dbj|BAF24552.1| Os09g0135400 [Oryza sativa Japonica Group]	115478085	NP_001062638			
	892	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_02g037770 [Sorghum bicolor] >gi|241924313|gb|EER97457.1| hypothetical protein SORBIDRAFT_02g037770 [Sorghum bicolor]	255761094	XP_002460936	547-567	ATTCACGGGGACGAACCTCCT/8	mtr-miR2647a
925	893	Zea mays	0.8738462	hypothetical protein LOC100279098 [Zea mays] >gi|195658887|gb|ACG48911.1| hypothetical protein [Zea mays]	226507742	NP_001145615			

926	894	Zea mays	0.8307692	hypothetical protein LOC100278263 [Zea mays] >gi|195650593|gb|ACG44764.1| hypothetical protein [Zea mays]	226495966	NP_001145067			

Table 6: Target Genes of Small RNA Molecules that are down regulated during NUE.

Nucleotide seq id no:	Protein seq id no:	Organism	% Identity	Annotation	Nucleotide NCBI GI number	Homologue NCBI Accession	miR Binding Position	miR sequence	miR name
	927	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_01g008450 [Sorghum bicolor] >gi|241917750|gb|EER90894.1| hypothetical protein SORBIDRAFT_01g008450 [Sorghum bicolor]	255761094	XP_002463896	426-446	GTGAAGTGTTTGGGGGAACTC/4	zma-miR395b
1022	928	Zea mays	0.946721311	unknown [Zea mays]	223949050	ACN28609			
1023	929	Zea mays	0.954918033	unknown [Zea mays]	224029894	ACN34023			
1024	930	Zea mays	0.942622951	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase [Zea mays]	195651448	ACG45192			

1025	931	Zea mays	0.946721311	ATP sulfurylase [Zea mays] >gi|2738750|gb|AAB94542.1| ATP sulfurylase [Zea mays]	162463127	NP_001104877			
	932	Oryza sativa Indica Group	0.799180328	hypothetical protein OsI_13470 [Oryza sativa Indica Group]	54362548	EAY91825			
1026	933	Oryza sativa Japonica Group	0.797131148	Os03g0743900 [Oryza sativa Japonica Group] >gi|30017582|gb|AAP13004.1| putative ATP sulfurylase [Oryza sativa Japonica Group] >gi|108711024|gb|ABF98819.1| Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthethase, putative, expressed [Oryza sativa Japonica Group] >gi|113549705|dbj|BAF13148.1| Os03g0743900 [Oryza sativa Japonica Group] >gi|215704581|dbj|BAG94214.1 unnamed	115455266	NP_001051234			

				protein product [Oryza sativa Japonica Group]					
1027	934	Hordeum vulgare subsp. vulgare	0.793032787	predicted protein [Hordeum vulgare subsp. vulgare] >gi|326502564|dbj|BAJ95345.1| predicted protein [Hordeum vulgare subsp. vulgare]	326491124	BAK05662			
1028	935	Oryza sativa Indica Group	0.797131148	plastidic ATP sulfurylase [Oryza sativa Indica Group]	3986152	BAA36274			
	936	Oryza sativa Japonica Group	0.770491803	hypothetical protein OsJ_12530 [Oryza sativa	54398660	EAZ28548			

				Japonica Group]					
	937	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_08g004650 [Sorghum bicolor] >gi|241942597|gb|EES15742.1| hypothetical protein SORBIDRAFT_08g004650 [Sorghum bicolor]	255761094	XP_002441904	352-372		
1029	938	Oryza sativa Japonica Group	0.705440901	Os12g0174100 [Oryza sativa Japonica Group] >gi|77553790|gb|ABA96586.1| Growth regulator protein, putative, expressed [Oryza sativa Japonica Group] >gi|255670095|dbj|BAF29304.2| Os12g0174100 [Oryza sativa Japonica Group]	115487595	NP_001066285			
	939	Oryza sativa Japonica Group	0.705440901	hypothetical protein OsJ_35390 [Oryza sativa Japonica Group]	54398660	EEE52851			
	940	Oryza sativa Indica Group	0.701688555	hypothetical protein OsI_37646 [Oryza sativa Indica Group]	54362548	EEC68940			

1030	941	Zea mays	1	unknown [Zea mays]	224029894	ACN34023	616-636		
1031	942	Zea mays	0.983640082	ATP sulfurylase [Zea mays] >gi|2738750|gb|AAB94542.1| ATP sulfurylase [Zea mays]	162463127	NP_001104877			
1032	943	Zea mays	0.940695297	unknown [Zea mays]	223949050	ACN28609			
1033	944	Zea mays	0.936605317	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase [Zea mays]	195651448	ACG45192			
	945	Sorghum bicolor	0.938650307	hypothetical protein SORBIDRAFT_01g008450 [Sorghum bicolor] >gi|241917750|gb|EER90894.1| hypothetical protein SORBIDRAFT_01g008450 [Sorghum bicolor]	255761094	XP_002463896			
1034	946	Hordeum vulgare subsp. vulgare	0.842535787	predicted protein [Hordeum vulgare subsp. vulgare] >gi|326502564|dbj|BAJ95345.1| predicted protein [Hordeum vulgare subsp. vulgare]	326491124	BAK05662			
	947	Oryza sativa Indica Group	0.795501022	hypothetical protein OsI_13470 [Oryza sativa Indica Group]	54362548	EAY91825			

1035	948	Oryza sativa Japonica Group	0.793456033	Os03g0743900 [Oryza sativa Japonica Group] >gi|30017582|gb|AAP13004.1| putative ATP sulfurylase [Oryza sativa Japonica Group] >gi|108711024|gb|ABF98819.1| Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthethase, putative, expressed [Oryza sativa Japonica Group] >gi|113549705|dbj|BAF13148.1| Os03g0743900 [Oryza sativa Japonica Group] >gi|215704581|dbj|BAG94214.1 unnamed protein product [Oryza sativa Japonica Group]	115455266	NP_001051234			
1036	949	Oryza sativa Indica Group	0.793456033	plastidic ATP sulfurylase [Oryza sativa Indica Group]	3986152	BAA36274			

	950	Oryza sativa Japonica Group	0.764826176	hypothetical protein OsJ_12530 [Oryza sativa Japonica Group]	54398660	EAZ28548			
	951	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_04g026710 [Sorghum bicolor] >gi|241932317|gb|EES05462.1| hypothetical protein SORBIDRAFT_04g026710 [Sorghum bicolor]	255761094	XP_002452486	1000-1020	GGAATCTTGATGATGCTGCAT/3	zma-miR172c
1037	952	Zea mays	0.880208333	unknown [Zea mays]	223974072	ACN31224			
1038	953	Zea mays	0.880208333	hypothetical protein LOC100276301 [Zea mays] >gi|195623072|gb|ACG33366.1 hypothetical protein [Zea mays]	226500051	NP_001143596			
1039	954	Zea mays	0.864583333	hypothetical protein LOC100277041 [Zea mays] >gi|195638130|gb|ACG38533.1 hypothetical protein [Zea mays] >gi|223942145|gb|ACN25156.1 unknown [Zea mays]	226492590	NP_001144184			

1040	955	Oryza sativa Japonica Group	0.776041667	Os02g0631000 [Oryza sativa Japonica Group] >gi|4938984|dbj|BAD26474.1| unknown protein [Oryza sativa Japonica Group] >gi|113537028|dbj|BAF09411.1| Os02g0631000 [Oryza sativa Japonica Group] >gi|215697023|dbj|BAG91017.1 unnamed protein product [Oryza sativa Japonica Group] >gi|218191219|gb|EEC73646.1| hypothetical protein OsI_08167 [Oryza sativa Indica Group] >gi|222623287|gb|EEE57419.1| hypothetical protein OsJ_07614 [Oryza sativa Japonica Group]	115447434	NP_001047497			

1041	956	Hordeum vulgare subsp. vulgare	0.760416667	predicted protein [Hordeum vulgare subsp. vulgare] >gi|326519272|dbj|BAJ96635.1| predicted protein [Hordeum vulgare subsp. vulgare]	326512283	BAJ96123			
1042	957	Zea mays	1	AP2 domain transcription factor [Zea mays]	148964889	ABR19871	869-889		
1043	958	Zea mays	0.96043956	AP2 domain transcription factor [Zea mays]	148964859	ABR19870			
	959	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_02g007000 [Sorghum bicolor] >gi|241922957|gb|EER96101.1| hypothetical protein SORBIDRAFT_02g007000 [Sorghum bicolor]	255761094	XP_002459580	1539-1559		
1044	960	Zea mays	0.85528757	sister of indeterminate spikelet 1 [Zea mays] >gi|223947941|gb|ACN28054.1 unknown [Zea mays]	225703093	NP_001139539			
1045	961	Zea mays	0.844155844	sister of indeterminate spikelet 1 [Zea mays]	224579291	ACN58224			
1046	962	Zea mays	0.742115028	floral homeotic protein [Zea mays] >gi|238015134|gb|AC	195653672	ACG46304			

				R38602.1| unknown [Zea mays]					
1047	963	Oryza sativa Japonica Group	1	Os01g0834500 [Oryza sativa Japonica Group] >gi|115456215|ref|NP_001051708.1| Os03g0818400 [Oryza sativa Japonica Group] >gi|297720551|ref|NP_001172637.1| Os01g0834601 [Oryza sativa Japonica Group] >gi|313103637|pdb|3IZ6|L Chain L, Localization Of The Small Subunit Ribosomal Proteins Into A 5.5 A Cryo-Em Map Of Triticum Aestivum Translating 80s Ribosome >gi|20805266|dbj|BAB92932.1| putative 40s ribosomal protein S23 [Oryza sativa Japonica Group] >gi|20805	115440880	NP_001044720	1121-1141		

				267|dbj|BAB92933.1| putative 40s ribosomal protein S23 [Oryza sativa Japonica Group] >gi|21671347|dbj|BAC02683.1| putative 40s ribosomal protein S23 [Oryza sativa Japonica Group] >gi|21671348|dbj|BAC02684.1| putative 40s ribosomal protein S23 [Oryza sativa Japonica Group] >gi|28876025|gb|AAO60034.1| 40S ribosomal protein S23 [Oryza sativa Japonica Group] >gi|29124115|gb|AAO65856.1| 40S ribosomal protein S23 [Oryza sativa Japonica Group] >gi|108711771|gb|ABF99566.1| 40S ribosomal protein S23, putative, expressed [Oryza sativa Japonica					

<table>
<tr><td></td><td></td><td></td><td></td><td>Group] >gi|113534251|dbj|BAF06634.1| Os01g0834500 [Oryza sativa Japonica Group] >gi|113550179|dbj|BAF13622.1| Os03g0818400 [Oryza sativa Japonica Group] >gi|125528286|gb|EAY76400.1 hypothetical protein OsI_04329 [Oryza sativa Indica Group] >gi|125546216|gb|EAY92355.1 hypothetical protein OsI_14082 [Oryza sativa Indica Group] >gi|215697420|dbj|BAG91414.1 unnamed protein product [Oryza sativa Japonica Group] >gi|215734943|dbj|BAG95665.1 unnamed protein product [Oryza sativa Japonica Group] >gi|255673847|dbj|BAH91367.1</td><td></td><td></td><td></td><td></td><td></td></tr>
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				Os01g0834601 [Oryza sativa Japonica Group] >gi|326501134|dbj|BAJ98798.1| predicted protein [Hordeum vulgare subsp. vulgare] >gi|326506086|dbj|BAJ91282.1| predicted protein [Hordeum vulgare subsp. vulgare]					

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<tr><td>1048</td><td>964</td><td>Zea mays</td><td>0.992957746</td><td>hypothetical protein LOC100192600 [Zea mays] >gi|242032479|ref|XP_002463634.1| hypothetical protein SORBIDRAFT_01g003410 [Sorghum bicolor] >gi|242059153|ref|XP_002458722.1| hypothetical protein SORBIDRAFT_03g039010 [Sorghum bicolor] >gi|242090801|ref|XP_002441233.1| hypothetical protein SORBIDRAFT_09g022840 [Sorghum bicolor] >gi|194691088|gb|ACF79628.1| unknown [Zea mays] >gi|194697612|gb|ACF82890.1| unknown [Zea mays] >gi|194702740|gb|ACF85454.1| unknown [Zea mays] >gi|195606082|gb|ACG24871.1 40S ribosomal protein S23 [Zea mays] >gi|19561</td><td>212722729</td><td>NP_001131287</td><td></td><td></td><td></td></tr>
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				8728|gb|ACG31194.1 40S ribosomal protein S23 [Zea mays] >gi|195619636|gb|ACG31648.1 40S ribosomal protein S23 [Zea mays] >gi|195625318|gb|ACG34489.1 40S ribosomal protein S23 [Zea mays] >gi|195628702|gb|ACG36181.1 40S ribosomal protein S23 [Zea mays] >gi|195657679|gb|ACG48307.1 40S ribosomal protein S23 [Zea mays] >gi|238012290|gb|ACR37180.1| unknown [Zea mays] >gi|241917488|gb|EER90632.1| hypothetical protein SORBIDRAFT_01g003410 [Sorghum bicolor] >gi|241930697|gb|EES03842.1| hypothetical protein SORBIDRAFT_03g039010 [Sorghum bicolor] >gi|24194					

				6518|gb|EES19663.1| hypothetical protein SORBIDRAFT_09g022840 [Sorghum bicolor]					
1049	965	Zea mays	0.985915493	40S ribosomal protein S23 [Zea mays]	195622025	ACG32843			
1050	966	Elaeis guineensis	0.978873239	40S ribosomal protein S23 [Elaeis guineensis] >gi|192910894|gb|ACF06555.1| 40S ribosomal protein S23 [Elaeis guineensis]	192910819	ACF06518			
1051	967	Elaeis guineensis	0.971830986	40S ribosomal protein S23 [Elaeis guineensis]	192910821	ACF06519			

1052	968	Solanum tuberosum	0.964788732	unknown [Solanum tuberosum]	77999292	ABB16993			
	969	Ricinus communis	0.964788732	40S ribosomal protein S23, putative [Ricinus communis] >gi|255568414|ref|XP_002525181.1| 40S ribosomal protein S23, putative [Ricinus communis] >gi|223535478|gb|EEF37147.1| 40S ribosomal protein S23, putative [Ricinus communis] >gi|223536832|gb|EEF38471.1| 40S ribosomal protein S23, putative [Ricinus communis]	255761086	XP_002523902			
1053	970	Vitis vinifera	0.964788732	PREDICTED: hypothetical protein [Vitis vinifera]	225439887	XP_002279025			
1054	971	Zea mays	1	unknown [Zea mays] >gi|223973927|gb|ACN31151.1 unknown [Zea mays] >gi|323388595|gb|ADX60102.1 SBP transcription factor [Zea mays]	223972764	ACN30570	882-902	AGAAGAGAGAGAGTACAGCCT/1	zma-miR529

1055	972	Zea mays	0.984615385	hypothetical protein LOC100278824 [Zea mays] >gi|195656399|gb|ACG47667.1 hypothetical protein [Zea mays]	226530074	NP_001145445			
	973	Sorghum bicolor	0.870769231	hypothetical protein SORBIDRAFT_05g017510 [Sorghum bicolor] >gi|241936618|gb|EES09763.1| hypothetical protein SORBIDRAFT_05g017510 [Sorghum bicolor]	255761094	XP_002450775			
	974	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_03g025410 [Sorghum bicolor] >gi|241927774|gb|EES00919.1| hypothetical protein SORBIDRAFT_03g025410 [Sorghum bicolor]	255761094	XP_002455799	45-65		
1056	975	Zea mays	0.893939394	unknown [Zea mays]	223946882	ACN27525			
1057	976	Zea mays	0.890151515	hypothetical protein LOC100278489 [Zea mays] >gi|195653155|gb|ACG46045.1 hypothetical protein [Zea mays]	226501393	NP_001145223			

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<tr><td>1058</td><td>977</td><td>Zea mays</td><td>1</td><td>unknown [Zea mays] >gi|323388573|gb|ADX60091.1 SBP transcription factor [Zea mays]</td><td>238908852</td><td>ACF86782</td><td>9910, 6-916</td><td></td><td></td></tr>
<tr><td>1059</td><td>978</td><td>Zea mays</td><td>0.997354497</td><td>squamosa promoter-binding-like protein 9 [Zea mays]</td><td>195651290</td><td>ACG45113</td><td></td><td></td><td></td></tr>
<tr><td></td><td>979</td><td>Sorghum bicolor</td><td>0.828042328</td><td>hypothetical protein SORBIDRAFT_02g028420 [Sorghum bicolor] >gi|241925948|gb|EER99092.1| hypothetical protein SORBIDRAFT_02g028420 [Sorghum bicolor]</td><td>255761094</td><td>XP_002462571</td><td></td><td></td><td></td></tr>
<tr><td>1060</td><td>980</td><td>Zea mays</td><td>0.756613757</td><td>hypothetical protein LOC100217104 [Zea mays] >gi|194697718|gb|ACF82943.1| unknown [Zea mays]</td><td>219363104</td><td>NP_001136945</td><td></td><td></td><td></td></tr>
<tr><td>1061</td><td>981</td><td>Zea mays</td><td>1</td><td>squamosa promoter-binding-like protein 11 [Zea mays] >gi|195627850|gb|ACG35755.1 squamosa promoter-binding-like protein 11 [Zea mays] >gi|195644948|gb|ACG41942.1 squamosa promoter-</td><td>226529809</td><td>NP_001149534</td><td>1348-1368</td><td></td><td></td></tr>
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				binding-like protein 11 [Zea mays]					
	982	Sorghum bicolor	0.876993166	hypothetical protein SORBIDRAFT_10g029190 [Sorghum bicolor] >gi|241917194|gb|EER90338.1| hypothetical protein SORBIDRAFT_10g029190 [Sorghum bicolor]	255761094	XP_002438971			
1062	983	Zea mays	1	hypothetical protein LOC100217104 [Zea mays] >gi|194697718|gb|ACF82943.1| unknown [Zea mays]	219363104	NP_001136945	973-993		
	984	Sorghum bicolor	0.817232376	hypothetical protein SORBIDRAFT_02g028420 [Sorghum bicolor] >gi|241925948|gb|EER99092.1| hypothetical protein SORBIDRAFT_02g028420 [Sorghum bicolor]	255761094	XP_002462571			

1063	985	Zea mays	0.759791123	unknown [Zea mays] >gi|323388573|gb|ADX60091.1 SBP transcription factor [Zea mays]	238908852	ACF86782			
1064	986	Zea mays	0.757180157	squamosa promoter-binding-like protein 9 [Zea mays]	195651290	ACG45113			
1065	987	Zea mays	1	SBP-domain protein 5 [Zea mays]	5931785	CAB56631	558-578		
	988	Sorghum bicolor	0.854103343	hypothetical protein SORBIDRAFT_07g027740 [Sorghum bicolor] >gi|241941121|gb|EES14266.1| hypothetical protein SORBIDRAFT_07g027740 [Sorghum bicolor]	255761094	XP_002444771			
1066	989	Zea mays	0.784194529	unknown [Zea mays]	219885132	ACL52941			
1067	990	Zea mays	1	MTA/SAH nucleosidase [Zea mays] >gi|195658647|gb|ACG48791.1 MTA/SAH nucleosidase [Zea mays] >gi|223973627|gb|ACN31001.1 unknown [Zea mays]	226529725	NP_001152658	1410-1430		
1068	991	Zea mays	0.884462151	unknown [Zea mays]	194699507	ACF83838			
1069	992	Zea mays	0.884462151	MTA/SAH nucleosidase [Zea mays]	195640251	ACG39594			

	993	Sorghum bicolor	0.884462151	hypothetical protein SORBIDRAFT_07g026190 [Sorghum bicolor] >gi|241942163|gb|EES15308.1| hypothetical protein SORBIDRAFT_07g026190 [Sorghum bicolor]	255761094	XP_002445813			
1070	994	Zea mays	0.900398406	unknown [Zea mays]	223974590	ACN31483			
1071	995	Oryza sativa Japonica Group	0.796812749	Os06g0112200 [Oryza sativa Japonica Group] >gi|7363290|dbj|BAA93034.1| methylthioadenosine/S-adenosyl homocysteine nucleosidase [Oryza sativa Japonica Group] >gi|32352128|dbj|BAC78557.1| hypothetical protein [Oryza sativa Japonica Group] >gi|113594632|dbj|BAF18506.1| Os06g0112200 [Oryza sativa Japonica Group] >gi|125595804|gb|EAZ35584.1| hypothetical protein OsJ_19870	115465985	NP_001056592			

				[Oryza sativa Japonica Group] >gi|215694661|dbj|BAG89852.1 unnamed protein product [Oryza sativa Japonica Group] >gi|215740802|dbj|BAG96958.1 unnamed protein product [Oryza sativa Japonica Group]					
1072	996	Oryza sativa	0.792828685	methylthioadenosine/S-adenosyl homocysteine nucleosidase [Oryza sativa]	18087496	AAL58883			
1073	997	Oryza sativa Indica Group	0.792828685	mta/sah nucleosidase [Oryza sativa Indica Group]	149390954	ABR25495			
1074	998	Hordeum vulgare subsp. vulgare	0.780876494	predicted protein [Hordeum vulgare subsp. vulgare] >gi|326534118|dbj|BAJ89409.1|	326512819	BAK03317			

				predicted protein [Hordeum vulgare subsp. vulgarc]					
	999	Oryza sativa Indica Group	0.784860558	hypothetical protein OsI_21350 [Oryza sativa Indica Group]	54362548	EAY99382			
1075	1000	Zea mays subsp. mays	1	teosinte glume architecture 1 [Zea mays subsp. mays]	72536147	AAX83872	1197-1217		
	1001	Zea mays subsp. mays	0.983796296	teosinte glume architecture 1 [Zea mays subsp. mays]		AAX83875			
1076	1002	Zea mays subsp. mays	0.990740741	teosinte glume architecture 1 [Zea mays subsp. mays] >gi|62467440|gb|AAX83874.1| teosinte glume architecture 1 [Zea mays subsp. mays]	62467433	AAX83873			
	1003	Sorghum bicolor	0.800925926	hypothetical protein SORBIDRAFT_07g026220 [Sorghum bicolor] >gi|241942165|gb|EES15310.1| hypothetical protein SORBIDRAFT_07g026220 [Sorghum bicolor]	255761094	XP_002445815			

	1004	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_02g038960 [Sorghum bicolor] >gi|241926544|gb|EER99688.1| hypothetical protein SORBIDRAFT_02g038960 [Sorghum bicolor]	255761094	XP_002463167	1112-1132	TAGCCAGGGATGATTTGCCTG/2	zma-miR1691
1077	1005	Zea mays	0.897009967	nuclear transcription factor Y subunit A-3 [Zea mays]	195634708	ACG36823			
1078	1006	Zea mays	0.890365449	hypothetical protein LOC100194182 [Zea mays] >gi|194695138|gb|ACF81653.1| unknown [Zea mays] >gi|195625280|gb|ACG34470.1 nuclear transcription factor Y subunit A-3 [Zea mays]	212723473	NP_001132701			
1079	1007	Zea mays	0.887043189	unknown [Zea mays]	224028448	ACN33300			
1080	1008	Zea mays	0.853820598	unknown [Zea mays]	194699259	ACF83714			
1081	1009	Zea mays	0.853820598	nuclear transcription factor Y subunit A-3 [Zea mays]	195609807	ACG26734			
1082	1010	Zea mays	0.850498339	nuclear transcription factor Y subunit A-3 [Zea mays] >gi|195609780|gb|ACG26720.1 nuclear transcription	226499901	NP_001147311			

				factor Y subunit A-3 [Zea mays]					
1083	1011	Zea mays	1	hypothetical protein LOC100194182 [Zea mays] >gi|194695138|gb|ACF81653.1| unknown [Zea mays] >gi|195625280|gb|ACG34470.1 nuclear transcription factor Y subunit A-3 [Zea mays]	212723473	NP_001132701	1108-1128		
1084	1012	Zea mays	0.996666667	unknown [Zea mays]	224028448	ACN33300			
1085	1013	Zea mays	0.98	nuclear transcription factor Y subunit A-3 [Zea mays]	195634708	ACG36823			
	1014	Sorghum bicolor	0.893333333	hypothetical protein SORBIDRAFT_02g038960 [Sorghum bicolor] >gi|241926544|gb|EER99688.1| hypothetical protein SORBIDRAFT_02g038960 [Sorghum bicolor]	255761094	XP_002463167			
1086	1015	Zea mays	0.853333333	unknown [Zea mays]	194699259	ACF83714			
1087	1016	Zea mays	0.856666667	nuclear transcription factor Y subunit A-3 [Zea mays]	195609807	ACG26734			

1088	1017	Zea mays	0.853333333	nuclear transcription factor Y subunit A-3 [Zea mays] >gi|195609780|gb|ACG26720.1 nuclear transcription factor Y subunit A-3 [Zea mays]	226499901	NP_001147311			
1089	1018	Zea mays	1	nuclear transcription factor Y subunit A-3 [Zea mays] >gi|195624530|gb|ACG34095.1 nuclear transcription factor Y subunit A-3 [Zea mays]	226502984	NP_001149075	979-999		
	1019	Sorghum bicolor	0.814545455	hypothetical protein SORBIDRAFT_04g034760 [Sorghum bicolor] >gi|241934478|gb|EES07623.1| hypothetical protein SORBIDRAFT_04g034760 [Sorghum bicolor]	255761094	XP_002454647			
	1020	Sorghum bicolor	1	hypothetical protein SORBIDRAFT_01g004290 [Sorghum bicolor] >gi|241917544|gb|EER90688.1| hypothetical protein SORBIDRAFT_01g004290 [Sorghum bicolor]	255761094	XP_002463690	946-966		
1090	1021	Zea mays	0.836633	unknown	194696171	ACF8217			

			663	[Zea mays]		0				

EXAMPLE 4

Verification of Expression of miRNAs Associated with Increased NUE

Following identification of dsRNAs potentially involved in improvement of maize NUE using bioinformatics tools, as described in Examples 1-2 above, the actual mRNA levels were determined using reverse transcription assay followed by quantitative Real-Time PCR (qRT-PCR) analysis. RNA levels were compared between different tissues, developmental stages, growth conditions and/or genetic backgrounds incorporated. A correlation analysis between mRNA levels in different experimental conditions/genetic backgrounds was applied and used as evidence for the role of the gene in the plant.

Methods

Mobile nutrients such as N reach their targets and are then recycled, often executed in the form of simultaneous import and export of the nutrients from leaves. This dynamic nutrient cycling is termed remobilization or retranslocation, and thus leaf analyses are highly recommended. For that reason, root and leaf samples were freshly excised from maize plants grown as described above on Murashige-Skoog without Ammonium Nitrate (NH_4NO_3) (Duchefa). Experimental plants were grown either under optimal ammonium nitrate concentrations (100%) and used as a control group, or under stressful conditions of 10% or 1% ammonium nitrate used as stress-induced groups. Total RNA was extracted from the different tissues, using mirVana^{TM} commercial kit (Ambion) following the protocol provided by the manufacturer. For measurement and verification of messenger RNA (mRNA) expression level of all genes, reverse transcription followed by quantitative real time PCR (qRT-PCR) was performed on total RNA extracted from each plant tissue (i.e., roots and leaves) from each experimental group as described above. To elaborate, reverse transcription was performed on 1 µg total RNA, using a miScript Reverse Transcriptase kit (Qiagen), following the protocol suggested by the manufacturer. Quantitative RT-PCR was performed on cDNA (0.1 ng/µl final concentration), using a miScript SYBR GREEN PCR (Qiagen) forward (based on the miR sequence itself) and reverse primers (supplied with the kit). All qRT-PCR reactions were performed in triplicates using an ABI7500 real-time PCR machine, following the recommended protocol for the machine. To normalize, the expression level of miRNAs associated with enhanced NUE between the different tissues and growth conditions of the maize plants, normalizer miRNAs were used for comparison. Normalizer miRNAs, which are miRNAs with unchanged expression level between tissues and growth conditions, were custom selected for each experiment. The normalization procedure consisted of second-degree polynomial fitting to a reference data (which is the median vector of all the data – excluding outliers) as described by Rosenfeld et al (2008, *Nat Biotechnol*, 26(4):462-469). A summary of primers for the differential miRNAs that was used in the qRT-PCR analysis is presented in Table 7a below. The results of the qRT-PCR analyses under different nitrogen concentrations (1% and 10% versus optimal 100%) are presented in Tables 7b-d below.

Table 7a: Primers of Small RNAs used for qRT-PCR Validation Analysis.

Primer Length	Primer Sequence/SEQ ID NO:	Small RNA Name
24	GGCAGAAGAGAGAGAGTACAGCCT/1091	Zma-miR529
23	GCTAGCCAGGGATGATTTGCCTG/1092	Zma-miR1691
21	AGGATGCTGACGCAATGGGAT/1093	Predicted zma mir 48486
25	TGGCTTAGATGACCATCAGCAAACA/1094	Zma-miR827
23	GCGTGAAGTGTTTGGGGGAACTC/1095	Zma-miR395b
22	CTAGCCAAGCATGATTTGCCCG/1096	Predicted zma mir 50601
23	CAGGATGTGAGGCTATTGGGGAC/1097	Predicted zma mir 48492
22	CCAAGTCGAGGGCAGACCAGGC/1098	Predicted zma mir 48879
21	ATTCACGGGGACGAACCTCCT/1099	Mtr-miR2647a
24	GGCGGAATCTTGATGATGCTGCAT/1100	Zma-miR172c

Table 7b: Results of qRT-PCR Validation Analysis on Differential Small RNAs – 1% Nitrogen vs. Control (100% Nitrogen).

p-value	Fold Change	Direction	Sequence/SEQ ID NO:	miR Name
3.20E-03	1.68	up	TTAGATGACCATCAGCAAACA/10	zma-miR827
3.60E-03	1.96	up	CCAAGTCGAGGGCAGACCAGGC/7	Predicted zma mir 48879
4.40E-02	1.55	up	AGGATGCTGACGCAATGGGAT/9	Predicted zma mir 48486
1.30E-03	-3.16	down	GTGAAGTGTTTGGGGGAACTC/4	zma-miR395b

Table 7c: Results of qRT-PCR Validation Analysis on Differential Small RNAs – 1% Nitrogen vs. 10% Nitrogen.

p-value	Fold Change	Direction	Sequence/SEQ ID NO:	miR Name
2.30E-02	2.42	up	AGGATGCTGACGCAATGGGAT/9	Predicted zma mir 48486
1.30E-02	1.62	up	TTAGATGACCATCAGCAAACA/10	zma-miR827
4.60E-02	1.57	up	AGGATGTGAGGCTATTGGGGAC/6	Predicted zma mir 48492

Table 7d: Results of qRT-PCR Validation Analysis on Differential Small RNAs – 10% Nitrogen vs. Control (100% Nitrogen).

p-value	Fold Change	Direction	Sequence/SEQ ID NO:	miR Name
4.50E-03	-3.71	down	GTGAAGTGTTTGGGGGAACTC/4	zma-miR395b

EXAMPLE 5

Gene Cloning and Creation of Binary Vectors for Plant Expression

Cloning Strategy – the best validated miRNAs are cloned into pORE-E1 binary vectors for the generation of transgenic plants. The full-length open reading frame (ORF) comprising of the hairpin sequence of each selected miRNA, is synthesized by Genscript (Israel). The resulting clone is digested with appropriate restriction enzymes and inserted into the Multi Cloning Site (MCS) of a similarly digested binary vector through ligation using T4 DNA ligase enzyme (Promega, Madison, WI, USA).

EXAMPLE 6

Generation of Transgenic Model Plants Expressing the NUE small RNAs

Arabidoposis thaliana transformation is performed using the floral dip procedure following a slightly modified version of the published protocol (ref). Briefly, T0 Plants are planted in small pots filled with soil. The pots are covered with aluminum foil and a plastic dome, kept at 4°C for 3-4 days, then uncovered and incubated in a growth chamber at 24°C under 16 hr light:8 hr dark cycles. A week prior to transformation all individual flowering stems are removed to allow for growth of multiple flowering stems instead. A single colony of Agrobacterium (GV3101) carrying the binary vectors (pORE-E1), harboring the NUE miRNA hairpin sequences with additional flanking sequences both upstream and downstream of it, is cultured in LB medium supplemented with kanamycin (50 mg/L) and gentamycin (25 mg/L). Three days prior to transformation, each culture is incubated at 28°C for 48 hrs, shaking at 180 rpm. The starter culture is split the day before transformation into two cultures, which are allowed to grow further at 28°C for 24 hours at 180 rpm. Pellets containing the agrobacterium cells are obtained by centrifugation of the cultures at 5000 rpm for 15 minutes. The pellets are resuspended in an infiltration medium (10 mM $MgCl_2$, 5% sucrose, 0.044 μM BAP (Sigma) and 0.03% Tween 20) in double-distilled water.

Transformation of T0 plants is performed by inverting each plant into the Agrobacterium suspension, keeping the flowering stem submerged for 5 minutes. Following inoculation, each plant is blotted dry for 5 minutes on both sides, and placed sideways on a fresh covered tray for 24 hours at 22°C. Transformed (transgenic) plants are then uncovered and transferred to a greenhouse for recovery and maturation. The transgenic T0 plants are grown in the greenhouse for 3-5 weeks until the seeds are ready, which are then harvested from plants and kept at room temperature until sowing.

EXAMPLE 7

Selection of Transgenic Arabidopsis Plants Expressing the NUE Genes According to Expression Level

Arabidopsis seeds are sown and sprayed with Basta (Bayer) on 1-2 weeks old seedlings, at least twice every few days. Only resistant plants, which are heterozygous for the transgene, survive. PCR on the genomic gene sequence is performed on the surviving seedlings using primers pORE-F2 (fwd, 5'-TTTAGCGATGAACTTCACTC-3', SEQ ID NO: 20) and a custom designed reverse primer based on each miR's sequence.

EXAMPLE 8

Evaluating Changes in Root Architecture in Transgenic Plants

Many key traits in modern agriculture can be explained by changes in the root architecture of the plant. Root size and depth have been shown to logically correlate with drought tolerance, since deeper root systems can access water stored in deeper soil layers. Correspondingly, a highly branched root system provides better coverage of the soil and therefore can effectively absorb all micro and macronutrients available, resulting in enhanced NUE.

To test whether the transgenic plants produce a modified root structure, plants can be grown in agar plates placed vertically. A digital picture of the plates is taken every few days and the maximal length and total area covered by the plant roots are assessed. From every construct created, several independent transformation events are checked in replicates. To assess significant differences between root features, a statistical test, such as a Student's t-test, is employed in order to identify enhanced root features and to provide a statistical value to the findings.

EXAMPLE 9

Testing for increased Nitrogen Use Efficiency (NUE)

To analyze whether the transgenic Arabidopsis plants are more responsive to nitrogen, plants are grown in two different nitrogen concentrations: (1) optimal nitrogen concentration (100% NH_4NO_3, which corresponds to 20.61 mM) or (2) nitrogen deficient conditions (1% or 10% NH_4NO_3, which corresponds to 0.2 and 2.06 mM, respectively). Plants are allowed to grow until seed production followed by an analysis of their overall size, time to flowering, yield, protein content of shoot and/or grain, and seed production. The parameters checked can be the overall size of the plant, wet and dry weight, the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Other parameters that may be tested are: the chlorophyll content of leaves (as nitrogen plant status and the degree of leaf greenness are highly correlated), amino acid and the total protein content of the seeds or other plant parts such as leaves or shoots and oil content. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher measured parameters levels than wild-type plants, are identified as nitrogen use efficient plants.

EXAMPLE 10

Method for Generating Transgenic Maize Plants with Enhanced or Reduced microRNA Regulation of Target Genes

Target prediction enables two contrasting strategies; an enhancement (positive) or a reduction (negative) of microRNA regulation. Both these strategies have been used in plants and have resulted in significant phenotype alterations. For complete *in-vivo* assessment of the phenotypic effects of the differential miRNAs in this invention, the inventors implement both over-expression and down-regulation methods on all miRNAs found to associate with NUE as listed in Table 1. Reduction of miRNA regulation of target genes can be accomplished in one of two approaches:

Expressing a microRNA-Resistant Target

In this method, silent mutations are introduced in the microRNA binding site of the target gene so that the DNA and resulting RNA sequences are changed to prevent microRNA binding, but the amino acid sequence of the protein is unchanged.

Expressing a Target-mimic Sequence

Plant microRNAs usually lead to cleavage of their targeted gene, with this cleavage typically occurring between bases 10 and 11 of the microRNA. This position is therefore especially sensitive to mismatches between the microRNA and the target. It was found that expressing a DNA sequence that could potentially be targeted by a microRNA, but contains three extra nucleotides (ATC) between the two nucleotides that are predicted to hybridize with bases 10-11 of the microRNA (thus creating a bulge in that position), can inhibit the regulation of that microRNA on its native targets (Franco-Zorilla JM et al., *Nat Genet* 2007; 39(8):1033-1037).

This type of sequence is referred to as a "target-mimic". Inhibition of the microRNA regulation is presumed to occur through physically capturing the microRNA by the target-mimic sequence and titering-out the microRNA, thereby reducing its abundance. This method was used to reduce the amount and, consequentially, the regulation of microRNA 399 in *Arabidopsis*.

Table 8 – miRNA-Resistant Target Examples for Selected down-regulated miRNAs of the Invention.

NCBI MiR Binding Site	Mutated Nucleotide SEQ ID NO:	ORF Nucleotide SEQ ID NO:	Original Nucleotide SEQ ID NO:	Protein SEQ ID NO:	Organism	Homolog NCBI Accession	WMD3 Targets	MiR sequence/ SEQ ID NO:	MiR name
							miR binding site: TC372606 -> not found on the master seq	TTAGATGACCATCAGCAAACA/10	zma-miR827
		1103	1102	1101	Zea mays	NP_001105530	TC372597		
1825 - 1845	1104								
1825 - 1845	1105								
1825 - 1845	1106								
1825 - 1845	1107								
1825 - 1845	1108								
1825 - 1845	1109								
1825 - 1845	1110								
1825 - 1845	1111								
1825 - 1845	1112								
1825 - 1845	1113								
		1116	1115	1114	Zea mays	NP_001130294	GRMZM2G013176_T02		
1017 - 1037	1117								
1017 - 1037	1118								
1017 - 1037	1119								
1017 - 1037	1120								
1017 - 1037	1121								
1017 -	1122								

1037									
1017 - 1037	1123								
1017 - 1037	1124								
							target: TC422488 of Mir Predicted zma mir 48486 is located in UTR	AGGATG CTGACG CAATGG GAT/9	Predicted zma mir 48486

Table 9 – miRNA-Resistant Target Examples for Selected up-regulated miRNAs of the Invention.

NCBI Mir Binding Site	Mutated Nucleotide SEQ ID NO:	ORF Nucleotide SEQ ID NO:	Original Nucleotide SEQ ID NO:	Protein SEQ ID NO:	Organism	Homolog NCBI Accession	WMD3 Targets	MiR sequence	MiR name
		1127	1126	1125	Zea mays	ACN34023	GRMZM2G051270_T01	GTGAA GTGTTT GGGGG AACTC/4	zma-miR395b
527 - 547	1128								
527 - 547	1129								
527 - 547	1130								
527 - 547	1131								
527 - 547	1132								
527 - 547	1133								
527 - 547	1134								
		1137	1136	1135	Zea mays	ACN30570	TC441933	AGAAG AGAGA GAGTAC AGCCT/1	zma-miR529
889 - 909	1138								
889 - 909	1139								

889 - 909	1140								
889 - 909	1141								
889 - 909	1142								
889 - 909	1143								
889 - 909	1144								
889 - 909	1145								
889 - 909	1146								
889 - 909	1147								
		1150	1149	1148	Zea mays	ACF86782	TC374118		
923 - 943	1151								
923 - 943	1152								
923 - 943	1153								
923 - 943	1154								
923 - 943	1155								
923 - 943	1156								
923 - 943	1157								
923 - 943	1158								
923 - 943	1159								
923 - 943	1160								
		1163	1162	1161	Zea mays	NP_001149534	GRMZM2G414805_T04		
1396 - 1416	1164								
1396 - 1416	1165								
1396 - 1416	1166								
1396 - 1416	1167								
1396 - 1416	1168								

1396 - 1416	1169								
1396 - 1416	1170								
1396 - 1416	1171								
1396 - 1416	1172								
1396 - 1416	1173								
		1176	1175	1174	Zea mays	NP_001136945	GRMZM2G126018_T01		
926 - 946	1177								
926 - 946	1178								
926 - 946	1179								
926 - 946	1180								
926 - 946	1181								
926 - 946	1182								
926 - 946	1183								
926 - 946	1184								
926 - 946	1185								
926 - 946	1186								
		1189	1188	1187	Zea mays	CAB56631	GRMZM2G160917_T01		
589 - 609	1190								
589 - 609	1191								
589 - 609	1192								
589 - 609	1193								
589 - 609	1194								
589 - 609	1195								
589 - 609	1196								
589 - 609	1197								
589 -	1198								

609									
589 - 609	1199								
								target: GRMZM2G101511_T01 of Mir zma-miR529 is located in UTR	
							target: TC374958 of Mir zma-miR1691 is located in UTR	TAGCCAGGGATGATTTGCCTG/2	zma-miR1691
								target: TC391807 of Mir zma-miR1691 is located in UTR	

Table 10 – Target Mimic Examples for Selected up-regulated miRNAs of the Invention

Full Target Mimic Nucleotide Seq/SEQ ID NO:	**Bulge in Target Binding Sequence/SEQ ID NO:**	**Bulge Reverse Complement miR/SEQ ID NO:**	**MiR sequence/SEQ ID NO:**	**MiR name**

1208	GAGTTCCTCCACTAAGCACTTCAT/1204	GAGTTCCCCCACTAAACACTTCAC/1200	GTGAAGTGTTTGGGGGAACTC/4	zma-miR395b
11	CTGCAGCATCACTATCAGGATTCT/1205	ATGCAGCATCACTATCAAGATTCC/1201	GGAATCTTGATGATGCTGCAT/3	zma-miR172e
12	CGAGTGTGCTCCTATCTCTCTTCT/1206	AGGCTGTACTCCTATCTCTCTTCT/1202	AGAAGAGAGAGAGTACAGCCT/1	zma-miR529
13	GTGGCAACTCACTATCCTTGGCTC/1207	CAGGCAAATCACTATCCCTGGCTA/1203	TAGCCAGGGATGATTTGCCTG/2	zma-miR1691

Table 11 – Target Mimic Examples for Selected up-regulated miRNAs of the Invention

Full Target Mimic Nucleotide Seq	**Bulge in Target Binding Sequence**	**Bulge Reverse Complement miR**	**MiR sequence**	**MiR name**
18	TGTTAGCTGATCTAGGTCATATAC/16	TGTTTGCTGATCTAGGTCATCTAA/14	TTAGATGACCATCAGCAAACA/10	zma-miR827

19	TTCCCCCTGCGCTATCAGCTTCCT/17	ATCCCATTGCGCTATCAGCATCCT/15	AGGATGCTGACGCAATGGGAT/9	Predicted zma mir 48486

Table 12 – Abbreviations of plant species

Common Name	**Organism Name**	**Abbreviation**
Peanut	Arachis hypogaea	ahy
Arabidopsis lyrata	Arabidopsis lyrata	aly
Rocky Mountain Columbine	Aquilegia coerulea	aqc
Tausch's goatgrass	Aegilops taushii	ata
Arabidopsis thaliana	Arabidopsis thaliana	ath
Grass	Brachypodium distachyon	bdi
Brassica napus canola ("liftit")	Brassica napus	bna
Brassica oleracea wild cabbage	Brassica oleracea	bol
Brassica rapa yellow mustard	Brassica rapa	bra
Clementine	Citrus clementine	ccl
Orange	Citrus sinensis	csi
Trifoliate orange	Citrus trifoliata	ctr
Glycine max	Glycine max	gma
Wild soybean	Glycine soja	gso
Barley	Hordeum vulgare	hvu
Lotus japonicus	Lotus japonicus	lja
Medicago truncatula - Barrel Clover ("tiltan")	Medicago truncatula	mtr
Oryza sativa	Oryza sativa	osa
European spruce	Picea abies	pab
Physcomitrella patens (moss)	Physcomitrella patens	ppt
Pinus taeda - Loblolly Pine	Pinus taeda	pta
Populus trichocarpa - black cotton wood	Populus trichocarpa	ptc
Castor bean ("kikayon")	Ricinus communis	rco
Sorghum bicolor Dura	Sorghum bicolor	sbi
tomato microtom	Solanum lycopersicum	sly
Selaginella moellendorffii	Selaginella moellendorffii	smo
Sugarcane	Saccharum officinarum	sof
Sugarcane	Saccharum spp	ssp
Triticum aestivum	Triticum aestivum	tae
cacao tree and cocoa tree	Theobroma cacao	tcc
Vitis vinifera Grapes	Vitis vinifera	vvi
corn	Zea mays	zma

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims.

All publications, patents and patent applications mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention. To the extent that section headings are used, they should not be construed as necessarily limiting.

WHAT IS CLAIMED IS:

1. A method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 10, 6-9, 21, 22, 23-37, 38-52, 1209, 1211, 1212, wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

2. A transgenic plant exogenously expressing a polynucleotide having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 10, 6-9, 23-37, wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of the plant.

3. The method of claim 1 or transgenic plant of claim 2, wherein said exogenous polynucleotide encodes a precursor of said nucleic acid sequence.

4. The method or transgenic plant of claim 3, wherein said precursor of said nucleic acid sequence is at least 60 % identical to SEQ ID NO: 21, 22, 38-52, 1209, 1211, 1212.

5. The method of claim 1 or the transgenic plant of claim 2, wherein said exogenous polynucleotide encodes a miRNA or a precursor thereof.

6. The method of claim 1 or the transgenic plant of claim 2, wherein said exogenous polynucleotide encodes a siRNA or a precursor thereof.

7. The method of claim 1 or the transgenic plant of claim 2, wherein said exogenous polynucleotide is selected from the group consisting of SEQ ID NO: 10, 6-9, 21, 22, 23-37, 38-52, 1209, 1211, 1212.

8. An isolated polynucleotide having a nucleic acid sequence at least 90 % identical to SEQ ID NO: 6, 7 and 9, wherein said nucleic acid sequence is capable of regulating nitrogen use efficiency of a plant.

9. The isolated polynucleotide of claim 8, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NO: 6, 7 and 9.

10. The isolated polynucleotide of claim 8, wherein said polynucleotide encodes a precursor of said nucleic acid sequence.

11. The isolated polynucleotide of claim 8, wherein said polynucleotide encodes a miRNA or a precursor thereof.

12. The isolated polynucleotide of claim 8, wherein said polynucleotide encodes a siRNA or a precursor thereof.

13. A nucleic acid construct comprising the isolated polynucleotide of claim 8-12 under the regulation of a cis-acting regulatory element.

14. The nucleic acid construct of claim 13, wherein said cis-acting regulatory element comprises a promoter.

15. The nucleic acid construct of claim 14, wherein said promoter comprises a tissue-specific promoter.

16. The nucleic acid construct of claim 15, wherein said tissue-specific promoter comprises a root specific promoter.

17. A method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a gene encoding an RNAi molecule having a nucleic acid sequence at least 90 % identical to

SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant.

18. A transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a gene encoding an RNAi molecule having a nucleic acid sequence at least 90 % identical to SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209.

19. An isolated polynucleotide which downregulates an activity or expression of a gene encoding an RNAi molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 4, 1-3, 5, 57-449, 454-846 and 53-56, 1209.

20. The method of claim 17, the transgenic plant of claim 18 or the isolated polynucleotide of claim 19, wherein said polynucleotide encodes a miRNA-Resistant Target as set forth in SEQ ID NO1104-1124.

21. The method of claim 17, the transgenic plant of claim 18 or the isolated polynucleotide of claim 19, wherein said isolated polynucleotide encodes a target mimic as set forth in SEQ ID NO: 18 or 19.

22. A nucleic acid construct comprising the isolated polynucleotide of claim 19 under the regulation of a cis-acting regulatory element.

23. The nucleic acid construct of claim 22, wherein said cis-acting regulatory element comprises a promoter.

24. The nucleic acid construct of claim 23, wherein said promoter comprises a tissue-specific promoter.

25. The nucleic acid construct of claim 24, wherein said tissue-specific promoter comprises a root specific promoter.

26. The method of claim 1 or 17, further comprising growing the plant under limiting nitrogen conditions.

27. The method of claim 1 or 17, further comprising growing the plant under abiotic stress.

28. The method of claim 27, wherein said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

29. The method of claim 1 or 17, or the plant of claim 2 or 18, being a monocotyledon.

30. The method of claim 1 or 17, or the plant of claim 2 or 18, being a dicotyledon.

31. A method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 927-1021, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

32. A transgenic plant exogenously expressing a polynucleotide encoding a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 927-1021, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

33. A nucleic acid construct comprising a polynucleotide encoding a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 927-1021, wherein said polypeptide is capable of regulating nitrogen use efficiency of

the plant, and wherein said polynucleotide is under a transcriptional control of a cis-acting regulatory element.

34. The method of claim 31, the transgenic plant of claim 32 or the nucleic acid construct of claim 33, wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 1022-1090.

35. The method of claim 31, the transgenic plant of claim 32 or the nucleic acid construct of claim 33, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 927-1021.

36. The nucleic acid construct of claim 33, wherein said cis-acting regulatory element comprises a promoter.

37. The nucleic acid construct of claim 36, wherein said promoter comprises a tissue-specific promoter.

38. The nucleic acid construct of claim 37, wherein said tissue-specific promoter comprises a root specific promoter.

39. The method of claim 31, further comprising growing the plant under limiting nitrogen conditions.

40. The method of claim 31, further comprising growing the plant under abiotic stress.

41. The method of claim 40, wherein said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

42. The method of claim 31, or the plant of claim 32, being a monocotyledon.

43. The method of claim 31, or the plant of claim 32, being a dicotyledon.

44. A method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 854-894, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

45. A transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 854-894, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

46. A nucleic acid construct comprising a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80 % homologous to SEQ ID NOs: 854-894, wherein said polypeptide is capable of regulating nitrogen use efficiency of a plant, said nucleic acid sequence being under the regulation of a cis-acting regulatory element.

47. The method of claim 44, the transgenic plant of claim 45 or the nucleic acid construct of claim 46, wherein said polynucleotide acts by a mechanism selected from the group consisting of sense suppression, antisense suppresion, ribozyme inhibition, gene disruption.

48. The nucleic acid construct of claim 46, wherein said cis-acting regulatory element comprises a promoter.

49. The nucleic acid construct of claim 48, wherein said promoter comprises a tissue-specific promoter.

50. The nucleic acid construct of claim 49, wherein said tissue-specific promoter comprises a root specific promoter.

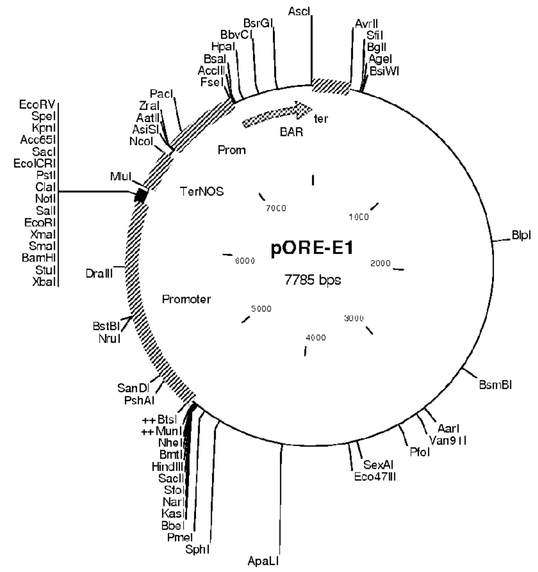
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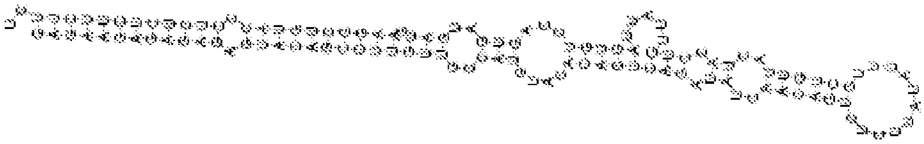
FIG. 1

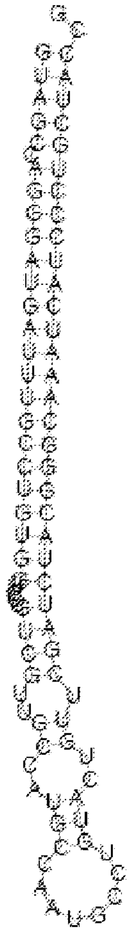
FIG. 2A



Pre-miR 529 (SEQ ID NO: 56)

FIG. 2B

Pre-miR169l (SEQ ID NO: 53)



Pre-predicted miR 48486
(SEQ ID NO: 1209)

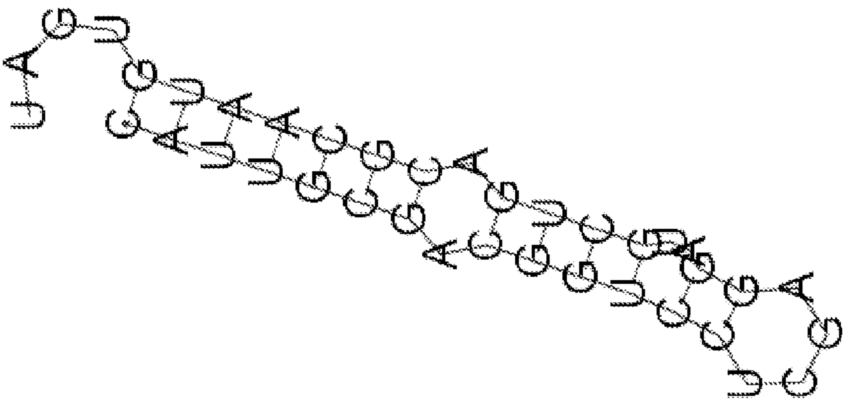


FIG. 2C

Pre-miR 827
(SEQ ID NO: 22)

FIG. 2D

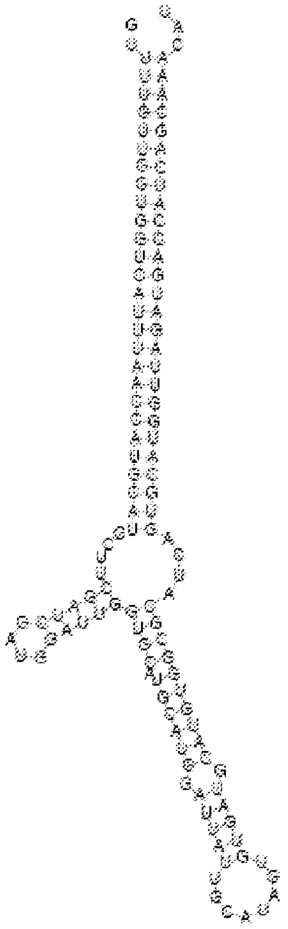
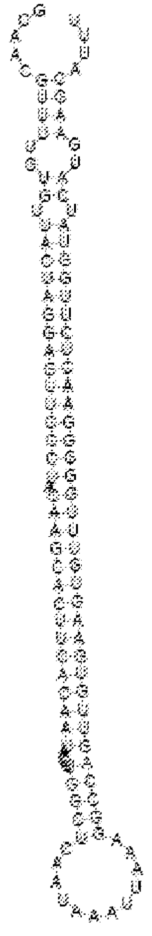


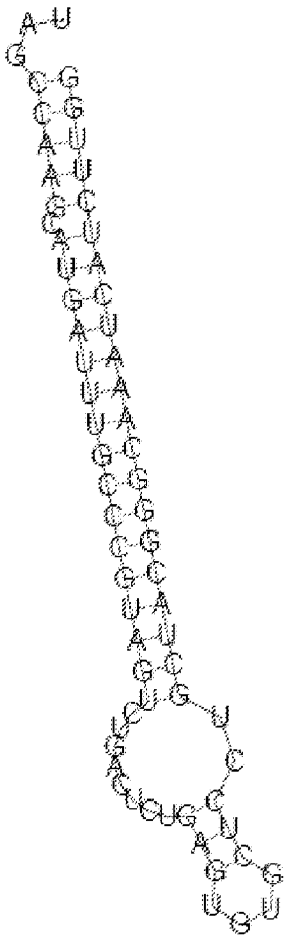
FIG. 2E

Pre-miR 395b
(SEQ ID NO: 55)



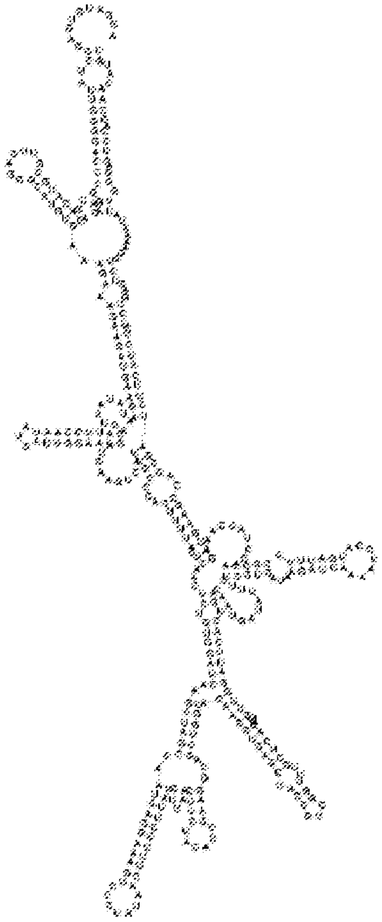
Pre- predicted miR 50601
(SEQ ID NO: 1210)

FIG. 2F



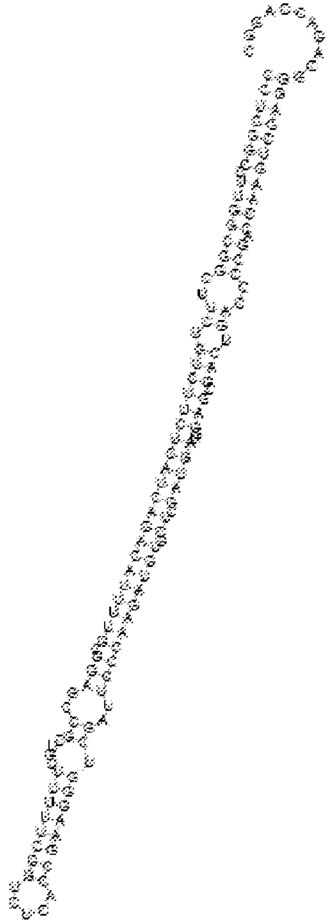
Pre-predicted miR 48492
(SEQ ID NO: 1212)

FIG. 2G



Pre-predicted miR48879
(SEQ ID NO: 1211)

FIG. 2H



Pre-miR 2467a
(SEQ ID NO: 21)

FIG. 2I

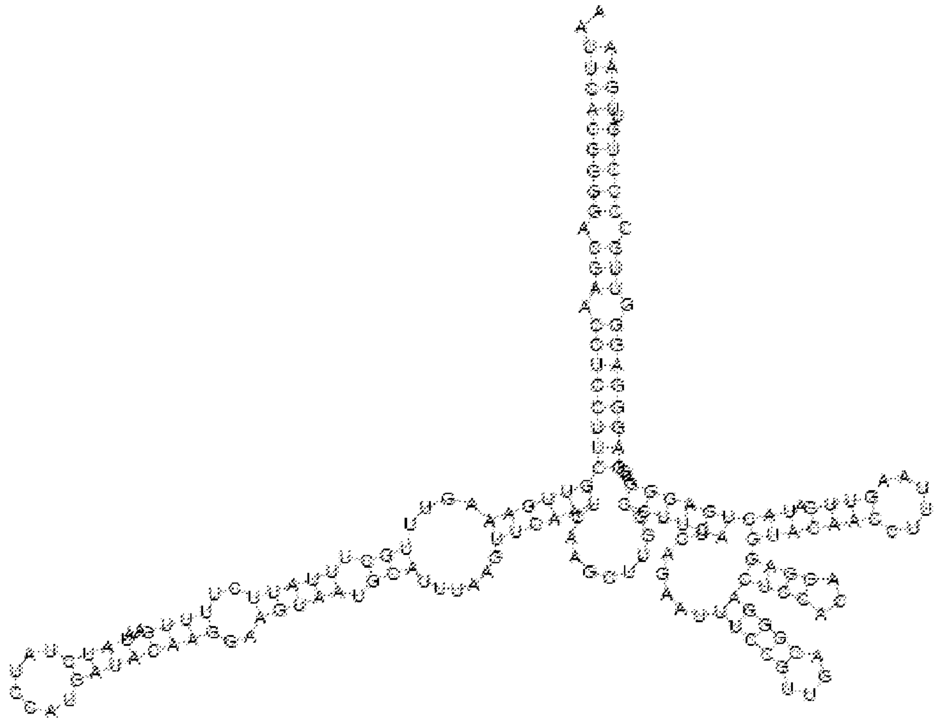
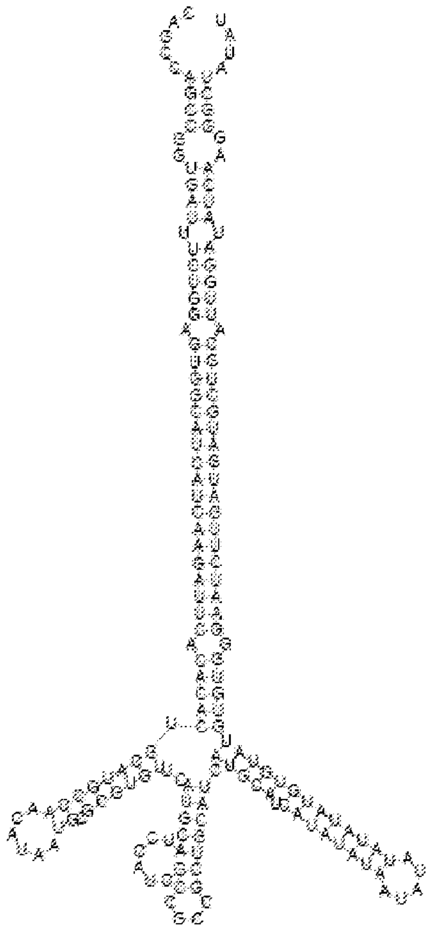


FIG. 2J

Pre-miR 172e
(SEQ ID NO: 54)



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<110> Rosetta Green Ltd.
Maor, Rudy
Nesher, Iris

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<151> 2010-10-25

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<400> 30
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<210> 33
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<210> 34
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<210> 35
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<213> Populus trichocarpa

<400> 35
ttagatgacc atcaacgaaa a 21

<210> 36
<211> 21
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<213> Saccharum ssp.

<400> 36
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<210> 37
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<213> Theobroma cacao

<400> 37
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<210> 38
<211> 194
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<213> Medicago truncatula

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ttgcccctgt tgaa 194

<210> 39
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<212> DNA
<213> Medicago truncatula

<400> 39
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catgatacaa ggaagtaatg catttaagtt caatcaagct tggccttcat cagaatttcc 120

gttgacggga ctccacagga ggtacaacct ttaagttgat actgagggat ggagggaggg 180

ttgcccctgt tgaa 194

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<211> 197
<212> DNA
<213> Arabidopsis lyrata

<400> 40
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gtttgttgat tgacatctat acatatcgat aatcctatcg tgttgataga tcgattggtt 120

tagatgacca tcaacaaacg ctttcgtggt tttgcatcgc ttcttgaaat cttgatcatg 180

tttttagcat ctttgta 197

<210> 41
<211> 177
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<213> Arabidopsis thaliana

<400> 41
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attgatatct acacatgttg atcatccttg tgttgatcga ttggtttaga tgaccatcaa   120

caaactcttt cgtggttttg catcgcttct tggaatctcg atcatgtttt tagcatc   177

<210> 42
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<212> DNA
<213> Brachypodium distachyon

<400> 42
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gtccgtgctt cggtgcttgt gccatgattt tgcatcatca caccggcgat ggttagatga   120

ccatcagcaa acatgttcgt gagacatgcc gtgcgtcctg agct   164

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<211> 100
<212> DNA
<213> Citrus sinensis

<400> 43
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ttagatgacc atcaacaaac atattcatgg tatggcatgc   100

<210> 44
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<212> DNA
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ttgttcaagc agtttttgga taatcgaacc gatagactac acccgcagaa atgatgttta   120

gatgaccatc aacaaacaac ttcatcttat tgcat   155

<210> 45
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<212> DNA

<213> Gossypium hirsutum

<400> 45
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tttcatctcg ccaattcttt gttcaagcag tttttggata atcgaaccga tagaatacac   120

ccgcagaaat gatgtttaga tgaccatcaa caaacaactt catcttattg catcaagtgt   180

tcaagattta ag   192

<210> 46
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<212> DNA
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ttgttcaagc agtttttgga taatcgaacc gatagactac acccgcagaa atgatgttta   120

gatgaccatc aacaaacaac ttcctcttat tgcat   155

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<211> 132
<212> DNA
<213> Oryza sativa

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tgatgtaaga tgaccgctag caaagatcca tttttgctgg tggctggctt aagatgacca   120

tcagcgaaaa tg   132

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gcagcagtcg gcttattggc tcttgggcac gcgtggttag atgaccatca gcaaaca   117

<210> 49

<211> 138
<212> DNA
<213> Oryza sativa

<400> 49
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taattgacga tgcagcagtc ggcttattgg ctcttgggca cgcgtggtta gatgaccatc 120

agcaaacaag ttcgtgag 138

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<212> DNA
<213> Populus trichocarpa

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aacgaaaaca ttcatg 76

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<212> DNA
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<400> 51
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gagtgtgatg ccatgaactc atcatggtca tgcatgtgtg catggttaga tgaccatcag 120

caaacatgtt 130

<210> 52
<211> 148
<212> DNA
<213> Theobroma cacao

<400> 52
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tggccttgta ccagttgcca gtaccaagtt cgtgtgcaga atgatgctta gatgaccatc 120

aacaaacact ttcatcgttt tgcattct 148

<210> 53

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

<400> 53
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gatctacggg caaatcatcc ctgctaccg   89

<210> 54
<211> 174
<212> DNA
<213> Zea mays

<400> 54
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atgcgcgtgt tcatgcatcc atcgccgccg ctgcatcatg catcatatat aatatatata   120

tatgtgtatg tgtgggaatc ttgatgatgc tgcattggat atcaagggct atat   174

<210> 55
<211> 114
<212> DNA
<213> Zea mays

<400> 55
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attaaaggcc agttgtgaag tgtttggggg aactcttggt atcatgaagc attt   114

<210> 56
<211> 126
<212> DNA
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<210> 66
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<210> 88
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<213> Festuca arundinacea

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<210> 99
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<210> 100
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gtatttactt atttatatgt gtgttggtga gatgtgtaaa caaagcaagc ccggcaagtc 240

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<213> Arabidopsis thaliana

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aatggattgt ctcatctaaa gccttgaatg tgggaaaaag gccattgttg ttcagccaag 120

gatgacttgc cggtagcttg tattatgatt actctatatt cgatttatat tatggagatg 180

atggtttata tatatttact tatctacata gttttagttg attttttttc gtacgtaata 240

taatacgaaa aagtatttac ttatttatat atgtgtgttg gggcaagaag tgtaaccaag 300

ctagcccggc aagtcatcta tggctatgca actgtctctt cctctcattc taggcttacg 360

atgacacgta aaaaatccca aatatcacta atatgatatg aatatggatg a 411

<210> 469
<211> 190
<212> DNA

<213> Arabidopsis thaliana

<400> 469
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tgcctgcgtt ttagaccata tatatcaaag actcactcga tcgatagtct tagagttggt 120

tggtcgtcag gcagtctcct tggctattca aacaattctc attctcttca ttcacatttc 180

tcttttttgg 190

<210> 470
<211> 206
<212> DNA
<213> Arabidopsis thaliana

<400> 470
gaaggagatg tcaaagatga atagaagaat catatttggt agccaaggat gacttgcctg 60

actctttgtg taaaatgttt agtgtcttgt ttgaagtcac tataagttgt atcaagcaat 120

gaccattttg cttataaaaa agatatcagg cagtctcctt ggctatcctt atatgttctt 180

ctctttcatc tcagacattc accttc 206

<210> 471
<211> 221
<212> DNA
<213> Arabidopsis thaliana

<400> 471
gagtataatg aggaagagag gtctaacatg gcgaaaagag tcatgtttag tagccaagga 60

tgacttgcct gatctttttc acctccatga ttcaatttgt aattcatggg ttttggatta 120

ttatacattc aaaagtataa taatttgaaa tcatgttgaa tcttgcgggt taggtttcag 180

gcagtctcct tggctatctt gacatgcttt tttcattcac g 221

<210> 472
<211> 213
<212> DNA
<213> Arabidopsis thaliana

<400> 472
ttagaaggag atgtcaaaga tgaataggag aacaatattt ggtagccaag gatgacttgc 60

ctgcttctct gaacaaaatg gtcgatgtca tgttttgaag tgactataag ttataccaag 120

aaatgaccat tttgtttata aatagacatc aggcagtctc cttggctatc cttatatgtt 180

cttctttctc aactcagata tttaccttca tcc 213

<210> 473
<211> 211
<212> DNA
<213> Arabidopsis thaliana

<400> 473
atgaagaaga gaggtctaat atggcgaaaa gagtcatgtt taatagccaa ggatgacttg 60

cctgatcttt ttcacctcca tgattcaatt ttaagttcgt ggattttgga ttattatgcg 120

tttaaaaggt ataataattt gagatcatgt tgaatcttgc gggttaggtt tcaggcagtc 180

tctttggcta tcttgacatg ctttcttcat c 211

<210> 474
<211> 212
<212> DNA
<213> Arabidopsis thaliana

<400> 474
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tgtttctttg agtaaaatgg gttagtgtca tgtttgacaa gtgactataa gttatatcaa 120

gcaatgacca ttttactcat caaaagacat caggcagtct ccttggctat ccttatatgt 180

tcttctctct catctcagac gtttaccttc at 212

<210> 475
<211> 215
<212> DNA
<213> Arabidopsis thaliana

<400> 475
gatgaagaag agaggtctaa catggcggaa agcgtcatgt ttagtagcca aggatgactt 60

gcctgatctt tttcgcctcc acgattcaat ttcaaattca tgcattttgg attattatac 120

cttttaaagt ataataggtc aaatatcatg ttgaatcttg cgggttaggt ttcaggcagt 180

ctctttggct atcttgacat gctttttcca tccat 215

<210> 476
<211> 106
<212> DNA
<213> Brachypodium distachyon

<400> 476
gagatagaga gtggaatgta gccaaggatg acttgccggg tatgtgcatg tacgcttcag 60

ggaattatat gcatccctgg tctgaatcca tgctgatatt tcccgg 106

<210> 477
<211> 151
<212> DNA
<213> Brachypodium distachyon

<400> 477
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tgttggggga attgcagctt tgttgagcct tgagttagcc ggcaggttgt ccttggctac 120

acctagttct cttcttctgg tgtttggccc t 151

<210> 478
<211> 187
<212> DNA
<213> Brachypodium distachyon

<400> 478
atggagatgg agagcctccc ttgattttgg tagccaagaa tgacttgcct atgcttgccc 60

tctgctaacc agctagccat gcatggtaac caatggacaa atttcttgtg gttggcgtgg 120

ttagtgtggt tgcatgggtg ggtcttcttg gctagccaga gcggctctca tccaccatgc 180

caggcca 187

<210> 479
<211> 164
<212> DNA
<213> Brachypodium distachyon

<400> 479
ccttacatgg tgataagggg tttggccctg atagccaagg atgacttgcc tgtgcatgtc 60

ctcccttgat cgcttgcata atttcatata tgcatgtgat ctcgatttat cacaggcagt 120 ctccttggct agcctgggtg cctcttatcc tccatgctag gcct 164

<210> 480
<211> 151
<212> DNA
<213> Brachypodium distachyon

<400> 480
gggccatgca ggacgaggca cagagcagga tgcagccaag gatgacttgc cggccggctg 60

gccggcaatg tcgccgccgg cgtgacatga tgcttgcccg gcaagtttgt ccttggctac 120

accttgctct ctgcccatca tgtgttgccc t 151

<210> 481
<211> 181
<212> DNA
<213> Brachypodium distachyon

<400> 481
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aaggatgact tgcctgtgtc atacttcaag gcttggcaac atgatgcatg agcctttgtt 120

gtagtctcat aggcagtctc cttggctagc ctgagtggct cttgcggctc atgccaggct 180

g 181

<210> 482
<211> 164
<212> DNA
<213> Brachypodium distachyon

<400> 482
cttgcatgag ggccagagcc tgcttcctcc ggtagccaag gatgacttgc ctatatttgc 60

tccttcagaa gtcctggtta attacatgcc aggtttcaga tgagtttggc gataggcagt 120

caccttggct agcctgagtg gctcttgcct cttatggaag gcct 164

<210> 483
<211> 183
<212> DNA
<213> Brachypodium distachyon

<400> 483
cttacatgga gataaggagc ctacctctgt tagccaggaa tggcttgcct acgcacacat 60

ttttcggttc atcacagggg caaaactaac ttggagatag cccctagtat gatggacgga 120

gtgtggctgc atggtcaagc cttcctgact aggagagtgc tcctcatccc ccatgctagg 180

ctg 183

<210> 484
<211> 174
<212> DNA
<213> Brachypodium distachyon

<400> 484
tctttgcatg gaagtaggag gccatctttg atagccaagg atgatttgcc tgtaaaaccg 60

attgtcgtcg cctctcggtg ccgttccagg cactcgaagg gagggcggca gcaacaggtt 120

ctatgggcaa gtcagcctgg ctacccgagt acctcttacc catattccat gcca 174

<210> 485
<211> 176
<212> DNA
<213> Brassica napus

<400> 485
agatgaatag aagaatcata tttggtagcc aaggatgact tgcctatttc ttgagagtaa 60

aatgggcatg gtgtcatgtt aaaagttact gtaggtagtt tcaatttgac cattttcctt 120

acaaatgata ttaggcagtc tccttggcta tccttatatg ttcttctctc tcatct 176

<210> 486
<211> 220
<212> DNA
<213> Brassica napus

<400> 486
gaaggagatg tcaaagatga ataggagatt tctatttggt agccaaggat gacttgccta 60

cttctttgcg aaggaaaatg gtcacggtgt catgtttgaa agtgaatata catttttaag 120

agtatatcaa ttagtgacca ttttgcgtat aaaaagatat taggcagtct ccttggctat 180

ccttatatgt tcttctttct catctcagac atttaccttc 220

<210> 487
<211> 277
<212> DNA
<213> Brassica napus

<400> 487
gtttcaggca gtctccttgg ctatcttgac atgctttttt cttccatgtt ataccttctt 60

tctttgtatt tttcgaatcc aaataatatt tttttctata aatttactac gaaaatcctt 120

taaacaatct ctaacaaagt atgttattag aaaactacca ctttttgcat ttattacaaa 180

tgcatgtacg tggtgagtgt atgcattctt tagaaggaaa tgtcaaaggt gaatagaaga 240

atcatatttg gtagccaagg atgacttgcc tatttct 277

<210> 488
<211> 201
<212> DNA
<213> Brassica napus

<400> 488
gtcaaagatg aataggagaa ttctatttgg tagccaagga tgacttgcct acttctttgc 60

gaaggaaaat ggtcacggtg tcatgtttga aagtgaatat atatttataa gagtatatca 120

attagtgacc attttgcgta taaaaagata ttaggcagtc tccttggcta tccttatatg 180

ttcttctttc tcatctcaga c 201

<210> 489
<211> 168
<212> DNA
<213> Brassica napus

<400> 489
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ctttaacacc atatcaaaga ctttatcgat agtctctgag ttggttaggc tgtaggcagt 120

ctccttggct attcagacac tcctctttct cctcatttca catttctc 168

<210> 490
<211> 176
<212> DNA
<213> Brassica napus

<400> 490
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cttagaccat atctatcaaa gactaaaaga ttgatagtct tcgatgaatt ggttaatcgg 120

taggcagtct cctcggctat tcagacagtt ctctttctcc tcatttcaca tttctc 176

<210> 491
<211> 174
<212> DNA
<213> Brassica napus

<400> 491
agagtcatgt ttagtagcca aggatgactt gcctgctctt tttcacctcc atgattcaat 60

tttatgtaca gttttggatt actatgcttc taaagagtat agtaattcaa aatcttgttg 120

aatctttgag ggtaacagtt tcaggcagtc tccttggcta tcttgacatg cttt 174

<210> 492
<211> 167
<212> DNA
<213> Brassica napus

<400> 492
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cgttgaaggg ttttggatta ttgtgcattc aacatgtata ataatttgaa atcatgttga 120

atctttgtgg gttaggtttc aggcagtctc cttggctatt ttgacat 167

<210> 493
<211> 155
<212> DNA
<213> Brassica napus

<400> 493
aaacggtgac atgaagaatg agaagttgtg tggtagccaa ggatgacttg cctgcgtctt 60

aacaccatat cacagacttt atcgatagtc tctgagttgg ttaggctgta ggcagtctcc 120

tcggctattc agacactcct ctttctcctc atttc 155

<210> 494
<211> 199

<212> DNA
<213> Brassica napus

<400> 494
catggcgaaa agagtcgtgt ttagtagcca aggatgactt gcctgctctt gttcacctcc 60

acgattcaac tttatacgtt gaagggtttt ggattattgt gcattcaaca tgtataataa 120

tttgaaatca tgttgaatct ttgtgggtta ggtttcaggc agtctccttg gctattttga 180

catacttttt tcatccatg 199

<210> 495
<211> 150
<212> DNA
<213> Festuca arundinacea

<400> 495
ggcacgaggg caaagcctta catggctgca agggccttac ctctgatagc caaggatgac 60

ttgcctatgt cttcttcctc cctcagatgc ctaattagcc ttggaggtgt ggggtctcat 120

gggcagtcac cttggctagc ctgagtggct 150

<210> 496
<211> 189
<212> DNA
<213> Gossypium herbacium

<400> 496
tatagagagg aagaaaaggt ctaacatgaa gataaagagt cttgtttggt agccaaggat 60

gacttgcctg cacctaatgt ccacgaggtt ttaatacatc aaaaaccctg gttgggtccc 120

aggcagtcac cttggctaac tagacaggct gttttcattc atgctaggcc tcatcttccg 180

ccccattgg 189

<210> 497
<211> 121
<212> DNA
<213> Glycine max

<400> 497
aagaggaaga gagagtgatg cagccaagga tgacttgccg gcgttattat ttgctcatgt 60

tcatgctcac cggtttcctt gccggcaagt tgtgtttggc tatgttttgc tctcttcttc 120 t 121

<210> 498
<211> 88
<212> DNA
<213> Glycine max

<400> 498
agattagtgg atgtgagcca aggatgactt gccggttgta taatagcacc cggtttaagt 60

ccttcttggt tcttatttac tattctta 88

<210> 499
<211> 120
<212> DNA
<213> Glycine max

<400> 499
gtcttgcatg aagaggtaga gagagtgctt ttgagccaag gatgacttgc cggcgtaatt 60

acgggtattg ccagcgagac atccttgttc acttatgctc tcttttcact catataagac 120

<210> 500
<211> 83
<212> DNA
<213> Hordeum vulgare

<400> 500
taacacgcca gaaataaagc caaggatgag ttgcctgatc atcaggactc atggaggtag 60

ggctttctgt ttttggtgag ttt 83

<210> 501
<211> 85
<212> DNA
<213> Medicago truncatula

<400> 501
gaatgcagcc aagggtgatt tgccggcaga tatatatgaa tattcataga gatgcatgtg 60

tcggcaagtt cctcttggct acatt 85

<210> 502
<211> 240

<212> DNA
<213> Medicago truncatula

<400> 502
agatgaagcc aaggatgact tgccggtata atagtaattt gccacaaatc tagatagcta 60

ttagctatgt ttggatgggc ggtgagatta acaaaattac agcagcattg tgattttgtt 120

gatgctttaa agtgtagttt ttatcaaaat tacagtggtt cactgtaatt atgagaatct 180

caccgtcaat ctaaatatgc atttagtttc atttccggca ggtcatcctt cggctatatt 240

<210> 503
<211> 139
<212> DNA
<213> Medicago truncatula

<400> 503
tttataagcc aaggatgact tgcctagcta aaaaccattt acattaattg gggacttaat 60

ttgtatatgt tatgtctgat cgatgatgag tatgtccctt gtttagttta ttagcaggca 120

ggtatcctag gctttttga 139

<210> 504
<211> 211
<212> DNA
<213> Medicago truncatula

<400> 504
atatgcagcc aaggatgact tgccggcgag cctctttcga tacttttatg acataattaa 60

tcatgtggat agccaaggta ctaaactcac tttgcactaa aacaaatatt tttgctttag 120

tgcaaactta gtttaggcgc ttcgcaacgg ctagtcaaat gtcctagttc caatgtgatt 180

ggttgtccgg caagtcgtct ctggctacgt a 211

<210> 505
<211> 77
<212> DNA
<213> Medicago truncatula

<400> 505
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ttgttcttga ctacatt 77

<210> 506
<211> 85
<212> DNA
<213> Medicago truncatula

<400> 506
gaatgcagcc aagggtgatt tgccggcaga tatatatgaa tattcataga gatgcatgtg 60

tcggcaagtt cctcttggct acatt 85

<210> 507
<211> 240
<212> DNA
<213> Medicago truncatula

<400> 507
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ttagctatgt ttggatgggc ggtgagatta acaaaattac agcagcattg tgattttgtt 120

gatgctttaa agtgtagttt ttatcaaaat tacagtggtt cactgtaatt atgagaatct 180

caccgtcaat ctaaatatgc atttagtttc atttccggca ggtcatcctt cggctatatt 240

<210> 508
<211> 100
<212> DNA
<213> Medicago truncatula

<400> 508
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gttgttgggt actcccggca ggtcatcctt cggctatatt 100

<210> 509
<211> 128
<212> DNA
<213> Oryza sativa

<400> 509
gaacggaatg cagccaagga tgacttgccg gtacgtgtat gcatgtttca aggtactata 60

tgtgcccccca actgttttag atccatgctg acattttccg gcaagttgtc cttggctacg 120

tcttgttc 128

<210> 510
<211> 112
<212> DNA
<213> Oryza sativa

<400> 510
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ctgaagcgcc ttggagttag ccggcaagtc tgtccttggc tacacctagc tc 112

<210> 511
<211> 103
<212> DNA
<213> Oryza sativa

<400> 511
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tataagttgg cgccggcaag tcatttcagg ctacatgttt gcc 103

<210> 512
<211> 132
<212> DNA
<213> Oryza sativa

<400> 512
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tatgctgtat tgccgtgtgt gatcgatcga tgcatggacc ggcaagttat tttctttggc 120

tacattacaa cc 132

<210> 513
<211> 170
<212> DNA
<213> Oryza sativa

<400> 513
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tcatctgcat tttgattatc ccctgatcag tcctgtcgtc aattatatgt gtgtgtagta 120

ctctgtactc atacatatat aggcatgtct tccttggcta ttcggagcgg 170

<210> 514
<211> 126
<212> DNA
<213> Oryza sativa

<400> 514
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gatcagtgtg gcctggctgg ttcagatgag ccgagatagg cagtctcctt ggctagcctg 120

agtggc 126

<210> 515
<211> 122
<212> DNA
<213> Oryza sativa

<400> 515
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tattcagaaa atgatccttt cagcaggttt catgggcagt ctccttggct agcctgagtg 120

at 122

<210> 516
<211> 108
<212> DNA
<213> Oryza sativa

<400> 516
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tgagccttga actggttcat aggcagtctc cttggctagt ctgagtcg 108

<210> 517
<211> 125
<212> DNA
<213> Oryza sativa

<400> 517
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tgcatttcta gctgctttct gcatatgtga tctcacaggc agtctccttg gctagcctga 120

gcggc 125

<210> 518
<211> 156
<212> DNA
<213> Oryza sativa

<400> 518
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attagcagca tggtttgagc attgcttgat cggttgatcg cttcgcttgc tctgcatgag 120

atcttacagg cagtctcctt ggctagtctg ggcggc 156

<210> 519
<211> 108
<212> DNA
<213> Oryza sativa

<400> 519
ttatctctga tagccaagga tgacttgcct gtgtcctccc tgaaggatta gcaatttaat 60

gatcctttaa gctggttcat gggcagtctc cttggctagc ctgagtgg 108

<210> 520
<211> 138
<212> DNA
<213> Oryza sativa

<400> 520
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aatggatgga ttgatcaagc tgcttgcagg ctcatgcata tatatgtaca ggcagtctcc 120

ttggctagcc cggctacc 138

<210> 521
<211> 177
<212> DNA
<213> Oryza sativa

<400> 521
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ccatctatca gccgttgcag atttgcagtg gcagattaaa gggtttcaga aagaaattct 120

tgtgatggat gtgcaatgtg gctgcatggg ccggtcttct tggctagcca gagtggc 177

<210> 522
<211> 173
<212> DNA
<213> Oryza sativa

<400> 522
ctccctttgg tagccaagaa tgacttgcct acgcttttgc cctctgttgg ctcatccatc 60

cgtctatcta tctgccatgg cagatggcag attaagggtt tctgaaagaa attcttgtga 120

taggatgtgc aatgaggctg catgggccgg tcttcttggc tagccagagt ggc 173

<210> 523
<211> 111
<212> DNA
<213> Populus trichocarpa

<400> 523
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ggcttctatt tggcacgccc ggccggcggg ttgtccttgg ctatatttgg t 111

<210> 524
<211> 166
<212> DNA
<213> Populus trichocarpa

<400> 524
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tttcattgat ggcattgcta gatagatata tatgatttcg taattcaaac ttttgggcca 120

ttgtctggtt gaaatgatcg gcaagctgtc cttggctatg tctcta 166

<210> 525
<211> 239
<212> DNA
<213> Populus trichocarpa

<400> 525
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ggtatttttc atcctaggtt tggctatata tatatatata tatagccagt taattgctat 120

aaatctcagc acatttatgt tttatatgtc tgcacacaga cacacacatc attgaatgtt 180

gatgttccac ctcctatgat cagtagtcaa tcggcaagtc atctctggct actcaactc 239

<210> 526
<211> 106
<212> DNA
<213> Populus trichocarpa

<400> 526
gagtagaatg cagccaagga tgacttgccg gcatttcctc ctaggtagct agcaagcctt 60

ctatttggca tgcctgtccg gcaggttgtc cttggctaaa ttttgt 106

<210> 527
<211> 118
<212> DNA
<213> Populus trichocarpa

<400> 527
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gaagatcaag gctgtcatta cttttccggc cggcaagttg cccttggcta cattgtac 118

<210> 528
<211> 123
<212> DNA
<213> Populus trichocarpa

<400> 528
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cagacatgta taatttcgaa acccctgttt cgtttcaggc agtctccttg gctaacttga 120

ctg 123

<210> 529
<211> 137
<212> DNA
<213> Populus trichocarpa

<400> 529
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agaaccaaat atgcatggaa ttatatgtaa tgaaactctt gtttgattgc caggcagtct 120

ccttggctag cctgaca 137

<210> 530
<211> 203
<212> DNA
<213> Populus trichocarpa

<400> 530
tcttgtttgg tagccaagga tgacttgcct gtagcctccc tcggattcat gaacacgagc 60

atttatgtgg tgctcaaaag aaaaggagag aatgatccca gctggcagcg acaaggtcaa 120

tccattgaag tagcgagaag caggtgattt atagctagaa tccacaagag gttcccagca 180

agtgtccttg gctaacgaga cgg 203

<210> 531
<211> 143
<212> DNA
<213> Populus trichocarpa

<400> 531
tcttgtttga tagccaagga tgacttgcct gctacataca agagatcatt atgcataaat 60

agaacgaaat atgtacatgg tattaattaa tgcagtgaaa actcttgttt ggttgccagg 120

cagtctcctt ggctaagctg aca 143

<210> 532
<211> 119
<212> DNA
<213> Populus trichocarpa

<400> 532
tcttgtttgg tagccaagga tgacttgcct gctcccttca aggaggtttc atgaaatgca 60

gacatgatct ctcgaaaccc ctgttgggtt tcaggcggtc tccttggcta acttgacag 119

<210> 533
<211> 104
<212> DNA
<213> Populus trichocarpa

<400> 533
ccttgcgtgg aagccaagga tgacttgcct gagaatttta ggaaggtttc tatatgaaag 60

ctttttatta gttttgcagg aagtcaacct tggctttcct atag 104

<210> 534
<211> 104
<212> DNA
<213> Populus trichocarpa

<400> 534
ccttgcgtgg aagccaagga tgacttgcct gagaatttta ggaaggtttc tatatgaaag 60

ctttttatta gttttgcagg aagtcaacct tggctttcct atag 104

<210> 535
<211> 115
<212> DNA
<213> Populus trichocarpa

<400> 535
tcttgttagt tagccaagga cgacttgcct gttcctagca atttgggatt tgccctggac 60

taagaggcag gaccctcatt ccgggtttca ggcagtctcc ttggctaggt tgaca 115

<210> 536
<211> 119
<212> DNA
<213> Populus trichocarpa

<400> 536
gagggtttgg tagccaagga tgacttgcct atttcctcca taaggcttta aaaagcatga 60

aatgtggttt agagctcaat tgaagggttc ataggcagtc tactttggtt atcctagct 119

<210> 537
<211> 122
<212> DNA
<213> Populus trichocarpa

<400> 537
gagggttggg tagccaagga cgacttgcct atttcctcca tggggtcctg aaaagaatga 60

aatactgtcg ttcagagctc attggtaggg ttcataggca gtctcctttg gctatcctaa 120

ct 122

<210> 538
<211> 110
<212> DNA
<213> Populus trichocarpa

<400> 538
cgtgtttggt agccaaggat gacttgccca ctccattgaa agagtttttc aagcatatgg 60

tagtgtagaa cttttctttg gttctgggca gtcatcttgg ctatgctgac 110

<210> 539
<211> 109
<212> DNA
<213> Populus trichocarpa

<400> 539
cgtgtttggt agccaaggat gacttgccca ctctatggaa agagttctca agcacacggc 60

agagaggacc cttacttcgg ctctgggcag tcaccttggc tatgctgac 109

<210> 540
<211> 118
<212> DNA
<213> Populus trichocarpa

<400> 540
tgctgttttc tagccaagga tgacttgctc gttagccctt gaaagatgtt tcaaatttag 60

gctgcatatg ctcagaacct tttctggct tcaggcaatc atcttggcta aatgacag 118

<210> 541
<211> 123
<212> DNA
<213> Populus trichocarpa

<400> 541
tcttgtttag tagccatgga tgaattgcct gcttccaaaa tgaggtgtca agccgagata 60

aacatacaag tttgatccct cattggggtt cccaggcagt catcagcttg gctaacttga 120

cag 123

<210> 542
<211> 118
<212> DNA
<213> Populus trichocarpa

<400> 542
tagtagaatg cagccaagaa tgatttgccg gcgccggcca gcacttgttg caaagcaact 60

aagcaagggc ttcaaatgtt tttggcaccc cggcaagttg ttcttggcta catttgga 118

<210> 543
<211> 92
<212> DNA
<213> Ricinus communis

<400> 543
gaatacagcc aaggatgact tgccggcatc aatttatata tatatatata tatatatata 60

tttatcggca agctgttctt ggctatattc at 92

<210> 544
<211> 93
<212> DNA
<213> Ricinus communis

<400> 544
taattcagcc aaggatgact tgccggcaca gcctatatat gtcttctact cacagctgct 60

agctaccggc aagttgttct tggctacatt gta 93

<210> 545
<211> 102
<212> DNA
<213> Sorghum bicolor

<400> 545
cagccaagga tgacttgccg gatatgtgca tgcatatgtt acaaggcagc atatgcaccc 60

tgttacaagc ctgcctgttc tccggcaagt tgtccttggc ta 102

<210> 546
<211> 126
<212> DNA
<213> Sorghum bicolor

<400> 546
tggcgagagc ctgcctttgg tagccaagga tgacttgcct acacggcctt gcgagttccg 60

gttgcatggc cagttcagtt gggtttgtgg gcggtcacct tggctagcct gagtggctct 120

tgcctg 126

<210> 547

<211> 103
<212> DNA
<213> Sorghum bicolor

<400> 547
tggcgagagc ctgcctttgg tagccaagga tgacttgcct acatggcatt gcgagttccg 60

gttgcatggc cagttcagct gagtttgtgg gcggtcacct tgg 103

<210> 548
<211> 109
<212> DNA
<213> Sorghum bicolor

<400> 548
tagccaagga tgacttgccg gcatttcttg ggtcggatga ctgagttgtt gagcctgggg 60

atgaacagac ccggatcgac ggccggccgg caagtcatct gtggctacg 109

<210> 549
<211> 148
<212> DNA
<213> Sorghum bicolor

<400> 549
cgatgagagc actgctctgg tagccaagga tgacttgcct gtggcctcca ctccacctgc 60

ggcaggaggc tcttcttctg cgcgcgcgtg tgtgtgtggt tgtcgatcgc aggcagtctc 120

cttggctagc ctcagcggct ctcatcct 148

<210> 550
<211> 152
<212> DNA
<213> Sorghum bicolor

<400> 550
gcgataagag tctgcccaga tagccaagga tgacttgcct gtggcctctt ggcttggctt 60

gagagcttat taactctgtg cacgtttaat ttgctcttct tgtggcctcg atcacaggca 120

gtctccttgg ctagtccggg cggctcttat ct 152

<210> 551
<211> 98
<212> DNA

<213> Sorghum bicolor

<400> 551
tagccaagga tgacttgcct agctatatgc ctgagagcct gtctcttggt ggtaaatttg   60

tatgtgctga gcatataggc atgtcttcct tggctact   98

<210> 552
<211> 169
<212> DNA
<213> Sorghum bicolor

<400> 552
gatggagagc ccccttttgc tagccaagaa tgacttgcct atgcatgccc tctgttggca   60

attcctccag ccatggagat tgcacaaggt gaatttttgc ggcatagatg atggatgcaa   120

tgtggctgca tgggcaggtc ttcttggcta gccagagtgc tctcatcca   169

<210> 553
<211> 123
<212> DNA
<213> Sorghum bicolor

<400> 553
tgtagccaag gatgacttgc cggccgatcg atgcctcatc cctgtccggg aacgtcatgc   60

atgtgatgca aactgtgagg ccgcatcgtc gatcgaccgg caggttcttc tctttggcta   120

cac   123

<210> 554
<211> 97
<212> DNA
<213> Sorghum bicolor

<400> 554
cagccaagga tgacttgccg gctcctcaaa tttgaagcgt cgtctaagct gctgaggctt   60

aataaaaact tagtcggcaa gtctgtcctt ggctaca   97

<210> 555
<211> 97
<212> DNA
<213> Sorghum bicolor

<400> 555
tgatagccaa ggatgacttg cctgtgtcct ttgtgccgaa ggatcagaaa tgtgagcctt 60

tgagatagat ggttcatagg cagtctcctt ggctagc 97

<210> 556
<211> 92
<212> DNA
<213> Sorghum bicolor

<400> 556
tagccaagga tgacttgcct atatcctctc taaaggatca gcaaatattg aggcttctag 60

tggtctcata tgggcagtct ccttggctag cc 92

<210> 557
<211> 93
<212> DNA
<213> Sorghum bicolor

<400> 557
ggtagccaag gatgacttgc ctatatcctc tatgaaggat cagcaaatat cgaggctttg 60

agtggtctca tgggcagtct ccttggctag cct 93

<210> 558
<211> 103
<212> DNA
<213> Sorghum bicolor

<400> 558
atagccaagg atgatttgcc tgtagcaacc tctgagtgct cctgctgcca tggcagtcag 60

gagcgccaag tgggtgcttc tccgggcaaa tcatctgggc tag 103

<210> 559
<211> 149
<212> DNA
<213> Solanum lycopersicum

<400> 559
ggtctataag gtttgcatga agttgaagag agtcaagttg cagccaagga tgacttgccg 60

gaccaaaagt tgtgaccatt ttctagttcc ggcaagttgt ttttggctat aagtttgctc 120

tcttcttctc atgttatcct cgttagacc 149

<210> 560
<211> 205
<212> DNA
<213> Solanum lycopersicum

<400> 560
ttttaatttg gtttcaggca gtctccttgg ctaccttgac atgctctttt cttttatgca 60

agatatcttt tcaaaataga agttttagtc atcgttaaaa tatcgagacg gggttacaag 120

tcttatttaa aagaagagaa gtctagcatg atgagaagag tcttatttgg tagccaagga 180

tgacttgcct gcaccgtact tgaaa 205

<210> 561
<211> 176
<212> DNA
<213> Solanum lycopersicum

<400> 561
gaagaggggt tttatatgaa gttgagagta ttatttagta gccaaggatg acttgcctac 60

ttcatttgat atatagttta aaataataat attgacaata tttgtcattt ggtcgtaggc 120

aagttatcct ggctatcttg acatgctcgt aatttttcat gtaagacctt atcttc 176

<210> 562
<211> 146
<212> DNA
<213> Saccharum ssp.

<400> 562
gtagccaagg atgacttgcc ggccgatgct tcgatggatc cctcatcccc gtccggccgg 60

gaacgtcgca cgtatgtatg tatgcgtgca tatgctgcga actgtgaggc atccatatcg 120

accggcaggt tcttctcttt ggctac 146

<210> 563
<211> 193
<212> DNA
<213> Theobroma cacao

<400> 563
ggaaatgagg ctatgtgctg cagccaagga tgacttgccg gaaaagctat attttacatt 60

atattaccct gttccctgat attaactata tgcttctgta tcaattttaa ctataaatta 120

ataaaattta taataaatgt tataagagtt tatcggcaag tcgtctctgg ctatatcact 180

gtttcatttt ctc 193

<210> 564
<211> 152
<212> DNA
<213> Theobroma cacao

<400> 564
agattaagag tcttgttggg tagccaagga tgacttgcct atatccaaaa aggattttga 60

ggaaagaaaa gctgaatctg ataaatctca tcagagtcct tttaatggtt tctgggcagt 120

ctcctttggc tatcctgact ggctcttatc tt 152

<210> 565
<211> 141
<212> DNA
<213> Theobroma cacao

<400> 565
aagaagagag cctcgctgga aagccaagaa tgacttgcct gcttcctcct tgaggtttca 60

aaatttcaat gaaactttta aaacccgcca ttctggctcg cgggcagtct tcttcgcttt 120

cttgacaggc tattcttttc c 141

<210> 566
<211> 144
<212> DNA
<213> Theobroma cacao

<400> 566
gataaagagt ctttgtttgg tagccaggga tgacttgcct acggcttttc aggtggttaa 60

tattgatgct atgattatga atgtaaaacc cctggctctg gtctgcaggc agtcaccttg 120

gctatgctaa caggctcttt tctc 144

<210> 567
<211> 139
<212> DNA

<213> Theobroma cacao

<400> 567
aggtaaagag tcatgcttgg tagccaagga tgacttgcct gcacctttcc ccaaggattc 60

aagtaaatgg ctaagaaacc tgaaactcct ttcaggttgc caggcagtca cctaggctaa 120

tctagcaggt tcttttccc 139

<210> 568
<211> 115
<212> DNA
<213> Theobroma cacao

<400> 568
aagataagag ttctgtttgg tagccaagga tgagttgcct gctccttcca agaggtttca 60

aatcttgttg ggttgccagg cattcacctt ggctaacttg actggctctt ttctt 115

<210> 569
<211> 141
<212> DNA
<213> Theobroma cacao

<400> 569
agataaagag tcttgtttga tagccaagga tgacttgcct gtacctcaca gcaggtttct 60

cttaggttaa aagttcttcc ttggaagccc ctgtctagtt tcaggcaatt atccttggct 120

aacctgacag gctcttctct a 141

<210> 570
<211> 132
<212> DNA
<213> Theobroma cacao

<400> 570
aagaggtaga cagtgtggtg cagccaagga tgacttgccg gctaatccct aggaggcatg 60

catttgcctt gtttctctgc tttagattat tccggctagt tgtccttggc tacggtgcgc 120

tgtcttcttc tc 132

<210> 571
<211> 122
<212> DNA

<213> Theobroma cacao

<400> 571
gagaggtaga gaatttagtg cagccaagga tgacttgccg gcgtagacaa tactcaaata   60

ctaattatta ttgtattttt ccggcaagtc tgtccttggc tacattggtt tctcttcttc   120

tc   122

<210> 572
<211> 124
<212> DNA
<213> Vitis vinifera

<400> 572
gagagtggaa tgcagccaag gatgacttgc cggaatttat atatagtgag aagagaagag   60

gctatatgct ttcacatata tagtgaaccc tggcaagttg tccttggcta catttgattc   120

tctt   124

<210> 573
<211> 90
<212> DNA
<213> Vitis vinifera

<400> 573
gggagtagaa tgcagccaag gatgacttgc cggagatggg gcattcctcg ttaatccggc   60

aagttgtcct tggctacatt gggctctctt   90

<210> 574
<211> 120
<212> DNA
<213> Vitis vinifera

<400> 574
gagtggaatg cagccaagaa tgatttgccg gaatttatat atagtgagaa gagaagaggc   60

tataggcttt cacatatata gtgaaccctg gcaagttgtc cttggctaca tttgattctc   120

<210> 575
<211> 149
<212> DNA
<213> Vitis vinifera

<400> 575
gtcttgtctg atagccaagg atgacttgcc tgccctatcc caagtgggtc aatttctttc 60

ttttttccaa gtagtgtttg atatttgata tatcatgaat ccggttgttt gggttccagg 120

cagtcacctt ggctaatttt acaggctct 149

<210> 576
<211> 122
<212> DNA
<213> Vitis vinifera

<400> 576
gagagtggag tgcagccaag gatgacttgc cggaattcac atatagagtg gaatgaggca 60

atagaccggc ctcttctcat ggtgtccctg gcaggttgtc cttggctacc tttcgctctc 120

tt 122

<210> 577
<211> 122
<212> DNA
<213> Vitis vinifera

<400> 577
gagagtggag tgcagccaag gatgacttgc cggaattcac atatagagtg gaatgaggca 60

agaggccggc ctcttcccat ggtgtccctg gcaggttgtc cttggctacc tttcgttctc 120

tt 122

<210> 578
<211> 102
<212> DNA
<213> Vitis vinifera

<400> 578
agagtggaag tgagccaagg atgacttgcc ggcagctgca gcaaggcatt aaggtttaac 60

tggccataac tggcaagcat ccgaggctct gtttcaccct ct 102

<210> 579
<211> 101
<212> DNA
<213> Vitis vinifera

<400> 579
tgagtggaat agagccaagg atgacttgcc ggcaactgca gcaaggcata gggtttaact 60

ggtcataact ggcaagcatc tgaggctcta tttcaccctc t 101

<210> 580
<211> 102
<212> DNA
<213> Vitis vinifera

<400> 580
agtgtggaat tgagccaagg atgacttgcc ggcagctgca gcaaggcatt aaggtttaac 60

tggctataac tggcaagcat ccgaggctct gtttcacccct ct 102

<210> 581
<211> 97
<212> DNA
<213> Vitis vinifera

<400> 581
agggtggaat agagccaagg atgacttgcc ggcatttgca gtaagtctat attaactgga 60

acagccggca tgtaatcctg gctctatttg gtcctct 97

<210> 582
<211> 99
<212> DNA
<213> Vitis vinifera

<400> 582
gaaagtggat tgcagccaag gatgacttgc cggcacttgg cattaggcac catcgatcat 60

cttcccggca agttgttcct ggctacattc tgctctctt 99

<210> 583
<211> 96
<212> DNA
<213> Vitis vinifera

<400> 583
agggaggaac aaagccaagg atgaattgcc ggcgatgaaa gtaggcagct ttgtccatgg 60

atcggcaatt tatttcttgg ctatgttggg ctctct 96

<210> 584
<211> 143
<212> DNA
<213> Vitis vinifera

<400> 584
ggttatgtgg tgcagccaag gatgacttgc cggcaactcc ctttattgta ctcatgcatg 60

ctcatactta tactgttgtg ggcatcattt aagtggcaaa aatggtggtc ggcgagtcat 120

tcttagctac atttctgcct cat 143

<210> 585
<211> 125
<212> DNA
<213> Vitis vinifera

<400> 585
gtctcgtctg gtagccaagg atgacttgcc taaatccacc aggtttcaaa acactgaatg 60

taattatcca caaagcgatt ccgtggtctt taggcagtca ttccttcggc taaactgacc 120

ggctc 125

<210> 586
<211> 248
<212> DNA
<213> Vitis vinifera

<400> 586
cgttgtttgg tagcgaagga tgacttgcct acagcctcct taaggtttca aaataccgag 60

cttgtctacc tttgatcaaa tgattcaaga aacaaaagaa aagaaaggcc atggcagcca 120

tccatcagag tcaacatgag aatcatgttc tatagaaatt ggagtcattc ttgagaatga 180

acacgacact attagcttgg aatctataat gtggtttatg gcaagtctcc ttggcacctg 240

atggcctc 248

<210> 587
<211> 134
<212> DNA
<213> Zea mays

<400> 587
atgaggtaga gaacgggatg cagccaagga tgacttgccg gctcctggaa cctggaggcg 60

tctcagcttg ctgtgctgtg gcttagaact tagtcggcaa gtctgtcctt ggctacacct 120

agttctcttc ctct 134

<210> 588
<211> 150
<212> DNA
<213> Zea mays

<400> 588
accagagctg attcgttcag tagccaagga tgacttgcct aggtatatat gcatgggcta 60

tggctacatg cctgagagcc agtctcttgt gacgctgagc atgtatagtg taggcatgtc 120

ttccttggct actcggagcg gctctagtca 150

<210> 589
<211> 140
<212> DNA
<213> Zea mays

<400> 589
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gttgttgcat gcatgccact atgccagtcc tgctgggttt gtgggcggtc tccttggcta 120

gcctgagtgg ctcttgcctg 140

<210> 590
<211> 128
<212> DNA
<213> Zea mays

<400> 590
caataagggc ctgcctctga tagccaagga tgacttgcct atgtcctttg tttacaaagg 60

atcagaattg tggacctttg tgttggttcg taggcagtct ccttggctag cctgagtggc 120

ccctattg 128

<210> 591
<211> 191
<212> DNA
<213> Zea mays

<400> 591
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tcatgcaagg accatctcgt gtcgaccgac gagcgagcga gcgatcgatc gatgagagga   120

tgacgaagct tggggtgtac gttggtctct cacgggcagt ctccttggct agccctgact   180

cactcttacc g   191

<210> 592
<211> 151
<212> DNA
<213> Zea mays

<400> 592
gcgataagag tctgtccaga tagccaagga tgacttgcct gtggcttctt ggcttggctt   60

ggctcgggca aaaccttgtg cacgttttat tgctcgcctc gtggcctcga tcacaggcag   120

tctccttggc tagtccgggc gggcccctta t   151

<210> 593
<211> 133
<212> DNA
<213> Zea mays

<400> 593
cgatgagagc actgctctgg tagccaagga tgacttgcct gtggcctcca tcagtcgcag   60

aggacgctgt tcttctgctt gtggttgtcg atcgcaggca gtctccttgg ctagcccgag   120

cggctctcat cca   133

<210> 594
<211> 138
<212> DNA
<213> Zea mays

<400> 594
gtagccaaga atgacttgcc tatgcacgcc ctctgttggc agttccgtcc ggcagccatg   60

gcgacggttg cacaaggtga gtttttgcgg cgtggatgat gcaatgtggc tgcatcggca   120

ggtcttcttg gctagcca   138

<210> 595

<211> 65
<212> DNA
<213> Zea mays

<400> 595
gtagccaagg atgacttgcc ggcattatat ttcttggccc gccggcaagt catctggggc 60

tacgc 65

<210> 596
<211> 126
<212> DNA
<213> Zea mays

<400> 596
gcagccaagg atgacttgcc gggtattttg agcatgcatg ttacagggga gcatatgcaa 60

tctgtttgga attttgagcc cataccgtgc ggtgcctgtc ttccggcaag ttgtccttgg 120

ctacat 126

<210> 597
<211> 149
<212> DNA
<213> Arabidopsis lyrata

<400> 597
ggagccacgg tcgctgtttg ctgctgtggc atcatcaaga ttcacatctg ttgatggacg 60

gtggtgattc gctctcccca aagttctcta tgaaaatgag aatcttgatg atgctgcatc 120

ggcaatcaac ggctattctt tttctctcc 149

<210> 598
<211> 146
<212> DNA
<213> Arabidopsis lyrata

<400> 598
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atctcctaaa ttagggtttt gatatgtata tgagaatctt gatgatgctg catcaacaat 120

cgacggctac aaaataccta aagctg 146

<210> 599

<211> 133
<212> DNA
<213> Arabidopsis lyrata

<400> 599
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tgaacccatt tataattata ttgttgatgt atgtatgaga atcttgatga tgctgcagct 120

gcaatcagtg gct 133

<210> 600
<211> 163
<212> DNA
<213> Arabidopsis lyrata

<400> 600
gattcagaat ttgaagttag tggcagtcat tgtttgctat tgcaacatct tcaagattca 60

gaaatcagat tcttttatgg gttttctttt gagcctatat tatttggttt gagaatcttg 120

atgatgctgc agcggcaatt aaatggctta tttatctagg gtt 163

<210> 601
<211> 133
<212> DNA
<213> Arabidopsis lyrata

<400> 601
gccagtagtc gcagatgcag caccattaag attcacaaga gatgtggttc cctttgtttt 60

tgcctctcga tccgaagaaa agggttcctt tcgagtggga atcttgatga tgctgcatca 120

gcaaatacat ggc 133

<210> 602
<211> 135
<212> DNA
<213> Aquilegia caerulea

<400> 602
gttggctctt tggagacgca gcatcatcta gttcgcacat gatgatgata ggcagtgatt 60

aagtcactca cttacgcatg atagaagttg tgatatgaga atcttgatga tgctgcatca 120

gcagttaggc gacta 135

<210> 603
<211> 108
<212> DNA
<213> Aquilegia caerulea

<400> 603
gtgcagcatc attaagattc acaaacccta agagccttat gatgggtttt gatattgatc 60

actcttatag gactttatag agatgggaat cttgatgatg ctgcatcg 108

<210> 604
<211> 54
<212> DNA
<213> Aegilops speltoides

<400> 604
aggatcttga tgatgctgca gagaaggctg taaaagcatc agtcaaatga ttaa 54

<210> 605
<211> 277
<212> DNA
<213> Aegilops tauschii

<400> 605
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gagcgtggta tcatcaagat tcacatccat catgcatctc cctctctctc tctctctctc 120

tctctctctc tctctctctc taggtctata tggggctata tggagctgga gacatataga 180

tgcatagata gataacatac tttggatgag aatcttgatg atgctgcatc cgcacacaag 240

cgcccatcac tatattcccc gctgattgct gattgat 277

<210> 606
<211> 102
<212> DNA
<213> Arabidopsis thaliana

<400> 606
tgctgtggca tcatcaagat tcacatctgt tgatggacgg tggtgattca ctctccacaa 60

agttctctat gaaaatgaga atcttgatga tgctgcatcg gc 102

<210> 607

<211> 95
<212> DNA
<213> Arabidopsis thaliana

<400> 607
aggcgcagca ccattaagat tcacatggaa attgataaat accctaaatt agggttttga 60

tatgtatatg agaatcttga tgatgctgca tcaac 95

<210> 608
<211> 133
<212> DNA
<213> Arabidopsis thaliana

<400> 608
agctactgtt cgctgttgga gcatcatcaa gattcacaaa tcatcaagta ttcgtgtaaa 60

taaacccatt tatgattaga tttttgatgt atgtatgaga atcttgatga tgctgcagct 120

gcaatcagtg gct 133

<210> 609
<211> 124
<212> DNA
<213> Arabidopsis thaliana

<400> 609
agtcattgtt tgctattgca acatcttcaa gattcagaaa tcagattctc ttatgggttt 60

tcttttgagc ctttattttt tggtttgaga atcttgatga tgctgcagcg gcaattaaat 120

ggct 124

<210> 610
<211> 125
<212> DNA
<213> Arabidopsis thaliana

<400> 610
gtagtcgcag atgcagcacc attaagattc acaagagatg tggttccctt tgctttcgcc 60

tctcgatccg cagaaaaggg ttccttatcg agtgggaatc ttgatgatgc tgcatcagca 120

aatac 125

<210> 611

<211> 141
<212> DNA
<213> Arabidopsis thaliana

<400> 611
agaatcctga tgatgctgca gcatttgtca acacttggtt cgtcgaggcc cgaccatcaa 60

accggtggtt ctcagccgcc ggaaacagtg agaatccgcc tccgctacca atgttgctgc 120

tgcccggaaa ttggtggttt g 141

<210> 612
<211> 153
<212> DNA
<213> Brachypodium distachyon

<400> 612
aggcggcacg cacagtcggc gcttgcaggt gcagcaccac caagattcac atcgggttct 60

ccagtcgtaa ttaattaacg aggagtacaa ccatgatgag aatcttgatg atgctgcatc 120

ggcaaccgct cgactactca tcatatcgtc aat 153

<210> 613
<211> 254
<212> DNA
<213> Brachypodium distachyon

<400> 613
gttcgcggcg accagtcggt gatttctgct gtggcatcat caagattcac acaaatgcat 60

gctagcttcg tctatgccat cctttctcat ctttcgatct cgatctcggc cctaattaag 120

taattatacc caattgtgga tcggccggat tggagatcga tggatgcgtg gagaggagct 180

agattagcta tagcttatgt gtgggaatct tgatgatgct gcatcggaca tcagtgacta 240

aaacaagtat ggca 254

<210> 614
<211> 93
<212> DNA
<213> Brachypodium distachyon

<400> 614
tggagccatc gggtcaaacc ggaatgaggc cggtgtggcg gcgggggcag ctgtcgtggt 60

ggcagttttg gagaatcctg atgatgctgc agc 93

<210> 615
<211> 119
<212> DNA
<213> Brassica oleracea

<400> 615
cgttttttgt aggcgcagca ccatcaagat tcacatggaa attgaaaaat ctcctaattt 60

ttaattaggg ttttgatatg tatatgagaa tcttgatgat gctgcatcaa caaccgacg 119

<210> 616
<211> 107
<212> DNA
<213> Brassica oleracea

<400> 616
tgtaggtgca gcaccattaa gattcacatg gaaattgaga aaaccctaat ttatattaat 60

tagggttctg atatgtatat gagaatcttg atgatgctgc atcaaca 107

<210> 617
<211> 119
<212> DNA
<213> Brassica rapa

<400> 617
cgttttttgt aggcgcagca ccatcaagat tcacatggaa attgaaaaat ctcctaattt 60

ttaattaggg ttttgatatg tatatgagaa tcttgatgat gctgcatcaa caaccgacg 119

<210> 618
<211> 107
<212> DNA
<213> Brassica rapa

<400> 618
tgtaggtgca gcaccattaa gattcacatg gaaattgaga aaaccctaat ttatattaat 60

tagggttctg atatgtatat gagaatcttg atgatgctgc atcaaca 107

<210> 619
<211> 162
<212> DNA

<213> Citrus sinensis

<400> 619
gtcaccttaa aacagtcgtt gctcgctgta gcagcgtcct caagattcac atccagtcta 60

aaggcaaaag cagcaatttt tcttcatttt tgcttgcctt ggtttttgtc agtgagaatc 120

ttgatgatgc tgcaacggcg attaatgact agctaccaac aa 162

<210> 620
<211> 162
<212> DNA
<213> Citrus sinensis

<400> 620
gtcaccttaa aacagtcgtt gctcgctgta gcagcgtcct caagattcac atccagtcta 60

aaggcaaaag cagcaatttt tcttcatttt tgcttgcctt ggtttttgtc agtgagaatc 120

ttgatgatgc tgcaacggcg attaatgact agctaccaac aa 162

<210> 621
<211> 127
<212> DNA
<213> Citrus sinensis

<400> 621
ttgctcgctg tagcagcgac gtcaagattc acatccagtc taaaggcaaa agcagcaatt 60

tttcttcagt ttggcttgcc tgggtttttg tcagtgagaa tcttgatgat gcggcaacgg 120

cgatgaa 127

<210> 622
<211> 163
<212> DNA
<213> Citrus sinensis

<400> 622
actgtttgca gttggagcac catcaagatt cacaaactat tagggttagt gagtggagat 60

aatggtggct attttatttt ttttggcccc ttgcttcact tcaaattgct ctttgttttg 120

gaatcttgat gatgctgcag cagcgataag tggctaaatt ata 163

<210> 623

<211> 125
<212> DNA
<213> Gossypium hirsutum

<400> 623
agtcactgtt tgctgttgga gcatcatcaa gattcacaat tttagggttc ttttttgatt   60

gatttgatca atcagccttt ttatgattga gaatcctgat gatgctgcag tggcaataag   120

tggct   125

<210> 624
<211> 159
<212> DNA
<213> Glycine max

<400> 624
ttaacagtcg ttatttgcgg atgtagcatc atcaagattc acatgcaagc gcaggtggtg   60

ggtgggactt gatgcaatct aagtgctgtg ccagccaagc cataggtctt ttggaactga   120

gaatcttgat gatgctgcat cagccataaa cgacttcac   159

<210> 625
<211> 153
<212> DNA
<213> Glycine max

<400> 625
ttgacagtcg ttgtttgcgg atgtagcatc atcaagattc acatgcaaat gaaggtgggt   60

gggactatga tgcaatccaa gtgctctgcc aatccatcgg tctttttgat gtgagaatct   120

tgatgatgct gcatcagcca taaacggctt taa   153

<210> 626
<211> 153
<212> DNA
<213> Glycine max

<400> 626
aaatcagtca ctgtttgccg gtggagcatc atcaagattc acaagcttta ggggcattaa   60

tttgtttgag gtggttcctt attgctccaa aaccaattag cccttttgct atgggaatct   120

tgatgatgct gcagcagcaa taaatgacta ata   153

<210> 627
<211> 150
<212> DNA
<213> Glycine max

<400> 627
aaaacagtcg ctgattgcag atggagcatc atcaagattc acaagcttca ggggtttttt 60

gtttggggtg gtcccttatt gctcccaaat gaattaagcc ctttgatatg ggaatcttga 120

tgatgctgca gcagcaataa acgactaaca 150

<210> 628
<211> 153
<212> DNA
<213> Glycine max

<400> 628
aaaacagtca ctgtttgccg gtggagcatc atcaagattc acaagcttta gggggcatta 60

atttgtttga ggtggtccct tattgatcca aaccaattag cccttttgct atgggaatct 120

tgatgatgct gcagcagcaa taaatgacta ata 153

<210> 629
<211> 133
<212> DNA
<213> Glycine max

<400> 629
gcggatgtag catcatcaag attcacatgc aaacgcaggt ggtgggtggg actgtgatgc 60

aatctaagtg ctactgtgcc aaccaaagcc ataggtcttt tggaagtgag aatcttgatg 120

atgctgcatc agc 133

<210> 630
<211> 148
<212> DNA
<213> Gossypium raimondii

<400> 630
agaatcttga tgatgctgca tgagagaaca gtggcattag tgtagtactg acctgaccgt 60

gcatttgcca cggccaatca gggacacgtt gtggaggatc gaattcaacc ggtttcacca 120 ttgttctttc ctcactagga aagaatct 148

<210> 631
<211> 240
<212> DNA
<213> Gossypium raimondii

<400> 631
aaaatcttga tgatgctgca tgaaaaaaca gtggcattag tgtagtactg acctgaccgt 60

gcatttgcca cggccaatca gggacacgtt gtggaggatc gaattcaacc ggtttcacca 120

ttgttctttc ctcactagga aaaaatctcg gatatgcact attccaaaaa ataggctgat 180

ctgaagtccc cgctaaccct tggaaagatg gaacactaaa tgttgcagct gcagggttct 240

<210> 632
<211> 255
<212> DNA
<213> Hordeum vulgare

<400> 632
atacagtcat gaatccaatc cactacatga aaccgccccg gcgcaagtcc gaaaacgctg 60

aaacgccgga ggagcaaaaa agatactggc ttcccagaac atttacagta tggcttcttt 120

ttcagcgggg gtggtggtgg tggtgttggt tgcttgacga cgatgatgga gccatcgggt 180

cgaaccggaa tgaggccgat ggggcggcgg gggcagctgc cgcggctgtt ttggagaatc 240

ctgatgatgc tgcag 255

<210> 633
<211> 90
<212> DNA
<213> Hordeum vulgare

<400> 633
atggagccat cgggtcgaac cggaatgagg ccgatggggc ggcgggggca gctgccgcgg 60

ctgttttgga gaatcctgat gatgctgcag 90

<210> 634
<211> 137
<212> DNA
<213> Hordeum vulgare

<400> 634
tggtggtggt gttggttgct tgacgacgat gatggagcca tcgggtcgaa ccggaatgag 60

gccgatgggg cggcgggggc agctgccgcg gctgttttgg agaatcctga tgatgctgca 120

gcggacgatg accacca 137

<210> 635
<211> 272
<212> DNA
<213> Hordeum vulgare

<400> 635
cttgggcagc atgggaaata cagtcatgaa tccaatccac tacatgaaac cgccccggcg 60

caagaccgaa aacgctgaaa cgccggagga gcaaaaaaga tactggcttc ccagaacatt 120

tacagtatgg cttctttttc agcgggggtg gtggtggtgg tgttggttgc ttgacgacga 180

tgatggagcc atcgggtcga accggaatga ggccgatggg gcggcggggg cagctgccgc 240

ggctgttttg gagaatcctg atgatgctgc ag 272

<210> 636
<211> 146
<212> DNA
<213> Manihot esculenta

<400> 636
attggcggat gcgtcaccat caagattcac aaaactatga aggcttcatc gggacggtga 60

gtgtacggcc ggcggcggtg gctcttctta cttaaaaggt ttcctttttc gtatgagaat 120

cttgatgatg ctgcatcggc aaatat 146

<210> 637
<211> 113
<212> DNA
<213> Medicago truncatula

<400> 637
gccggtggag catcatcagg attcacaaga ttttgaaggg tttaatttgt tttgattgtt 60

tcaaatagat tagccctttg acatatgaga atcctgatga tgctgcagct gca 113

<210> 638
<211> 45
<212> DNA
<213> Medicago truncatula

<400> 638
atgcagaatc tctgagaatt gtgaggaatc ttgatgattc tgcac 45

<210> 639
<211> 109
<212> DNA
<213> Oryza sativa

<400> 639
gtgtttgcgg gcgtggcatc atcaagattc acatccatgc atatatcaca agacgcacat 60

atacatccga tttggctgag aatcttgatg atgctgcatc cgcagacaa 109

<210> 640
<211> 238
<212> DNA
<213> Oryza sativa

<400> 640
gtgatttctg acgtggcatc atcaagattc acacattaca ttgcatgcat gcatatgtct 60

atgcatcttt gagcttgttg ttctgatctc aacaacctag ctagctaata tttctctcct 120

ggccctgacc tgcatgatgc atggttgcac gcatggagag agaagagaga gatcgaagct 180

aattaaacgc atgtgtatat atgtgtggga atcttgatga tgctgcatcg gaaattaa 238

<210> 641
<211> 111
<212> DNA
<213> Oryza sativa

<400> 641
cttgttgcgg gtgcagcgtc atcaagattc acgtgtgccg cacggcacac gtatcggttt 60

tcaagtgtag tcatcgtgcg tgaatcttga tgatgctgca ccagcaaaga g 111

<210> 642
<211> 130
<212> DNA
<213> Oryza sativa

<400> 642
aaacagtcgg tgcttgcagg tgcagcacca tcaagattca catcgagttc atccctaaac 60

gagatcgagg ttggctgact atatgtgatg agaatcttga tgatgctgca tcagcaaacg 120

ctcgactact 130

<210> 643
<211> 297
<212> DNA
<213> Oryza sativa

<400> 643
atgcaaatac agtcatgaat cccaattaat taatcactac aagaaaccac ccggccggcc 60

cgccggcgca aagacgaaaa cgttgaaacg ccggcgacgg ccaagaaaaa aaaatttgcc 120

ggcttcccgg caaaatttac agtggtggtg atggcttctt tcctttttat caatggtggt 180

ggtgatggcg gcttgacgac gaagacgacg gcgccgtcgg gtcgaaccgg agggtggcag 240

tgtgttaggc agcagctgct gtcgtggcgg ctttggagaa tcctgatgat gctgcag 297

<210> 644
<211> 62
<212> DNA
<213> Oryza sativa

<400> 644
ggcagtgtgt taggcagcag ctgctgtcgt ggcggctttg gagaatcctg atgatgctgc 60

ag 62

<210> 645
<211> 53
<212> DNA
<213> Oryza sativa

<400> 645
agaatcctga tgatgctgca gcggaggacg acgacggcga cgacgaggag gag 53

<210> 646
<211> 318
<212> DNA
<213> Oryza sativa

<400> 646
ggtagcacgg tcacgattcg tggtttcgca ctcaaaaatg aagataaaag aatcatgagc 60

gtgagaattc tgatcataac caggtggaac atagagaggg atatcatatg gagaaggtcc 120

ctctctggac aaacgacgaa tgttatcagc aagcggcggt ggatgcacgg tgaggtgtcg 180

cctccaccag aataggtggc agtcaggcgg tcggggggaa gtagaactgg tggtggccgg 240

gaaatggatg ggggcgggag gaaggcgagc gggcggcgtc ggcgacggtg cccgtagaga 300

atcctgatga tgctgcag 318

<210> 647
<211> 248
<212> DNA
<213> Picea glauca

<400> 647
gcttatgcaa gacgaggctt ccaacttgtc acgtgaagat caacctagtg acaagttcaa 60

tgagtggtca ctgggttttt tcccgtaagt gttaatcaaa gctggtgctg ttgctgaatg 120

caaaatattc tttgtctgca ttaatgcagg ctggaacaag aaatgaaatc cccttttctg 180

cagccattct ggagaaggac tagttgttga agaatatatt tggggtgaga atcctgatga 240

tgctgcac 248

<210> 648
<211> 139
<212> DNA
<213> Populus trichocarpa x Populus deltoides

<400> 648
gtttgcgggt ggagcatcat caagattcac atgcaaatgc acggccggtg atgttaagag 60

ttaaatcttt ctttgtttct gttcatctgc caaagttctt tggaagtgag aatcttgatg 120

atgctgcatc ggcaataaa 139

<210> 649
<211> 139
<212> DNA
<213> Populus trichocarpa x Populus deltoides

<400> 649
tattgccgat gcagcatcat caagattctc acttccaaag aactttggca gatgaacaga   60

aacaaagaaa gatttaactc ttaacatcac cggccgtgca tttgcatgtg aatcttgatg   120

atgctccacc cgcaaacaa   139

<210> 650
<211> 68
<212> DNA
<213> Picea sitchensis

<400> 650
ctgtagccaa tcatgtgaag gaacagcagc tgaaattatt tggggtgaga atcctgatga   60

tgctgcac   68

<210> 651
<211> 129
<212> DNA
<213> Populus trichocarpa

<400> 651
ttgtttgcag gtgcagcatc atcaagattc acattcaaat agatgtaccg aagctataca   60

gctatgtagc tagctagcaa tgtataatca ttgtaggtga gaatcttgat gatgctgcat   120

cagccataa   129

<210> 652
<211> 140
<212> DNA
<213> Populus trichocarpa

<400> 652
ttgtttgcgg gtggagcatc atcaagattc acatgcaaat gcacggccgg tgatgttaag   60

agttaaatct ttctttgttt ctgttcatct gccaaagttc tttggaagtg agaatcttga   120

tgatgctgca tcggcaataa   140

<210> 653
<211> 128
<212> DNA
<213> Populus trichocarpa

<400> 653
ttgtttgcag gtgcagcatc atcaagattc acattcaaac agatgtacgg cagctagcta 60

gctagataga tagacagcaa tgtatttctt tgaaggtgag aatcttgatg atgctgcatc 120

agccataa 128

<210> 654
<211> 182
<212> DNA
<213> Populus trichocarpa

<400> 654
gcattggcgg atgcggcatc atcaagattc acaagcttta aggcttgagt gagaggggtg 60

gcatacggtc acctccttta gcaagcttta aggcttgagt gagaggggtg gcatacggtc 120

acctccttta gtccaaaggg tccttttta tgggaatctt gatgatgctg catcggcaaa 180

ta 182

<210> 655
<211> 133
<212> DNA
<213> Populus trichocarpa

<400> 655
atattggccg atgcggcagc atcaagattc acaaacttta aggcttgagt tggggtggta 60

cacggtcacc tcctttactc gaaaggttcc ttaatttctg atgggaatct tgatgatgct 120

gcatcggcaa ata 133

<210> 656
<211> 161
<212> DNA
<213> Populus trichocarpa

<400> 656
ttgtttgcgg gtgctgcatc accaagattc acatgcaaat gcatggccga tgatatatgt 60

tagaaatttt ttttatataa aaaagatatc tttctttctt tctgatcatc tgccaaagtt 120

ctttggaagt gagaatcttg atgatgctgc atcggcaata a 161

<210> 657

<211> 143
<212> DNA
<213> Populus trichocarpa

<400> 657
ctgtttgcct atggagcatc atcaagattc acaagcttta ttagggctag tgtgtggtga 60

tgatggtggc ttttggtggt cccttttttt caatccaata gccctttgaa ttgggaatct 120

tgatgatgct gcagcggcaa taa 143

<210> 658
<211> 143
<212> DNA
<213> Populus trichocarpa

<400> 658
ctgtttgccg atggagcacc atcaagattc acaaacttta ttagggctaa taagtggtga 60

tgatggtggc ttttggtggt cccttcgttt caacccaata gccatttgaa ttgggaatct 120

tgatgatgct gcagcggcaa taa 143

<210> 659
<211> 125
<212> DNA
<213> Populus trichocarpa

<400> 659
atgtggtgaa ggcagcaagt cgcgggttgt tgttggcgaa atggttctgt tggttgaatg 60

gaagagtagc tgaaggaaca gttttggtcg aagaagagaa tcctgatgat gctgcaacac 120

agagc 125

<210> 660
<211> 144
<212> DNA
<213> Ricinus communis

<400> 660
ctgatggagc atcatcaaga ttcacaaact ttatctaggg ctagtgggtt gttgtggtcc 60

cttttctttt tcttttttc tttttctctt gcttcaatcc aatagtccct ttgatatggg 120

aatcttgatg atgctgcagc ggca 144

<210> 661
<211> 102
<212> DNA
<213> Sorghum bicolor

<400> 661
gtgcagcatc atcaagattc acatccagct catcctcggt gatatgctat atacataaat 60

atatgcgtat gtgatgagat gagaatcttg atgatgctgc at 102

<210> 662
<211> 170
<212> DNA
<213> Sorghum bicolor

<400> 662
gcgtggcatc atcaagattc acacactgct tgcaaatgca tacatgcatc tctgccgcct 60

tctttgcctg ccattaatag cagttttact acatgtttta gctgctgctg catcatatat 120

gcctctgtga atatatatgt gtatgtgtgg gaatcttgat gatgctgcat 170

<210> 663
<211> 119
<212> DNA
<213> Sorghum bicolor

<400> 663
gtgcagcacc atcaagattc acatggtcca actcatgcat cttcagtgat gctcatgtga 60

tggctcgcag ttgctatata tgcatatgtg atgagatgag aatcttgatg atgctgcat 119

<210> 664
<211> 88
<212> DNA
<213> Sorghum bicolor

<400> 664
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atgcatgaga atcttgatga tgctgcat 88

<210> 665
<211> 115
<212> DNA

<213> Sorghum bicolor

<400> 665
tcggagccga ctctctgcag gtgcagcagc atcaaggttc gccagcagca agcgatcgat 60

cgaggcgtgt gtgtgtgaat cttgatgatg ctgcaccagc aatgagccgg ccggc 115

<210> 666
<211> 118
<212> DNA
<213> Sorghum bicolor

<400> 666
gcggcatcat caggattcac accgggtaaa caccgttggg tgggtgcagt tacccatgca 60

catatatgca ggtctggctc tatctgttgc ttgcgtgaga atcctgatga tgctgcac 118

<210> 667
<211> 106
<212> DNA
<213> Solanum lycopersicum

<400> 667
atgtggcata atcaagattc acgtgaaaag ttgcaaattg gttatataat tgatgaaatt 60

aatggctggc tatttgaaac tcacgagaat cttgatgatg ctgcat 106

<210> 668
<211> 135
<212> DNA
<213> Solanum lycopersicum

<400> 668
atgtagcatc atcaagattc atacatgaaa attaagaggc aaggttaaat atgtagcttt 60

aatttgaaat gaaaaatata atatatcatg accatgtcta tttatttcaa agtgagaatc 120

ttgatgatgc tgcat 135

<210> 669
<211> 300
<212> DNA
<213> Saccharum officinarum

<400> 669
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ccgaaccaca cccaccggtg gcggcgcatg gccagcccgc caccatttca ccgttcagct 120

cagacgccgt ctccactctc cagctcaaca ggaggactgg gggagtctgt caggcggttg 180

gggggaagcg gagctgctgg tagccgaaga acacttgccg ggggccaccg gacggcacgc 240

tgccggcggc tgtggccgcg tccacgccgg tggcggtaga gaatcctgat gatgctgcag 300

<210> 670
<211> 93
<212> DNA
<213> Solanum tuberosum

<400> 670
gtgcagcacc atcaagattc acatagaaaa tatggactat gaaatgaaat atgcccaatt 60

tttgaataca tgagaatctt gatgatgctg cat 93

<210> 671
<211> 100
<212> DNA
<213> Triticum aestivum

<400> 671
agaatcctga tgatgctgca gcggacgacg gcagggcggc aggaggagga gctgctgctg 60

ccacctgcca tgcccagctg ggaacagccc ctgcaggcct 100

<210> 672
<211> 118
<212> DNA
<213> Triticum aestivum

<400> 672
agaatcctga tgatgctgca gcggatgacg atgacgaaga gaacagcggc aatggcaggg 60

tgtgaggagg agctgctgtc accttccatg cccagctagg agcacccccc tcaggcct 118

<210> 673
<211> 54
<212> DNA
<213> Triticum aestivum

<400> 673
aggatcttga tgatgctgca gagaaggctg taaaagcatc agtcaaatga ttaa 54

<210> 674
<211> 240
<212> DNA
<213> Theobroma cacao

<220>
<221> misc_feature
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<223> n is a, c, g, or t

<400> 674
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gcgtttgcca tgcccaatcg gggagacctt gcggaggacc taattcaact cgattcacca 120

ttgctctttc ctcgctagga aagaatctag gatatccact attccaaaaa ataggctgat 180

ctgacggccc tactggtcct ttgaaaggtg gaccacccac tgttgcagca gcagggttct 240

<210> 675
<211> 154
<212> DNA
<213> Theobroma cacao

<400> 675
acagtcactg tttgctgatg gagcatcatc aagattcaca aaactttttt tagggctaat 60

gatcaatggt gaagatcatg cttcactata caatcagccc tttgaatatg tatgggaatc 120

ttgatgatgc tgcagcggca ataaatggct aaat 154

<210> 676
<211> 160
<212> DNA
<213> Theobroma cacao

<400> 676
atcagtcgtt ttttgctgct gcagcattat caagattcat atgcaaatat agtacggcag 60

ccgtggtccc ggtaccgcga ttgttttttt tcagatgcca tagcttttat ttgagcatga 120

gaatcttgat gatgctgcat cggccataaa tgacttcaca 160

<210> 677

<211> 163
<212> DNA
<213> Theobroma cacao

<400> 677
caatctgtca gtgtttgcag atgcggcatc atcaagattc acaaacttta gtaagggctt 60

cttttggagg ccggggagtg gtaaccaatc acctccttta ctcgaaagtt acctttcaaa 120

tgggaatctt gatgatgctg catcagcaaa catattggct att 163

<210> 678
<211> 129
<212> DNA
<213> Theobroma cacao

<400> 678
ggagcagtcg ttgtttgcaa atgtggcatc atcaagattc acatgcaacg tacatatata 60

tttatatata ttatatggtt ttggcctgag aatcctgatg atgctgcatt ggcaatgaat 120

ggctagatg 129

<210> 679
<211> 189
<212> DNA
<213> Theobroma cacao

<400> 679
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ggtgatggat aatacaaact ctcttctttt tttctcccct tcccctttct tttcccttct 120

cctttatgcc aaagttgttt ggaaagtgag aatcttgatg atgctgcatc ggcaataaac 180

gactataca 189

<210> 680
<211> 110
<212> DNA
<213> Vitis vinifera

<400> 680
tattgccgat gcagcatcat caagattctc atccttgaaa agtttggcag agataacatc 60

accaccgtgc atttgcatgt gaatcttgat gatgctacat gcgcaaacaa 110

<210> 681
<211> 118
<212> DNA
<213> Vitis vinifera

<400> 681
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atcgctgccg cgccgggctt tcgcatgtga atcttgatga tgctacacct gcaaacaa 118

<210> 682
<211> 138
<212> DNA
<213> Vitis vinifera

<400> 682
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ggtgactttt gtggtccctt cctacactcc gatggctctt tgatgtggga atcttgatga 120

tgctgcagcg gcaataaa 138

<210> 683
<211> 109
<212> DNA
<213> Vitis vinifera

<400> 683
gttagctgat gcagcatcat caagattcac acccaatgga agggcagtga tgcaatctct 60

gccaaagatt ttgagatgag aatcttgatg atgctgcatt cgcagtgaa 109

<210> 684
<211> 83
<212> DNA
<213> Zea mays

<400> 684
gcgtggcatc atcaagattc acaacccatc aatccgaacc actgatttgg aatgcatgya 60

tgagaatctt gatgatgctg cat 83

<210> 685
<211> 126
<212> DNA

<213> Zea mays

<400> 685
gtgcagcacc atcaagattc acatcgtcca actcatgcat catgcatata tgcatcttca   60

atgatgcgtg cctcgcatgt gtgtgtatat atatatgatg agatgagaat cttgatgatg   120

ctgcat   126

<210> 686
<211> 123
<212> DNA
<213> Zea mays

<400> 686
gtgcagcacc accaagattc acatccaact ctcacgcatc ttcagtgatg catgcatgct   60

ctgtgatgtc tcgcagcagc tatatgcata tgtgatgaga tgagaatctt gatgatgctg   120

cat   123

<210> 687
<211> 74
<212> DNA
<213> Zea mays

<400> 687
gtgcagcacc atcaagattc acatccccag ctcgatctgt gcatgatgag atgagaatct   60

tgatgatgct gcat   74

<210> 688
<211> 135
<212> DNA
<213> Zea mays

<400> 688
gagtggcatc atcaagattc acacactgca tgccaacata atgcgcgtgt tcatgcatcc   60

atcgccgccg ctgcatcatg catcatatat aatatatata tatgtgtatg tgtgggaatc   120

ttgatgatgc tgcat   135

<210> 689
<211> 455
<212> DNA

<213> Zea mays

<400> 689
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gccatgccca ggaggggaac ggctggggac acgccggctc ggaccggttc tcctcttcct 120

gcataggcgc ctccctgagg ttcacaaaga agcctggaca aggagatgca tacagatgtg 180

gatgctgggg ccgcatcgat ctgctgtgag gatggacagg ccactggggg cccattggct 240

gagaaacaat ggagcttgaa gcttcaggag aattacaact taatccaaaa ccagtcaggg 300

taccatcact tctgagatca tgcacgttag gttgtgaaat cctcaaattc agatcaagga 360

tgtctccatc aaccacatct ttctcaattg caggtggaag tgggacatct ccatcatagg 420

aaacagaatc aaagttccta acagcatccg gtcca 455

<210> 690
<211> 81
<212> DNA
<213> Zea mays

<400> 690
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agaatcctga tgatgctgca t 81

<210> 691
<211> 111
<212> DNA
<213> Arabidopsis lyrata

<400> 691
gccaaatgtc cccatgagtt ccctttaacg cttcattgtt aaatactcaa agccacattg 60

gtttgtatat aacactgaag tgtttggggg gactcttggt gccattttgg c 111

<210> 692
<211> 166
<212> DNA
<213> Arabidopsis lyrata

<400> 692
atgacagagc tacaagaaga aagtcaaatg tcttcatgag ttccctttaa cgcttcattg 60

ttaatattca aactacattt atttccataa atgtttgatc gatttgtata taacactgaa 120

gtgtttgggg ggacttttgg tgtcattctg gcgtagttac gattat 166

<210> 693
<211> 140
<212> DNA
<213> Arabidopsis lyrata

<400> 693
acaaaatata attcgactag atgtcctcta gagttctccc gaacacttca ttggaaattt 60

gttattcggt aaactaccaa ttaattccac tgaagtgttt gggggaactc cggatgtcat 120

ttggtgatgt caagccatgt 140

<210> 694
<211> 105
<212> DNA
<213> Arabidopsis lyrata

<400> 694
gtcggatgtt tcctagagtt cctctgagca cttcattgga gataccatct tttatcaaat 60

ggttttctac tgaagtgttt gggggaactc ccggactcat tcgat 105

<210> 695
<211> 127
<212> DNA
<213> Arabidopsis lyrata

<400> 695
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caatcgatcg attcaatcaa tctgacgaac actgaagtgt ttggggggac tctaggtgac 120

atatggc 127

<210> 696
<211> 105
<212> DNA
<213> Arabidopsis lyrata

<400> 696
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agtattctac tgaagtgttt gggggaactc ctggactcat tcgat 105

<210> 697
<211> 135
<212> DNA
<213> Arabidopsis lyrata

<400> 697
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tctaagatct atcgaccgat aaatcaatct gatgaacact gaagtgtttg gggggactct 120

aggtgacatc ttggc 135

<210> 698
<211> 93
<212> DNA
<213> Arabidopsis lyrata

<400> 698
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tactgaagtg tttggaggaa ctccagatga tat 93

<210> 699
<211> 100
<212> DNA
<213> Aquilegia caerulea

<400> 699
tggagttcct cctgccgctt cagtaatgat ctattaattc ctagctagtt aactagtttt 60

tgacaatctt aattactgaa gggtttggag gaactctaag 100

<210> 700
<211> 80
<212> DNA
<213> Aquilegia caerulea

<400> 700
cctggagttt ctcctgccgc ttcaggaacg atcaattgca aaatttgtta ttactgaagg 60

gtttggagga actctgggtg 80

<210> 701

<211> 93
<212> DNA
<213> Arabidopsis thaliana

<400> 701
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cactgaagtg tttgggggaa ctcccggacc cat   93

<210> 702
<211> 100
<212> DNA
<213> Arabidopsis thaliana

<400> 702
atgtccccat gagttccctt taacgcttca ttgttaaata ctcaaagcca cattggtttg   60

tatacaacac tgaagtgttt ggggggactc ttggtgtcat   100

<210> 703
<211> 100
<212> DNA
<213> Arabidopsis thaliana

<400> 703
atgtccacat gagttccctt taacgcttca ttgttgaata ctcaaagcca cattggtttg   60

tatataacac tgaagtgttt ggggggactc ttggtgtcat   100

<210> 704
<211> 100
<212> DNA
<213> Arabidopsis thaliana

<400> 704
atgtcctcta gagttctcct gaacacttca ttggaaattt gttattcagt aagctaacag   60

ttaattccac tgaagtgttt gggggaactc ccgatgtcat   100

<210> 705
<211> 95
<212> DNA
<213> Arabidopsis thaliana

<400> 705
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tctactgaag tgtttggggg aactcccggg ctgat 95

<210> 706
<211> 112
<212> DNA
<213> Arabidopsis thaliana

<400> 706
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gatcaatcaa tctgatgaac actgaagtgt ttggggggac tctaggtgac at 112

<210> 707
<211> 181
<212> DNA
<213> Brachypodium distachyon

<400> 707
caggagatga atggttggtt gtcaactgga gttctcctca aatcacttca gtagctagct 60

agctagcttg tgcctcattg tttcattgcc gctgtttata agtgtgcatg gagctggaga 120

gccgtgcaca gtgaagtgtt tgggggaact ccgggtggca accaacaata ctgatatcac 180

c 181

<210> 708
<211> 238
<212> DNA
<213> Brachypodium distachyon

<400> 708
acttcacaag aagctattcc tagggctatt gtgaagtgtt tgggggaact cttgatgtca 60

ccaagcttcc atttgtagat gtttctctca agccaaaaga gatacatcag ccggcatcgg 120

accacgtttg gtattaccat gagttccctg caagcacttc acgaggccca attatgatgg 180

ctactgtgaa gtgtttgggg gaactcttgg tgtcaccaag cttacacaaa taaaaaga 238

<210> 709
<211> 126
<212> DNA
<213> Brachypodium distachyon

<400> 709
ggcggcagac cacgtttggt aataccatga gttccctgca agcacttcat gaggcctaat 60

tctaagggct actgtgaagt gtttggggga actcttggtg ttaccaagct tttacaacaa 120

aaggag 126

<210> 710
<211> 148
<212> DNA
<213> Brachypodium distachyon

<400> 710
agctcctgga cgaacggttg gttgtttcct ggggttccct ccaaacactt cagcaggtcg 60

gctttcctat actagctcac aggctgaagg gtgaagtgtt tggggaactc taggtgacaa 120

ccgccatttt atcaaggtca aactgctg 148

<210> 711
<211> 150
<212> DNA
<213> Brachypodium distachyon

<400> 711
gttggttgtc acctggagtt ctcctcaaat cacttcagta gctagctagc ttgtgcctcc 60

ttgttgcatt gccactgttt tataagtgtg cttggggcca gagagctgtg cacagtgaag 120

tgtttggggg aactctgggt ggcaaccagc 150

<210> 712
<211> 96
<212> DNA
<213> Brachypodium distachyon

<400> 712
gtttggtgtc cccgggagtt cccttcaaac actttacgaa gcatctttct aagactattt 60

gtgaagtgtt tgggggaact ctcggtgtca ccaagc 96

<210> 713
<211> 89
<212> DNA
<213> Brachypodium distachyon

<400> 713
ggtgttacca ggagtttcct gcaaacactt cacgagtgcc tattttaatg ggttgttgtg 60

aagtgtttgg gggaactctt gatgtcacc 89

<210> 714
<211> 76
<212> DNA
<213> Brachypodium distachyon

<400> 714
accatgagtt ccctgcaagc acttcacgag gccgttttct gagggctact gtgaagtgtt 60

tgggggaact cttggt 76

<210> 715
<211> 90
<212> DNA
<213> Brachypodium distachyon

<400> 715
tggtattatc atgaattccc tacaagcact tcacaagaag ctattcctag ggctattgtg 60

aagtgtttgg gggaactctt gatgtcacca 90

<210> 716
<211> 88
<212> DNA
<213> Brachypodium distachyon

<400> 716
ggtattctca tgagtttccc gcaagcactt cacgaggccg ttttctgagg gctactgtga 60

agtgtttggg ggaactcttg gtctcacc 88

<210> 717
<211> 86
<212> DNA
<213> Brachypodium distachyon

<400> 717
gtactaccat gagttccctg caagcacttc atgaggccca attctgaggg ctactgtgaa 60

gtgtttgggg gaactcttgg tgttac 86

<210> 718
<211> 96
<212> DNA
<213> Brachypodium distachyon

<400> 718
gtttggtatt atcatgagtt ccctgcaagc acttcacgag gcactatccc aagggctact 60

gtgaagtgtt tgggggaact cttggtgtca ccaagc 96

<210> 719
<211> 95
<212> DNA
<213> Brachypodium distachyon

<400> 719
tggtattacc atgagttcct ttgcaagcat ttcacgtacg aggcactatc ccaagggcta 60

ttgtgaagtg tttgggggaa ctcttggtgt cacca 95

<210> 720
<211> 90
<212> DNA
<213> Brachypodium distachyon

<400> 720
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aagtgtttgg gggaactctt ggtgtcacca 90

<210> 721
<211> 101
<212> DNA
<213> Citrus sinensis

<400> 721
atgtctccgg gagttcctcc gatcacttca ttggggctat atgatcattt agacaaaatt 60

tgtcacccca ctgaagtgtt tgggggaact ctgggtgcca c 101

<210> 722
<211> 186
<212> DNA
<213> Gossypium hirsutum

<400> 722

cttttcctc gaacaactgt aacggaacgg gtgagacgga gaagggaaag gtggtgtcca 60

tttgaagcga aatcggatca tccgcaatgg aggatttagt aaaacccagg gacagacccg 120

atttagtatg aaataaatcc attgaaaccc taaaagggaa attttttgaa gtgtttgggg 180

gaactt 186

<210> 723
<211> 84
<212> DNA
<213> Gossypium hirsutum

<400> 723
gagttcccct gaccacttca ttggggatat attaaaaacc ttaactgagg aaattttttc 60

ctactaaagt gtttagggga actc 84

<210> 724
<211> 107
<212> DNA
<213> Gossypium hirsutum

<400> 724
gagttcccct gatcacttca ctggggttat ggggtctgct cttctcttct cagagccttg 60

ttaaaaggga ggtctccgat gacctactga agtgtttggg ggaactc 107

<210> 725
<211> 67
<212> DNA
<213> Glycine max

<400> 725
gagttcctct gaacgcttca tgtgattggc tagttatagg cctttgatga agtgtttggg 60

ggaactc 67

<210> 726
<211> 135
<212> DNA
<213> Medicago truncatula

<400> 726
tttttgttga ttgtttctta gagttccttt gaacgcttca tgcatgagaa tatgtatttg 60

gtctaatatc cattagaaaa gatagttctt catcaatgaa gtgtttgggg gaactcttgg 120

gttcaaccag cacca 135

<210> 727
<211> 124
<212> DNA
<213> Medicago truncatula

<400> 727
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gaaattatgg atagttcttg ttcaatgaag tatttggggg aactcttgga attgaatcaa 120

cata 124

<210> 728
<211> 97
<212> DNA
<213> Medicago truncatula

<400> 728
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gatagtcttt tcttctatga agtgtttggg ggaactc 97

<210> 729
<211> 95
<212> DNA
<213> Medicago truncatula

<400> 729
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atagttcttc ttaaatgaag tgtttggggg aactc 95

<210> 730
<211> 100
<212> DNA
<213> Medicago truncatula

<400> 730
gagttccttt gaacgcttca tgcatgagaa tatctatcta tttggtttaa aatccattag 60

gatagatagt tcttcttaaa tgaagtgttt gggggaactc 100

<210> 731
<211> 98
<212> DNA
<213> Medicago truncatula

<400> 731
gagttccttt gaacgcttca tgcatgagaa atatctcttt ggtttaaaat ccattagaaa 60

agatagtatt ttcttctatg aagtgtttgg gggaactc 98

<210> 732
<211> 63
<212> DNA
<213> Medicago truncatula

<400> 732
gagttcctct gaacgcttca tataagaggt tatccatctt cattgaagtg tttgggggaa 60

ctc 63

<210> 733
<211> 101
<212> DNA
<213> Medicago truncatula

<400> 733
gactttctct gaacacttca tacaagaggt tatccatcta atctaaaagt cattagatat 60

ttacgatggg tcgttcttca atgaagtgtt tgggggaact t 101

<210> 734
<211> 76
<212> DNA
<213> Medicago truncatula

<400> 734
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gtgtttgggg gaactc 76

<210> 735
<211> 76
<212> DNA
<213> Medicago truncatula

<400> 735
gagttcctct gaatgcttca aacatgagac aatctatatg gatagttctt gttcaatgaa 60

gtgtttgggg gaactc 76

<210> 736
<211> 98
<212> DNA
<213> Medicago truncatula

<400> 736
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agatagtatt ttcttctatg aagtgtttgg gggaactc 98

<210> 737
<211> 101
<212> DNA
<213> Medicago truncatula

<400> 737
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aaaagatagc cattttttca atgaagtgtt tgggggaact c 101

<210> 738
<211> 100
<212> DNA
<213> Medicago truncatula

<400> 738
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aaaagatagt tcttcttaaa tgaagtgttt gggggaactc 100

<210> 739
<211> 101
<212> DNA
<213> Medicago truncatula

<400> 739
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aaaagatagc cattttttca atgaagtgtt tgggggaact c 101

<210> 740
<211> 83
<212> DNA
<213> Medicago truncatula

<400> 740
gagttcctct gaactcttca tctaaagggc tatagcaaga aagaaaggaa aatccttgta 60

tgatgaagtg tttgggggaa ctc 83

<210> 741
<211> 72
<212> DNA
<213> Medicago truncatula

<400> 741
gagttccctt aaacatttca ttaaggactc aatttcttct cttcaacctt gttgaagcgt 60

ttgggggaac tc 72

<210> 742
<211> 105
<212> DNA
<213> Medicago truncatula

<400> 742
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gaaaaatagt tcttcttaaa tgaagtgttt gggggaactc ttggg 105

<210> 743
<211> 111
<212> DNA
<213> Medicago truncatula

<400> 743
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attagaaaag atagccattt tttcaatgaa gtgtttgggg gaactcttgg a 111

<210> 744
<211> 142
<212> DNA
<213> Oryza sativa

<400> 744

ttgtccactg gagttctcct caatccactt cagtagatag ctatggctag gcctcattgc 60

attgcactgt tacataactg tgatcatggg gccaaaagct agctatgtat agtgaagtgc 120

ttgggggaac tccagttgac ac 142

<210> 745
<211> 142
<212> DNA
<213> Oryza sativa

<400> 745
ttgtccactg gagttctcct caatccactt cagtagatag ctatggctag gcctcattgc 60

attgcactgt tacataactg tgatcatggg gccaaaagct agctatgtat agtgaagtgc 120

ttgggggaac tccagttgac ac 142

<210> 746
<211> 86
<212> DNA
<213> Oryza sativa

<400> 746
gagtccctag gagttccttt caagcacttt acgacacact gtattgagag ttgtcgtgaa 60

gtgtttgggg gaactcttag tgtcgc 86

<210> 747
<211> 89
<212> DNA
<213> Oryza sativa

<400> 747
gtattatcaa gagttctctt taagcacttc atacgacacc attatttata gggttgttgt 60

gaagtgtttg gaggaactct cggtgtcat 89

<210> 748
<211> 88
<212> DNA
<213> Oryza sativa

<400> 748
gtattgtcgt gagttccctt caagcacttc acgtggcact atctcaatgc ctactatgtg 60

aagtgtttgg gggaactctc gatatcac 88

<210> 749
<211> 88
<212> DNA
<213> Oryza sativa

<400> 749
gtattatcga gagttccctt caaccacttc acgtggcact gtttcaaggc ctattgtgtg 60

aagtgtttgg gggaactctc gatatcac 88

<210> 750
<211> 82
<212> DNA
<213> Oryza sativa

<400> 750
ttatcgcggg ttcccttcaa tcacttcaca tggtactatt tcaaggccta ctatgtgaat 60

tgtttggggg aactctcgat gt 82

<210> 751
<211> 86
<212> DNA
<213> Oryza sativa

<400> 751
gtatcaccgt gagttccctt cgaacacttc acgtggcact atttcaatgc ctattgtgaa 60

gtgtttgggg gaactctcga tgtcat 86

<210> 752
<211> 112
<212> DNA
<213> Oryza sativa

<400> 752
ttgttacctg gagtttcctc aacacacttc acatctgcta ggccctatta caattgcgca 60

atgtggagtc tgcaattggt agtgaagtgt ttgggggaac tctaggtggc ac 112

<210> 753
<211> 99
<212> DNA

<213> Oryza sativa

<400> 753
gttttaccgg gagttctctt caagcacttc acgtagagct ttctattgac atggagcttt 60

agaacaatgt gaagtgtttg ggggaactct tggtaccaa 99

<210> 754
<211> 112
<212> DNA
<213> Oryza sativa

<400> 754
gtgttcccaa gagttccttg caagcacttc acatagaact tctgttactc tcatgtaaca 60

ttgggaactt gagaagctac tgtgaagtgt ttgggggaac tctaggtggc ac 112

<210> 755
<211> 99
<212> DNA
<213> Oryza sativa

<400> 755
gttttatcgg gagtttcctt caagcacttc acgtagagct ttctattgat atggagcttt 60

ggaacaatgt gaagtgtttg ggggaactct tgataccaa 99

<210> 756
<211> 94
<212> DNA
<213> Oryza sativa

<400> 756
gcgttccttc caagcacttc acacagagct tttatttctc tcacatcgat tgagaactta 60

attagaagct tttgtgaagt gtttggggga actc 94

<210> 757
<211> 120
<212> DNA
<213> Oryza sativa

<400> 757
gagttctcct caaatcactt cagtagatag ctagctaggc ttcattgcat tacactgtta 60

caaaactgtg agcatggggc caaaagctag ttgtatatag tgaagtgttt gggggaactc 120

<210> 758
<211> 66
<212> DNA
<213> Oryza sativa

<400> 758
gagttccctt caagcacttc acgacgcact atttagagag ttgttgtgaa gtgtttgggg 60

gaactc 66

<210> 759
<211> 69
<212> DNA
<213> Oryza sativa

<400> 759
gagttctctt taagcacttc atacgacacc attattgtta gggttgttat gaagtgtttg 60

gaggaactc 69

<210> 760
<211> 68
<212> DNA
<213> Oryza sativa

<400> 760
gagttccctt caagcacttc acgtggcact atttcaatgc gtaccgtgtg aagtgtttgg 60

gggaactc 68

<210> 761
<211> 68
<212> DNA
<213> Oryza sativa

<400> 761
gagttccctt caagcacttc acatgacact atttcaatgt ctattatgtg aagtgtttgg 60

gggaactc 68

<210> 762
<211> 68
<212> DNA
<213> Oryza sativa

<400> 762
gagttccctt caaccacttc acgtggcact attttaggac ctactatgtg aagtgtttgg 60

gggaactc 68

<210> 763
<211> 86
<212> DNA
<213> Oryza sativa

<400> 763
gtatcaccgt gagttccctt caagcacttc acgtggcact atttcaatgc ctattgtgaa 60

gtgtttgggg gaactctcga tgttcc 86

<210> 764
<211> 143
<212> DNA
<213> Oryza sativa

<400> 764
ttatccactg gagttctcct caaaccactt cagcagatag ctagctaggc ctcattgcat 60

tgcaccactg ttgcataact atgagcatgg ggccaaaagt tagctgctta tagtgaagtg 120

tttggggaaa ctccggttgg caa 143

<210> 765
<211> 86
<212> DNA
<213> Oryza sativa

<400> 765
acactgccag gaattccctt caagcaattc atgaaacaat attttgagag ttgttgtgaa 60

gcgtttgggg gaaatctcag tgtcgc 86

<210> 766
<211> 69
<212> DNA
<213> Oryza sativa

<400> 766
gaattctctt taagcacttc atacgacaca attatttcaa gggttgttgt gaagtatttg 60

gcggaactc 69

<210> 767
<211> 69
<212> DNA
<213> Oryza sativa

<400> 767
gagttctctt taatcatttc acatggcact attttaaggc ctactgtgtg aagtgtttgg 60

gggattctc 69

<210> 768
<211> 96
<212> DNA
<213> Oryza sativa

<400> 768
atttggtatc gccatgagtt ctcttcaaac tcttcatacg acactaattc aagtgatgtt 60

gtgaagtgtt tggagtagct cttggtgtca ccaaac 96

<210> 769
<211> 110
<212> DNA
<213> Oryza sativa

<400> 769
tggccccagg agttccttgc aagcacttca catagaactt cagttactct catacaacat 60

tgtgattttg agaagctatt gtgaagtgtt tgggggaact ctcggtgcca 110

<210> 770
<211> 103
<212> DNA
<213> Picea abies

<400> 770
ctcacagctg gttctcaatg ccgggagttc cttcaatcac ttcgccgaat ccgaaagcat 60

ttcactgaag tgtttggagg aacttcgggc gtcactgaac tgc 103

<210> 771
<211> 226
<212> DNA

<213> Populus trichocarpa

<400> 771
ggtcaccctg agttcctcct agcttcttca gtacccgtgg aaagctaatg ctacaattat 60

cttgagctgg taagactggc aggtgtcaga tgtggatgtg ttaaaggtaa tattattgat 120

tatttacggc gccattcaag tatttgttct actgttagag gatttaatca agtatatgtg 180

gtattactcc tgatttgctg aagggtttgg aggaactcta ggtgct 226

<210> 772
<211> 98
<212> DNA
<213> Populus trichocarpa

<400> 772
gtgtccccta gagttccctt gagcacttca ctgggaccct tcagaccgaa agagtattat 60

ctttcccact gaagtgtttg ggggaactcc tggtgtca 98

<210> 773
<211> 101
<212> DNA
<213> Populus trichocarpa

<400> 773
gtgtccccta gagttcctct gagcacttca ttgggaatct tcgattaaat gaaagagtat 60

tatcattcct actgaagtgt ttgggggaac tcctggtgtc a 101

<210> 774
<211> 101
<212> DNA
<213> Populus trichocarpa

<400> 774
gtgtccccta gagttcctct gagcacttca ctgggaattt ccgatcaaat gaaagagtat 60

tatcattcct actgaagtgt ttgggggaac tcctggtgtc a 101

<210> 775
<211> 113
<212> DNA
<213> Populus trichocarpa

<400> 775
ctgtcccccg gagtttccct gaccacttca ctggggctat aattctactc ttcgtgttta 60

agggtagagg caacccttcc tcactgaagt gtttggggga actctgggtg gca 113

<210> 776
<211> 113
<212> DNA
<213> Populus trichocarpa

<400> 776
ctgtcccccg gagtttccct gaccacttca ctggggctat aattctactc ctcgtgttta 60

agggtagagg caacccttcc tcactgaagt gtttggggga actctgggag gca 113

<210> 777
<211> 102
<212> DNA
<213> Populus trichocarpa

<400> 777
gtgtccccta gagttcctct gagcacttca ttggggatct tccatcgacc tgaaagagta 60

ttatcattcc tactgaagtg tttgggggaa ctcctggtgt ca 102

<210> 778
<211> 102
<212> DNA
<213> Populus trichocarpa

<400> 778
gtgtccccta gagttcctct gagcacttca ttggggatct tccatcgacc tgaaagagta 60

ttatcattcc tactgaagtg tttgggggaa ctcctggtgt ca 102

<210> 779
<211> 102
<212> DNA
<213> Populus trichocarpa

<400> 779
gtgtccccta gagttcctct gagcacttca atggggatct tccatcgacc tgaaagagta 60

ttatcattcc tactgaagtg tttgggggaa ctcctggtgt ca 102

<210> 780
<211> 102
<212> DNA
<213> Populus trichocarpa

<400> 780
gtgtccccta gagttcctct gagcacttca atggggatct tccatcgacc tgaaagagta 60

ttatcattcc tactgaagtg tttgggggaa ctcctggtgt ca 102

<210> 781
<211> 74
<212> DNA
<213> Ricinus communis

<400> 781
ctagagttcc cttgaacact tcactgggac gaaaatccat tcttccaact gaagtgtttg 60

ggggaactct tggt 74

<210> 782
<211> 97
<212> DNA
<213> Ricinus communis

<400> 782
ctggagttcc cctggccgct tcattggggc tattatatac ccttaattat acatgtgtta 60

ttcctgccct actgaagtgt ttgggggaac tctaggt 97

<210> 783
<211> 82
<212> DNA
<213> Ricinus communis

<400> 783
ctagagttcc cttgagcact tcactgggat gaaaaaaggt ccagtcttcc ttcctactga 60

agtgtttggg ggaactcctg gt 82

<210> 784
<211> 87
<212> DNA
<213> Ricinus communis

<400> 784

ctagagttcc cttgaccact tcattgtgga ttattcttca agctcaagga gttggtttac 60

actgaagtgt ttgggggaac tcctggt 87

<210> 785
<211> 74
<212> DNA
<213> Ricinus communis

<400> 785
ctagagttcc cttgaacact tcactgggac gaaaatccat tcttccaact gaagtgtttg 60

ggggaactct tggt 74

<210> 786
<211> 150
<212> DNA
<213> Sorghum bicolor

<400> 786
ggttggttgg ttgtcacctg gagttctcca caaactactt cagtagcaac acacacccct 60

agtttaatgc accgtgtttg catgtttgtg tggagctgtg tgtgtacata gtgaagtgtt 120

tgggggaact ctgggtggca atcagcaatt 150

<210> 787
<211> 105
<212> DNA
<213> Sorghum bicolor

<400> 787
gttaggtttg gtgtccctag gagttctctg caagcacttc acgaggcatc gttttgagag 60

cttttgtgaa gtgtttgggg gaactcttag tgtcacaaat cattt 105

<210> 788
<211> 73
<212> DNA
<213> Sorghum bicolor

<400> 788
gagttcccta caagcacttc acgagacctt ggcttaataa agggttgttt gtgaagtgtt 60

tgggggaact ctt 73

<210> 789
<211> 103
<212> DNA
<213> Sorghum bicolor

<400> 789
tcaagtttgg tgtccccagg agttctctgc aaacacttca caaagcactt ttttagagct 60

tttgtgaagt gtttggggga actcttggtg ccactgatca ttt 103

<210> 790
<211> 105
<212> DNA
<213> Sorghum bicolor

<400> 790
attaggtttg gtgtccccgg gagttctctg caagcacttc acgaggcact attttgagag 60

cttttgtgaa gtgtttgggg gaactcttga tgccactaac cattt 105

<210> 791
<211> 122
<212> DNA
<213> Sorghum bicolor

<400> 791
acaatgtttg gtgttaccac gagttccctt caagcacttc atgaggcacc attaaataac 60

tctatttaag attaggtgta atatgaagtg tttgggggaa ctcttggtga tactcaacat 120

cg 122

<210> 792
<211> 68
<212> DNA
<213> Sorghum bicolor

<400> 792
gttccctaaa agcacttcac gagaccttgg cttaataaag ggcccttgtg aagtgtttgg 60

gggaactc 68

<210> 793
<211> 81
<212> DNA

<213> Sorghum bicolor

<400> 793
gttcccttca agcacttcac atgaggcacc attcaaactc tgtttaagat taggtgtaat   60

gtgaagtgtt tgggggaact c   81

<210> 794
<211> 97
<212> DNA
<213> Sorghum bicolor

<400> 794
gttccctgca aacacttcac aagctagacc atatatagta tgcccttgca caatgtggta   60

tccagttacc tagctagtga agtgtttggg ggaactc   97

<210> 795
<211> 87
<212> DNA
<213> Sorghum bicolor

<400> 795
gttcccttca agcacttcac atgaagctct ttgcattata ttggcggatg tagcattgag   60

accaatgtga agtgtttggg ggaactc   87

<210> 796
<211> 80
<212> DNA
<213> Sorghum bicolor

<400> 796
gttcccttca agcacttcac atgaagcttc acattggcag atgtagtctt gagaccaatg   60

tgaagtgttt ggaggaactc   80

<210> 797
<211> 84
<212> DNA
<213> Sorghum bicolor

<400> 797
gttcccttca agcacttcac atggagcatt atttgtcttg gagaaagctt aatttgatgc   60

attgtgaagt gcttggggga actc   84

<210> 798
<211> 94
<212> DNA
<213> Solanum demissum

<400> 798
atgttcccta gagttccctt gaccgcttca ttagggttaa ctactttgtt gtttgatgcc 60

ctgctgaagt gtttggggga actcccgggc tcac 94

<210> 799
<211> 199
<212> DNA
<213> Solanum lycopersicum

<400> 799
agggcttact ttgatgttgg aagccttgct gaagtgtttg ggggaactcc cgggttgact 60

ttgaaaatta cgcaaacaag tatatataaa tgcatgagta cgtattagct aaagatgatg 120

agtacaatat tgattcatgt acctttggag ttcccttgac cacttcatga gagcttaata 180

tttgattgtt tgaagtcct 199

<210> 800
<211> 101
<212> DNA
<213> Solanum lycopersicum

<400> 800
ttaaggtgtt ccctagagtt cccttgacca cttcatgagg gcttactttg atgttagaag 60

cgttgctgaa gtgtttgggg gaactcctgg gttgacttta a 101

<210> 801
<211> 77
<212> DNA
<213> Triticum aestivum

<400> 801
cttacagtgg gttccttgca agcacttcat gaggcattat taaaaatgcc actgtgaagt 60

gtttggggga actcttg 77

<210> 802
<211> 124
<212> DNA
<213> Triticum aestivum

<400> 802
ctgaagtgtt tgggggaact cttggtgtca ccaagcattt agtagacatt ggccacatat 60

cataagagag atgcatcaat gggctgaatg tttggtctta ccatgggttc cttgcaagca 120

cttc 124

<210> 803
<211> 123
<212> DNA
<213> Theobroma cacao

<400> 803
agagagtcag ctgtcctctg gagttcccct gaccacttca ctagaggttt cctggaccct 60

taataggaag aaacctgacc tactgaagtg tttgggggaa ctcctgttgg cacctgacaa 120

tgt 123

<210> 804
<211> 117
<212> DNA
<213> Theobroma cacao

<400> 804
tatgccaggt gcccactaga gttcccctgg gcacttcagt tgatttcttt agagctcaaa 60

acctcttacc tgtctactga agtgtttggg ggaactccgg ttgccatctg agacagt 117

<210> 805
<211> 92
<212> DNA
<213> Vitis vinifera

<400> 805
gtcccctaga gttcccttga tcacttcact agggagcttc gctagtttta atgacttcct 60

actgaagtgt ttgggggaac tcctggtacc ga 92

<210> 806
<211> 90

<212> DNA
<213> Vitis vinifera

<400> 806
gtcccctaga gttcccctta ccacttcact ggggatcttc tctaatgaat gcctacgtac 60

tgaagtgttt gggggaactc ctggtgccat 90

<210> 807
<211> 92
<212> DNA
<213> Vitis vinifera

<400> 807
gtcccctaga gttcccttga ccacttcact ggggaccttc tctagttata atgacttcct 60

actgaagtgt ttgggggaac tcctggtgcc at 92

<210> 808
<211> 86
<212> DNA
<213> Vitis vinifera

<400> 808
gccccctaga gttcccctga ccacttcatt ggggatcttc tctaatgact tcctactgaa 60

gtgtttgggg gaactcctgg tgtcat 86

<210> 809
<211> 92
<212> DNA
<213> Vitis vinifera

<400> 809
ctcccctaga gttcccttga ccacttcact ggggaccttc tctaattata atgacttcct 60

actgaagtgt ttgggggaac tcctggtgcc at 92

<210> 810
<211> 86
<212> DNA
<213> Vitis vinifera

<400> 810
gtaccctaga gttcccctga ccacttcact ggggatcttc tctaatgact tcccactgaa 60

gtgtttgggg gaactcctgg tgtcat 86

<210> 811
<211> 86
<212> DNA
<213> Vitis vinifera

<400> 811
gtcccctaga gttcccctga gcacttcatt ggggatcctt agttttcaat tcctactgaa 60

gtgtttgggg gaactcccgg tgtcat 86

<210> 812
<211> 92
<212> DNA
<213> Vitis vinifera

<400> 812
gtcccctaga gttcccttga ccacttcact ggggaccttc tctaattata atgacttcct 60

actgaagtgt ttgggggaac tcctggtgct at 92

<210> 813
<211> 86
<212> DNA
<213> Vitis vinifera

<400> 813
gccccctaga gttcccctga ccacttcact ggggatcttc tgtaatgact tcctactgaa 60

gtgtttgggg gaactcctgg tgtcat 86

<210> 814
<211> 86
<212> DNA
<213> Vitis vinifera

<400> 814
gccccctaga gttcccctga ccacttcact ggggatcttc tttaatgact tcctactgaa 60

gtgtttgggg gaactcctgg tgtcat 86

<210> 815
<211> 92
<212> DNA

<213> Vitis vinifera

<400> 815
tcccctagag ttcccttgac cacttcactg gggaccttct ctaattataa tgacttccta   60

ctgaagtgtt tgggggaact cctggtgcca tt   92

<210> 816
<211> 87
<212> DNA
<213> Vitis vinifera

<400> 816
gccccctaga gttcccctga ccacttcact gggggatctt ctgtaatgac ttcctactga   60

agtgtttggg ggaactcctg gtgtcat   87

<210> 817
<211> 92
<212> DNA
<213> Vitis vinifera

<400> 817
gtcccctaga gttcccttga acacttcact ggggaccttc tctagttata atgacttcct   60

actgaagtgt ttgggggaac tcctggtgcc at   92

<210> 818
<211> 137
<212> DNA
<213> Vitis vinifera

<400> 818
ggccttgaga gttcccccaa cccctccagt atgaccatct ctcttcttct tttaatttgt   60

tcatcaaatc ttcttctact atctatttcc agggtgattt cctctactga agagtctgga   120

ggaactcttg gtgccac   137

<210> 819
<211> 149
<212> DNA
<213> Zea mays

<400> 819
tattggttgg ttgtcacctg gagttctcct caaaccactt cagttgctgc acctagctag   60

tttaatggca ctgtgcttgc gtgcaagcgg ccggagctgt gtgtagctag tgaagtgttt 120

gggggaactc tgggtgtcaa tcagcaatt 149

<210> 820
<211> 138
<212> DNA
<213> Zea mays

<400> 820
tcttggttgg ttctcccttg gagttccctg caaacacttc accagctagg ccatagtgcc 60

ggcccttgca caatgttgta tctgatcacc tagctagtgt gaagtgtttg gaggaactct 120

aggtgttatc cagcaatg 138

<210> 821
<211> 66
<212> DNA
<213> Zea mays

<400> 821
agttctatgc aagcacttca cgaggcattg tttcaagagc ttttgtgaag tgtttggggg 60

aactct 66

<210> 822
<211> 85
<212> DNA
<213> Zea mays

<400> 822
agttcccttc aagcacttca catgaggcac cattcaaata acacatttca agattaggtg 60

catgtgaagt gtttggggga actct 85

<210> 823
<211> 70
<212> DNA
<213> Zea mays

<400> 823
agttacctac aagcacgtct cgataccttg gcttaataaa ggccagttgt gaagtgtttg 60

ggggaactct 70

<210> 824
<211> 66
<212> DNA
<213> Zea mays

<400> 824
agttctatgc aagcacttca cgaggcattg tttcaagagc ttttgtgaag tgtttggggg 60

aactct 66

<210> 825
<211> 85
<212> DNA
<213> Zea mays

<400> 825
agttcccttc aagcacttca catgaggcac cattcaaata acacatttca agattaggtg 60

catgtgaagt gtttggggga actct 85

<210> 826
<211> 70
<212> DNA
<213> Zea mays

<400> 826
agttccctac aagcacttca cgataccttg gcttaataaa ggccagttgt gaagtgtttg 60

ggggaactct 70

<210> 827
<211> 85
<212> DNA
<213> Zea mays

<400> 827
agttcccttc aagcacttca catgaggcac cattcaaata acacatttca agattaggtg 60

catgtgaagt gtttggggga actct 85

<210> 828
<211> 84
<212> DNA
<213> Zea mays

<400> 828
agtttccttc aagcacttca catggagcat tctgtcttag agaaagctta atttattgca 60

ttgtgaagtg tttgaggaaa ctct 84

<210> 829
<211> 81
<212> DNA
<213> Zea mays

<400> 829
agttccttcc aaacacttca ccagctaggc catgcacaag atgaacccac attaggctag 60

tgaagtgttt ggaggaactc t 81

<210> 830
<211> 82
<212> DNA
<213> Zea mays

<400> 830
agttcctttc aaacacttca catggagctt ctcattggtg gatatattct tgagacccgt 60

gtgaagtgtt tggaggaact ct 82

<210> 831
<211> 66
<212> DNA
<213> Zea mays

<400> 831
agttctctac aagcacttca cgaggcttcg tactgagagc ttttgtgaag tgtttggggg 60

aactct 66

<210> 832
<211> 226
<212> DNA
<213> Zea mays

<400> 832
agttctcttc aagcacttca cgaggcatca cactgagagc ttttgtgaag tgtttggggg 60

aactcttggt gtcacaaatc atttgcattt gcttgatgtt agtcatgcac catgtgatat 120 gagataaagg acatggcaac gttttgtgtt actaggagtt ccctacaagc acttcatgag 180

accttgactt aataaagggc cattgtgaag tgtttgggtg aactct 226

<210> 833
<211> 89
<212> DNA
<213> Zea mays

<400> 833
agttcccttc aagcacttca catgaggcac cattcaaatg acaactccat ttaagattat 60

gtgtaatgtg aagtgtttgg gggaactct 89

<210> 834
<211> 125
<212> DNA
<213> Aquilegia caerulea

<400> 834
agagatgaga gatatgttga cagaagagag agagcacaac ccatcatcag ctaaagagag 60

tcttttcttt tgttgggagt gtgctctttg ctcttctgtc atcatcacca aatctctctc 120

tctct 125

<210> 835
<211> 107
<212> DNA
<213> Brachypodium distachyon

<400> 835
cgtcaaggtt aaagggagaa gagagagagt acagccttaa ttaagctcga tcgatctgtc 60

ttgtatcaag gctgtaccct ctctcttctt ctcttagctt cttgatg 107

<210> 836
<211> 120
<212> DNA
<213> Festuca arundinacea

<400> 836
tggtcgtggc tggcaccgtg ggtggtggta tcccatggct gagtacttga cagaagagag 60

agagcacagc ttgagtcggc ggcgacccct gtgagacacc cgcctggagg gagctctgga 120

<210> 837
<211> 138
<212> DNA
<213> Oryza sativa

<400> 837
atcgtgaagg ctaaatggag aagagagaga gtacagcttt gggcggttta gttgttagat 60

ggtggaagta cttgcgacgc ctactaccct tttcaccaag gctgtacgct ccctcttctt 120

ctcttagctt tttatgat 138

<210> 838
<211> 149
<212> DNA
<213> Physcomitrella patens

<400> 838
ctcccctttt ctacattcaa gccgggtttc gaagagagag agcacagccc tggacttttc 60

tcatgtgacc gattttagcg gtacatggtg cactgtcatc gggctgttct ctctctcttc 120

tagaccctac ttggatgtgt ttctactgc 149

<210> 839
<211> 149
<212> DNA
<213> Physcomitrella patens

<400> 839
ttcagccgta ctacacccaa gccgggattc gaagagagag agcacagccc gtaactttca 60

ctaaagacca cttattgtgg ttcattggag atttgatgtc gggctgtgct ctctcttttc 120

cagtccctac tcggatgtgt cgccatcac 149

<210> 840
<211> 151
<212> DNA
<213> Physcomitrella patens

<400> 840
ttcagcttta ctacatccaa gccaggattc gaagagagag agcacagccc cgttactttt 60

gctgaaagaa tacttcctgt gatccattgg gaatttgatg ttgggctgtg ctctctcttt 120 tccagtccct acctggatgt gctgccattg c 151

<210> 841
<211> 136
<212> DNA
<213> Physcomitrella patens

<400> 841
ctagcttctc cacaatttct caccctcgtt gggatcagaa gagagagagc acagccccgat 60

gtccaatgtt caggtcgaat gggctgtgct ctctctcttc ttgctccaac ttgggtgcta 120

cacgcatcta gggtac 136

<210> 842
<211> 122
<212> DNA
<213> Physcomitrella patens

<400> 842
tcagcaattt actcactcat gctgggatca gaagagagag agtacagccc aagagcaacc 60

gcttagttgg aatgggctgt gctctctctc ttctggttcc aacctgagtg catgtcggtt 120

gt 122

<210> 843
<211> 122
<212> DNA
<213> Physcomitrella patens

<400> 843
tgcacaattt tctcactcat gctgggatca gaagagagag agtacagccc aacggccgat 60

gttcagttgg aacgggctgt gctctctctc ttcttgttcc aacctgggtg catttccgtt 120

ct 122

<210> 844
<211> 149
<212> DNA
<213> Physcomitrella patens

<400> 844
tcaccttttt ctacattcaa gctggggttc gaagagagag agcacagtcc cagacttttc 60

actcacgacc actttgagtg tcttatggtg aacagtagtc gggctgtact ctctcttttc 120

cagtccctac tcgaatgtgt ttctatcgc 149

<210> 845
<211> 174
<212> DNA
<213> Brachypodium distachyon

<400> 845
tctttgcatg gaagtaggag gccatctttg atagccaagg atgatttgcc tgtaaaaccg 60

attgtcgtcg cctctcggtg ccgttccagg cactcgaagg gagggcggca gcaacaggtt 120

ctatgggcaa gtcagcctgg ctacccgagt acctcttacc catattccat gcca 174

<210> 846
<211> 103
<212> DNA
<213> Sorghum bicolor

<400> 846
atagccaagg atgatttgcc tgtagcaacc tctgagtgct cctgctgcca tggcagtcag 60

gagcgccaag tgggtgcttc tccgggcaaa tcatctgggc tag 103

<210> 847
<211> 111
<212> DNA
<213> Sorghum bicolor

<400> 847
aaacagtcgg tgcttgcagg tgcagcacca tcaagattca catccccagc tcgatctgtg 60

catgatgaga tgagaatctt gatgatgctg catcagcaaa cactcactta c 111

<210> 848
<211> 83
<212> DNA
<213> Zea mays

<400> 848
gcgtggcatc atcaagattc acaacccatc aatccgaacc actgatttgg aatgcatgya 60

tgagaatctt gatgatgctg cat 83

<210> 849
<211> 208
<212> DNA
<213> Sorghum bicolor

<400> 849
gcactatttt gagagctttt gtgaagtgtt tgggggaact cttgatgcca ctaaccattt 60

gctagaggtt ggccaagtgt gtgctacatg agccaagtgt gtgctacatg aaatgatttg 120

aagacaaatc acatttggaa attatatatc aagtttggtg tccccaggag ttctctgcaa 180

acacttcaca aagcactttt ttagagct 208

<210> 850
<211> 104
<212> DNA
<213> Sorghum bicolor

<400> 850
tcaagtttgg tgtcccccag gagttctctg caaacacttc acaaagcact tttttagagc 60

ttttgtgaag tgtttggggg aactcttggt gccactgatc attt 104

<210> 851
<211> 81
<212> DNA
<213> Zea mays

<400> 851
gagttccttt caaacacttc acatggagct tctcattggt cgatatattc ttgagacccg 60

tgtgaagtgt ttggaggaac t 81

<210> 852
<211> 257
<212> DNA
<213> Zea mays

<400> 852
gtgaagtgtt tggaggaact ctaggtgtta tccagcaatg tttcatagtt tgtgaaactg 60

taaaaggttt tggtaagacg atgatcagat ttggtgttat catgagttcc tttcaaacac 120

ttcacatgca gcttctcatt ggtggatata ttcttgagac ccgtgtgaag tgtttggagg 180 aactcttgat accaataagt ttttccccca aatataatag ctggttgctt ccccggagtt 240

ccttccaaac acttcac 257

<210> 853
<211> 84
<212> DNA
<213> Zea mays

<400> 853
gagtttcctt caagcacttc acatggagca ttctgtctta gagaaagctt aatttattgc 60

attgtgaagt gtttgaggaa actc 84

<210> 854
<211> 307
<212> PRT
<213> Zea mays

<400> 854

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

Leu Ser Ala Cys Cys Ser Pro Val Pro Cys Pro Ser Val Ala Ala Pro
20 25 30

Cys Ser Phe Phe Leu Ala Leu Gly Leu Glu Ala Pro Leu Ala Ala Cys
35 40 45

Val Ala Pro Ser Ser Pro Pro Phe Pro Met Ala Ala Leu Ser Pro Ser
50 55 60

Ser Pro Ser Ser Ala Gln Arg Arg Ile Ser Leu Leu Val Thr Ala Arg
65 70 75 80

Arg Ala Pro Ser Ala Ala Ala Leu Ser Pro Ala Ser Phe Ser Leu Arg
85 90 95

Gln Leu Ala Leu Ala Cys Ala Ala Pro Leu Arg Ser Ser Arg Arg Ser
100 105 110

Ser Ser Pro Ile Cys Ala Gln Pro Arg Thr Pro Leu Arg Ser Ala Arg
115 120 125

Ser Ala Ala Val Leu Ser Pro Gly Ser Leu Cys Pro Phe Ser Thr Ala
130 135 140

Pro Cys Ser Leu Asp Ala His Ala Ala Phe Arg Arg Pro Ser Pro Cys
145 150 155 160

Arg Val Leu Cys Ala Gln Ser Arg Pro Thr Ala Trp Leu Trp Pro Pro
165 170 175

Ser Cys Leu Gly Phe Val His Pro Ser Leu Phe Ser Leu Gly Lys Lys
180 185 190

Lys Leu Trp Met Leu Gly Pro Arg Leu Asp Gln Val Phe Arg Phe Gly
195 200 205

Arg His Arg Leu Ser Ser Phe Ile Ile Ala Ser Cys Ser Ser Ala Ser
210 215 220

Leu Ile Val Pro Met Leu Asn Thr Ala Ile Pro Ala Val Pro Arg Phe
225 230 235 240

Arg Cys Val Arg Leu Asn Val Gly Pro Arg Phe His Asp Val Thr His
245 250 255

Pro Arg Cys Glu Thr Leu Thr Leu Ile Ile Pro Cys Ser Ile Ser Ser
260 265 270

Ser Ser Phe Ala Ser Asp Leu Ala Arg Arg Ser Arg Ser Pro Asp Val
275 280 285

Arg Ser Arg Thr Ser Ala Glu Gly Arg Arg Cys Ser Gly Asn Tyr Gln
290 295 300

Ile Glu Leu

305

<210> 855
<211> 2319
<212> PRT
<213> Zea mays

<400> 855

Met Ser Thr Gln Arg Asp His Val Asp Pro Leu Leu Glu Glu Ile Pro
1 5 10 15

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

Met Lys Ile Ala Glu Lys Met Phe Leu Lys Met Lys Glu Glu Asp Ala
35 40 45

Arg Lys Lys Ala Glu Glu Glu Glu Ser Arg Arg Lys Ala Glu Glu Asp
50 55 60

Lys Gly Lys Gly Thr Phe Asp Tyr Asn Asp Asp Leu Val Asp Leu Leu
65 70 75 80

Val Ser Lys Val Leu Ser Lys Val Ser Leu Asn Thr Glu Gly Ser Ser
85 90 95

Thr Lys Ser Lys Gly Asn Asp Phe Ser Lys Val Gln Phe Asp Tyr Ser
100 105 110

Arg Asn Tyr Ile Pro Asn Phe Ser Ser Ala Pro Leu Gly Lys Leu Pro
115 120 125

Thr Leu Ser Glu Leu Asn Tyr Asp Glu Trp Ala Asp Lys Met Lys Ser
130 135 140

His Leu Ile Gly Val His Pro Ser Leu Trp Glu Ile Val Asn Val Gly
145 150 155 160

Met Tyr Lys Pro Ala Gln Gly Glu Glu Met Thr Pro Glu Met Met Gln
165 170 175

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

Cys Pro Glu Glu Tyr Arg Lys Val Gln Gly Arg Glu Asp Ala Arg Asp
195 200 205

Ile Trp Asn Ile Leu Arg Met Ser His Glu Gly Asp Pro Lys Ala Lys
210 215 220

Arg His Arg Val Glu Ala Leu Glu Ser Glu Leu Ala Arg Tyr Asp Trp
225 230 235 240

Thr Lys Gly Glu Ser Leu Gln Ser Leu Phe Asp Arg Leu Met Val Leu
245 250 255

Val Asn Lys Ile Arg Val Leu Gly Ser Glu Asp Trp Ser Asp Ser Lys
260 265 270

Val Thr Arg Leu Phe Met Arg Ala Tyr Lys Glu Lys Asp Lys Ser Leu
275 280 285

Ala Arg Met Ile Arg Asp Arg Asp Asp Tyr Glu Asp Met Thr Pro His
290 295 300

Gln Leu Phe Ala Lys Ile Gln Gln His Glu Ser Glu Glu Ala Pro Ile
305 310 315 320

Lys Thr Arg Asp Ser His Ala Leu Ile Thr Asn Glu Gln Asp Asn Leu
325 330 335

Lys Lys Ser Lys Asp His Lys Ala Lys Lys Val Val Glu Thr Ser Ser
340 345 350

Asp Glu Asp Ser Ser Ser Asp Glu Asp Thr Ala Met Phe Ile Lys Thr
355 360 365

Phe Lys Lys Phe Val Arg Lys Asn Asp Lys Phe Gln Arg Lys Gly Lys
370 375 380

Lys Arg Ala Cys Tyr Glu Cys Gly Gln Thr Gly His Phe Ile Ala Asp
385 390 395 400

Cys Pro Asn Lys Lys Glu Gln Glu Ala Lys Lys Glu Tyr Lys Lys Asp
405 410 415

Lys Phe Lys Lys Gly Gly Lys Thr Lys Gly Tyr Phe Lys Lys Lys Lys
420 425 430

Tyr Gly Gln Ala His Ile Gly Glu Glu Trp Asn Ser Asp Asp Glu Ser
435 440 445

Ser Ser Ser Glu Glu Glu Glu Val Val Ala Asn Val Ala Ile Gln Ser
450 455 460

Thr Ser Ser Ala Gln Leu Phe Thr Asn Leu Gln Asp Asp Ser Tyr Ile
465 470 475 480

Pro Thr Cys Leu Met Ala Lys Gly Asp Lys Val Thr Leu Phe Ser Asn
485 490 495

Asp Phe Ser Asn Asp Asp Asp Asp Asp Gln Ile Ala Met Lys Asn Lys
500 505 510

Met Ile Lys Glu Phe Gly Leu Asn Gly Tyr Asn Val Ile Thr Lys Leu
515 520 525

Met Glu Lys Leu Asp Lys Arg Lys Ala Thr Leu Asp Ala Gln Glu Asp
530 535 540

Leu Leu Ile Leu Glu Lys Glu Arg Asn Leu Glu Leu Gln Glu Leu Ile
545 550 555 560

His Asn Lys Asp Ile Glu Val Ile Asn Leu Lys Thr Ser Ile Asp Asn
565 570 575

Leu Ala Asn Glu Lys Asn Ala Leu Glu Ser Ser Met Leu Ser Leu Asn
580 585 590

Val Gln Asn Gln Glu Leu Gln Val Gln Leu Glu Asn Cys Lys Asn Ile
595 600 605

Asn Ala Pro Thr Leu Val Phe Glu Ser Lys Ser Ser Ser Asn Asp Asn
610 615 620

Ser Cys Lys His Cys Ala Lys Tyr His Ala Ser Cys Cys Leu Thr Asn
625 630 635 640

His Ala Arg Lys His Ser Pro Gln Val Lys Val Glu Glu Ile Leu Lys
645 650 655

Arg Cys Ser Ser Asn Asp Gly Leu Lys Lys Val Glu Pro Lys Tyr Lys
660 665 670

Ser Leu Lys Pro Asn Asn Gly Arg Arg Gly Leu Gly Phe Asn Ser Ser
675 680 685

Lys Glu Asn Pro Ser Thr Val His Lys Gly Trp Arg Ser Pro Lys Phe
690 695 700

Ile Glu Gly Thr Thr Leu Tyr Asp Ala Leu Gly Arg Ile His Ser Ser
705 710 715 720

Asn Asp Lys Ser Ser Gln Val Tyr Ser Ser Gly Gly Ser Ser Trp Val
725 730 735

Leu Asp Ser Gly Cys Thr Asn His Met Thr Gly Glu Lys Asp Met Phe
740 745 750

His Thr Leu Gln Leu Thr Gln Glu Ala Gln Glu Ile Val Phe Gly Asp
755 760 765

Ser Gly Lys Ser Lys Val Ile Gly Ile Gly Lys Ile Pro Ile Ser Asp
770 775 780

Gln Gln Ser Leu Ser Asn Val Leu Leu Val Asp Ser Leu Ser Tyr Asn
785 790 795 800

Leu Leu Ser Val Ser Gln Leu Cys Gly Met Gly Tyr Asn Cys Leu Phe
805 810 815

Ser Asp Val Asp Val Lys Ile Leu Arg Arg Glu Asp Ser Ser Val Ala
820 825 830

Phe Thr Gly Arg Leu Lys Gly Lys Leu Tyr Leu Val Asp Phe Thr Thr
835 840 845

Ser Lys Val Thr Pro Glu Thr Cys Leu Val Ala Lys Ser Asp Lys Gly
850 855 860

Trp Leu Trp His Arg Arg Leu Ala His Val Gly Met Arg Asn Leu Ala
865 870 875 880

Lys Leu Gln Lys Asp Asn His Ile Ile Gly Leu Thr Asn Val Val Phe
885 890 895

Glu Lys Asp Arg Val Cys Gly Ala Cys Gln Ala Gly Lys Gln His Gly
900 905 910

Val Pro His Gln Ser Lys Asn Val Val Thr Thr Lys Arg Pro Leu Glu
915 920 925

Leu Leu His Met Asp Leu Phe Gly Pro Val Ala Tyr Ile Ser Ile Gly
930 935 940

Gly Ser Lys Tyr Gly Leu Val Ile Val Asp Asp Phe Ser Arg Phe Thr
945 950 955 960

Trp Val Phe Phe Leu Ser Asp Lys Gly Glu Thr Gln Glu Ile Leu Lys
965 970 975

Lys Phe Met Arg Arg Ala Gln Asn Glu Phe Glu Leu Lys Ile Lys Lys
980 985 990

Val Arg Ser Asp Asn Gly Thr Glu Phe Lys Asn Thr Gly Val Glu Glu
995 1000 1005

Phe Leu Gly Glu Glu Gly Ile Lys His Glu Phe Ser Val Pro Tyr
1010 1015 1020

Thr Pro Gln Gln Asn Gly Val Val Glu Arg Lys Asn Arg Thr Leu
1025 1030 1035

Ile Glu Ala Ala Arg Thr Met Leu Asp Glu Tyr Lys Thr Pro Asp
1040 1045 1050

Asn Phe Trp Ala Glu Ala Val Asn Thr Ala Cys His Ala Ile Asn
1055 1060 1065

Arg Leu Tyr Leu His Lys Ile Tyr Lys Lys Thr Ala Tyr Glu Leu
1070 1075 1080

Leu Thr Gly Asn Lys Pro Lys Val Asp Tyr Phe Arg Val Phe Gly
1085 1090 1095

Cys Lys Cys Phe Ile Leu Asn Lys Lys Val Lys Ser Ser Lys Phe
1100 1105 1110

Ala Pro Arg Val Asp Glu Gly Phe Leu Leu Gly Tyr Ala Ser Asn
1115 1120 1125

Ala His Gly Tyr Arg Val Phe Asn Asn Ser Thr Gly Leu Val Glu
1130 1135 1140

Ile Ala Ile Asp Val Thr Phe Asp Glu Ser Asn Gly Ser Gln Gly
1145 1150 1155

His Val Ser Asn Asp Thr Val Gly Asn Glu Lys Leu Pro Cys Glu
1160 1165 1170

Ser Ile Lys Lys Leu Ala Ile Gly Glu Val Arg Pro Gln Glu Arg
1175 1180 1185

Asp Asp Glu Glu Gly Thr Leu Trp Met Thr Asn Glu Val Val Asp
1190 1195 1200

Val Gly Ala Arg Val Val Ser Asp Asn Val Ser Thr Gln Ala Asn
1205 1210 1215

Pro Ser Thr Ser Ser His Pro Asn His Glu Glu Asn His Gln Arg
1220 1225 1230

Met Pro Thr Val Val Glu Asp Glu Gln Glu Asn Ile Asp Gly Glu
1235 1240 1245

Val Pro Leu Asp Gln Val Thr Asn Glu Glu Glu Gln Ile Gln Arg
1250 1255 1260

His Pro Ser Val Pro His Pro Arg Val His His Thr Ile Gln Arg
1265 1270 1275

Asp His Pro Val Asp Asn Ile Leu Gly Ser Ile Arg Arg Gly Val
1280 1285 1290

Thr Thr Arg Ser Arg Leu Ala Asn Phe Cys Glu Phe Tyr Ser Phe
1295 1300 1305

Val Ser Ser Leu Glu Pro Leu Lys Val Glu Glu Ala Leu Asp Asp
1310 1315 1320

Pro Asp Trp Ile Thr Ala Met Gln Glu Glu Leu Asn Asn Phe Thr
1325 1330 1335

Arg Asn Glu Val Trp Ser Leu Val Gln Arg Pro Lys Gln Asn Val
1340 1345 1350

Ile Gly Thr Lys Trp Val Phe Arg Asn Lys Gln Asp Glu Asn Gly
1355 1360 1365

Val Val Thr Lys Asn Lys Ala Arg Leu Val Ala Gln Gly Tyr Thr
1370 1375 1380

Gln Val Glu Gly Leu Asp Phe Gly Glu Thr Tyr Ala Pro Val Ala
1385 1390 1395

Arg Leu Glu Ser Ile Arg Ile Leu Ile Ala Tyr Ala Thr Asn His
1400 1405 1410

Asp Phe Lys Leu Tyr Gln Met Asp Val Lys Ser Ala Phe Leu Asn
1415 1420 1425

Gly Pro Leu Gln Glu Arg Val Tyr Val Glu Gln Pro Pro Gly Phe
1430 1435 1440

Glu Asp Pro Lys Lys Pro Asn His Val Tyr Leu Leu His Lys Ala
1445 1450 1455

Leu Tyr Gly Leu Lys Gln Ala Pro Arg Ala Trp Tyr Asp Cys Leu
1460 1465 1470

Lys Asp Phe Leu Ile Lys Asn Gly Phe Thr Ile Gly Lys Ala Asp
1475 1480 1485

Ser Thr Leu Phe Thr Arg Lys Val Asp Asn Glu Leu Phe Val Cys
1490 1495 1500

Gln Ile Tyr Val Asp Asp Ile Ile Phe Gly Ser Thr Asn Glu Lys
1505 1510 1515

Phe Cys Glu Glu Phe Ser Lys Val Met Thr Asn Arg Phe Glu Met
1520 1525 1530

Ser Met Met Gly Glu Leu Lys Tyr Phe Leu Gly Phe Gln Val Lys
1535 1540 1545

Gln Leu Lys Glu Gly Thr Phe Leu Cys Gln Thr Lys Tyr Thr Gln
1550 1555 1560

Asp Met Leu Lys Lys Phe Gly Met Glu Lys Ala Lys His Ala Lys
1565 1570 1575

Thr Pro Met Pro Ser Asn Gly His Leu Asp Leu Asn Glu Glu Gly
1580 1585 1590

Lys Pro Val Asp Gln Lys Leu Tyr Arg Ser Met Ile Gly Ser Leu
1595 1600 1605

Leu Tyr Leu Cys Ala Ser Arg Pro Asp Ile Met Leu Ser Val Cys
1610 1615 1620

Met Cys Ala Arg Phe Gln Ala Asn Pro Lys Asp Cys His Leu Val
1625 1630 1635

Ala Val Lys Arg Ile Leu Arg Tyr Leu Val His Thr Gln Asn Leu
1640 1645 1650

Gly Leu Trp Tyr Pro Lys Gly Ser Phe Phe Asp Leu Leu Gly Tyr
1655 1660 1665

Ser Asp Ser Asp Tyr Ala Gly Cys Lys Val Asp Arg Lys Ser Thr
1670 1675 1680

Thr Gly Thr Cys Gln Phe Leu Gly Arg Ser Leu Val Ser Trp Ser
1685 1690 1695

Ser Lys Lys Gln Asn Cys Val Ala Leu Ser Thr Ala Glu Ala Glu
1700 1705 1710

Tyr Ile Ala Ala Gly Ala Cys Cys Ala Gln Leu Leu Trp Met Lys
1715 1720 1725

Gln Thr Leu Arg Asp Phe Gly Cys Glu Phe Asn Lys Ile Pro Leu
1730 1735 1740

Leu Cys Asp Asn Glu Ser Ala Ile Lys Leu Ala Asn Asn Pro Val
1745 1750 1755

Gln His Ser Arg Thr Lys His Ile Asp Ile Arg Arg His Phe Leu
1760 1765 1770

Arg Asp His Glu Ala Lys Gly Asp Ile Glu Leu Phe His Ala Trp
1775 1780 1785

Glu Pro Ala Ser Asp Asp Asp Gly Gly Lys Asp Asp Ala Val Asp
1790 1795 1800

Leu Pro Pro Ala Ser Ala Pro Val Ile Arg Gly Leu Val Leu His
1805 1810 1815

Arg Ala Glu Ala Arg Arg Ala Gly Asn Glu Pro Val Thr Asp Phe
1820 1825 1830

Thr Ala Ser Gly Gly Ser Ala Leu Leu Gln Asp Leu Arg Phe Gln
1835 1840 1845

Asn Pro Val Leu Arg Ile Arg Asp Ala Arg Ile Asp Gly Asn Arg
1850 1855 1860

Phe Trp Thr Leu His His Val Asp Phe Tyr Asn Ser Val Ile Leu
1865 1870 1875

Pro Lys Lys His Gln Pro Ile Leu His Gln Arg Tyr Ile Asn Trp
1880 1885 1890

Glu Gly Cys Glu Ala Ile Gly Asp Pro Glu Met Ser Gln Ala Leu
1895 1900 1905

Arg Ala Cys Glu Arg Lys Gln Met Lys Asn Ile Met Thr Phe Gln
1910 1915 1920

Tyr Asp Trp Asn Asp Glu Val Ile Ala Gln Phe Tyr Ser Thr Leu
1925 1930 1935

Trp Ile Lys Leu Ala Asp Glu Glu Ser His Tyr Asn Tyr Pro Phe
1940 1945 1950

Leu Asn Phe Phe Ile Glu Gly Ser Trp Tyr Lys Val Ser Tyr Arg
1955 1960 1965

Arg Phe Ala His Ile Leu Gly Phe Ser Asp Glu Asp Ile Ser Gly
1970 1975 1980

Asp Lys Ile Lys Ile His Asp Phe Arg Gln Pro Thr Arg Asp Glu
1985 1990 1995

Ala Lys Asp Leu His Leu Ser Glu Ser Gly Lys Tyr Trp Glu Ser
2000 2005 2010

Thr Asn Ile His Lys Tyr Tyr Cys Tyr Ile Asn Ser Leu Cys Arg
2015 2020 2025

Met Thr Leu Ile Pro Lys Gly Gly Asn Gln Met Asn Ile Leu Gly
2030 2035 2040

Glu Ser Lys Val Leu Leu Ser Phe Met Lys Pro Asn Ser Ser Glu
2045 2050 2055

Arg Ile Asn Val Phe Asp Met Ile Trp Gln Glu Ile Ile His Ala
2060 2065 2070

Ala Cys Phe Pro Leu Lys Gly Cys Leu His Ala Pro Phe Ile Met
2075 2080 2085

Lys Met Ile Glu Val Val Thr Gln Phe Arg Phe Glu Lys Gly Thr
2090 2095 2100

Arg His Gln Ser Tyr Thr Pro Phe Trp Ile Asp Pro Asn Asn Pro
2105 2110 2115

Ala Gly Arg Leu Arg Lys Ala Pro Ser Ser Ser Arg Gly His Thr
2120 2125 2130

Ser Ala Gly Pro Ser Ala Gly Ala Gly Ala Ala Ala Gly Ala Ser
2135 2140 2145

Arg Pro Ser Pro Gly Arg Gly Ser Pro Thr Pro Arg Gly Arg Gly
2150 2155 2160

Arg Gly Arg Gly Arg Gly Arg Gly Met Gly Ala Arg Leu Ala His
2165 2170 2175

Gly Phe Ala Ala Phe Phe Ser Met Cys Arg Asn Ile Ala Ala Asp
2180 2185 2190

Val His Glu Val Ala Arg Arg Gln Arg Glu Thr Asp Asp Asn Leu
2195 2200 2205

Arg Arg Gln Ala Ser Ala Leu Gly Thr Pro Phe Ala Pro Arg Ser
2210 2215 2220

Pro Asp Val Pro Leu His Pro Pro Pro Pro Asp Val Asn Glu Trp
2225 2230 2235

Tyr Gln Gln Ala Tyr Gly Val Pro Phe Ser Ser Ala Asp Asp Val
2240 2245 2250

Glu Glu Glu Thr Phe Phe Asp Asp Pro Glu Gln Phe Asp Pro Pro
2255 2260 2265

Pro Tyr His Gly Asp Pro Gly Gln Ser Ser Ser Tyr Pro Pro Pro
2270 2275 2280

Gln Asp Pro Ser Gly Ser Ala Pro Pro Pro Ala Gln Ser Gly Glu
2285 2290 2295

Glu His Phe Ala Tyr Asp Leu Ala Gln His Leu Phe Ala Pro His
2300 2305 2310

Gln Pro Pro Pro His Trp
2315

<210> 856
<211> 627
<212> PRT
<213> Eulaliopsis binata

<400> 856

Met Pro Gly Leu Pro Leu Pro Gln Pro Leu Asn Gln Asn Ile Gly Arg
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Arg Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Lys Leu Ala Ala Glu Arg Asp Leu
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

Ala Val Lys Asn Pro Leu Phe Ile Gln Arg Cys Leu Leu Tyr Asn Ile
65 70 75 80

His Ala Arg Arg Lys Lys Arg Ile Gln Ile Thr Ile Ser Leu Ser Arg
85 90 95

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

Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro

115 120 125

Ile Tyr Arg Phe Ser Arg Val Arg Leu Leu Thr Ser Phe Ser Glu Leu
130 135 140

Gly Asn Lys Asp Asn Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
145 150 155 160

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

Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn
180 185 190

His Val Glu Gly Ser Pro Leu Gln Met Leu Glu Gly Lys Cys Ser Trp
195 200 205

Gly Lys Ile Pro Thr Asn Leu Leu Ala Ser Ser Leu Glu Ser Cys Val
210 215 220

Asn Leu Ser Leu Gly His Ile Val Glu Leu Ala Ser Lys Ile Thr Met
225 230 235 240

Arg Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Ser Cys Leu
245 250 255

Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr Gln Leu Gln
260 265 270

Leu Cys Met Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Leu Ser
275 280 285

Pro Tyr Ser Ser Tyr Leu Tyr Asp Asp Val Pro Pro Ser Ser Leu Ser
290 295 300

Asp Ile Ile Arg Leu Arg Ser Gly Asn Val Leu Phe Asn Tyr Lys Tyr
305 310 315 320

His Asn Asn Thr Met Gln Glu Thr Glu Val Thr Glu Asp Phe Cys Cys
325 330 335

Pro Phe Cys Tyr Val Arg Cys Gly Ser Phe Lys Gly Leu Gly Cys His
340 345 350

Leu Asn Ser Ser His Asp Leu Phe His Tyr Glu Phe Trp Ile Ser Glu
355 360 365

Asp Tyr Gln Ile Val Asn Val Ser Leu Lys Ala Asp Ala Trp Arg Thr
370 375 380

Glu Leu Ile Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr
385 390 395 400

Arg Ser Arg Phe Lys Lys Arg Arg Arg Ser Lys Thr Thr Thr Asp Lys
405 410 415

Ile Arg His Val His Ser His Ile Met Glu Ser Gly Ser Pro Glu Asp
420 425 430

Ala Gln Ala Gly Ser Glu Asp Asn Cys Val Gln Gly Glu Asn Gly Thr
435 440 445

Ser Val Ala Asn Ala Ser Ile Asp Pro Ala Gln Ser Leu His Gly Ser
450 455 460

Asn Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu
465 470 475 480

Ser Glu Arg Ala Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln
485 490 495

Phe Phe His Ser His Arg Ala Gln Pro Met Ala Leu Glu Gln Val Phe
500 505 510

Ser Asp Arg Asp Ser Glu Asp Glu Val Asp Asp Asp Ile Ala Asp Phe

515 520 525

Glu Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu
530 535 540

Lys Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val
545 550 555 560

Leu Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Gln Leu
565 570 575

His Gly Arg Gln Leu Val Gln Asn Pro Ala Gln Leu Arg Gly Trp Arg
580 585 590

Phe Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr
595 600 605

Met Asp Thr Cys Asn Thr Val Leu Gln Ser Phe Gln Glu Glu Ser Thr
610 615 620

Gly Leu Lys
625

<210> 857
<211> 626
<212> PRT
<213> Zea mays

<400> 857

Met Pro Gly Leu Pro Leu Pro Gln Ser Leu Asn Lys Asn Ile Gly Cys
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Gln Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Lys Leu Thr Ala Glu Lys Asp Leu
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

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

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

Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro
115 120 125

Ile Tyr Arg Phe Ser Arg Val Cys Leu Leu Thr Ser Phe Ser Glu His
130 135 140

Gly Asn Lys Asp Ser Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
145 150 155 160

Ser Leu Ser Thr Ser Arg Ala Cys Asn Leu Asp Ile Ile Phe Ile Ser
165 170 175

Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn
180 185 190

His Val Glu Ala Ser Ser Leu Gln Met Leu Glu Gly Lys Cys Ser Trp
195 200 205

Gly Lys Ile Pro Thr Asn Leu Leu Ala Ser Ser Leu Glu Ser Cys Val
210 215 220

Asn Leu Ser Leu Gly His Ile Val Glu Leu Ala Ser Lys Val Thr Met
225 230 235 240

Arg Ser Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Asn Cys Leu
245 250 255

Thr Phe Cys Ser His Lys Val Asp Ala Val Gly Ser Tyr Lys Leu Gln
260 265 270

Leu Cys Met Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Leu Ser
275 280 285

Pro His Ser Ser Tyr Ser Tyr Asn Asp Val Pro Pro Ser Ser Leu Ser
290 295 300

Asp Ile Ile Arg Leu Arg Ser Gly Asn Val Leu Phe Asn Tyr Lys Tyr
305 310 315 320

Tyr Ser Asn Thr Met Gln Glu Thr Glu Val Thr Glu Asp Phe Ser Cys
325 330 335

Pro Phe Cys Tyr Val Arg Cys Gly Ser Phe Lys Gly Leu Gly Cys His
340 345 350

Leu Asn Ser Ser His Asp Leu Phe His Tyr Glu Phe Trp Ile Ser Glu
355 360 365

Glu Tyr Gln Val Val Asn Val Ser Leu Lys Ala Asp Ala Trp Arg Thr
370 375 380

Glu Leu Phe Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr
385 390 395 400

Arg Ser Arg Phe Lys Lys Arg Arg Arg Ser Lys Thr Thr Met Glu Lys
405 410 415

Ile Arg His Val His Ser His Ile Met Glu Ser Gly Ser Pro Gly Asp
420 425 430

Glu Ala Gly Ser Glu Asp Asn Phe Val Gln Gly Glu Asn Gly Thr Ser
435 440 445

Val Ala Asn Ala Ser Ile Asp Pro Ala Gln Ser Leu His Gly Ser Asn
    450   455   460

Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu Ser
465   470   475   480

Glu Arg Ser Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln Phe
                485   490   495

Phe His Ser His Arg Ala Gln Pro Met Gln Leu Glu Gln Val Phe Ser
            500   505   510

Asp Arg Asp Ser Gly Asp Glu Val Asp Asp Asp Ile Ala Asp Phe Glu
        515   520   525

Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu Lys
    530   535   540

Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val Leu
545   550   555   560

Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Gln Leu His
                565   570   575

Gly Arg Gln Leu Ile Gln Asn Pro Ala Leu Leu Trp Gly Trp Arg Phe
            580   585   590

Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr Met
        595   600   605

Asn Thr Cys Asn Thr Val Leu Gln Ile Leu Gln Glu Glu Ser Thr Gly
    610   615   620

Leu Lys
625

<210> 858
<211> 626

<212> PRT
<213> Zea mays

<400> 858

Met Pro Gly Leu Pro Leu Pro Gln Ser Leu Asn Gln Asn Ile Gly Cys
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Gln Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Lys Leu Thr Ala Glu Lys Asp Leu
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

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

Ser Thr Asn Thr Glu Leu Gln Thr His Tyr Val Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro
115 120 125

Ile Tyr Arg Phe Ser Arg Val Cys Leu Leu Thr Ser Phe Ser Glu His
130 135 140

Gly Asn Lys Asp Asn Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
145 150 155 160

Ser Leu Ser Thr Ser Arg Ala Cys Asn His Asp Ile Ile Phe Ile Ser
165 170 175

Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn

180 185 190

His Val Glu Asp Ser Ser Leu Gln Met Leu Glu Gly Lys Cys Ser Trp
195 200 205

Gly Lys Ile Pro Thr Asn Leu Leu Ala Ser Ser Leu Glu Ser Cys Val
210 215 220

Asn Leu Ser Leu Gly His Ile Val Glu Leu Ala Ser Lys Val Thr Met
225 230 235 240

Arg Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Ser Cys Leu
245 250 255

Thr Phe Cys Ser His Lys Val Asp Ala Val Gly Ser Tyr Lys Leu Gln
260 265 270

Leu Cys Met Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Leu Ser
275 280 285

Pro Tyr Ser Ser Tyr Ser Tyr Asn Asp Val Pro Pro Ser Ser Leu Ser
290 295 300

Asp Ile Ile Arg Leu Arg Ser Gly Asn Val Leu Phe Asn Tyr Lys Tyr
305 310 315 320

Tyr Asn Asn Thr Met Gln Glu Thr Glu Val Thr Glu Asp Phe Ser Cys
325 330 335

Pro Phe Cys Tyr Val Arg Cys Gly Ser Phe Lys Gly Leu Gly Cys His
340 345 350

Leu Asn Ser Ser His Asp Leu Phe His Tyr Glu Phe Trp Ile Ser Glu
355 360 365

Glu Tyr Gln Val Val Asn Val Ser Leu Lys Ala Asp Ala Trp Arg Thr
370 375 380

Glu Leu Phe Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr
385 390 395 400

Arg Ser Arg Phe Lys Lys Arg Arg Arg Ser Lys Asn Thr Met Glu Lys
405 410 415

Ile Arg His Val His Ser His Ile Met Glu Ser Gly Ser Pro Glu Asp
420 425 430

Glu Ala Gly Ser Glu Asp Asn Phe Val Gln Gly Glu Asn Gly Thr Ser
435 440 445

Val Ala Asn Ala Ser Ile Asp Pro Ala Gln Ser Leu His Gly Ser Asn
450 455 460

Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu Ser
465 470 475 480

Glu Arg Ser Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln Phe
485 490 495

Phe His Ser His Arg Ala Gln Pro Met Gln Leu Glu Gln Val Phe Ser
500 505 510

Asp Arg Asp Ser Glu Asp Glu Val Asp Asp Asp Ile Ala Asp Phe Glu
515 520 525

Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu Lys
530 535 540

Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val Leu
545 550 555 560

Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Gln Leu His
565 570 575

Gly Arg Gln Leu Ile Gln Asn Pro Ala Leu Leu Trp Gly Trp Arg Phe

580 585 590

Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr Met
595 600 605

Asn Thr Cys Asn Thr Val Leu Gln Ile Leu Gln Glu Glu Ser Thr Gly
610 615 620

Leu Lys
625

<210> 859
<211> 629
<212> PRT
<213> Dendrocalamus latiflorus

<400> 859

Met Pro Gly Leu Pro Leu Pro Ala Arg Asp Ala Ala Asn Ile Gly Cys
1 5 10 15

Gly Phe Gly Tyr Pro Arg Ser Ala Asp Gln Met Cys Arg Gln Gln Ser
20 25 30

Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Asn Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

Ala Ile Lys Asn Pro Ala Phe Leu Gln Arg Cys Leu Leu Tyr Lys Ile
65 70 75 80

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

Gly Ala Asn Thr Glu Leu Gln Glu His Asn Ile Phe Pro Leu Tyr Ala
100 105 110

Leu Leu Ala Arg Pro Thr Ser Asn Val Ser Leu Glu Gly His Ser Pro
115 120 125

Tyr Arg Phe Ser Arg Ala Cys Leu Leu Thr Ser Phe Asn Glu Phe Gly
130 135 140

Asn Lys Asp His Thr Glu Ala Thr Phe Met Ile Pro Asp Val Lys Asn
145 150 155 160

Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser Cys
165 170 175

Gly Gln Ala Gly Gln Thr Leu Gly Glu Asn Thr Phe Ser Gly Asn His
180 185 190

Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys Cys Phe Trp Gly
195 200 205

Lys Ile Pro Ile Cys Leu Leu Gly Ser Ser Leu Glu Asn Asp Val Asp
210 215 220

Leu Thr Leu Gly His Thr Val Glu Leu Ala Ser Thr Val Ser Met Ser
225 230 235 240

Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Ser Cys Leu Thr
245 250 255

Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser His Gln Leu Gln Val
260 265 270

Ser Ile Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Glu Ser Pro
275 280 285

Tyr Ser Ser Tyr Ser Tyr Ser Asp Val Pro Pro Ser Ser Leu Pro His
290 295 300

Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn Tyr Lys Tyr Tyr
305 310 315 320

Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp Phe Ser Cys Pro
325 330 335

Phe Cys Leu Val Ser Cys Gly Ser Phe Lys Gly Leu Gly Cys His Leu
340 345 350

Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp Ile Ser Glu Glu
355 360 365

Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Ala Trp Arg Thr Glu
370 375 380

Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr Cys
385 390 395 400

Ser Arg Phe Lys Lys Arg Arg Arg Phe Glu Ile Thr Thr Glu Lys Ile
405 410 415

Ser His Val His Pro His Ile Val Asp Ser Gly Ser Pro Glu Asp Ala
420 425 430

Gln Ala Gly Ser Glu Asp Asp Tyr Ala Gln Arg Glu Asn Gly Ile Ser
435 440 445

Val Ala His Ala Ser Val Asp Pro Ala Asn Ser Leu His Gly Ser Asn
450 455 460

Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu Ser
465 470 475 480

Val Glu Arg Ala Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln
485 490 495

Phe Phe His Ser His Arg Ala Gln Pro Met Ala Leu Glu Gln Val Phe
500 505 510

Ser Asp Arg Asp Ser Glu Asp Glu Val Asp Asp Asp Ile Ala Asp Phe
515 520 525

Glu Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu
530 535 540

Lys Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val
545 550 555 560

Leu Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Arg Leu
565 570 575

His Gly Gln Gln Leu Val Gln Asn Ser Ala Leu Leu Arg Cys Trp Arg
580 585 590

Phe Phe Met Ile Lys Leu Trp Asn His Ser Leu Leu Asp Ala Arg Thr
595 600 605

Met Asn Thr Cys Asn Thr Ile Leu Glu Gly Tyr Gln Asn Glu Ser Pro
610 615 620

Asp Pro Lys Gln Thr
625

<210> 860
<211> 638
<212> PRT
<213> Triticum aestivum

<400> 860

Met Pro Gly Leu Pro Leu Pro Gln Ser Leu Asn Gln Asn Ile Gly Cys
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Gln Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Ser Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

His Ala Ser Arg Lys Lys Arg Ile Gln Ile Thr Val Ser Leu Ser Arg
85 90 95

Gly Thr Asn Thr Glu Leu Pro Glu Gln Asn Ile Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Thr Pro Thr Ser Asn Ile Ser Leu Glu Gly His Ser Pro
115 120 125

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

Gly Asn Lys Gly Arg Thr Lys Ala Thr Phe Ile Ile Pro Asp Ile Lys
145 150 155 160

Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser
165 170 175

Cys Val Ser Glu Gly Gln Val Gly Glu Asn Arg Gly Glu His Asn Cys
180 185 190

Ser Val Asp His Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys
195 200 205

Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Gly Ser Ser Leu Glu
210 215 220

Asn Cys Val Thr Leu Asn Leu Gly His Thr Val Glu Leu Ala Ser Ala
225 230 235 240

Val Ser Met Ser Pro Ser Phe Leu Glu Pro Lys Phe Met Glu Gln Asp

245 250 255

Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr
260 265 270

Gln Leu Gln Val Gly Ile Ser Ala Gln Glu Ala Gly Ala Lys Asp Met
275 280 285

Ser Glu Ser Pro Tyr Ser Ser Tyr Ser Tyr Ser Gly Val Pro Pro Ser
290 295 300

Ser Leu Pro His Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn
305 310 315 320

Phe Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp
325 330 335

Phe Ala Cys Pro Phe Cys Leu Val Lys Cys Gly Ser Tyr Lys Gly Leu
340 345 350

Gly Cys His Leu Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp
355 360 365

Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Val
370 375 380

Trp Arg Thr Glu Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr
385 390 395 400

Phe Ser Tyr Ser Ser Arg Phe Lys Lys Arg Arg Arg Leu Gly Met Leu
405 410 415

Gly Thr Thr Ala Glu Lys Ile Ser His Val His Pro His Ile Met Asp
420 425 430

Ser Asp Ser Pro Glu Asp Ala Gln Ala Val Ser Glu Asp Asp Phe Val
435 440 445

Gln Arg Glu Glu Asp Asp Ile Ser Ala Pro Arg Ala Ser Val Asp Pro
450 455 460

Ala Gln Ser Leu His Gly Ser Asn Leu Ser Pro Pro Thr Val Leu Gln
465 470 475 480

Phe Gly Lys Thr Arg Lys Leu Ser Ala Glu Arg Ala Asp Pro Arg Asn
485 490 495

Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln
500 505 510

Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu
515 520 525

Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Lys Arg Met Leu Glu Asp
530 535 540

Phe Val Asp Val Thr Asp Asp Glu Lys Leu Ile Met His Met Trp Asn
545 550 555 560

Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp
565 570 575

Ala Cys Glu Ala Phe Ser Arg Leu His Gly Lys His Leu Val Gln Asn
580 585 590

Pro Pro Leu Leu Trp Ser Trp Arg Phe Leu Met Ile Lys Leu Trp Asn
595 600 605

His Ser Leu Leu Asp Ala Arg Ala Met Asn Val Cys Gly Thr Ile Leu
610 615 620

Gln Gly Tyr Gln Asn Glu Ser Gly Leu Asp Pro Lys Lys Met
625 630 635

<210> 861

<211> 606
<212> PRT
<213> Oryza sativa Japonica Group

<400> 861

Tyr Gln Met Cys Arg His Gln Pro Arg Ala Arg Leu Ser Pro Asp Glu
1 5 10 15

Gln Leu Ala Ala Glu Glu Ser Phe Ala Leu Tyr Cys Lys Pro Val Glu
20 25 30

Leu Tyr Asn Ile Ile Gln Arg Arg Ser Ile Lys Asn Pro Ala Phe Leu
35 40 45

Gln Arg Cys Leu Leu Tyr Lys Ile His Ala Arg Arg Lys Lys Arg Ser
50 55 60

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

Gln Asn Ile Phe Pro Leu Tyr Val Leu Leu Ala Arg Pro Thr Asn Asn
85 90 95

Val Ser Leu Glu Gly His Ser Pro Ile Tyr Arg Phe Ser Arg Ala Cys
100 105 110

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

Thr Phe Val Ile Pro Asp Val Lys Asn Leu Ala Thr Ser Arg Ala Cys
130 135 140

Ser Leu Asn Ile Ile Leu Ile Ser Cys Gly Arg Ala Glu Gln Thr Phe
145 150 155 160

Asp Asp Asn Asn Cys Ser Gly Asn His Val Glu Gly Ser Thr Leu Gln
165 170 175

Lys Leu Glu Gly Lys Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu
180 185 190

Ala Ser Ser Leu Gly Asn Cys Val Ser Leu Ser Leu Gly His Thr Val
195 200 205

Glu Met Ser Ser Thr Val Glu Met Thr Pro Ser Phe Leu Glu Pro Lys
210 215 220

Phe Leu Glu Asp Asp Ser Cys Leu Thr Phe Cys Ser Gln Lys Val Asp
225 230 235 240

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

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

Asp Val Pro Pro Ser Ser Leu Thr His Ile Ile Arg Leu Arg Ser Gly
275 280 285

Asn Val Leu Phe Asn Tyr Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr
290 295 300

Glu Val Thr Glu Asp Phe Ser Cys Pro Phe Cys Leu Val Pro Cys Gly
305 310 315 320

Ser Phe Lys Gly Leu Gly Cys His Leu Asn Ala Ser His Asp Leu Phe
325 330 335

His Tyr Glu Phe Trp Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser
340 345 350

Leu Lys Thr Asp Ser Trp Arg Thr Glu Leu Leu Ala Glu Gly Val Asp
355 360 365

Pro Arg His Gln Thr Phe Ser Tyr Arg Ser Arg Phe Lys Lys Arg Lys
370 375 380

Arg Val Glu Ile Ser Ser Asp Lys Ile Arg His Val His Pro His Ile
385 390 395 400

Val Asp Ser Gly Ser Pro Glu Asp Ala Gln Ala Gly Ser Glu Asp Asp
405 410 415

Tyr Val Gln Arg Glu Asn Gly Ser Ser Val Ala His Ala Ser Val Asp
420 425 430

Pro Ala Asn Ser Leu His Gly Ser Asn Leu Ser Ala Pro Thr Val Leu
435 440 445

Gln Phe Gly Lys Thr Arg Lys Leu Ser Val Glu Arg Ala Asp Pro Arg
450 455 460

Asn Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala
465 470 475 480

Gln Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp
485 490 495

Glu Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp
500 505 510

Asp Phe Val Asp Val Thr Lys Asp Glu Lys Leu Ile Met His Met Trp
515 520 525

Asn Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro
530 535 540

Trp Ala Cys Glu Ala Phe Ser Gln Phe His Gly Gln Glu Leu Val Gln
545 550 555 560

Asn Pro Ala Leu Leu Trp Cys Trp Arg Phe Phe Met Val Lys Leu Trp
565 570 575

Asn His Ser Leu Leu Asp Ala Arg Ala Met Asn Ala Cys Asn Thr Ile
580 585 590

Leu Glu Gly Tyr Leu Asn Gly Ser Ser Asp Pro Lys Lys Asn
595 600 605

<210> 862
<211> 604
<212> PRT
<213> Oryza sativa Japonica Group

<400> 862

Met Cys Arg His Gln Pro Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu
1 5 10 15

Ala Ala Glu Glu Ser Phe Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr
20 25 30

Asn Ile Ile Gln Arg Arg Ser Ile Lys Asn Pro Ala Phe Leu Gln Arg
35 40 45

Cys Leu Leu Tyr Lys Ile His Ala Arg Arg Lys Lys Arg Ser Leu Ile
50 55 60

Thr Ile Ser Leu Ser Gly Gly Thr Asn Lys Glu Leu Arg Ala Gln Asn
65 70 75 80

Ile Phe Pro Leu Tyr Val Leu Leu Ala Arg Pro Thr Asn Asn Val Ser
85 90 95

Leu Glu Gly His Ser Pro Ile Tyr Arg Phe Ser Arg Ala Cys Leu Leu
100 105 110

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

Val Ile Pro Asp Val Lys Asn Leu Ala Thr Ser Arg Ala Cys Ser Leu
130 135 140

Asn Ile Ile Leu Ile Ser Cys Gly Arg Ala Glu Gln Thr Phe Asp Asp
145 150 155 160

Asn Asn Cys Ser Gly Asn His Val Glu Gly Ser Thr Leu Gln Lys Leu
165 170 175

Glu Gly Lys Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Ala Ser
180 185 190

Ser Leu Gly Asn Cys Val Ser Leu Ser Leu Gly His Thr Val Glu Met
195 200 205

Ser Ser Thr Val Glu Met Thr Pro Ser Phe Leu Glu Pro Lys Phe Leu
210 215 220

Glu Asp Asp Ser Cys Leu Thr Phe Cys Ser Gln Lys Val Asp Ala Thr
225 230 235 240

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

Lys Asp Met Ser Glu Ser Pro Tyr Ser Val Tyr Ser Tyr Asn Asp Val
260 265 270

Pro Pro Ser Ser Leu Thr His Ile Ile Arg Leu Arg Ser Gly Asn Val
275 280 285

Leu Phe Asn Tyr Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val
290 295 300

Thr Glu Asp Phe Ser Cys Pro Phe Cys Leu Val Pro Cys Gly Ser Phe
305 310 315 320

Lys Gly Leu Gly Cys His Leu Asn Ala Ser His Asp Leu Phe His Tyr
325 330 335

Glu Phe Trp Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys

340 345 350

Thr Asp Ser Trp Arg Thr Glu Leu Leu Ala Glu Gly Val Asp Pro Arg
355 360 365

His Gln Thr Phe Ser Tyr Arg Ser Arg Phe Lys Lys Arg Lys Arg Val
370 375 380

Glu Ile Ser Ser Asp Lys Ile Arg His Val His Pro His Ile Val Asp
385 390 395 400

Ser Gly Ser Pro Glu Asp Ala Gln Ala Gly Ser Glu Asp Asp Tyr Val
405 410 415

Gln Arg Glu Asn Gly Ser Ser Val Ala His Ala Ser Val Asp Pro Ala
420 425 430

Asn Ser Leu His Gly Ser Asn Leu Ser Ala Pro Thr Val Leu Gln Phe
435 440 445

Gly Lys Thr Arg Lys Leu Ser Val Glu Arg Ala Asp Pro Arg Asn Arg
450 455 460

Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln Pro
465 470 475 480

Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu Val
485 490 495

Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp Phe
500 505 510

Val Asp Val Thr Lys Asp Glu Lys Leu Ile Met His Met Trp Asn Ser
515 520 525

Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp Ala
530 535 540

Cys Glu Ala Phe Ser Gln Phe His Gly Gln Glu Leu Val Gln Asn Pro
545 550 555 560

Ala Leu Leu Trp Cys Trp Arg Phe Phe Met Val Lys Leu Trp Asn His
565 570 575

Ser Leu Leu Asp Ala Arg Ala Met Asn Ala Cys Asn Thr Ile Leu Glu
580 585 590

Gly Tyr Leu Asn Gly Ser Ser Asp Pro Lys Lys Asn
595 600

<210> 863
<211> 601
<212> PRT
<213> Eulaliopsis binata

<400> 863

Met Cys Leu Gln His Cys Ser Ala Arg Leu Ser Pro Asp Glu Gln Leu
1 5 10 15

Ala Ala Glu Lys Ser Phe Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr
20 25 30

Asn Ile Ile Gln Arg Arg Ala Val Lys Asn Pro Pro Phe Ile Gln Arg
35 40 45

Ser Leu Leu Tyr Lys Ile Gln Ala Arg Arg Lys Lys Arg Ile Gln Ile
50 55 60

Thr Val Ser Leu Ser Ala Ser Thr Asn Thr Gln Ala Gln Asn Ile Phe
65 70 75 80

Pro Leu Tyr Val Leu Leu Ala Arg Pro Thr Ser Asn Ile Ser Leu Asp
85 90 95

Gly His Ser Pro Ile Tyr Arg Phe Ser Arg Val Ser Leu Leu Thr Asn
100 105 110

Phe Ser Glu Phe Gly Asn Glu Gly Lys Thr Glu Ala Thr Phe Ile Ile
115 120 125

Pro Asn Val Lys Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Ser Ile
130 135 140

Ile Phe Ile Ser Cys Gly Gln Val Gly Gln Ile Ile Gly Glu Asp Ser
145 150 155 160

Cys Ser Gly Asn Asp Val Leu Arg Ser Ser Leu Gln Lys Leu Glu Gly
165 170 175

Lys Cys Ser Trp Gly Lys Ile Leu Thr Asn Arg Leu Ala Ser Ser Leu
180 185 190

Glu Gln Cys Val Thr Leu Ser Thr Gly Asp Ala Val Asp Leu Ala Ser
195 200 205

Thr Val Thr Met Asn Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln
210 215 220

Asp Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser
225 230 235 240

Tyr Gln Leu Gln Val Ser Ile Ser Ala Glu Glu Ala Gly Ala Arg Glu
245 250 255

Leu Leu Leu Ser Pro Tyr Tyr Cys Asn Tyr Ser Tyr Asn Asn Val Pro
260 265 270

Pro Ser Leu Leu Pro Glu Ile Ile Arg Leu Arg Ala Gly Asn Val Leu
275 280 285

Phe Asn Tyr Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr
290 295 300

Glu Asp Phe Ser Cys Pro Phe Cys Leu Val Pro Cys Gly Ser Phe Lys
305 310 315 320

Gly Leu Gly Cys His Leu Asn Ser Thr His Asp Leu Phe His Tyr Glu
325 330 335

Phe Trp Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Val
340 345 350

Asp Ala Trp Lys Thr Glu Phe Val Ala Glu Gly Val Asp Pro Arg His
355 360 365

Gln Thr Phe Ser Tyr Cys Ser Arg Phe Lys Lys Arg Arg Arg Leu Glu
370 375 380

Thr Thr Ala Lys Lys Ile Arg His Val His Pro His Ile Met Glu Pro
385 390 395 400

Gly Ser His Glu Asp Ala Gln Ala Gly Ser Glu Asp Asp Tyr Val Gln
405 410 415

Arg Glu Asn Gly Leu Ser Val Glu His Ala Ser Val Asp His Ser Gln
420 425 430

Pro Val His Gly Ser Asn Leu Ser Pro Pro Thr Val Leu Gln Phe Gly
435 440 445

Lys Ser Arg Lys Leu Ser Ala Glu Arg Ser Asp Pro Arg Asn Arg Gln
450 455 460

Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln Pro Met
465 470 475 480

Pro Leu Glu Gln Val Phe Ser Asp His Asp Ser Glu Asp Glu Val Asp
485 490 495

Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp Phe Val
500 505 510

Asp Val Thr Lys Asp Glu Lys Leu Ile Met His Met Trp Asn Ser Phe
515 520 525

Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp Ala Cys
530 535 540

Glu Ala Phe Ser Arg Cys His Gly Gln Arg Leu Val Gln Asn Pro Ala
545 550 555 560

Leu Leu Trp Gly Trp Arg Phe Phe Met Ile Lys Leu Trp Ser His Ser
565 570 575

Leu Leu Asp Ala Arg Ala Met Asn Thr Cys Asn Thr Ile Leu Gln Gly
580 585 590

Tyr Gln Asp Gly Ser Ser Asp Pro Lys
595 600

<210> 864
<211> 637
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 864

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

Glu Phe Ser Tyr Pro Gln Ser Ala Asp Gln Met Arg Gln Gln Gln Leu
20 25 30

Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Ser Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

Ala Ile Arg Asn Pro Ala Phe Leu Gln Arg Cys Leu His Tyr Lys Ile

65 70 75 80

His Ala Ser Arg Lys Lys Arg Ile Gln Ile Thr Val Ser Leu Ser Arg
85 90 95

Gly Thr Asn Thr Glu Leu Pro Glu Gln Asn Val Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Thr Pro Thr Thr Asn Ile Ser Leu Glu Gly His Ser Pro
115 120 125

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

Gly Ser Lys Gly Arg Thr Lys Ala Thr Phe Thr Ile Pro Asp Ile Lys
145 150 155 160

Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser
165 170 175

Cys Val Ser Glu Gly Gln Val Glu Glu Asn Val Gly Glu His Asn Cys
180 185 190

Ser Val Asn His Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys
195 200 205

Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Gly Ser Ser Leu Glu
210 215 220

Asn Cys Val Thr Leu Asn Leu Gly His Thr Val Glu Leu Ala Ser Ala
225 230 235 240

Val Ser Met Ser Pro Ser Phe Leu Glu Pro Lys Phe Met Glu Gln Asp
245 250 255

Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr
260 265 270

Gln Leu Gln Val Gly Ile Ser Ala Gln Glu Ala Gly Ala Arg Asp Met
275 280 285

Ser Glu Ser Pro Tyr Ser Ser Tyr Ser Tyr Ser Gly Val Pro Pro Ser
290 295 300

Ser Leu Pro His Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn
305 310 315 320

Phe Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp
325 330 335

Phe Ala Cys Pro Phe Cys Leu Val Lys Cys Gly Ser Tyr Lys Gly Leu
340 345 350

Gly Cys His Leu Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp
355 360 365

Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Val
370 375 380

Trp Arg Thr Glu Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr
385 390 395 400

Phe Ser Tyr Ser Ser Arg Leu Lys Lys Arg Arg Arg Leu Gly Met Leu
405 410 415

Gly Thr Thr Ala Glu Lys Ile Ser His Val His Pro His Ile Met Asp
420 425 430

Ser Asp Ser Pro Glu Asp Ala Gln Ala Val Ser Glu Gly Asp Phe Val
435 440 445

Gln Arg Glu Glu Asp Asp Ile Ser Ala Pro Arg Ala Ser Val Asp Pro
450 455 460

Ala Gln Ser Leu His Asp Ser Asn Leu Ser Pro Pro Thr Val Leu Gln

465 470 475 480

Phe Gly Lys Thr Arg Lys Leu Ser Ala Glu Arg Ala Asp Pro Arg Asn
485 490 495

Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln
500 505 510

Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu
515 520 525

Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp
530 535 540

Phe Val Asp Val Thr Asn Asp Glu Lys Leu Ile Met His Met Trp Asn
545 550 555 560

Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp
565 570 575

Ala Cys Glu Ala Phe Ser Arg Leu His Gly Lys His Leu Val Gln Asn
580 585 590

Pro Pro Leu Leu Trp Ser Trp Arg Phe Leu Met Ile Lys Leu Trp Asn
595 600 605

His Ser Leu Leu Asp Ala Arg Ala Met Asn Val Cys Gly Thr Ile Leu
610 615 620

Gln Gly Tyr Gln Asn Glu Ser Ser Asp Pro Lys Asn Ile
625 630 635

<210> 865
<211> 637
<212> PRT
<213> Hordeum vulgare

<400> 865

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

Glu Phe Ser Tyr Pro Gln Ser Ala Asp Gln Met Arg His Gln Gln Leu
20 25 30

Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Ser Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

His Ala Ser Arg Lys Lys Arg Ile Gln Ile Thr Val Ser Leu Ser Arg
85 90 95

Gly Thr Asn Thr Glu Leu Pro Glu Gln Asn Val Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Thr Pro Thr Thr Asn Ile Ser Leu Glu Gly His Ser Pro
115 120 125

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

Gly Ser Lys Gly Arg Thr Lys Ala Thr Phe Thr Ile Pro Asp Ile Lys
145 150 155 160

Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser
165 170 175

Cys Val Ser Glu Gly Gln Val Glu Glu Asn Val Gly Glu His Asn Cys
180 185 190

Ser Val Asn His Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys
195 200 205

Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Gly Ser Ser Leu Glu
210 215 220

Asn Cys Val Thr Leu Asn Leu Gly His Thr Val Glu Leu Ala Ser Ala
225 230 235 240

Val Ser Met Ser Pro Ser Phe Leu Glu Pro Lys Phe Met Glu Gln Asp
245 250 255

Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr
260 265 270

Gln Leu Gln Val Gly Ile Ser Ala Gln Glu Ala Gly Ala Arg Asp Met
275 280 285

Ser Glu Ser Pro Tyr Ser Ser Tyr Ser Tyr Ser Gly Val Pro Pro Ser
290 295 300

Ser Leu Pro His Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn
305 310 315 320

Phe Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp
325 330 335

Phe Ala Cys Pro Phe Cys Leu Val Lys Cys Gly Ser Tyr Lys Gly Leu
340 345 350

Gly Cys His Leu Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp
355 360 365

Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Val
370 375 380

Trp Arg Thr Glu Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr
385 390 395 400

Phe Ser Tyr Ser Ser Arg Phe Lys Lys Arg Arg Arg Leu Gly Met Leu
405 410 415

Gly Thr Thr Ala Glu Lys Ile Ser His Val His Pro His Ile Met Asp
420 425 430

Ser Asp Ser Pro Glu Asp Ala Gln Ala Val Ser Glu Gly Asp Phe Val
435 440 445

Gln Arg Glu Glu Asp Asp Ile Ser Ala Pro Arg Ala Ser Val Asp Pro
450 455 460

Ala Gln Ser Leu His Asp Ser Asn Leu Ser Pro Pro Thr Val Leu Gln
465 470 475 480

Phe Gly Lys Thr Arg Lys Leu Ser Ala Glu Arg Ala Asp Pro Arg Asn
485 490 495

Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln
500 505 510

Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu
515 520 525

Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp
530 535 540

Phe Val Asp Val Thr Asn Asp Glu Lys Leu Ile Met His Met Trp Asn
545 550 555 560

Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp
565 570 575

Ala Cys Glu Ala Phe Ser Arg Leu His Gly Lys His Leu Val Gln Asn
580 585 590

Pro Pro Leu Leu Trp Gly Trp Arg Phe Leu Met Ile Lys Leu Trp Asn
595 600 605

His Ser Leu Leu Asp Ala Arg Ala Met Asn Val Cys Gly Thr Ile Leu
610 615 620

Gln Gly Tyr Gln Asn Glu Ser Ser Asp Pro Lys Ser Ile
625 630 635

<210> 866
<211> 626
<212> PRT
<213> Zea mays

<400> 866

Met Pro Gly Leu Pro Leu Pro Gln Ser Leu Asn Gln Asn Ile Gly Cys
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Gln Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Lys Leu Thr Ala Glu Lys Asp Leu
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

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

Ser Thr Asn Thr Glu Leu Gln Thr His Tyr Val Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro
115 120 125

Ile Tyr Arg Phe Ser Arg Val Cys Leu Leu Thr Ser Phe Ser Glu His

130 135 140

Gly Asn Lys Asp Asn Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
145 150 155 160

Ser Leu Ser Thr Ser Arg Ala Cys Asn His Asp Ile Ile Phe Ile Ser
165 170 175

Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn
180 185 190

His Val Glu Asp Ser Ser Leu Gln Met Leu Glu Gly Lys Cys Ser Trp
195 200 205

Gly Lys Ile Pro Thr Asn Leu Leu Ala Ser Ser Leu Glu Ser Cys Val
210 215 220

Asn Leu Ser Leu Gly His Ile Val Glu Leu Ala Ser Lys Val Thr Met
225 230 235 240

Arg Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Ser Cys Leu
245 250 255

Thr Phe Cys Ser His Lys Val Asp Ala Val Gly Ser Tyr Lys Leu Gln
260 265 270

Leu Cys Met Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Leu Ser
275 280 285

Pro Tyr Ser Ser Tyr Ser Tyr Asn Asp Val Pro Pro Ser Ser Leu Ser
290 295 300

Asp Ile Ile Arg Leu Arg Ser Gly Asn Val Leu Phe Asn Tyr Lys Tyr
305 310 315 320

Tyr Asn Asn Thr Met Gln Glu Thr Glu Val Thr Glu Asp Phe Ser Cys
325 330 335

Pro Phe Cys Tyr Val Arg Cys Gly Ser Phe Lys Gly Leu Gly Cys His
340 345 350

Leu Asn Ser Ser His Asp Leu Phe His Tyr Glu Phe Trp Ile Ser Glu
355 360 365

Glu Tyr Gln Val Val Asn Val Ser Leu Lys Ala Asp Ala Trp Arg Thr
370 375 380

Glu Leu Phe Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr
385 390 395 400

Arg Ser Arg Phe Lys Lys Arg Arg Arg Ser Lys Asn Thr Met Glu Lys
405 410 415

Ile Arg His Val His Ser His Ile Met Glu Ser Gly Ser Pro Glu Asp
420 425 430

Glu Ala Gly Ser Glu Asp Asn Phe Val Gln Gly Glu Asn Gly Thr Ser
435 440 445

Val Ala Asn Ala Ser Ile Asp Pro Ala Gln Ser Leu His Gly Ser Asn
450 455 460

Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu Ser
465 470 475 480

Glu Arg Ser Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln Phe
485 490 495

Phe His Ser His Arg Ala Gln Pro Met Gln Leu Glu Gln Val Phe Ser
500 505 510

Asp Arg Asp Ser Glu Asp Glu Val Asp Asp Asp Ile Ala Asp Phe Glu
515 520 525

Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu Lys

530 535 540

Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val Leu
545 550 555 560

Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Gln Leu His
565 570 575

Gly Arg Gln Leu Ile Gln Asn Pro Ala Leu Leu Trp Gly Trp Arg Phe
580 585 590

Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr Met
595 600 605

Asn Thr Cys Asn Thr Val Leu Gln Ile Leu Gln Glu Glu Ser Thr Gly
610 615 620

Leu Lys
625

<210> 867
<211> 626
<212> PRT
<213> Zea mays

<400> 867

Met Pro Gly Leu Pro Leu Pro Gln Ser Leu Asn Lys Asn Ile Gly Cys
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Gln Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Lys Leu Thr Ala Glu Lys Asp Leu
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

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

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

Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro
        115                 120                 125

Ile Tyr Arg Phe Ser Arg Val Cys Leu Leu Thr Ser Phe Ser Glu His
    130                 135                 140

Gly Asn Lys Asp Ser Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
145                 150                 155                 160

Ser Leu Ser Thr Ser Arg Ala Cys Asn Leu Asp Ile Ile Phe Ile Ser
                165                 170                 175

Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn
            180                 185                 190

His Val Glu Ala Ser Ser Leu Gln Met Leu Glu Gly Lys Cys Ser Trp
        195                 200                 205

Gly Lys Ile Pro Thr Asn Leu Leu Ala Ser Ser Leu Glu Ser Cys Val
    210                 215                 220

Asn Leu Ser Leu Gly His Ile Val Glu Leu Ala Ser Lys Val Thr Met
225                 230                 235                 240

Arg Ser Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Asn Cys Leu
                245                 250                 255

Thr Phe Cys Ser His Lys Val Asp Ala Val Gly Ser Tyr Lys Leu Gln
            260                 265                 270
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Leu Cys Met Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Leu Ser
275 280 285

Pro His Ser Ser Tyr Ser Tyr Asn Asp Val Pro Pro Ser Ser Leu Ser
290 295 300

Asp Ile Ile Arg Leu Arg Ser Gly Asn Val Leu Phe Asn Tyr Lys Tyr
305 310 315 320

Tyr Ser Asn Thr Met Gln Glu Thr Glu Val Thr Glu Asp Phe Ser Cys
325 330 335

Pro Phe Cys Tyr Val Arg Cys Gly Ser Phe Lys Gly Leu Gly Cys His
340 345 350

Leu Asn Ser Ser His Asp Leu Phe His Tyr Glu Phe Trp Ile Ser Glu
355 360 365

Glu Tyr Gln Val Val Asn Val Ser Leu Lys Ala Asp Ala Trp Arg Thr
370 375 380

Glu Leu Phe Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr
385 390 395 400

Arg Ser Arg Phe Lys Lys Arg Arg Arg Ser Lys Thr Thr Met Glu Lys
405 410 415

Ile Arg His Val His Ser His Ile Met Glu Ser Gly Ser Pro Gly Asp
420 425 430

Glu Ala Gly Ser Glu Asp Asn Phe Val Gln Gly Glu Asn Gly Thr Ser
435 440 445

Val Ala Asn Ala Ser Ile Asp Pro Ala Gln Ser Leu His Gly Ser Asn
450 455 460

Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu Ser
465 470 475 480

Glu Arg Ser Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln Phe
485 490 495

Phe His Ser His Arg Ala Gln Pro Met Gln Leu Glu Gln Val Phe Ser
500 505 510

Asp Arg Asp Ser Gly Asp Glu Val Asp Asp Asp Ile Ala Asp Phe Glu
515 520 525

Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu Lys
530 535 540

Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val Leu
545 550 555 560

Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Gln Leu His
565 570 575

Gly Arg Gln Leu Ile Gln Asn Pro Ala Leu Leu Trp Gly Trp Arg Phe
580 585 590

Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr Met
595 600 605

Asn Thr Cys Asn Thr Val Leu Gln Ile Leu Gln Glu Glu Ser Thr Gly
610 615 620

Leu Lys
625

<210> 868
<211> 627
<212> PRT
<213> Eulaliopsis binata

<400> 868

Met Pro Gly Leu Pro Leu Pro Gln Pro Leu Asn Gln Asn Ile Gly Arg
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Arg Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Lys Leu Ala Ala Glu Arg Asp Leu
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

Ala Val Lys Asn Pro Leu Phe Ile Gln Arg Cys Leu Leu Tyr Asn Ile
65 70 75 80

His Ala Arg Arg Lys Lys Arg Ile Gln Ile Thr Ile Ser Leu Ser Arg
85 90 95

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

Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro
115 120 125

Ile Tyr Arg Phe Ser Arg Val Arg Leu Leu Thr Ser Phe Ser Glu Leu
130 135 140

Gly Asn Lys Asp Asn Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
145 150 155 160

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

Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn
180 185 190

His Val Glu Gly Ser Pro Leu Gln Met Leu Glu Gly Lys Cys Ser Trp

195 200 205

Gly Lys Ile Pro Thr Asn Leu Leu Ala Ser Ser Leu Glu Ser Cys Val
210 215 220

Asn Leu Ser Leu Gly His Ile Val Glu Leu Ala Ser Lys Ile Thr Met
225 230 235 240

Arg Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Ser Cys Leu
245 250 255

Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr Gln Leu Gln
260 265 270

Leu Cys Met Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Leu Ser
275 280 285

Pro Tyr Ser Ser Tyr Leu Tyr Asp Asp Val Pro Pro Ser Ser Leu Ser
290 295 300

Asp Ile Ile Arg Leu Arg Ser Gly Asn Val Leu Phe Asn Tyr Lys Tyr
305 310 315 320

His Asn Asn Thr Met Gln Glu Thr Glu Val Thr Glu Asp Phe Cys Cys
325 330 335

Pro Phe Cys Tyr Val Arg Cys Gly Ser Phe Lys Gly Leu Gly Cys His
340 345 350

Leu Asn Ser Ser His Asp Leu Phe His Tyr Glu Phe Trp Ile Ser Glu
355 360 365

Asp Tyr Gln Ile Val Asn Val Ser Leu Lys Ala Asp Ala Trp Arg Thr
370 375 380

Glu Leu Ile Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr
385 390 395 400

Arg Ser Arg Phe Lys Lys Arg Arg Arg Ser Lys Thr Thr Thr Asp Lys
405 410 415

Ile Arg His Val His Ser His Ile Met Glu Ser Gly Ser Pro Glu Asp
420 425 430

Ala Gln Ala Gly Ser Glu Asp Asn Cys Val Gln Gly Glu Asn Gly Thr
435 440 445

Ser Val Ala Asn Ala Ser Ile Asp Pro Ala Gln Ser Leu His Gly Ser
450 455 460

Asn Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu
465 470 475 480

Ser Glu Arg Ala Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln
485 490 495

Phe Phe His Ser His Arg Ala Gln Pro Met Ala Leu Glu Gln Val Phe
500 505 510

Ser Asp Arg Asp Ser Glu Asp Glu Val Asp Asp Asp Ile Ala Asp Phe
515 520 525

Glu Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu
530 535 540

Lys Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val
545 550 555 560

Leu Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Gln Leu
565 570 575

His Gly Arg Gln Leu Val Gln Asn Pro Ala Gln Leu Arg Gly Trp Arg
580 585 590

Phe Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr

595 600 605

Met Asp Thr Cys Asn Thr Val Leu Gln Ser Phe Gln Glu Glu Ser Thr
610 615 620

Gly Leu Lys
625

<210> 869
<211> 629
<212> PRT
<213> Dendrocalamus latiflorus

<400> 869

Met Pro Gly Leu Pro Leu Pro Ala Arg Asp Ala Ala Asn Ile Gly Cys
1 5 10 15

Gly Phe Gly Tyr Pro Arg Ser Ala Asp Gln Met Cys Arg Gln Gln Ser
20 25 30

Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Asn Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

Ala Ile Lys Asn Pro Ala Phe Leu Gln Arg Cys Leu Leu Tyr Lys Ile
65 70 75 80

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

Gly Ala Asn Thr Glu Leu Gln Glu His Asn Ile Phe Pro Leu Tyr Ala
100 105 110

Leu Leu Ala Arg Pro Thr Ser Asn Val Ser Leu Glu Gly His Ser Pro
115 120 125

Tyr Arg Phe Ser Arg Ala Cys Leu Leu Thr Ser Phe Asn Glu Phe Gly
130 135 140

Asn Lys Asp His Thr Glu Ala Thr Phe Met Ile Pro Asp Val Lys Asn
145 150 155 160

Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser Cys
165 170 175

Gly Gln Ala Gly Gln Thr Leu Gly Glu Asn Thr Phe Ser Gly Asn His
180 185 190

Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys Cys Phe Trp Gly
195 200 205

Lys Ile Pro Ile Cys Leu Leu Gly Ser Ser Leu Glu Asn Asp Val Asp
210 215 220

Leu Thr Leu Gly His Thr Val Glu Leu Ala Ser Thr Val Ser Met Ser
225 230 235 240

Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln Asp Ser Cys Leu Thr
245 250 255

Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser His Gln Leu Gln Val
260 265 270

Ser Ile Ser Ala Gln Glu Ala Gly Ala Arg Asp Met Ser Glu Ser Pro
275 280 285

Tyr Ser Ser Tyr Ser Tyr Ser Asp Val Pro Pro Ser Ser Leu Pro His
290 295 300

Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn Tyr Lys Tyr Tyr
305 310 315 320

Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp Phe Ser Cys Pro
325 330 335

Phe Cys Leu Val Ser Cys Gly Ser Phe Lys Gly Leu Gly Cys His Leu
340 345 350

Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp Ile Ser Glu Glu
355 360 365

Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Ala Trp Arg Thr Glu
370 375 380

Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr Phe Ser Tyr Cys
385 390 395 400

Ser Arg Phe Lys Lys Arg Arg Arg Phe Glu Ile Thr Thr Glu Lys Ile
405 410 415

Ser His Val His Pro His Ile Val Asp Ser Gly Ser Pro Glu Asp Ala
420 425 430

Gln Ala Gly Ser Glu Asp Asp Tyr Ala Gln Arg Glu Asn Gly Ile Ser
435 440 445

Val Ala His Ala Ser Val Asp Pro Ala Asn Ser Leu His Gly Ser Asn
450 455 460

Leu Ser Pro Pro Thr Val Leu Gln Phe Gly Lys Thr Arg Lys Leu Ser
465 470 475 480

Val Glu Arg Ala Asp Pro Arg Asn Arg Gln Leu Leu Gln Lys Arg Gln
485 490 495

Phe Phe His Ser His Arg Ala Gln Pro Met Ala Leu Glu Gln Val Phe
500 505 510

Ser Asp Arg Asp Ser Glu Asp Glu Val Asp Asp Asp Ile Ala Asp Phe
515 520 525

Glu Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu
530 535 540

Lys Leu Ile Met His Met Trp Asn Ser Phe Val Arg Lys Gln Arg Val
545 550 555 560

Leu Ala Asp Gly His Ile Pro Trp Ala Cys Glu Ala Phe Ser Arg Leu
565 570 575

His Gly Gln Gln Leu Val Gln Asn Ser Ala Leu Leu Arg Cys Trp Arg
580 585 590

Phe Phe Met Ile Lys Leu Trp Asn His Ser Leu Leu Asp Ala Arg Thr
595 600 605

Met Asn Thr Cys Asn Thr Ile Leu Glu Gly Tyr Gln Asn Glu Ser Pro
610 615 620

Asp Pro Lys Gln Thr
625

<210> 870
<211> 638
<212> PRT
<213> Triticum aestivum

<400> 870

Met Pro Gly Leu Pro Leu Pro Gln Ser Leu Asn Gln Asn Ile Gly Cys
1 5 10 15

Glu Tyr Ala Tyr Pro Gly Ser Thr Gly Gln Ala Phe Arg Gln Gln Leu
20 25 30

Arg Thr Ala Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Ser Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

His Ala Ser Arg Lys Lys Arg Ile Gln Ile Thr Val Ser Leu Ser Arg
                85                  90                  95

Gly Thr Asn Thr Glu Leu Pro Glu Gln Asn Ile Phe Pro Leu Tyr Val
            100                 105                 110

Leu Leu Ala Thr Pro Thr Ser Asn Ile Ser Leu Glu Gly His Ser Pro
        115                 120                 125

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

Gly Asn Lys Gly Arg Thr Lys Ala Thr Phe Ile Ile Pro Asp Ile Lys
145                 150                 155                 160

Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser
                165                 170                 175

Cys Val Ser Glu Gly Gln Val Gly Glu Asn Arg Gly Glu His Asn Cys
            180                 185                 190

Ser Val Asp His Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys
        195                 200                 205

Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Gly Ser Ser Leu Glu
    210                 215                 220

Asn Cys Val Thr Leu Asn Leu Gly His Thr Val Glu Leu Ala Ser Ala
225                 230                 235                 240

Val Ser Met Ser Pro Ser Phe Leu Glu Pro Lys Phe Met Glu Gln Asp
                245                 250                 255

Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr
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260 265 270

Gln Leu Gln Val Gly Ile Ser Ala Gln Glu Ala Gly Ala Lys Asp Met
275 280 285

Ser Glu Ser Pro Tyr Ser Ser Tyr Ser Tyr Ser Gly Val Pro Pro Ser
290 295 300

Ser Leu Pro His Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn
305 310 315 320

Phe Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp
325 330 335

Phe Ala Cys Pro Phe Cys Leu Val Lys Cys Gly Ser Tyr Lys Gly Leu
340 345 350

Gly Cys His Leu Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp
355 360 365

Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Val
370 375 380

Trp Arg Thr Glu Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr
385 390 395 400

Phe Ser Tyr Ser Ser Arg Phe Lys Lys Arg Arg Arg Leu Gly Met Leu
405 410 415

Gly Thr Thr Ala Glu Lys Ile Ser His Val His Pro His Ile Met Asp
420 425 430

Ser Asp Ser Pro Glu Asp Ala Gln Ala Val Ser Glu Asp Asp Phe Val
435 440 445

Gln Arg Glu Glu Asp Asp Ile Ser Ala Pro Arg Ala Ser Val Asp Pro
450 455 460

Ala Gln Ser Leu His Gly Ser Asn Leu Ser Pro Pro Thr Val Leu Gln
465 470 475 480

Phe Gly Lys Thr Arg Lys Leu Ser Ala Glu Arg Ala Asp Pro Arg Asn
485 490 495

Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln
500 505 510

Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu
515 520 525

Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Lys Arg Met Leu Glu Asp
530 535 540

Phe Val Asp Val Thr Asp Asp Glu Lys Leu Ile Met His Met Trp Asn
545 550 555 560

Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp
565 570 575

Ala Cys Glu Ala Phe Ser Arg Leu His Gly Lys His Leu Val Gln Asn
580 585 590

Pro Pro Leu Leu Trp Ser Trp Arg Phe Leu Met Ile Lys Leu Trp Asn
595 600 605

His Ser Leu Leu Asp Ala Arg Ala Met Asn Val Cys Gly Thr Ile Leu
610 615 620

Gln Gly Tyr Gln Asn Glu Ser Gly Leu Asp Pro Lys Lys Met
625 630 635

<210> 871
<211> 606
<212> PRT
<213> Oryza sativa Japonica Group

<400> 871

Tyr Gln Met Cys Arg His Gln Pro Arg Ala Arg Leu Ser Pro Asp Glu
1   5   10   15

Gln Leu Ala Ala Glu Glu Ser Phe Ala Leu Tyr Cys Lys Pro Val Glu
            20   25   30

Leu Tyr Asn Ile Ile Gln Arg Arg Ser Ile Lys Asn Pro Ala Phe Leu
        35   40   45

Gln Arg Cys Leu Leu Tyr Lys Ile His Ala Arg Arg Lys Lys Arg Ser
    50   55   60

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

Gln Asn Ile Phe Pro Leu Tyr Val Leu Leu Ala Arg Pro Thr Asn Asn
                85   90   95

Val Ser Leu Glu Gly His Ser Pro Ile Tyr Arg Phe Ser Arg Ala Cys
            100   105   110

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

Thr Phe Val Ile Pro Asp Val Lys Asn Leu Ala Thr Ser Arg Ala Cys
    130   135   140

Ser Leu Asn Ile Ile Leu Ile Ser Cys Gly Arg Ala Glu Gln Thr Phe
145   150   155   160

Asp Asp Asn Asn Cys Ser Gly Asn His Val Glu Gly Ser Thr Leu Gln
                165   170   175

Lys Leu Glu Gly Lys Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu
            180   185   190

Ala Ser Ser Leu Gly Asn Cys Val Ser Leu Ser Leu Gly His Thr Val
195 200 205

Glu Met Ser Ser Thr Val Glu Met Thr Pro Ser Phe Leu Glu Pro Lys
210 215 220

Phe Leu Glu Asp Asp Ser Cys Leu Thr Phe Cys Ser Gln Lys Val Asp
225 230 235 240

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

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

Asp Val Pro Pro Ser Ser Leu Thr His Ile Ile Arg Leu Arg Ser Gly
275 280 285

Asn Val Leu Phe Asn Tyr Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr
290 295 300

Glu Val Thr Glu Asp Phe Ser Cys Pro Phe Cys Leu Val Pro Cys Gly
305 310 315 320

Ser Phe Lys Gly Leu Gly Cys His Leu Asn Ala Ser His Asp Leu Phe
325 330 335

His Tyr Glu Phe Trp Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser
340 345 350

Leu Lys Thr Asp Ser Trp Arg Thr Glu Leu Leu Ala Glu Gly Val Asp
355 360 365

Pro Arg His Gln Thr Phe Ser Tyr Arg Ser Arg Phe Lys Lys Arg Lys
370 375 380

Arg Val Glu Ile Ser Ser Asp Lys Ile Arg His Val His Pro His Ile
385 390 395 400

Val Asp Ser Gly Ser Pro Glu Asp Ala Gln Ala Gly Ser Glu Asp Asp
405 410 415

Tyr Val Gln Arg Glu Asn Gly Ser Ser Val Ala His Ala Ser Val Asp
420 425 430

Pro Ala Asn Ser Leu His Gly Ser Asn Leu Ser Ala Pro Thr Val Leu
435 440 445

Gln Phe Gly Lys Thr Arg Lys Leu Ser Val Glu Arg Ala Asp Pro Arg
450 455 460

Asn Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala
465 470 475 480

Gln Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp
485 490 495

Glu Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp
500 505 510

Asp Phe Val Asp Val Thr Lys Asp Glu Lys Leu Ile Met His Met Trp
515 520 525

Asn Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro
530 535 540

Trp Ala Cys Glu Ala Phe Ser Gln Phe His Gly Gln Glu Leu Val Gln
545 550 555 560

Asn Pro Ala Leu Leu Trp Cys Trp Arg Phe Phe Met Val Lys Leu Trp
565 570 575

Asn His Ser Leu Leu Asp Ala Arg Ala Met Asn Ala Cys Asn Thr Ile
580 585 590

Leu Glu Gly Tyr Leu Asn Gly Ser Ser Asp Pro Lys Lys Asn
595 600 605

<210> 872
<211> 604
<212> PRT
<213> Oryza sativa Japonica Group

<400> 872

Met Cys Arg His Gln Pro Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu
1 5 10 15

Ala Ala Glu Glu Ser Phe Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr
20 25 30

Asn Ile Ile Gln Arg Arg Ser Ile Lys Asn Pro Ala Phe Leu Gln Arg
35 40 45

Cys Leu Leu Tyr Lys Ile His Ala Arg Arg Lys Lys Arg Ser Leu Ile
50 55 60

Thr Ile Ser Leu Ser Gly Gly Thr Asn Lys Glu Leu Arg Ala Gln Asn
65 70 75 80

Ile Phe Pro Leu Tyr Val Leu Leu Ala Arg Pro Thr Asn Asn Val Ser
85 90 95

Leu Glu Gly His Ser Pro Ile Tyr Arg Phe Ser Arg Ala Cys Leu Leu
100 105 110

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

Val Ile Pro Asp Val Lys Asn Leu Ala Thr Ser Arg Ala Cys Ser Leu
130 135 140

Asn Ile Ile Leu Ile Ser Cys Gly Arg Ala Glu Gln Thr Phe Asp Asp
145 150 155 160

Asn Asn Cys Ser Gly Asn His Val Glu Gly Ser Thr Leu Gln Lys Leu
165 170 175

Glu Gly Lys Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Ala Ser
180 185 190

Ser Leu Gly Asn Cys Val Ser Leu Ser Leu Gly His Thr Val Glu Met
195 200 205

Ser Ser Thr Val Glu Met Thr Pro Ser Phe Leu Glu Pro Lys Phe Leu
210 215 220

Glu Asp Asp Ser Cys Leu Thr Phe Cys Ser Gln Lys Val Asp Ala Thr
225 230 235 240

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

Lys Asp Met Ser Glu Ser Pro Tyr Ser Val Tyr Ser Tyr Asn Asp Val
260 265 270

Pro Pro Ser Ser Leu Thr His Ile Ile Arg Leu Arg Ser Gly Asn Val
275 280 285

Leu Phe Asn Tyr Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val
290 295 300

Thr Glu Asp Phe Ser Cys Pro Phe Cys Leu Val Pro Cys Gly Ser Phe
305 310 315 320

Lys Gly Leu Gly Cys His Leu Asn Ala Ser His Asp Leu Phe His Tyr
325 330 335

Glu Phe Trp Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys
340 345 350

Thr Asp Ser Trp Arg Thr Glu Leu Leu Ala Glu Gly Val Asp Pro Arg

355 360 365

His Gln Thr Phe Ser Tyr Arg Ser Arg Phe Lys Lys Arg Lys Arg Val
370 375 380

Glu Ile Ser Ser Asp Lys Ile Arg His Val His Pro His Ile Val Asp
385 390 395 400

Ser Gly Ser Pro Glu Asp Ala Gln Ala Gly Ser Glu Asp Asp Tyr Val
405 410 415

Gln Arg Glu Asn Gly Ser Ser Val Ala His Ala Ser Val Asp Pro Ala
420 425 430

Asn Ser Leu His Gly Ser Asn Leu Ser Ala Pro Thr Val Leu Gln Phe
435 440 445

Gly Lys Thr Arg Lys Leu Ser Val Glu Arg Ala Asp Pro Arg Asn Arg
450 455 460

Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln Pro
465 470 475 480

Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu Val
485 490 495

Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp Phe
500 505 510

Val Asp Val Thr Lys Asp Glu Lys Leu Ile Met His Met Trp Asn Ser
515 520 525

Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp Ala
530 535 540

Cys Glu Ala Phe Ser Gln Phe His Gly Gln Glu Leu Val Gln Asn Pro
545 550 555 560

Ala Leu Leu Trp Cys Trp Arg Phe Phe Met Val Lys Leu Trp Asn His
565 570 575

Ser Leu Leu Asp Ala Arg Ala Met Asn Ala Cys Asn Thr Ile Leu Glu
580 585 590

Gly Tyr Leu Asn Gly Ser Ser Asp Pro Lys Lys Asn
595 600

<210> 873
<211> 601
<212> PRT
<213> Eulaliopsis binata

<400> 873

Met Cys Leu Gln His Cys Ser Ala Arg Leu Ser Pro Asp Glu Gln Leu
1 5 10 15

Ala Ala Glu Lys Ser Phe Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr
20 25 30

Asn Ile Ile Gln Arg Arg Ala Val Lys Asn Pro Pro Phe Ile Gln Arg
35 40 45

Ser Leu Leu Tyr Lys Ile Gln Ala Arg Arg Lys Lys Arg Ile Gln Ile
50 55 60

Thr Val Ser Leu Ser Ala Ser Thr Asn Thr Gln Ala Gln Asn Ile Phe
65 70 75 80

Pro Leu Tyr Val Leu Leu Ala Arg Pro Thr Ser Asn Ile Ser Leu Asp
85 90 95

Gly His Ser Pro Ile Tyr Arg Phe Ser Arg Val Ser Leu Leu Thr Asn
100 105 110

Phe Ser Glu Phe Gly Asn Glu Gly Lys Thr Glu Ala Thr Phe Ile Ile
115 120 125

Pro Asn Val Lys Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Ser Ile
130 135 140

Ile Phe Ile Ser Cys Gly Gln Val Gly Gln Ile Ile Gly Glu Asp Ser
145 150 155 160

Cys Ser Gly Asn Asp Val Leu Arg Ser Ser Leu Gln Lys Leu Glu Gly
165 170 175

Lys Cys Ser Trp Gly Lys Ile Leu Thr Asn Arg Leu Ala Ser Ser Leu
180 185 190

Glu Gln Cys Val Thr Leu Ser Thr Gly Asp Ala Val Asp Leu Ala Ser
195 200 205

Thr Val Thr Met Asn Pro Ser Phe Leu Glu Pro Lys Phe Leu Glu Gln
210 215 220

Asp Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser
225 230 235 240

Tyr Gln Leu Gln Val Ser Ile Ser Ala Glu Glu Ala Gly Ala Arg Glu
245 250 255

Leu Leu Leu Ser Pro Tyr Tyr Cys Asn Tyr Ser Tyr Asn Asn Val Pro
260 265 270

Pro Ser Leu Leu Pro Glu Ile Ile Arg Leu Arg Ala Gly Asn Val Leu
275 280 285

Phe Asn Tyr Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr
290 295 300

Glu Asp Phe Ser Cys Pro Phe Cys Leu Val Pro Cys Gly Ser Phe Lys
305 310 315 320

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Gly Leu Gly Cys His Leu Asn Ser Thr His Asp Leu Phe His Tyr Glu
                325                 330                 335

Phe Trp Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Val
            340                 345                 350

Asp Ala Trp Lys Thr Glu Phe Val Ala Glu Gly Val Asp Pro Arg His
        355                 360                 365

Gln Thr Phe Ser Tyr Cys Ser Arg Phe Lys Lys Arg Arg Arg Leu Glu
    370                 375                 380

Thr Thr Ala Lys Lys Ile Arg His Val His Pro His Ile Met Glu Pro
385                 390                 395                 400

Gly Ser His Glu Asp Ala Gln Ala Gly Ser Glu Asp Asp Tyr Val Gln
                405                 410                 415

Arg Glu Asn Gly Leu Ser Val Glu His Ala Ser Val Asp His Ser Gln
            420                 425                 430

Pro Val His Gly Ser Asn Leu Ser Pro Pro Thr Val Leu Gln Phe Gly
        435                 440                 445

Lys Ser Arg Lys Leu Ser Ala Glu Arg Ser Asp Pro Arg Asn Arg Gln
    450                 455                 460

Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln Pro Met
465                 470                 475                 480

Pro Leu Glu Gln Val Phe Ser Asp His Asp Ser Glu Asp Glu Val Asp
                485                 490                 495

Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp Phe Val
            500                 505                 510

Asp Val Thr Lys Asp Glu Lys Leu Ile Met His Met Trp Asn Ser Phe
        515                 520                 525
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Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp Ala Cys
530 535 540

Glu Ala Phe Ser Arg Cys His Gly Gln Arg Leu Val Gln Asn Pro Ala
545 550 555 560

Leu Leu Trp Gly Trp Arg Phe Phe Met Ile Lys Leu Trp Ser His Ser
565 570 575

Leu Leu Asp Ala Arg Ala Met Asn Thr Cys Asn Thr Ile Leu Gln Gly
580 585 590

Tyr Gln Asp Gly Ser Ser Asp Pro Lys
595 600

<210> 874
<211> 637
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 874

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

Glu Phe Ser Tyr Pro Gln Ser Ala Asp Gln Met Arg Gln Gln Gln Leu
20 25 30

Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Ser Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

His Ala Ser Arg Lys Lys Arg Ile Gln Ile Thr Val Ser Leu Ser Arg

85 90 95

Gly Thr Asn Thr Glu Leu Pro Glu Gln Asn Val Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Thr Pro Thr Thr Asn Ile Ser Leu Glu Gly His Ser Pro
115 120 125

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

Gly Ser Lys Gly Arg Thr Lys Ala Thr Phe Thr Ile Pro Asp Ile Lys
145 150 155 160

Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser
165 170 175

Cys Val Ser Glu Gly Gln Val Glu Glu Asn Val Gly Glu His Asn Cys
180 185 190

Ser Val Asn His Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys
195 200 205

Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Gly Ser Ser Leu Glu
210 215 220

Asn Cys Val Thr Leu Asn Leu Gly His Thr Val Glu Leu Ala Ser Ala
225 230 235 240

Val Ser Met Ser Pro Ser Phe Leu Glu Pro Lys Phe Met Glu Gln Asp
245 250 255

Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr
260 265 270

Gln Leu Gln Val Gly Ile Ser Ala Gln Glu Ala Gly Ala Arg Asp Met
275 280 285

Ser Glu Ser Pro Tyr Ser Ser Tyr Ser Tyr Ser Gly Val Pro Pro Ser
290 295 300

Ser Leu Pro His Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn
305 310 315 320

Phe Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp
325 330 335

Phe Ala Cys Pro Phe Cys Leu Val Lys Cys Gly Ser Tyr Lys Gly Leu
340 345 350

Gly Cys His Leu Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp
355 360 365

Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Val
370 375 380

Trp Arg Thr Glu Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr
385 390 395 400

Phe Ser Tyr Ser Ser Arg Leu Lys Lys Arg Arg Arg Leu Gly Met Leu
405 410 415

Gly Thr Thr Ala Glu Lys Ile Ser His Val His Pro His Ile Met Asp
420 425 430

Ser Asp Ser Pro Glu Asp Ala Gln Ala Val Ser Glu Gly Asp Phe Val
435 440 445

Gln Arg Glu Glu Asp Asp Ile Ser Ala Pro Arg Ala Ser Val Asp Pro
450 455 460

Ala Gln Ser Leu His Asp Ser Asn Leu Ser Pro Pro Thr Val Leu Gln
465 470 475 480

Phe Gly Lys Thr Arg Lys Leu Ser Ala Glu Arg Ala Asp Pro Arg Asn

485 490 495

Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln
500 505 510

Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu
515 520 525

Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp
530 535 540

Phe Val Asp Val Thr Asn Asp Glu Lys Leu Ile Met His Met Trp Asn
545 550 555 560

Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp
565 570 575

Ala Cys Glu Ala Phe Ser Arg Leu His Gly Lys His Leu Val Gln Asn
580 585 590

Pro Pro Leu Leu Trp Ser Trp Arg Phe Leu Met Ile Lys Leu Trp Asn
595 600 605

His Ser Leu Leu Asp Ala Arg Ala Met Asn Val Cys Gly Thr Ile Leu
610 615 620

Gln Gly Tyr Gln Asn Glu Ser Ser Asp Pro Lys Asn Ile
625 630 635

<210> 875
<211> 637
<212> PRT
<213> Hordeum vulgare

<400> 875

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

Glu Phe Ser Tyr Pro Gln Ser Ala Asp Gln Met Arg His Gln Gln Leu
20 25 30

Arg Ala Arg Leu Ser Pro Asp Glu Gln Leu Ala Ala Glu Glu Ser Phe
35 40 45

Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
50 55 60

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

His Ala Ser Arg Lys Lys Arg Ile Gln Ile Thr Val Ser Leu Ser Arg
85 90 95

Gly Thr Asn Thr Glu Leu Pro Glu Gln Asn Val Phe Pro Leu Tyr Val
100 105 110

Leu Leu Ala Thr Pro Thr Thr Asn Ile Ser Leu Glu Gly His Ser Pro
115 120 125

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

Gly Ser Lys Gly Arg Thr Lys Ala Thr Phe Thr Ile Pro Asp Ile Lys
145 150 155 160

Asn Leu Ser Thr Ser Arg Ala Cys Asn Leu Asn Ile Ile Leu Ile Ser
165 170 175

Cys Val Ser Glu Gly Gln Val Glu Glu Asn Val Gly Glu His Asn Cys
180 185 190

Ser Val Asn His Val Glu Gly Ser Ala Leu Gln Lys Leu Glu Gly Lys
195 200 205

Cys Phe Trp Gly Lys Ile Pro Ile Asp Leu Leu Gly Ser Ser Leu Glu
210 215 220

Asn Cys Val Thr Leu Asn Leu Gly His Thr Val Glu Leu Ala Ser Ala
225 230 235 240

Val Ser Met Ser Pro Ser Phe Leu Glu Pro Lys Phe Met Glu Gln Asp
245 250 255

Ser Cys Leu Thr Phe Cys Ser His Lys Val Asp Ala Thr Gly Ser Tyr
260 265 270

Gln Leu Gln Val Gly Ile Ser Ala Gln Glu Ala Gly Ala Arg Asp Met
275 280 285

Ser Glu Ser Pro Tyr Ser Ser Tyr Ser Tyr Ser Gly Val Pro Pro Ser
290 295 300

Ser Leu Pro His Ile Ile Arg Leu Arg Ala Gly Asn Val Leu Phe Asn
305 310 315 320

Phe Lys Tyr Tyr Asn Asn Thr Met Gln Lys Thr Glu Val Thr Glu Asp
325 330 335

Phe Ala Cys Pro Phe Cys Leu Val Lys Cys Gly Ser Tyr Lys Gly Leu
340 345 350

Gly Cys His Leu Asn Ser Ser His Asp Leu Phe His Phe Glu Phe Trp
355 360 365

Ile Ser Glu Glu Cys Gln Ala Val Asn Val Ser Leu Lys Thr Asp Val
370 375 380

Trp Arg Thr Glu Leu Val Ala Glu Gly Val Asp Pro Arg His Gln Thr
385 390 395 400

Phe Ser Tyr Ser Ser Arg Phe Lys Lys Arg Arg Arg Leu Gly Met Leu
405 410 415

Gly Thr Thr Ala Glu Lys Ile Ser His Val His Pro His Ile Met Asp
420 425 430

Ser Asp Ser Pro Glu Asp Ala Gln Ala Val Ser Glu Gly Asp Phe Val
435 440 445

Gln Arg Glu Glu Asp Asp Ile Ser Ala Pro Arg Ala Ser Val Asp Pro
450 455 460

Ala Gln Ser Leu His Asp Ser Asn Leu Ser Pro Pro Thr Val Leu Gln
465 470 475 480

Phe Gly Lys Thr Arg Lys Leu Ser Ala Glu Arg Ala Asp Pro Arg Asn
485 490 495

Arg Gln Leu Leu Gln Lys Arg Gln Phe Phe His Ser His Arg Ala Gln
500 505 510

Pro Met Ala Leu Glu Gln Val Phe Ser Asp Arg Asp Ser Glu Asp Glu
515 520 525

Val Asp Asp Asp Ile Ala Asp Phe Glu Asp Arg Arg Met Leu Asp Asp
530 535 540

Phe Val Asp Val Thr Asn Asp Glu Lys Leu Ile Met His Met Trp Asn
545 550 555 560

Ser Phe Val Arg Lys Gln Arg Val Leu Ala Asp Gly His Ile Pro Trp
565 570 575

Ala Cys Glu Ala Phe Ser Arg Leu His Gly Lys His Leu Val Gln Asn
580 585 590

Pro Pro Leu Leu Trp Gly Trp Arg Phe Leu Met Ile Lys Leu Trp Asn
595 600 605

His Ser Leu Leu Asp Ala Arg Ala Met Asn Val Cys Gly Thr Ile Leu
610 615 620

Gln Gly Tyr Gln Asn Glu Ser Ser Asp Pro Lys Ser Ile
625 630 635

<210> 876
<211> 696
<212> PRT
<213> Sorghum bicolor

<400> 876

Met Val Asn Phe Gly Lys Lys Leu Met Ala Asp Gln Leu Glu Glu Trp
1 5 10 15

Arg Glu Tyr Tyr Ile Asn Tyr Lys Met Met Lys Lys Lys Val Lys Gln
20 25 30

Tyr Val Gln Gln Thr Gln Thr Gly Gly Lys Asn Arg Asp Gln Val Leu
35 40 45

Lys Glu Phe Ser Arg Met Leu Asp Asp Gln Ile Glu Lys Val Val Leu
50 55 60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Arg Arg Ile Glu Lys Leu
65 70 75 80

Gly Val Gln Arg Ala Met Leu Met Gln Gln Ser Asp Val Ser Gln Ile
85 90 95

Cys Gln Leu Arg Gln Ala Tyr Arg Glu Val Gly Tyr Asp Leu Val Lys
100 105 110

Leu Leu Arg Phe Leu Asp Met Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Lys Phe Thr Asp Tyr Tyr Val
130 135 140

Ser Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Ile Phe Lys

145 150 155 160

Gln Val Gly Val Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ala
165 170 175

Tyr Leu Gln Asp His Gln Gly Tyr Leu Ala Asn Ile Tyr Asp Tyr Pro
180 185 190

Ser Leu Ile Leu Lys Asp Pro Val Ile Glu Gln Ile Asn His Ser Val
195 200 205

Gln Lys Leu Thr His Ser Thr Ser Phe Leu Gln Phe Leu Gly Gln His
210 215 220

Ala Leu Ile Val Pro Glu Asp Met Gln Ser Gly Ser Asp Leu Asp Asp
225 230 235 240

Asp Lys Asp Tyr His Phe Leu Ser Leu Leu Leu Asn Leu Val Asn Thr
245 250 255

Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp Asp
260 265 270

Tyr Ser Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile Ile
275 280 285

Gly Ser Met Ala Val Ala Gln Ile Phe Ser Ser Val Tyr Phe Ser Ala
290 295 300

Trp Ser Asn Lys Ser Tyr Phe Arg Pro Leu Val Phe Ser Ser Ile Met
305 310 315 320

Leu Phe Leu Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn Ser
325 330 335

Leu Thr Ala Leu Ile Val Gly Arg Leu Leu Cys Gly Leu Gly Ser Ala
340 345 350

Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys Ser
355 360 365

Arg Met Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly Met
370 375 380

Ala Cys Gly Pro Gly Leu Ala Gly Leu Leu Gln Thr Lys Phe Lys Ile
385 390 395 400

Tyr Gly Leu Thr Phe Asn Gln Asn Thr Leu Pro Gly Trp Val Met Cys
405 410 415

Val Ala Trp Leu Ala Tyr Leu Phe Trp Leu Trp Ile Ser Phe Lys Glu
420 425 430

Pro Gly His Ile Ala Ser Glu Asn Ser Val Asn Thr Gln Ser Ser Asp
435 440 445

Ser Gly Arg Pro Val Ser Gly Asn Leu Glu Asp Gly Val Arg Glu Pro
450 455 460

Leu Leu Ile Asp Ala Lys Ala Gly Pro Asp Asp Asp Val Glu Asp Asn
465 470 475 480

Asp Asp Asn Asp Asp Asp Pro Glu Glu Ser His Arg Pro Ala Thr Ser
485 490 495

Leu Ala Ala Ala Tyr Arg Leu Leu Thr Pro Ser Val Lys Val Gln Leu
500 505 510

Leu Ile Tyr Phe Met Leu Lys Phe Ala Met Glu Ile Leu Leu Ser Glu
515 520 525

Ser Ser Val Val Thr Thr Phe Tyr Phe Lys Trp Thr Thr Ser Thr Val
530 535 540

Ala Ile Phe Leu Ala Val Leu Gly Leu Thr Val Leu Pro Val Asn Val

545 550 555 560

Ile Val Gly Ser Tyr Val Thr Asn Leu Phe Gln Asp Arg Gln Ile Leu
565 570 575

Val Ala Ser Glu Ile Met Val Leu Ile Gly Ile Val Met Ser Phe Arg
580 585 590

Phe Thr Pro His Tyr Ser Val Pro Gln Tyr Val Thr Ser Ala Leu Ile
595 600 605

Thr Phe Val Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu
610 615 620

Ser Arg Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly Gly
625 630 635 640

Leu Leu Ser Thr Glu Ala Gly Thr Leu Ala Arg Val Ala Ala Asp Met
645 650 655

Thr Ile Thr Ala Ala Gly Asn Leu Gly Gln Ser Arg Leu Leu Asn Ala
660 665 670

Thr Leu Leu Pro Ser Leu Val Ile Cys Leu Ala Ser Ile Val Ala Thr
675 680 685

Phe Cys Thr Tyr Asn Ser Leu Tyr
690 695

<210> 877
<211> 692
<212> PRT
<213> Zea mays

<400> 877

Met Val Asn Phe Gly Lys Lys Leu Met Ala Asp Gln Leu Glu Glu Trp
1 5 10 15

Arg Glu Tyr Tyr Ile Asn Tyr Lys Met Met Lys Lys Lys Val Lys Gln
20 25 30

Tyr Val Gln Gln Thr Gln Thr Gly Gly Lys Asn Arg Asp Gln Val Leu
35 40 45

Lys Glu Phe Ser Arg Met Leu Asp Asp Gln Ile Glu Lys Ile Val Leu
50 55 60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Arg Arg Ile Glu Asn Leu
65 70 75 80

Gly Glu Gln Arg Val Val Leu Met Glu Arg Ser Asp Val Ser Gln Ile
85 90 95

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

Leu Leu Arg Phe Leu Asp Ser Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Lys Phe Thr Asp Tyr Tyr Val
130 135 140

Ser Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Ile Phe Lys
145 150 155 160

Gln Val Gly Val Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ser
165 170 175

Tyr Leu Gln Asp His Gln Gly Ser Leu Ala Asn Ile Tyr Asp Tyr Pro
180 185 190

Ser Leu Ile Leu Lys Asp Pro Val Ile Glu Gln Ile Asn His Ser Val
195 200 205

Gln Lys Leu Thr His Ser Thr Ser Phe Leu Gln Phe Leu Gly Gln His
210 215 220

Ala Leu Ile Val Pro Gly Asp Met Gln Ser Gly Ser Asp Leu Gly Asp
225 230 235 240

Asp Lys Asp Tyr His Phe Leu Ser Leu Leu Leu Asn Leu Val Asn Thr
245 250 255

Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp Asp
260 265 270

Tyr Ser Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile Ile
275 280 285

Gly Ser Met Ala Val Ala Gln Ile Phe Ser Ser Val Tyr Phe Ser Ala
290 295 300

Trp Ser Asn Arg Ser Tyr Phe Arg Pro Leu Val Phe Ser Cys Ile Met
305 310 315 320

Leu Phe Leu Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn Ser
325 330 335

Leu Thr Val Leu Ile Ala Gly Arg Leu Leu Cys Gly Leu Gly Ser Ala
340 345 350

Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys Thr
355 360 365

Arg Leu Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly Met
370 375 380

Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Lys Phe Lys Ile
385 390 395 400

Tyr Gly Leu Thr Phe Asn Gln Asn Thr Leu Pro Gly Trp Val Met Cys
405 410 415

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Leu Ala Trp Ile Ala Tyr Leu Phe Trp Leu Trp Ile Ser Phe Lys Glu
        420                 425                 430

Pro Gly His Ile Ala Thr Glu Asn Ser Val Ser Thr Gln Ser Ser Asp
    435                 440                 445

Ser Gly Arg Arg Val Ser Gly Asn Leu Glu Gly Gly Leu Gly Glu Pro
    450                 455                 460

Leu Leu Ile Asp Ala Lys Ala Gly Gln Asp Glu Asp Asp Glu Asp Asn
465                 470                 475                 480

Asp Asp Pro Glu Glu Ser His Thr Pro Ala Thr Ser Leu Ala Ala Ala
                485                 490                 495

Tyr Arg Leu Leu Thr Pro Ser Val Lys Val Gln Leu Leu Ile Tyr Phe
            500                 505                 510

Met Leu Lys Phe Ala Met Glu Ile Leu Leu Ser Glu Ser Ser Val Val
        515                 520                 525

Thr Thr Phe Tyr Phe Lys Trp Thr Thr Ser Thr Val Ala Ile Phe Leu
    530                 535                 540

Ala Val Leu Gly Leu Thr Val Leu Pro Val Asn Val Ile Val Gly Ser
545                 550                 555                 560

Tyr Val Thr Asn Leu Phe Gln Asp Arg Gln Ile Leu Val Ala Ser Glu
                565                 570                 575

Ile Met Val Leu Ile Gly Ile Val Met Ser Phe Cys Phe Thr Pro His
            580                 585                 590

Tyr Ser Val Pro Gln Tyr Val Thr Ser Ala Leu Ile Thr Phe Val Phe
        595                 600                 605

Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu Ser Arg Val Met
    610                 615                 620
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Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly Gly Leu Leu Ser Thr
625 630 635 640

Glu Ala Gly Thr Leu Ala Arg Val Ala Ala Asp Met Thr Ile Thr Ala
645 650 655

Ala Gly Tyr Leu Gly Gln Gly Arg Leu Leu Asn Ala Thr Leu Leu Pro
660 665 670

Ser Leu Val Ile Cys Leu Ala Ser Ile Val Ala Thr Phe Cys Thr Tyr
675 680 685

Asn Ser Leu Tyr
690

<210> 878
<211> 692
<212> PRT
<213> Zea mays

<400> 878

Met Val Asn Phe Gly Lys Lys Leu Met Ala Asp Gln Leu Glu Glu Trp
1 5 10 15

Arg Glu Tyr Tyr Ile Asn Tyr Lys Met Met Lys Lys Lys Val Lys Gln
20 25 30

Tyr Val Gln Gln Thr Gln Thr Gly Gly Lys Asn Arg Asp Gln Val Leu
35 40 45

Lys Glu Phe Ser Arg Met Leu Asp Asp Gln Ile Glu Lys Ile Val Leu
50 55 60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Arg Arg Ile Glu Asn Leu
65 70 75 80

Gly Glu Gln Arg Val Val Leu Met Glu Arg Ser Asp Val Ser Gln Ile

85 90 95

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

Leu Leu Arg Phe Leu Asp Ser Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Lys Phe Thr Asp Tyr Tyr Val
130 135 140

Ser Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Ile Phe Lys
145 150 155 160

Gln Val Gly Val Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ser
165 170 175

Tyr Leu Gln Asp His Gln Gly Ser Leu Ala Asn Ile Tyr Asp Tyr Pro
180 185 190

Ser Leu Ile Leu Lys Asp Pro Val Ile Glu Gln Ile Asn His Ser Val
195 200 205

Gln Lys Leu Thr His Ser Thr Ser Phe Leu Gln Phe Leu Gly Gln His
210 215 220

Ala Leu Ile Val Pro Gly Asp Met Gln Ser Gly Ser Asp Leu Gly Asp
225 230 235 240

Asp Lys Asp Tyr His Phe Leu Ser Leu Leu Leu Asn Leu Val Asn Thr
245 250 255

Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp Asp
260 265 270

Tyr Ser Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile Ile
275 280 285

Gly Ser Met Ala Val Ala Gln Ile Phe Ser Ser Val Tyr Phe Ser Ala
290 295 300

Trp Ser Asn Arg Ser Tyr Phe Arg Pro Leu Val Phe Ser Cys Ile Met
305 310 315 320

Leu Phe Leu Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn Ser
325 330 335

Leu Thr Val Leu Ile Ala Gly Arg Leu Leu Cys Gly Leu Gly Ser Ala
340 345 350

Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys Thr
355 360 365

Arg Leu Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly Met
370 375 380

Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Lys Phe Lys Ile
385 390 395 400

Tyr Gly Leu Thr Phe Asn Gln Asn Thr Leu Pro Gly Trp Val Met Cys
405 410 415

Leu Ala Trp Ile Ala Tyr Leu Phe Trp Leu Trp Ile Ser Phe Lys Glu
420 425 430

Pro Gly His Ile Ala Thr Glu Asn Ser Val Ser Thr Gln Ser Ser Asp
435 440 445

Ser Gly Arg Arg Val Ser Gly Asn Leu Glu Gly Gly Leu Gly Glu Pro
450 455 460

Leu Leu Ile Asp Ala Lys Ala Gly Gln Asp Glu Asp Asp Glu Asp Asn
465 470 475 480

Asp Asp Pro Glu Glu Ser His Thr Pro Ala Thr Ser Leu Ala Ala Ala

485 490 495

Tyr Arg Leu Leu Thr Pro Ser Val Lys Val Gln Leu Leu Ile Tyr Phe
500 505 510

Met Leu Lys Phe Ala Met Glu Ile Leu Leu Ser Glu Ser Ser Val Val
515 520 525

Thr Thr Phe Tyr Phe Lys Trp Thr Thr Ser Thr Val Ala Ile Phe Leu
530 535 540

Ala Val Leu Gly Leu Thr Val Leu Pro Val Asn Val Ile Val Gly Ser
545 550 555 560

Tyr Val Thr Asn Leu Phe Gln Asp Arg Gln Ile Leu Val Ala Ser Glu
565 570 575

Ile Met Val Leu Ile Gly Ile Val Met Ser Phe Cys Phe Thr Pro His
580 585 590

Tyr Ser Val Pro Gln Tyr Val Thr Ser Ala Leu Ile Thr Phe Val Phe
595 600 605

Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu Ser Arg Val Met
610 615 620

Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Val Gly Leu Leu Ser Thr
625 630 635 640

Glu Ala Gly Thr Leu Ala Arg Val Ala Ala Asp Met Thr Ile Thr Ala
645 650 655

Ala Gly Tyr Leu Gly Gln Gly Arg Leu Leu Asn Ala Thr Leu Leu Pro
660 665 670

Ser Leu Val Ile Cys Leu Ala Ser Ile Val Ala Thr Phe Cys Thr Tyr
675 680 685

Asn Ser Leu Tyr
690

<210> 879
<211> 697
<212> PRT
<213> Oryza sativa Japonica Group

<400> 879

Met Val Asn Phe Gly Lys Arg Leu Met Ala Asp Gln Leu Glu Glu Trp
1 5 10 15

Lys Glu Tyr Tyr Ile Asn Tyr Lys Met Met Lys Lys Lys Val Lys Gln
20 25 30

Tyr Val Gln Gln Thr Gln Asn Gly Gly Arg Asn Arg Glu Gln Val Leu
35 40 45

Lys Glu Phe Ser Arg Met Leu Asp Asp Gln Ile Glu Lys Ile Val Leu
50 55 60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Ser Arg Ile Glu Lys Leu
65 70 75 80

Gly Glu Glu Arg Ala Leu Leu Met Glu Gln Ala Asp Ala Ser Gln Ile
85 90 95

Ser Glu Leu Arg Glu Ala Tyr Arg Glu Val Gly Ile Asp Leu Met Lys
100 105 110

Leu Leu Arg Phe Val Asp Met Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Lys Phe Thr Asp Tyr Tyr Val
130 135 140

Ser Thr Arg Ala Asn His Pro Cys Ser Gln Leu Gln Gln Ile Phe Lys
145 150 155 160

Gln Val Gly Ile Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ala
165 170 175

Phe Leu Gln Asp His Gln Gly Asn Phe Pro Ser Ile Tyr Asp His Pro
180 185 190

Ser Ile Thr Leu Lys Asp Pro Ile Ile Glu Gln Ile Asn His Ser Val
195 200 205

Gln Lys Leu Thr His Ala Thr Asn Leu Leu Gln Phe Ile Gly Gln His
210 215 220

Ala Leu Ile Ile Pro Glu Asp Met His Ser Gly Ser Glu Asp Leu Val
225 230 235 240

Asp Asp Gln Ser Tyr His Phe Met Ser Leu Leu Leu Asn Leu Ala Asn
245 250 255

Thr Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp
260 265 270

Asp Tyr Ser Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile
275 280 285

Ile Gly Ser Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser
290 295 300

Ala Trp Ser Asn Lys Ser Tyr Phe Arg Pro Leu Val Phe Ser Ser Ile
305 310 315 320

Met Leu Phe Leu Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Val Asn
325 330 335

Ser Leu Thr Val Leu Ile Val Gly Arg Leu Leu Cys Gly Leu Gly Ser
340 345 350

Ala Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys
355 360 365

Thr Arg Leu Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly
370 375 380

Met Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Asn Phe Lys
385 390 395 400

Ile Tyr Gly Phe Thr Phe Asp Gln Asn Thr Leu Pro Gly Trp Ile Met
405 410 415

Cys Leu Ala Trp Ile Thr Tyr Leu Phe Trp Leu Trp Ile Ser Phe Lys
420 425 430

Glu Pro Asp His Ile Val Arg Glu Asn Ser Val Asn Thr Pro Ser Ser
435 440 445

Asp Ser Gly His Arg Arg Asn Ser Asn Leu Glu Asp Gly Leu Ala Gln
450 455 460

Pro Phe Leu Ile Asp Ala Lys Glu Ser Leu Asp Glu Asn Gly Glu Asp
465 470 475 480

Asn Asp Glu Asn Glu Glu Asp Pro Glu Asp Ser His Lys Pro Ala Thr
485 490 495

Ser Leu Ala Ala Ala Tyr Arg Leu Leu Thr Pro Ser Val Lys Val Gln
500 505 510

Leu Leu Ile Tyr Phe Met Leu Lys Phe Ala Met Glu Ile Leu Leu Ser
515 520 525

Glu Ser Ser Val Val Thr Thr Phe Tyr Phe Asn Trp Ser Thr Ser Thr
530 535 540

Val Ala Met Phe Leu Ala Val Leu Gly Leu Thr Val Leu Pro Val Asn
545 550 555 560

Val Ile Val Gly Ser Tyr Val Thr Asn Leu Phe Gln Asp Arg Gln Ile
565 570 575

Leu Val Ala Ser Glu Ile Met Val Leu Ile Gly Ile Ala Met Ser Phe
580 585 590

Arg Phe Thr Ser His Tyr Ser Val Pro Gln Tyr Val Ser Ser Ala Leu
595 600 605

Ile Thr Phe Val Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu
610 615 620

Leu Ser Arg Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly
625 630 635 640

Gly Leu Leu Ser Thr Glu Ala Gly Thr Leu Ala Arg Val Ala Ala Asp
645 650 655

Met Thr Ile Thr Ala Ala Gly Tyr Leu Gly Gln Asn Ser Leu Leu Asn
660 665 670

Val Thr Leu Leu Pro Ser Phe Val Ile Cys Val Ala Ser Ile Val Ala
675 680 685

Thr Phe Cys Thr Tyr Asn Ser Leu Tyr
690 695

<210> 880
<211> 697
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 880

Met Val Asn Phe Gly Lys Val Leu Val Ser Asp Gln Leu Glu Glu Trp
1 5 10 15

Lys Glu Tyr Tyr Ile Asn Tyr Lys Met Met Lys Lys Lys Val Lys Gln

20 25 30

Tyr Val Gln Gln Thr Gln Ser Gly Gly Arg Asn His Glu Gln Val Leu
35 40 45

Lys Glu Phe Ser Arg Met Leu Asp Glu Gln Ile Glu Lys Val Val Leu
50 55 60

Phe Leu Leu Lys Gln Gln Gly His Leu Ala Ser Arg Ile Glu Lys Leu
65 70 75 80

Gly Gln Gln Arg Ala Ile Leu Thr Glu His Cys Asp Ile Ser Gln Val
85 90 95

Ser Gln Val Arg Glu Ala Tyr Arg Gln Val Gly Leu Asp Leu Val Lys
100 105 110

Leu Leu Arg Phe Val Asp Met Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Arg Phe Thr Asp Tyr Tyr Val
130 135 140

Ser Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Pro Ile Phe Lys
145 150 155 160

Gln Val Gly Ile Val Ala Val Ala Gly Ala Leu Thr Arg Asn Leu Ala
165 170 175

Ser Leu Gln Asp His Gln Gly Ser Phe Ile Ser Ile Tyr Asp His Pro
180 185 190

Ser Ile Thr Leu Lys Asp Pro Val Ile Glu Gln Ile Asn Asn Ser Val
195 200 205

Gln Lys Leu Thr Asn Ser Thr Thr Phe Leu Lys Phe Leu Gly Gln His
210 215 220

Ala Leu Ile Val Pro Glu Asp Val Gln Thr Ser Ser Glu Asp Leu Val
225 230 235 240

Asp Asp Gln Ser Tyr His Phe Met Ser Leu Met Leu Asn Leu Val Asn
245 250 255

Thr Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp
260 265 270

Asp Tyr Ser Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile
275 280 285

Ile Gly Ser Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser
290 295 300

Ala Trp Ser Asn Lys Ser Tyr Phe Arg Pro Leu Val Phe Ser Ser Ile
305 310 315 320

Met Leu Phe Ser Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn
325 330 335

Ser Leu Thr Val Leu Ile Val Gly Arg Leu Leu Cys Gly Leu Gly Ser
340 345 350

Ala Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys
355 360 365

Ile Arg Leu Lys Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly
370 375 380

Met Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Glu Phe Lys
385 390 395 400

Ile Tyr Glu Val Thr Phe Asn Gln Asn Thr Leu Pro Gly Trp Ile Met
405 410 415

Cys Phe Ala Trp Val Ala Asn Leu Val Trp Leu Trp Ile Ser Phe Lys

420 425 430

Glu Pro Asp His Phe Ala Gln Glu Asn Ala Leu Ser Thr Gln Ser Ser
435 440 445

Glu Ser Gly His Gly Arg Ser Asp Asn Leu Glu Ser Gly Leu Ala Gln
450 455 460

Pro Leu Leu Thr Glu Ala Lys Glu Arg Arg Asn Glu Asn Ala Glu Asp
465 470 475 480

Asn Gly Asp Asn Glu Glu Gly Arg Lys Glu Ser His Lys Pro Ala Thr
485 490 495

Ser Ile Ala Ala Ala Tyr Arg Leu Leu Thr Pro Ser Val Lys Val Gln
500 505 510

Leu Leu Ile Tyr Phe Met Leu Lys Phe Ala Met Glu Ile Leu Leu Ser
515 520 525

Glu Ser Ser Val Val Thr Thr Phe Tyr Phe Asn Trp Ser Thr Ser Thr
530 535 540

Val Ala Ile Phe Leu Ala Val Leu Gly Leu Thr Val Leu Pro Val Asn
545 550 555 560

Val Ile Val Gly Ser Tyr Ile Thr Asn Leu Phe Gln Asp Arg Gln Ile
565 570 575

Leu Val Ala Ser Glu Ile Met Val Leu Ile Gly Ile Ala Ser Ser Phe
580 585 590

His Phe Ser Ser Ser Tyr Cys Val Ala Gln Tyr Val Val Ser Ala Leu
595 600 605

Ile Thr Phe Val Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu
610 615 620

Leu Ser Arg Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly
625 630 635 640

Gly Leu Leu Ser Thr Glu Ala Gly Thr Leu Ala Arg Val Ala Ala Asp
645 650 655

Met Thr Ile Thr Ala Ala Gly Tyr Leu Gly Gln Ser Gln Leu Leu Asn
660 665 670

Ala Thr Leu Leu Pro Ser Leu Val Ile Cys Val Ala Ser Ile Ala Ala
675 680 685

Thr Phe Gly Thr Tyr Asn Thr Leu Tyr
690 695

<210> 881
<211> 725
<212> PRT
<213> Oryza sativa Japonica Group

<400> 881

Met Gly Ile Val Gly Asn Val Thr Val Arg Lys Ser Ser Lys Lys Leu
1 5 10 15

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

Phe Gly Lys Lys Leu Met Ala Asp Gln Val Glu Glu Trp Lys Gly Tyr
35 40 45

Tyr Ile Asn Tyr Lys Leu Met Lys Lys Met Leu Lys Gln Tyr Val Gln
50 55 60

Gln Thr Gln Leu Gly Gly Lys Asp Arg Glu Gln Val Leu Lys Glu Phe
65 70 75 80

Ser Arg Ile Leu Asp Glu Gln Ile Glu Arg Ile Val Leu Phe Leu Leu
85 90 95

Gln Gln Gln Gly His Leu Ala Asn Arg Ile Glu Glu Leu Gly Glu Gln
100 105 110

Arg Ala Ala Leu Leu Glu Gln His Asp Ile Ser Gln Val Phe Gln Leu
115 120 125

Arg Glu Ala Tyr Arg Glu Val Gly Arg Asp Leu Ile Lys Leu Leu Arg
130 135 140

Phe Val Asp Met Asn Ala Thr Gly Ile Arg Lys Ile Leu Lys Lys Phe
145 150 155 160

Asp Lys Arg Phe Gly Tyr Arg Phe Thr Asp Tyr Tyr Val Thr Thr Arg
165 170 175

Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Val Phe Lys Gln Val Gly
180 185 190

Ile Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ala Tyr Leu Gln
195 200 205

Asp His Glu Gly Ser Val Leu Ser Ile Tyr Asp His Pro Ser Val Thr
210 215 220

Leu Lys Asp Pro Ile Ile Asp Gln Val Asn His Ala Val Gln Lys Leu
225 230 235 240

Thr His Ala Thr Ser Phe Leu Gln Phe Leu Gly Gln His Ala Leu Ile
245 250 255

Ile Gln Glu Asp Val Gln Ser Gly Ser Glu Asp Leu Val Asp Asp Gln
260 265 270

Ser Tyr His Phe Met Ser Leu Ile Leu Asn Leu Val Asn Thr Phe Leu
275 280 285

Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp Asp Tyr Ala
    290   295   300

Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile Ile Gly Ser
305   310   315   320

Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser Ala Trp Ser
                325   330   335

Asn Arg Ser Tyr Phe Arg Pro Leu Val Phe Ser Ser Ile Met Leu Phe
            340   345   350

Ala Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn Ser Leu Thr
        355   360   365

Val Leu Leu Ile Gly Arg Leu Leu Cys Gly Leu Gly Ser Ala Arg Ala
    370   375   380

Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys Ile Arg Leu
385   390   395   400

Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly Met Ala Cys
                405   410   415

Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Arg Phe Lys Ile Tyr Ser
            420   425   430

Leu Thr Phe Asp Gln Ser Thr Leu Pro Gly Trp Val Met Cys Ile Ala
        435   440   445

Trp Leu Val Tyr Leu Leu Trp Leu Trp Ile Ser Phe Lys Glu Pro Gly
    450   455   460

His Phe Ala Lys Ser Ser Asp Thr Ala Gln Pro Ala Glu Ser Gly His
465   470   475   480

Gln Val Asn Ala Asn Leu Glu Glu Gly Leu Ala Gln Pro Leu Leu Thr
                485   490   495

Gly Ser Glu Glu Gly Gln Asp Gln Asn Ala Glu Asp Asn Asp Asp Asn
500 505 510

Glu Glu Glu Ser Lys Asn Ser His Gly Pro Ala Thr Ser Ile Ser Ser
515 520 525

Ala Tyr Lys Leu Leu Thr Pro Ser Val Lys Val Gln Leu Leu Ile Tyr
530 535 540

Phe Met Leu Lys Tyr Ala Met Glu Ile Leu Leu Ser Glu Ser Ser Val
545 550 555 560

Ile Thr Thr Tyr Tyr Phe Asn Trp Ser Thr Ser Ala Val Ala Ile Phe
565 570 575

Leu Ala Ile Leu Gly Cys Thr Val Leu Pro Val Asn Ala Ile Val Gly
580 585 590

Ser Tyr Ile Thr Asn Leu Phe Glu Asp Arg Gln Ile Leu Val Ala Ser
595 600 605

Glu Ile Met Val Leu Ile Gly Ile Ile Met Ser Phe Arg Tyr Thr Pro
610 615 620

His Tyr Ser Val Pro Gln Tyr Val Leu Ser Ala Leu Ile Thr Phe Val
625 630 635 640

Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu Ser Arg Val
645 650 655

Met Ser Ser Arg Leu Ala Arg Gly Thr Tyr Asn Gly Gly Leu Leu Ser
660 665 670

Thr Glu Ala Gly Thr Leu Ala Arg Val Val Ala Asp Ala Thr Ile Thr
675 680 685

Ala Ala Gly Tyr Leu Gly Pro Asp Leu Leu Leu Asn Ile Thr Leu Leu
690 695 700

Pro Pro Leu Val Ile Cys Ile Ala Ser Leu Val Ala Thr Phe Cys Thr
705 710 715 720

Tyr Asn Thr Leu Tyr
725

<210> 882
<211> 696
<212> PRT
<213> Oryza sativa Japonica Group

<400> 882

Met Val Asn Phe Gly Lys Lys Leu Met Ala Asp Gln Val Glu Glu Trp
1 5 10 15

Lys Gly Tyr Tyr Ile Asn Tyr Lys Leu Met Lys Lys Met Leu Lys Gln
20 25 30

Tyr Val Gln Gln Thr Gln Leu Gly Gly Lys Asp Arg Glu Gln Val Leu
35 40 45

Lys Glu Phe Ser Arg Ile Leu Asp Glu Gln Ile Glu Arg Ile Val Leu
50 55 60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Asn Arg Ile Glu Glu Leu
65 70 75 80

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

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

Leu Leu Arg Phe Val Asp Met Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Arg Phe Thr Asp Tyr Tyr Val
130 135 140

Thr Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Val Phe Lys
145 150 155 160

Gln Val Gly Ile Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ala
165 170 175

Tyr Leu Gln Asp His Glu Gly Ser Val Leu Ser Ile Tyr Asp His Pro
180 185 190

Ser Val Thr Leu Lys Asp Pro Ile Ile Asp Gln Val Asn His Ala Val
195 200 205

Gln Lys Leu Thr His Ala Thr Ser Phe Leu Gln Phe Leu Gly Gln His
210 215 220

Ala Leu Ile Ile Gln Glu Asp Val Gln Ser Gly Ser Glu Asp Leu Val
225 230 235 240

Asp Asp Gln Ser Tyr His Phe Met Ser Leu Ile Leu Asn Leu Val Asn
245 250 255

Thr Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp
260 265 270

Asp Tyr Ala Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile
275 280 285

Ile Gly Ser Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser
290 295 300

Ala Trp Ser Asn Arg Ser Tyr Phe Arg Pro Leu Val Phe Ser Ser Ile
305 310 315 320

Met Leu Phe Ala Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn

325 330 335

Ser Leu Thr Val Leu Leu Ile Gly Arg Leu Leu Cys Gly Leu Gly Ser
340 345 350

Ala Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys
355 360 365

Ile Arg Leu Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly
370 375 380

Met Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Arg Phe Lys
385 390 395 400

Ile Tyr Ser Leu Thr Phe Asp Gln Ser Thr Leu Pro Gly Trp Val Met
405 410 415

Cys Ile Ala Trp Leu Val Tyr Leu Leu Trp Leu Trp Ile Ser Phe Lys
420 425 430

Glu Pro Gly His Phe Ala Lys Ser Ser Asp Thr Ala Gln Pro Ala Glu
435 440 445

Ser Gly His Gln Val Asn Ala Asn Leu Glu Glu Gly Leu Ala Gln Pro
450 455 460

Leu Leu Thr Gly Ser Glu Glu Gly Gln Asp Gln Asn Ala Glu Asp Asn
465 470 475 480

Asp Asp Asn Glu Glu Glu Ser Lys Asn Ser His Gly Pro Ala Thr Ser
485 490 495

Ile Ser Ser Ala Tyr Lys Leu Leu Thr Pro Ser Val Lys Val Gln Leu
500 505 510

Leu Ile Tyr Phe Met Leu Lys Tyr Ala Met Glu Ile Leu Leu Ser Glu
515 520 525

Ser Ser Val Ile Thr Thr Tyr Tyr Phe Asn Trp Ser Thr Ser Ala Val
530 535 540

Ala Ile Phe Leu Ala Ile Leu Gly Cys Thr Val Leu Pro Val Asn Ala
545 550 555 560

Ile Val Gly Ser Tyr Ile Thr Asn Leu Phe Glu Asp Arg Gln Ile Leu
565 570 575

Val Ala Ser Glu Ile Met Val Leu Ile Gly Ile Ile Met Ser Phe Arg
580 585 590

Tyr Thr Pro His Tyr Ser Val Pro Gln Tyr Val Leu Ser Ala Leu Ile
595 600 605

Thr Phe Val Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu
610 615 620

Ser Arg Val Met Ser Ser Arg Leu Ala Arg Gly Thr Tyr Asn Gly Gly
625 630 635 640

Leu Leu Ser Thr Glu Ala Gly Thr Leu Ala Arg Val Val Ala Asp Ala
645 650 655

Thr Ile Thr Ala Ala Gly Tyr Leu Gly Pro Asp Leu Leu Leu Asn Ile
660 665 670

Thr Leu Leu Pro Pro Leu Val Ile Cys Ile Ala Ser Leu Val Ala Thr
675 680 685

Phe Cys Thr Tyr Asn Thr Leu Tyr
690 695

<210> 883
<211> 696
<212> PRT
<213> Oryza sativa Indica Group

<400> 883

Met Val Asn Phe Gly Lys Lys Leu Met Ala Asp Gln Val Glu Glu Trp
1   5   10   15

Lys Gly Tyr Tyr Ile Asn Tyr Lys Leu Met Lys Lys Met Leu Lys Gln
            20   25   30

Tyr Val Gln Gln Thr Gln Leu Gly Gly Lys Asp Arg Glu Gln Val Leu
        35   40   45

Lys Glu Phe Ser Arg Ile Leu Asp Glu Gln Ile Glu Arg Ile Val Leu
    50   55   60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Asn Arg Ile Glu Glu Leu
65   70   75   80

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

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

Leu Leu Arg Phe Val Asp Met Asn Ala Thr Gly Ile Arg Lys Ile Leu
        115   120   125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Arg Phe Thr Asp Tyr Tyr Val
    130   135   140

Thr Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Val Phe Lys
145   150   155   160

Gln Val Gly Ile Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Ala
                165   170   175

Tyr Leu Gln Asp His Glu Gly Ser Val Leu Ser Ile Tyr Asp His Pro
            180   185   190

Ser Val Thr Leu Lys Asp Pro Ile Ile Asp Gln Val Asn His Ala Val
195 200 205

Gln Lys Leu Thr His Ala Thr Ser Phe Leu Gln Phe Leu Gly Gln His
210 215 220

Ala Leu Ile Ile Gln Glu Asp Val Gln Ser Gly Ser Glu Asp Leu Val
225 230 235 240

Asp Asp Gln Ser Tyr His Phe Met Ser Leu Ile Leu Asn Leu Val Asn
245 250 255

Thr Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp
260 265 270

Asp Tyr Ala Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile
275 280 285

Ile Gly Ser Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser
290 295 300

Ala Trp Ser Asn Arg Ser Tyr Phe Arg Pro Leu Val Phe Ser Ser Ile
305 310 315 320

Met Leu Phe Ala Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn
325 330 335

Ser Leu Thr Val Leu Leu Ile Gly Arg Leu Leu Cys Gly Leu Gly Ser
340 345 350

Ala Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys
355 360 365

Ile Arg Leu Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly
370 375 380

Met Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Thr Arg Phe Lys
385 390 395 400

Ile Tyr Ser Leu Thr Phe Asp Gln Ser Thr Leu Pro Val Trp Val Met
405 410 415

Cys Ile Ala Trp Leu Val Tyr Leu Leu Trp Leu Trp Ile Ser Phe Thr
420 425 430

Glu Pro Gly His Phe Ala Lys Ser Ser Asp Thr Ala Gln Pro Ala Glu
435 440 445

Ser Gly His Gln Val Asn Ala Asn Leu Glu Glu Gly Leu Ala Gln Pro
450 455 460

Leu Leu Thr Gly Ser Glu Glu Gly Gln Asp Gln Asn Ala Glu Asp Asn
465 470 475 480

Asp Asp Asn Glu Glu Glu Ser Lys Asn Ser His Gly Pro Ala Thr Ser
485 490 495

Ile Ser Ser Ala Tyr Lys Leu Leu Thr Pro Ser Val Lys Val Gln Leu
500 505 510

Leu Ile Tyr Phe Met Leu Lys Tyr Ala Met Glu Ile Leu Leu Ser Glu
515 520 525

Ser Ser Val Ile Thr Thr Tyr Tyr Phe Asn Trp Ser Thr Ser Ala Val
530 535 540

Ala Ile Phe Leu Ala Ile Leu Gly Cys Thr Val Leu Pro Val Asn Ala
545 550 555 560

Ile Val Gly Ser Tyr Ile Thr Asn Leu Phe Glu Asp Arg Gln Ile Leu
565 570 575

Val Ala Ser Glu Ile Met Val Leu Ile Gly Ile Ile Met Ser Phe Arg
580 585 590

Tyr Thr Pro His Tyr Ser Val Pro Gln Tyr Val Leu Ser Ala Leu Ile
595 600 605

Thr Phe Val Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu
610 615 620

Ser Arg Val Met Ser Ser Arg Leu Ala Arg Gly Thr Tyr Asn Gly Gly
625 630 635 640

Leu Leu Ser Thr Glu Ala Gly Thr Leu Ala Arg Val Val Ala Asp Ala
645 650 655

Thr Ile Thr Ala Ala Gly Tyr Leu Gly Pro Asp Leu Leu Leu Asn Ile
660 665 670

Thr Leu Leu Pro Pro Leu Val Ile Cys Ile Ala Ser Leu Val Ala Thr
675 680 685

Phe Cys Thr Tyr Asn Thr Leu Tyr
690 695

<210> 884
<211> 696
<212> PRT
<213> Sorghum bicolor

<400> 884

Met Val Asn Phe Gly Lys Lys Leu Met Ala Asp Gln Val Glu Glu Trp
1 5 10 15

Lys Gly Tyr Tyr Ile Asn Tyr Lys Leu Met Lys Lys Met Leu Lys Gln
20 25 30

Tyr Val Gln Gln Thr Gln His Gly Gly Lys Asp Arg Glu Gln Val Leu
35 40 45

Lys Asp Phe Ser Arg Ile Leu Asp Asp Gln Ile Glu Arg Ile Val Leu
50 55 60

Phe Leu Leu Gln Gln Gln Gly His Leu Ala Ser Arg Ile Glu Glu Leu
65 70 75 80

Gly Glu Lys Arg Ile Val Leu Leu Glu Glu Tyr Asp Ile Ser Gln Val
85 90 95

Tyr Gln Leu His Asp Ala Tyr Arg Glu Val Gly Leu Asp Leu Ile Lys
100 105 110

Leu Leu Arg Phe Val Asp Val Asn Ala Thr Gly Ile Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Lys Phe Thr Asp Tyr Tyr Val
130 135 140

Thr Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Val Phe Lys
145 150 155 160

Gln Val Gly Ile Val Ala Val Val Gly Ala Leu Ser Arg Asn Leu Glu
165 170 175

Tyr Leu Gln His His Glu Gly Ser Phe Val Ser Ile Tyr Asp Arg Pro
180 185 190

Ala Val Thr Leu Lys Asp Pro Ile Ile Asp Gln Val Asn Asn Ala Val
195 200 205

Gln Lys Leu Thr His Ala Thr Asn Phe Met Gln Phe Leu Gly Gln His
210 215 220

Ser Leu Ile Val Gln Glu Asp Ala Gln Ser Gly Ser Glu Asp Leu Val
225 230 235 240

Asp Asp Gln Ser Tyr His Phe Met Ser Leu Met Leu Asn Leu Val Asn
245 250 255

Thr Phe Leu Tyr Met Val Asn Thr Tyr Ile Ile Val Pro Thr Ala Asp

260 265 270

Asp Tyr Ala Val Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Ile
275 280 285

Ile Gly Ser Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser
290 295 300

Ala Trp Ser Asn Lys Ser Tyr Phe Lys Pro Leu Val Phe Ser Ser Ile
305 310 315 320

Met Leu Phe Leu Gly Asn Leu Leu Tyr Ala Leu Ala Tyr Asp Leu Asn
325 330 335

Ser Leu Ile Val Leu Leu Ile Gly Arg Leu Leu Cys Gly Leu Gly Ser
340 345 350

Ala Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys
355 360 365

Met Arg Leu Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly
370 375 380

Met Ala Cys Gly Pro Ala Leu Ala Gly Phe Leu Gln Ile Lys Phe Lys
385 390 395 400

Ile Tyr Ser Leu Thr Phe Asn Gln Ser Thr Leu Pro Gly Trp Val Met
405 410 415

Cys Ile Ala Trp Phe Ile Tyr Leu Leu Trp Leu Trp Leu Thr Phe Lys
420 425 430

Glu Pro Glu His Phe Thr Lys Thr Leu Val Ser Glu Gln Pro Ser Glu
435 440 445

Ser Gly Cys Gln Gly Asn Ser Asn Leu Glu Glu Gly Leu Ala Gln Pro
450 455 460

Leu Leu Val Gly Ile Glu Gln Arg Gln Glu Glu Asn Ser Glu Asp Asn
465 470 475 480

Asp Asp Thr Glu Leu Ala Ser Glu Ser Ser His Glu Pro Ala Thr Ser
485 490 495

Ile Ala Ser Ala Tyr Arg Leu Leu Thr Pro Ser Val Lys Ala Gln Leu
500 505 510

Leu Ile Tyr Phe Met Leu Lys Tyr Ala Met Glu Ile Leu Leu Ser Glu
515 520 525

Ser Ser Val Val Thr Thr Tyr Tyr Phe Ser Trp Thr Thr Ser Val Val
530 535 540

Ala Ile Phe Leu Ala Ile Leu Gly Leu Thr Val Leu Pro Val Asn Ala
545 550 555 560

Ile Val Gly Ser Tyr Ile Thr Asn Leu Phe Glu Asp Arg Gln Ile Leu
565 570 575

Leu Ala Ser Glu Val Met Val Leu Ile Gly Ile Ile Met Ser Phe Arg
580 585 590

Phe Thr Pro His Tyr Ser Ile Pro Gln Tyr Val Ile Ser Ala Leu Ile
595 600 605

Thr Phe Val Phe Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu
610 615 620

Ser Arg Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly Gly
625 630 635 640

Leu Leu Ser Thr Glu Ala Gly Thr Leu Ala Arg Val Val Ala Asp Ala
645 650 655

Thr Ile Thr Ala Ala Gly Tyr Leu Gly Thr Asp Leu Leu Leu Asn Ile

660 665 670

Thr Leu Val Pro Ser Leu Val Ile Cys Ile Val Ser Ile Ala Ala Thr
675 680 685

Leu Tyr Thr Tyr Asn Asn Leu Tyr
690 695

<210> 885
<211> 698
<212> PRT
<213> Vitis vinifera

<400> 885

Met Val Ala Phe Gly Lys Lys Leu Lys Glu Arg Gln Ile Gln Glu Trp
1 5 10 15

Gln Gly Tyr Tyr Ile Asn Tyr Lys Leu Met Lys Lys Lys Val Lys Gln
20 25 30

Tyr Val Gln Gln Ile Glu Gly Gly Ala Gln Asn Arg Arg His Val Leu
35 40 45

Lys Asp Phe Ser Arg Met Leu Asp Thr Gln Ile Glu Lys Ile Val Leu
50 55 60

Phe Leu Leu Glu Gln Gln Gly Leu Leu Ala Ser Arg Ile Ala Lys Leu
65 70 75 80

Gly Glu Gln His Asp Ala Leu Gln Gln Gln Pro Asp Ile Ser Gln Ile
85 90 95

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

Leu Leu Phe Phe Val Glu Ile Asn Ala Ile Gly Leu Arg Lys Ile Leu
115 120 125

Lys Lys Phe Asp Lys Arg Phe Gly Tyr Arg Phe Thr Asp Tyr Tyr Val
130 135 140

Lys Thr Arg Ala Asn His Pro Tyr Ser Gln Leu Gln Gln Val Phe Lys
145 150 155 160

His Val Gly Val Gly Ala Val Val Gly Ala Ile Ser Arg Asn Leu Gly
165 170 175

Asp Leu Gln Asp Arg Gln Gly Ser Tyr Leu Ser Ile Tyr Asp Gln Pro
180 185 190

Ala Leu Pro Leu Gln Asp Pro Val Ile Asp Ser Ile Lys Ala Ala Val
195 200 205

Asp Arg Leu Thr His Ser Thr Asn Phe Leu His Phe Leu Ala Gln His
210 215 220

Ala Leu Ile Met Gln Glu Glu Leu Pro Thr Ala Val Glu Glu His Val
225 230 235 240

Asp Asp Gln Arg Tyr His Phe Met Ser Leu Leu Leu Asn Leu Ala Asn
245 250 255

Thr Phe Leu Tyr Met Val Asn Thr Tyr Ile Val Val Pro Thr Ala Asp
260 265 270

Asn Tyr Ser Met Ser Leu Gly Ala Ala Ala Thr Val Cys Gly Val Val
275 280 285

Ile Gly Ala Met Ala Val Ala Gln Val Phe Ser Ser Val Tyr Phe Ser
290 295 300

Ala Trp Ser Asn Lys Ser Tyr Tyr Arg Pro Leu Ile Phe Ser Ser Ile
305 310 315 320

Val Leu Phe Val Gly Asn Thr Met Tyr Ala Leu Ala Tyr Asp Leu Asp
325 330 335

Ser Ile Val Val Leu Leu Leu Gly Arg Leu Phe Cys Gly Leu Gly Ser
340 345 350

Ala Arg Ala Val Asn Arg Arg Tyr Ile Ser Asp Cys Val Pro Leu Lys
355 360 365

Ile Arg Met Gln Ala Ser Ala Gly Phe Val Ser Ala Ser Ala Leu Gly
370 375 380

Met Ala Cys Gly Pro Ala Leu Ala Gly Leu Leu Gln Ile Asn Phe Lys
385 390 395 400

Ile Tyr Lys Ile Thr Phe Asn Glu Asp Thr Leu Pro Gly Trp Val Met
405 410 415

Ala Val Ala Trp Leu Val Tyr Leu Ile Trp Leu Trp Ile Ser Phe Lys
420 425 430

Glu Pro Val Arg Glu Thr Gln Glu Ser Asn Ile Gln Gln Glu Ser Asn
435 440 445

Ala Glu Pro Val Glu Asn Asp Ala Leu Glu Lys Gly Leu Ala Gln Pro
450 455 460

Leu Leu Leu Ser Ser Glu Asp Lys Gln Glu Asp Glu Asp Gly Asp Gln
465 470 475 480

Asp Asn Asp Val Ser Glu Glu Ala Pro Glu Glu Ser Arg Gly Pro Ala
485 490 495

Thr Ser Ile Gly Ser Ala Tyr Arg Leu Leu Thr Pro Ser Val Lys Val
500 505 510

Gln Leu Leu Ile Tyr Phe Met Leu Lys Tyr Ala Met Glu Ile Leu Leu
515 520 525

Ser Glu Ser Ser Val Val Thr Thr Tyr Tyr Phe Asn Trp Ser Thr Ser
530 535 540

Thr Val Ala Ile Phe Leu Ala Cys Leu Gly Leu Thr Val Leu Pro Val
545 550 555 560

Asn Ile Ala Val Gly Ser Tyr Ile Ser Asn Met Phe Glu Asp Arg Gln
565 570 575

Ile Leu Leu Ala Ser Glu Ile Met Val Leu Ile Gly Ile Leu Leu Ser
580 585 590

Phe Asn Ile Ile Ile Pro Tyr Ser Val Pro Gln Tyr Val Cys Ser Gly
595 600 605

Leu Ile Met Phe Val Ser Ala Glu Val Leu Glu Gly Val Asn Leu Ala
610 615 620

Leu Leu Ser Arg Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn
625 630 635 640

Gly Gly Leu Leu Ser Thr Glu Ala Gly Thr Ile Ala Arg Val Ile Ala
645 650 655

Asp Gly Thr Ile Thr Leu Val Gly Tyr Leu Gly Glu Ser Lys Leu Leu
660 665 670

Asn Ile Thr Leu Leu Pro Ser Leu Leu Ile Cys Ile Ser Ser Ile Ile
675 680 685

Ala Thr Phe Phe Thr Tyr Asn Ser Leu Tyr
690 695

<210> 886
<211> 542
<212> PRT
<213> Sorghum bicolor

<400> 886

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

Ala Pro Ala Pro Ala Pro Glu Pro Gln Thr Pro Pro Ala Glu Pro Val
20 25 30

Thr Lys Gly Arg Gly Leu Arg Arg Trp Arg Arg Ile Pro Arg Glu Gln
35 40 45

His His Glu Gly Ser Pro Ala Ser Pro Gly Ala Gly Thr Gly Ala Gly
50 55 60

Ala Thr Ala Gly Glu Asp Leu Ala Ala Gln Leu His Lys Arg Arg Tyr
65 70 75 80

Gly Pro Ala Ala Asp Glu Pro Lys Gly Lys Gln Asp Ala Ala Ala Ala
85 90 95

Glu Glu Val Glu Ser Ser Val Ala Ser Val Glu Ser Ser Phe Val Pro
100 105 110

Leu Glu Ala Ser Pro Pro Pro Ala Pro Ala Pro Ala Leu Thr Arg Leu
115 120 125

Asp Pro Asn Leu Gly His Leu Ile Ala Thr Ala Gly Phe Ser Val Gly
130 135 140

Ala Gly Gly Ala Asp Ser Asp Asn Ser Asp Asp Arg Thr Ser Lys Ser
145 150 155 160

Ser Thr Ala Ala Ser Ala Pro Arg His Asp Phe Ser Ser Val Gly Phe
165 170 175

Gly Arg Glu Arg Asp Arg Ala Arg Ser Arg Ala Pro Gly Ala Ala His
180 185 190

Gly Lys Gly Ile Arg Ala Ala Arg Val Arg Gly Ala Ser Ala Arg Val

195 200 205

Ala Ser Ser Pro Ala Glu Ala Glu Asn Ser Arg Ser Ser Val Glu Ser
210 215 220

Asn Leu Arg Ser Ser Asn Ala Ala His Ala Arg Arg Ser Ser Ser Gly
225 230 235 240

Val Thr Ser Asn Gly Val His Lys Val Leu Phe Pro Asp Gly His Gln
245 250 255

Ser Asp Asp Glu Pro Pro Ser Ala Asp Leu Arg Tyr Ala Thr Gly Gly
260 265 270

Phe Tyr Lys Glu Asn Gly Ser Val Ile Gly Arg Leu Ala Asn Cys Asp
275 280 285

Ser Asp Ser Asn Asn His Ile Phe Asp Glu Ala Ser Ala Gly Lys Phe
290 295 300

Glu Asn Gly Gly Thr His Ser Gly Leu Asp Pro Tyr Ala Glu Ser Val
305 310 315 320

Ala Leu Leu Gln Ser Ala Gln Glu Ala Leu Glu Asn Glu Ile Gln Lys
325 330 335

Phe Val Glu Ile Arg Glu Glu Thr Asp Glu Asp Ser Thr Thr His Gln
340 345 350

Ser Glu Ile Glu Trp Ser Ser Ser Pro Val Glu Glu Leu Asn Glu Lys
355 360 365

Ile Lys Met Leu Glu Ser Lys Leu Glu Glu Ala Thr Met Val Ile Asn
370 375 380

Lys Gln Asp Ser Lys Ile Ile Glu Leu Asp Ala Leu Ser Gln Val Gln
385 390 395 400

Pro Gln Asn Thr Ile Ala Cys Asn Asn Asp Leu Leu Ser Leu Pro Ser
405 410 415

Asp Val Asp Gln Leu Leu Leu Glu Lys Leu Glu Ala Glu Ile Gln Cys
420 425 430

Phe Ile Leu Thr Arg Ala Trp Gln Asp Trp Lys Leu Leu Thr Lys Asp
435 440 445

Gln Phe Ala Leu Asn Glu Thr Gln Lys Ser Leu Leu Ala Asp His Lys
450 455 460

Ser Leu Glu Thr Lys Leu Arg His Ala Glu Asn Arg Ala Met Met Leu
465 470 475 480

Glu Glu Met Val Asp Lys Leu Glu Ser Gln Cys Lys Glu Leu Ser Glu
485 490 495

Thr Ser Glu Val Leu Lys Leu Gln Ala Arg Ala Ser Arg Val Ser Leu
500 505 510

Phe Cys Ser Val Gln Phe Val Leu Leu Cys Leu Ala Met Gly Thr Leu
515 520 525

Leu Val Arg Phe Leu Pro Ser Ser Pro Asp Val Val Pro Thr
530 535 540

<210> 887
<211> 538
<212> PRT
<213> Zea mays

<400> 887

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

Ser Leu Ala Leu Ala Pro Glu Pro Gln Thr Arg Pro Ala Glu Pro Val
20 25 30

Thr Lys Gly Arg Gly Leu Arg Arg Trp Arg Arg Ile Pro Arg Glu Gln
35 40 45

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

Ala Ser Ala Gly Glu Asp Leu Ala Ala Gln Leu His Lys Arg Arg Tyr
65 70 75 80

Gly Pro Ala Ala Asp Glu Pro Lys Gly Lys Gln Asp Pro Ala Ala Ala
85 90 95

Glu Glu Val Glu Ser Ser Val Ala Ser Val Glu Ser Ser Phe Val Pro
100 105 110

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

Gly His Leu Ile Ala Thr Ala Gly Phe Ser Val Gly Ala Gly Gly Ala
130 135 140

Asp Ser Asp Asn Ser Asp Asp Arg Thr Ser Lys Leu Ser Thr Ala Ala
145 150 155 160

Ser Ala Pro Arg His Asp Phe Ser Ser Val Gly Phe Gly Arg Glu Arg
165 170 175

Asp Arg Ala Arg Ser Arg Ala Pro Gly Ala Ala His Gly Lys Gly Ile
180 185 190

Arg Ala Ala Arg Val Arg Gly Ala Thr Met Arg Val Ala Ser Ser Pro
195 200 205

Ala Glu Ala Gly Asn Ser Arg Ser Ser Val Glu Ser Asn Leu Arg Ser
210 215 220

Ser Asn Ala Ala His Ala Arg Arg Ser Ser Ala Gly Val Thr Ser Asn
225   230   235   240

Gly Val His Lys Ile Leu Phe Pro Asp Gly His Gln Ser Asp Asp Glu
                245   250   255

Pro Pro Ser Gly Asp Met Arg Tyr Gly Thr Gly Arg Phe Tyr Lys Glu
            260   265   270

Asn Gly Ser Ile Glu Gly Arg Leu Gly Asn Cys Asp Ser Asp Ser Asn
        275   280   285

His His Thr Phe Asp Glu Ala Ser Val Gly Lys Phe Glu Asn Gly Gly
    290   295   300

Thr His Ser Gly Leu Asp Leu Tyr Gly Glu Ser Met Ala Leu Leu Gln
305   310   315   320

Ser Ala Gln Glu Ala Leu Glu Asn Glu Ile Gln Lys Phe Val Glu Ile
                325   330   335

Arg Lys Glu Thr Asp Glu Asp Ser Thr Ala His Gln Ser Glu Ile Glu
            340   345   350

Trp Ser Ser Ser Pro Val Glu Glu Leu Asn Glu Lys Ile Lys Met Leu
        355   360   365

Glu Leu Lys Leu Glu Glu Ala Thr Met Leu Ile Asn Glu Arg Asp Ser
    370   375   380

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

Val Ala Cys Asn Asn Tyr Pro Leu Ser Leu Gln Ser Asp Val Asp Arg
                405   410   415

Leu Phe Leu Glu Lys Met Glu Ala Glu Ile Gln Cys Phe Ile Leu Thr
            420   425   430

Arg Ala Ser Gln Asp Trp Lys Leu Leu Thr Met Asp Gln Phe Ala Leu
435 440 445

Asn Glu Ala Gln Lys Ser Leu Leu Ser Asp His Lys Ser Leu Glu Thr
450 455 460

Lys Leu Arg His Ala Glu Asn Arg Ala Met Met Leu Glu Glu Met Val
465 470 475 480

Asp Lys Leu Glu Ser Gln Cys Lys Ala Leu Ser Glu Thr Ser Glu Val
485 490 495

Leu Lys Leu Gln Ala Gly Ala Ser Arg Ala Ser Leu Phe Cys Ser Ile
500 505 510

Gln Phe Val Leu Leu Cys Ile Ala Ile Gly Thr Leu Leu Val Arg Phe
515 520 525

Leu Ser Ser Ser Pro Glu Ile Val Pro Thr
530 535

<210> 888
<211> 532
<212> PRT
<213> Zea mays

<400> 888

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

Val Pro Ala Pro Ala Pro Gln Thr Arg Pro Ala Glu Pro Val Thr Lys
20 25 30

Gly Arg Gly Leu Arg Arg Trp Arg Arg Ile Pro Arg Glu Gln His His
35 40 45

Glu Gly Ser Pro Val Ser Pro Gly Leu Gly Asn Ser Ala Gly Ala Ser

50 55 60

Ala Gly Glu Asp Leu Ala Ala Gln Leu His Lys Arg Arg Tyr Gly Pro
65 70 75 80

Ala Asp Asp Lys Pro Lys Gly Lys Gln Asp Ala Ala Ala Glu Glu Val
85 90 95

Glu Ser Ser Val Ala Ser Val Lys Ser Ser Phe Val Pro Leu Glu Val
100 105 110

Ser Pro Pro Pro Pro Pro Thr Leu Thr Arg Leu Asp Pro Asn Leu Gly
115 120 125

His Leu Ile Ala Thr Thr Gly Phe Ser Val Gly Ala Gly Gly Ala Asp
130 135 140

Ser Asp Asn Ser Asp Asp Arg Thr Ser Lys Ser Ser Thr Ala Ala Ser
145 150 155 160

Ala Pro Arg His Asp Phe Ser Ser Val Gly Phe Gly Arg Glu Arg Asp
165 170 175

Arg Ala Arg Ser Arg Ala Pro Ser Ala Ala His Gly Lys Ser Ile Arg
180 185 190

Ala Ala Arg Val Arg Gly Ala Ser Ser Thr Ala Glu Ala Asp His Ser
195 200 205

Arg Ser Ser Val Glu Ser Asn Leu Arg Ser Ser Asn Ala Ala His Ala
210 215 220

Arg Arg Ser Ile Thr Asp Val Thr Ser Asn Gly Val His Lys Val Leu
225 230 235 240

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

Arg Tyr Ala Thr Gly Gly Val Cys Lys Glu Asn Gly Ser Val Val Gly
260 265 270

Ile Leu Gly Asn Cys Asp Thr Gly Ser Asn Asn His Thr Phe Asp Glu
275 280 285

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

Pro Tyr Val Glu Ser Met Ala Leu Leu Gln Ser Ala Gln Glu Ala Leu
305 310 315 320

Glu Asn Glu Ile Gln Lys Phe Val Glu Ile Arg Lys Glu Thr Asp Glu
325 330 335

Asp Ser Thr Ile His Gln Ser Glu Ile Glu Trp Ser Ser Ser Pro Val
340 345 350

Glu Glu Leu Asn Glu Lys Ile Lys Met Leu Glu Trp Lys Leu Glu Glu
355 360 365

Ala Thr Met Leu Ile Lys Glu Arg Asp Ser Lys Ile Leu Glu Leu Asp
370 375 380

Ala Leu Ser Gln Val Gln Pro His Asp Thr Ile Ala Cys Asn Asp Asp
385 390 395 400

Leu Leu Ser Leu Gln Ser Asp Ala Asp Gln Leu Leu Leu Glu Lys Met
405 410 415

Glu Ala Glu Ile Gln Cys Phe Ile Leu Thr Arg Ala Ser His Asp Trp
420 425 430

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

Leu Leu Thr Asp His Lys Ser Leu Glu Thr Lys Leu Arg His Ala Glu

450 455 460

Asn Arg Ala Met Met Leu Glu Asp Met Val Asp Lys Leu Asp Ser Gln
465 470 475 480

Cys Lys Glu Leu Ser Glu Ile Ser Glu Val Leu Lys Leu Gln Ala Arg
485 490 495

Ala Ser Arg Ala Ser Leu Phe Cys Ser Val Gln Phe Ile Leu Leu Cys
500 505 510

Ile Ala Ile Gly Thr Ile Leu Val Arg Phe Leu Pro Pro Ser Pro Glu
515 520 525

Ile Val Pro Thr
530

<210> 889
<211> 532
<212> PRT
<213> Zea mays

<400> 889

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

Val Ala Ala Pro Ala Pro Gln Thr Arg Pro Ala Glu Pro Val Thr Lys
20 25 30

Gly Arg Gly Leu Arg Arg Trp Arg Arg Ile Pro Arg Glu Gln His His
35 40 45

Glu Gly Ser Pro Val Ser Pro Gly Leu Gly Asn Ser Ala Gly Ala Ser
50 55 60

Ala Gly Glu Asp Leu Ala Ala Gln Leu His Lys Arg Arg Tyr Gly Pro
65 70 75 80

Ala Asp Asp Lys Pro Lys Gly Lys Gln Asp Ala Ala Ala Glu Glu Val
85 90 95

Glu Ser Ser Val Ala Ser Val Lys Ser Ser Phe Val Pro Leu Glu Ala
100 105 110

Ser Pro Pro Pro Pro Pro Thr Leu Thr Arg Leu Asp Pro Asn Leu Gly
115 120 125

His Leu Ile Ala Thr Thr Gly Phe Ser Val Gly Ala Gly Gly Ala Asp
130 135 140

Ser Asp Asn Ser Asp Asp Arg Thr Ser Lys Ser Ser Thr Ala Ala Ser
145 150 155 160

Ala Pro Arg His Asp Phe Ser Ser Val Gly Phe Gly Arg Glu Arg Asp
165 170 175

Arg Ala Arg Ser Arg Ala Pro Ser Ala Ala His Gly Lys Ser Ile Arg
180 185 190

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

Arg Ser Ser Val Glu Ser Asn Leu Arg Ser Ser Asn Ala Ala His Ala
210 215 220

Arg Arg Ser Ile Thr Asp Val Thr Ser Asn Gly Val His Lys Val Leu
225 230 235 240

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

Arg Tyr Ala Thr Gly Gly Val Cys Lys Glu Asn Gly Ser Val Val Gly
260 265 270

Ile Leu Gly Asn Cys Asp Thr Gly Ser Asn Asn His Thr Phe Asp Glu
275 280 285

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

Pro Tyr Val Glu Ser Met Ala Leu Leu Gln Ser Ala Gln Glu Ala Leu
305 310 315 320

Glu Asn Glu Ile Gln Lys Phe Val Glu Ile Arg Lys Glu Thr Asp Glu
325 330 335

Asp Ser Thr Ile His Gln Ser Glu Ile Glu Trp Ser Ser Ser Pro Val
340 345 350

Glu Glu Leu Asn Glu Lys Ile Lys Met Leu Glu Trp Lys Leu Glu Glu
355 360 365

Ala Thr Met Leu Ile Lys Glu Arg Asp Ser Lys Ile Leu Glu Leu Asp
370 375 380

Ala Leu Ser Gln Val Gln Pro His Asp Thr Ile Ala Cys Asn Asp Asp
385 390 395 400

Leu Leu Ser Leu Gln Ser Asp Ala Asp Gln Leu Leu Leu Glu Lys Met
405 410 415

Glu Ala Glu Ile Gln Cys Phe Ile Leu Thr Arg Ala Ser His Asp Trp
420 425 430

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

Phe Leu Thr Asp His Lys Ser Leu Glu Thr Lys Leu Arg His Ala Glu
450 455 460

Asn Arg Ala Met Met Leu Glu Asp Met Val Asp Lys Leu Asp Ser Gln
465 470 475 480

Cys Lys Glu Leu Ser Glu Ile Ser Glu Val Leu Lys Leu Gln Ala Arg
485 490 495

Ala Ser Arg Ala Ser Leu Phe Phe Ser Val Gln Phe Val Leu Leu Cys
500 505 510

Ile Ala Ile Gly Thr Ile Leu Val Arg Phe Leu Pro Ser Ser Pro Glu
515 520 525

Ile Val Pro Thr
530

<210> 890
<211> 507
<212> PRT
<213> Zea mays

<400> 890

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

Ile Asn Lys Lys Val Val Thr Arg Trp Arg Pro Leu Lys Leu Val Tyr
20 25 30

Asp His Asp Ile Arg Leu Gly Gln Val Pro Glu Lys Cys Ser Phe Arg
35 40 45

Thr Leu Arg Glu Phe Val Ala Lys Arg Phe Pro Ser Ser Lys Ala Val
50 55 60

Leu Ile Lys Tyr Lys Asp Ala Asp Gly Asp Leu Val Thr Ile Thr Ser
65 70 75 80

Thr Glu Glu Leu Arg Leu Ala Glu Leu Phe Ile Asp Lys Val Gly His
85 90 95

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

Arg Leu His Leu Val Glu Val Ser Pro Glu Gln Glu Pro Thr Leu Pro
115 120 125

Leu Glu Glu Glu Lys Leu Glu Glu Asp Glu Glu Leu Leu Ile Asn Gly
130 135 140

Glu Asp Ser Thr Leu His Ala Leu Ala Val Val Thr Asp Ala Glu Val
145 150 155 160

Val Lys Gln Asp Val Glu Asn Arg Ser Ala Asp Gln Ser Val Glu Thr
165 170 175

Gly Lys Asn Asp Cys Gly His Ala Glu Cys Lys Glu Ala Glu Ile Asp
180 185 190

Asp Trp Leu Leu Gln Phe Ala Asp Leu Phe Arg Asn Gln Val Gly Ile
195 200 205

Asp Ala Asp Ala His Leu Asp Leu His Glu Leu Gly Met Glu Leu Cys
210 215 220

Ser Glu Ala Leu Glu Glu Thr Val Thr Ser Met Glu Ala Gln Val Leu
225 230 235 240

Phe Glu Leu Ala Ala Ser Lys Phe Gln Glu Val Ala Ala Leu Ala Leu
245 250 255

Phe Asn Trp Gly Asn Val His Met Cys Glu Ala Arg Lys Arg Ile Pro
260 265 270

Leu Asp Glu Ser Ala Pro Lys Glu Val Met Ala Ala Gln Leu Arg Thr
275 280 285

Ala Tyr Tyr Trp Val Lys Glu Arg Tyr Ala Leu Ala Gly His Lys Tyr
290 295 300

Glu Glu Ala Leu Lys Ile Lys Pro Asp Phe His Glu Gly Leu Leu Ala

305 310 315 320

Leu Gly Gln Gln His Phe Glu Thr Ala Lys Leu His Trp Ser Tyr Ala
325 330 335

Leu Ala Asp Lys Ala Asp Leu Ser Thr Trp Asp Ser Leu Glu Thr Phe
340 345 350

Lys Leu Phe Asp Ser Ala Glu Gln Asn Met Arg Ala Ala Thr Glu Met
355 360 365

Trp Glu Lys Val Glu Glu Gln Arg Met Ala Glu Leu Lys Glu Pro Gly
370 375 380

Ala Cys Asp Lys Asp Gly Val Leu Arg Lys Arg Gln His Gly Ala Gly
385 390 395 400

Gly Gln Pro Glu Leu Thr Pro Glu Glu Ala Ala Glu Gln Ala Ala Val
405 410 415

Met Arg Gln Gln Ile His Leu Phe Trp Gly Asn Met Leu Phe Glu Arg
420 425 430

Ser Gln Val Glu Phe Lys Leu Ser Val Gly Asp Trp Lys Thr Asn Leu
435 440 445

Asp Ala Ser Val Glu Arg Phe Lys Leu Ala Gly Ala Ser Glu Ser Asp
450 455 460

Ile Leu Thr Val Leu Lys Asn His Phe Ser Asn Val Ala Ser Glu Cys
465 470 475 480

Glu Glu Lys Lys Val Met Thr Ser Gly Thr Glu Ile Ser Gln Thr Asn
485 490 495

Asp Asn Val Glu Asp Lys Cys Val Val Glu Thr
500 505

<210> 891
<211> 544
<212> PRT
<213> Oryza sativa Japonica Group

<400> 891

Met Ser Lys Phe Asn Pro Ser Pro Pro Ser Pro Lys Leu Val Pro Phe
1 5 10 15

Ser Asn Ser Pro Pro Ser Ser Ala Asn Ala Ser Ala Ala Glu Ser Ser
20 25 30

Gln Lys Val Thr Pro Thr Pro Leu Val Pro Ser Ser Leu Ser Leu Lys
35 40 45

Asp Lys Ala Leu Met Asp Lys Lys Val Val Thr Arg Ser Arg Pro Leu
50 55 60

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

Cys Ser Phe Arg Thr Leu Arg Glu Val Val Ala Ser Arg Phe Pro Ser
85 90 95

Ser Lys Ala Val Leu Ile Lys Tyr Lys Asp Ala Asp Gly Asp Leu Val
100 105 110

Thr Ile Thr Cys Ser Ala Glu Leu Arg Leu Ala Glu Ser Cys Val Asp
115 120 125

Ile Ala Gly Ser Glu Val Ile Glu Asp Gly Ala Arg His Gly Gln Lys
130 135 140

Leu Pro Met Leu Arg Leu His Ile Val Glu Val Ser Pro Asp Gln Glu
145 150 155 160

Pro Pro Met Pro Thr Glu Glu Glu Lys Leu Glu Gln Asp Asn Glu Leu
165 170 175

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

Thr Asp Ala Glu Val Thr Lys Gln Asp Val Glu Asn Val Val Ala Glu
195 200 205

Ala Glu Gln Asn Thr Leu Thr Gly Lys Lys Asp Cys Gly His Ala Glu
210 215 220

Cys Lys Glu Ala Glu Ile Asp Asp Trp Leu Leu Gln Phe Ala Asp Leu
225 230 235 240

Phe Arg Asn Gln Val Gly Val Asp Ala Asp Ala His Leu Asp Leu His
245 250 255

Glu Leu Gly Met Glu Leu Cys Ser Glu Ala Leu Glu Glu Thr Val Thr
260 265 270

Ser Glu Glu Ala Gln Ala Leu Phe Glu Met Ala Ala Ala Lys Phe Gln
275 280 285

Glu Val Ala Ala Leu Ala Leu Phe Asn Trp Gly Asn Val His Met Cys
290 295 300

Ala Ala Arg Lys Arg Ile Pro Leu Asp Glu Ser Ala Pro Lys Lys Val
305 310 315 320

Met Ser Ala Gln Leu Cys Thr Ala Tyr Asp Trp Val Arg Asp Arg Tyr
325 330 335

Ala Leu Ala Gly Ser Lys Tyr Glu Glu Ala Leu Lys Ile Lys Pro Asp
340 345 350

Phe Tyr Glu Gly Leu Leu Ala Leu Gly Gln Gln His Phe Glu Thr Ala
355 360 365

Lys Leu His Trp Ser Phe Ala Leu Ala Asp Lys Val Asp Leu Ser Ala
370 375 380

Trp Asp Ser Ser Gln Thr Phe Lys Leu Phe Asp Ser Ala Glu His Lys
385 390 395 400

Met Arg Ala Ala Thr Glu Met Trp Glu Lys Val Glu Glu Gln Arg Met
405 410 415

Ala Glu Leu Lys Glu Pro Ser Ser Glu Ala Leu Lys Lys Arg Lys Lys
420 425 430

Gln His Asn Ala Asp Gly Gln Gly Glu Leu Thr Pro Glu Glu Ala Ala
435 440 445

Glu Gln Ala Ala Val Met Arg Gln Gln Ile His Leu Phe Trp Gly Asn
450 455 460

Met Leu Phe Glu Arg Ser Gln Val Glu Phe Lys Leu Asp Ile Ala Asp
465 470 475 480

Trp Lys Lys Asn Leu Asp Ala Ser Ile Glu Arg Phe Lys Leu Ala Gly
485 490 495

Ala Ser Glu Ser Asp Ile Ser Ala Val Leu Lys Asn His Phe Ser Asn
500 505 510

Thr Val Ser Glu Cys Glu Asp Lys Lys Ile Met Thr Leu Asp Thr Gly
515 520 525

Ile Ser Gln Ile Ser Asn Asn Ile Glu Asp Lys Cys Ile Leu Glu Ser
530 535 540

<210> 892
<211> 325
<212> PRT
<213> Sorghum bicolor

<400> 892

Met Ala Met Val Gln Pro Ala Asp Thr Ala Val Lys Ala Asn Glu Ile
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Leu Ala Arg Phe Arg Pro Ile Ala Pro Lys Pro Thr Leu Ala Thr Ala
20 25 30

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

Ala Ala Asn Arg Val Leu Cys His Leu Gln Ser Arg Pro Cys Arg Ala
50 55 60

Arg Lys Arg Gly Arg Pro Thr Val Val Pro Val Ser Pro Pro Lys Ser
65 70 75 80

Gly Ser Gly Ala Gln Ser Pro Ala Lys Arg Lys Arg Ala Ala Thr Pro
85 90 95

Tyr Pro Pro Leu Arg Cys Ala Ala Ala Thr Ala Cys Ser Ala Ser Ala
100 105 110

Val Val Pro Val Ser Ala Arg Leu Pro Leu Ala Ser Leu Pro Pro Ala
115 120 125

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

Asp Val Pro Val Glu Arg Asp Leu Leu Arg Lys Leu Leu Glu Pro Lys
145 150 155 160

Val Ile Ser Pro Arg Ala Val Arg Pro Val Cys Ser Ala Ile His Val
165 170 175

Gly Cys Ile His Arg Thr Asp Ala Thr Cys Thr Ala Ala Ala Ser Lys
180 185 190

Thr Ala Ala Gln Val Glu Ala Glu Leu Glu Val Asp Ala Leu Pro Ala

195 200 205

Val Val Ser Asp Ser Ser Asn Arg Val Arg Leu Val Asn Asp Ala Tyr
210 215 220

Lys Glu Met Val Gly Gln Pro Glu Cys Pro Trp Leu Tyr Ala Val Ala
225 230 235 240

Ala Thr Ser Arg Arg Ile Ser Gly Glu Val Ala Leu Val Val Ala Asp
245 250 255

Gln Ser Ser Leu Pro Glu Thr Tyr Gly Val Phe Thr Cys Thr Ala Lys
260 265 270

Ile Glu Trp Glu Asp Asp Gly Lys Val Thr Ser Ile Ala Val Pro Cys
275 280 285

Asp Val Ser Arg Leu His Cys Glu Ser Arg Asp Tyr Leu Phe Thr Trp
290 295 300

Arg Phe Arg Thr Ala Asp Ala Asp Ala Ser Val Gly His Ser Ser Glu
305 310 315 320

Glu Ile Ser Glu Ser
325

<210> 893
<211> 327
<212> PRT
<213> Zea mays

<400> 893

Met Ala Met Val Gln Pro Ala Asp Thr Ala Val Lys Ala Asn Glu Ile
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Leu Ala Arg Phe Arg Pro Ile Ala Pro Lys Pro Thr Leu Ala Ala Ala
20 25 30

Ala Ala Ala Ala Ala Ala Pro Val Ala Gln Ala Ala Ala Glu Gly Val
35 40 45

Val Ala Ala Asn Arg Val Leu Cys His Leu Gln Ser Arg Pro Cys Arg
50 55 60

Ala Arg Lys Arg Gly Arg Pro Thr Val Val Pro Val Ser Pro Lys Ser
65 70 75 80

Gly Ala Gln Pro Pro Ala Lys Arg Arg Arg Ala Ser Thr Pro Tyr Pro
85 90 95

Pro Leu Arg Cys Ala Ala Ala Thr Thr Gly Ala His Val Ser Ala Val
100 105 110

Val Pro Gly Ser Ala Arg Leu Pro Pro Ala Ser Ala Gly Val Glu Asp
115 120 125

Ile Ala Lys Ala Ala Ala Ala Ala Ala Thr Glu Glu Gly Arg Asp Val
130 135 140

Pro Val Glu Arg Asp Leu Leu Arg Lys Leu Leu Glu Pro Arg Val Ile
145 150 155 160

Ser Pro Arg Ala Val Arg Pro Val Trp Ser Ala Ile His Val Gly Cys
165 170 175

Ile His Arg Thr Asp Asp Ala Ala Cys Thr Asp Ala Ala Val Ser Lys
180 185 190

Thr Ala Val Gln Val Glu Ala Glu Leu Glu Val Asp Ala Leu Pro Ala
195 200 205

Val Val Ser Asp Ser Gly Asn Arg Val Arg Leu Val Asn Asp Ala Tyr
210 215 220

Lys Glu Met Val Gly Gln Pro Glu Cys Pro Trp Leu Asp Ala Val Ala
225 230 235 240

Ala Thr Ser Arg Arg Ile Ser Gly Glu Val Ala Leu Val Val Ala Asp
245 250 255

Arg Ser Ser Leu Pro Asp Ser Tyr Gly Ala Phe Thr Cys Thr Ala Lys
260 265 270

Ile Glu Trp Glu Asp Asp Gly Lys Val Thr Ser Ile Ala Ala Pro Cys
275 280 285

Asp Val Ser Arg Leu Gln Cys Glu Ser Arg Asp Tyr Leu Phe Ala Trp
290 295 300

Arg Phe Arg Thr Ala Ala Ala Asp Ala Asp Ala Ser Val Gly His Ser
305 310 315 320

Ser Glu Glu Ile Ser Glu Ser
325

<210> 894
<211> 312
<212> PRT
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<400> 894

Met Ala Met Val Gln Ala Ala Asp Ala Ala Val Lys Ala Asn Glu Ile
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20 25 30

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

Cys Arg Ala Arg Lys Arg Gly Arg Pro Gly Pro Ala Val Val Ala Pro
50 55 60

Ser Pro Glu Ser Gly Leu Gln Pro Pro Ala Lys Arg Lys Arg Ala Thr

65 70 75 80

Thr Pro Tyr Pro Pro Leu Arg Cys Arg Gly Pro Arg Ala Ser Ala Ala
85 90 95

Val Pro Gly Ser Ala Gly Leu Pro Leu Ala Ser Ala Ser Leu Pro Pro
100 105 110

Ala Gly Ala Gly Thr Ala Glu Asp Leu Ala Lys Val Ala Ala Glu Gly
115 120 125

Arg Asp Val Pro Val Glu Arg Asp Leu Leu Arg Lys Leu Leu Glu Pro
130 135 140

Lys Val Ile Ser Pro Arg Ala Val Arg Pro Val Cys Ser Ala Ile His
145 150 155 160

Val Gly Cys Ile His Arg Ala Asp Ala Thr Cys Thr Ala Ala Val Ser
165 170 175

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

Ala Val Val Ser Asp Ala Ser Asn Arg Val Arg Leu Val Asn Asp Ala
195 200 205

Tyr Lys Glu Met Val Gly Gln Pro Glu Cys Pro Trp Leu Asp Ala Val
210 215 220

Ala Ala Thr Ser Arg Arg Ile Ser Gly Glu Val Ala Leu Val Val Ala
225 230 235 240

Asn Gln Ser Ser Leu Pro Glu Ser Tyr Gly Val Phe Thr Cys Thr Ala
245 250 255

Lys Ile Glu Trp Glu Asp Asp Gly Lys Val Ala Ser Ile Asp Val Pro
260 265 270

Cys Asp Val Ser Arg Leu Gln Cys Glu Ser Arg Glu Tyr Leu Phe Val
275 280 285

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290 295 300

Ser Ser Glu Glu Ile Ser Glu Ser
305 310

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<213> Zea mays

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<212> DNA
<213> Eulaliopsis binata

<400> 896
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gtacaaatac tgagttgcag gcacatgata tctttcctct ttatgttctg ttagctagac 420

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gtgggcaagt cggacaaagt aatggtgaag ataactgctc tgggaaccat gtggaaggtt 660

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<211> 2073
<212> DNA
<213> Zea mays

<400> 897
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ccaactaatt tacttgcttc atctttggag agttgtgtca atttaagttt gggacatatt 720

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caagacaatt gcttgacatt ttgctctcat aaggttgatg ctgtgggttc atataaacta 840

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gagtaacttt ttattgataa tttcattcat atctattgtc aattgtatta atggtttttta 2040

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<212> DNA

<213> Dendrocalamus latiflorus

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<213> Sorghum bicolor

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Ala Val Gly Val Gly Ser Ala Lys Val Gly Val Arg Val Gly Val Lys
35 40 45

Ala Gly Thr Ala Glu Ala Lys Ala Val Ala Gln Arg Arg Gly Val Arg
50 55 60

Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp Leu
65 70 75 80

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

Ala Glu Leu Pro His Arg Leu Arg Leu Ser Arg Val Asp Lys Glu Trp
100 105 110

Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe Met
115 120 125

Arg Glu His Glu Phe Leu Gln Ala Leu His Phe Asn Ala Ile Arg Gly
130 135 140

Ala Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser Leu
145 150 155 160

Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg Val
165 170 175

Ala Leu Val Asp Gln Arg Asp Arg Pro Ile Ala Val Leu Ser Asp Ile
180 185 190

Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly
195 200 205

Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn Ala
210 215 220

Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val Ile Glu Pro Ile Lys
225 230 235 240

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

Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu
260 265 270

Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg
275 280 285

Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu His
290 295 300

Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp Arg
305 310 315 320

Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro Glu
325 330 335

Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro
340 345 350

Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn
355 360 365

Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr Glu
370 375 380

Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met
385 390 395 400

Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala Ala
405 410 415

Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg Lys
420 425 430

Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys
435 440 445

Asn Arg Glu Asn Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys
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Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser Ser
465 470 475 480

Lys Leu Arg Glu Pro Val Ala Ala
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Val Ala Ala Val Gly Ser Ala Lys Val Gly Ala Arg Val Gly Leu Lys
35 40 45

Ala Gly Ile Ala Ala Pro Ala Pro Ala Ala Gly Arg Gly Val Arg Cys
50 55 60

Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Gln Leu Val Asp Leu Val
65 70 75 80

Ala Pro Glu Glu Gly Gly Arg Arg Ala Ala Leu Arg Arg Glu Ala Ala
85 90 95

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

His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe Met Arg
115 120 125

Glu His Glu Phe Leu Gln Thr Leu His Phe Asn Ala Ile Arg Gly Gln
130 135 140

Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser Val Gly

145 150 155 160

Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg Val Ala
165 170 175

Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp Ile Glu
180 185 190

Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr
195 200 205

Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn Ala Gly
210 215 220

Asp Trp Leu Ile Gly Gly Asp Leu Glu Ile Ile Glu Pro Ile Lys Tyr
225 230 235 240

Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser Pro Ala Gln Leu Arg Glu
245 250 255

Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg
260 265 270

Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Lys
275 280 285

Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu His Pro
290 295 300

Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp Arg Met
305 310 315 320

Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro Glu Ser
325 330 335

Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr
340 345 350

Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe
355 360 365

Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr Glu Lys
370 375 380

Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala
385 390 395 400

Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala Ala Tyr
405 410 415

Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg Lys Asp
420 425 430

Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn
435 440 445

Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val
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Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser Ser Lys
465 470 475 480

Leu Arg Glu Pro Ile Ala Ala
485

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Val Lys Ala Gly Thr Ser Arg Thr Ala Ala Val Ala Arg Leu Gly Val
50 55 60

Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp
65 70 75 80

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

Ala Ala Glu Leu Pro His Arg Leu Arg Leu Gly Arg Val Asp Lys Glu
100 105 110

Trp Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe
115 120 125

Met Arg Glu His Glu Phe Leu Gln Ala Leu His Phe Asn Ala Ile Arg
130 135 140

Gly Gln Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser
145 150 155 160

Val Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg
165 170 175

Val Ala Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp
180 185 190

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Val Ala Arg Thr Trp
195 200 205

Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
210 215 220

Ala Gly Asp Trp Leu Val Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
225 230 235 240

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

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
260 265 270

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
275 280 285

Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu
290 295 300

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp
305 310 315 320

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
325 330 335

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
340 345 350

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
355 360 365

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr
370 375 380

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
385 390 395 400

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
405 410 415

Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg
420 425 430

Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala
435 440 445

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp
450 455 460

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser
465 470 475 480

Ser Lys Leu Arg Glu Pro Val Ala Ala
485

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<400> 930

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Val Ala Ala Val Gly Ser Ala Lys Val Gly Ala Arg Val Gly Leu Lys
35 40 45

Ala Gly Ile Ala Ala Pro Ala Pro Ala Ala Gly Arg Gly Val Arg Phe
50 55 60

Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Gln Leu Val Asp Leu Val
65 70 75 80

Ala Pro Glu Glu Gly Gly Arg Arg Ala Ala Leu Arg Arg Glu Ala Ala
85 90 95

Glu Leu Pro His Arg Leu Arg Leu Gly Arg Val Asp Lys Glu Trp Val

100 105 110

His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe Met Arg
115 120 125

Glu His Glu Phe Leu Gln Thr Leu His Phe Asn Ala Ile Arg Gly Gln
130 135 140

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

Asp Ala Gln Arg Arg Ala Ile Leu Ala Asp Gly Ala Thr Arg Val Ala
165 170 175

Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp Ile Glu
180 185 190

Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr
195 200 205

Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn Ala Gly
210 215 220

Asp Trp Leu Ile Gly Gly Asp Leu Glu Ile Ile Glu Pro Ile Lys Tyr
225 230 235 240

Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser Pro Ala Gln Leu Arg Glu
245 250 255

Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg
260 265 270

Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Lys
275 280 285

Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu His Pro
290 295 300

Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp Arg Met
305 310 315 320

Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro Glu Ser
325 330 335

Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr
340 345 350

Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe
355 360 365

Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr Glu Lys
370 375 380

Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala
385 390 395 400

Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala Ala Tyr
405 410 415

Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg Lys Asp
420 425 430

Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn
435 440 445

Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val
450 455 460

Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser Ser Lys
465 470 475 480

Leu Arg Glu Pro Ile Ala Ala
485

<210> 931

<211> 489
<212> PRT
<213> Zea mays

<400> 931

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

Gln Pro Gly Arg Asp Arg Ala Val Ala Val Ala Val Ala Pro Ala Pro
20 25 30

Gly Pro Ala Arg Val Ala Val Ala Ala Val Gly Ser Ala Lys Leu Gly
35 40 45

Val Lys Ala Gly Thr Ser Arg Thr Ala Ala Val Ala Arg Leu Gly Val
50 55 60

Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp
65 70 75 80

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

Ala Ala Glu Leu Pro His Arg Leu Arg Leu Gly Arg Val Asp Lys Glu
100 105 110

Trp Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe
115 120 125

Met Arg Asp Asp Glu Phe Leu Gln Thr Leu His Phe Asn Ala Ile Arg
130 135 140

Gly Gln Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser
145 150 155 160

Val Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg
165 170 175

Val Ala Val Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp
180 185 190

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp
195 200 205

Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
210 215 220

Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
225 230 235 240

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

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
260 265 270

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
275 280 285

Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Pro
290 295 300

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp
305 310 315 320

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
325 330 335

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
340 345 350

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
355 360 365

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr
370 375 380

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
385 390 395 400

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
405 410 415

Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg
420 425 430

Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala
435 440 445

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp
450 455 460

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser
465 470 475 480

Ser Lys Leu Arg Glu Pro Ile Ala Ala
485

<210> 932
<211> 477
<212> PRT
<213> Oryza sativa Indica Group

<400> 932

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
20 25 30

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

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

50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Val Arg Leu Gly Arg
85 90 95

Val Glu Thr Glu Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro
100 105 110

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
115 120 125

Asn Ala Ile Arg Gly Gly Asp Gly Ala Met Val Asn Met Ser Val Pro
130 135 140

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

Gly Ala Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
165 170 175

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
180 185 190

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
195 200 205

Ala Ile Thr Asn Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val
210 215 220

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
225 230 235 240

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
245 250 255

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
260 265 270

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

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
290 295 300

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
305 310 315 320

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
325 330 335

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
340 345 350

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
355 360 365

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
370 375 380

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro
385 390 395 400

Phe Lys Val Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe
405 410 415

Asp Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met
420 425 430

Arg Thr Leu Ala Lys Asn Arg Gln Ser Pro Pro Asp Gly Phe Met Cys
435 440 445

Pro Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro

450 455 460

Ser Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470 475

<210> 933
<211> 477
<212> PRT
<213> Oryza sativa Japonica Group

<400> 933

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
20 25 30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Val Arg Leu Gly Arg
85 90 95

Val Glu Thr Glu Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro
100 105 110

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
115 120 125

Asn Ala Ile Arg Gly Gly Asp Gly Ala Met Val Asn Met Ser Val Pro
130 135 140

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

Gly Ala Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
165 170 175

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
180 185 190

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
195 200 205

Ala Ile Thr Asn Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val
210 215 220

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
225 230 235 240

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
245 250 255

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
260 265 270

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

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
290 295 300

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
305 310 315 320

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
325 330 335

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
340 345 350

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
355 360 365

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
370 375 380

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro
385 390 395 400

Phe Lys Val Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe
405 410 415

Asp Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met
420 425 430

Arg Thr Leu Ala Lys Asn Cys Gln Ser Pro Pro Asp Gly Phe Met Cys
435 440 445

Pro Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro
450 455 460

Ser Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470 475

<210> 934
<211> 473
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 934

Met Ala Thr Gln Ala Ala Phe Ala Val Arg Phe Pro Gln Leu Ala Arg
1 5 10 15

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

Val Arg Gly Val Gly Arg Ala Ala Ala Ala Ala Ala Arg Gly Val Arg

35 40 45

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

Leu Val Ala Pro Glu Glu Gly Gly Arg Arg Ala Ala Leu Arg Arg Glu
65 70 75 80

Ala Ala Ala Leu Pro His Arg Val Arg Leu Gly Arg Val Asp Thr Glu
85 90 95

Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Arg Gly Phe
100 105 110

Met Arg Glu Thr Glu Phe Leu Gln Ala Leu His Phe Asn Ala Val Arg
115 120 125

Gly Ala Asp Gly Ser Leu Val Asn Met Ser Val Pro Ile Val Leu Ala
130 135 140

Leu Asp Asp Ala Gln Arg Arg Ala Ile Gln Ala Ser Ala Ala Thr Ser
145 150 155 160

Val Ala Leu Val Asp Ala His Asp Arg Pro Val Ala Val Leu Arg Asp
165 170 175

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp
180 185 190

Gly Thr Thr Ala Arg Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
195 200 205

Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
210 215 220

Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser Pro Ala Gln Leu
225 230 235 240

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
245 250 255

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
260 265 270

Arg Arg Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu
275 280 285

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Val
290 295 300

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
305 310 315 320

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
325 330 335

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
340 345 350

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Gly His Pro Thr
355 360 365

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
370 375 380

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
385 390 395 400

Ala Tyr Asp Thr Lys His Asn Lys Met Asn Phe Phe Asp Pro Ser Arg
405 410 415

Lys Glu Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Ser Leu Ala
420 425 430

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp

435 440 445

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Ala Pro Pro Glu Gly Ser
450 455 460

Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470

<210> 935
<211> 476
<212> PRT
<213> Oryza sativa Indica Group

<400> 935

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
20 25 30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Val Arg Leu Gly Arg
85 90 95

Val Glu Thr Glu Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro
100 105 110

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
115 120 125

Asn Ala Ile Arg Gly Gly Asp Gly Ala Met Val Asn Met Ser Val Pro
130 135 140

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

Gly Ala Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
165 170 175

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
180 185 190

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
195 200 205

Ala Ile Thr Asn Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val
210 215 220

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
225 230 235 240

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
245 250 255

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
260 265 270

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

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
290 295 300

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
305 310 315 320

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
325 330 335

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
340 345 350

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
355 360 365

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
370 375 380

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro
385 390 395 400

Phe Lys Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp
405 410 415

Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg
420 425 430

Thr Leu Ala Lys Asn Arg Gln Ser Pro Pro Asp Gly Phe Met Cys Pro
435 440 445

Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro Ser
450 455 460

Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470 475

<210> 936
<211> 461
<212> PRT
<213> Oryza sativa Japonica Group

<400> 936

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro

20 25 30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Gly Gly Ala Ser Pro
85 90 95

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
100 105 110

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

Ile Val Leu Pro Leu Gly Asp Ala Gln Arg Arg Ala Ile Glu Ala Ser
130 135 140

Gly Val Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
145 150 155 160

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
165 170 175

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
180 185 190

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

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
210 215 220

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
225 230 235 240

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
245 250 255

Met Thr Asp Thr Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro
260 265 270

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
275 280 285

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
290 295 300

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
305 310 315 320

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
325 330 335

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
340 345 350

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
355 360 365

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro
370 375 380

Phe Lys Val Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe
385 390 395 400

Asp Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met
405 410 415

Arg Thr Leu Ala Lys Asn Cys Gln Ser Pro Pro Asp Gly Phe Met Cys

420 425 430

Pro Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro
435 440 445

Ser Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
450 455 460

<210> 937
<211> 533
<212> PRT
<213> Sorghum bicolor

<400> 937

Met Ser Leu Ala Ser Ala Gly Ala Ala Ala Ala Arg Lys Pro Ala Ala
1 5 10 15

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

Ala Arg Arg Arg Ala Val Ala Ala Ala Ala Ala Leu Leu Leu Ala Leu
35 40 45

Val Tyr Ala Ala Gly Leu Leu Val Phe Leu Leu Gly Gly Arg Leu Ser
50 55 60

Gly Gly Gly Ala Thr Ala Gly Gly Pro Gly Pro Ala Ala Val Thr Val
65 70 75 80

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

His Ala Gln Leu Arg Leu Met Thr Ser His Tyr Gln Asn Ser Gly Asp
100 105 110

Pro Trp Met Pro Cys Val Asn Ser Arg Leu Thr Arg Ser Glu Leu Pro
115 120 125

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Pro Ser Asn Gly Tyr Leu Met Ile Glu Ala Asn Gly Gly Leu Asn Gln
    130                 135                 140


Gln Arg Leu Ser Ile Cys Asp Ala Val Ala Val Ala Ser Leu Leu Asn
145                 150                 155                 160


Ala Thr Leu Val Ile Pro Thr Phe His Leu Asn Ser Val Trp Arg Asp
                165                 170                 175


Pro Ser Lys Phe Gly Asp Ile Phe Asp Glu Asp His Phe Ile Glu Thr
            180                 185                 190


Leu Lys Glu His Val Arg Val Val Lys Lys Leu Pro Glu Asp Val Leu
        195                 200                 205


Leu Arg Phe Asn His Asn Ile Ser Ser Ile Pro Asn Met Arg Thr Lys
    210                 215                 220


Ala Tyr Ser Ser Pro Asn His Tyr Val Gln Asn Val Leu Pro Lys Leu
225                 230                 235                 240


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


Leu Ser Val Pro Leu Asn Ile Gln Ala Leu Arg Cys Leu Val Asn Tyr
            260                 265                 270


His Ala Leu Arg Phe Ala Glu Pro Ile Arg Ile Leu Ser Asp Asp Leu
        275                 280                 285


Val Gly Arg Met Thr Lys Lys Ser Leu Leu Thr Gly Gly Lys Tyr Val
    290                 295                 300


Ser Val His Leu Arg Phe Glu Glu Asp Met Val Ala Phe Ser Cys Cys
305                 310                 315                 320


Thr Tyr Asp Gly Gly Trp Arg Glu Lys Thr Glu Met Asp Asn Ala Arg
                325                 330                 335
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Glu Arg Ser Trp Arg Gly Lys Phe Arg Arg His Gly Arg Val Ile Asn
340 345 350

Pro Glu Ala Asn Arg Arg Asp Gly Lys Cys Pro Leu Thr Pro Leu Glu
355 360 365

Val Gly Met Met Leu Arg Gly Met Gly Phe Asp Asn Thr Thr Ser Leu
370 375 380

Tyr Val Ala Ser Gly Lys Ile Tyr Asn Ser Glu Lys Tyr Met Ala Pro
385 390 395 400

Leu Arg Gln Met Phe Pro Leu Leu Thr Thr Lys Asp Ser Leu Ala Leu
405 410 415

Pro Glu Glu Leu Ala Gln Phe Lys Gly His Ser Ser Gln Leu Ala Ala
420 425 430

Leu Asp Tyr Thr Val Cys Val Gln Ser Glu Val Phe Val Thr Thr Gln
435 440 445

Gly Gly Asn Phe Pro His Phe Leu Met Gly His Arg Arg Tyr Leu Phe
450 455 460

Gly Gly Asn Ala Lys Thr Ile Lys Pro Asp Lys Arg Lys Leu Val Leu
465 470 475 480

Ser Phe Asp Asp Pro Asn Ile Arg Trp Asp Gln Phe Lys Gln Asn Met
485 490 495

Gln Glu Ile Leu His His Ser Asp Met Lys Ser Ile Ala Phe Arg Lys
500 505 510

Pro Asn Asp Ser Val Tyr Thr Phe Pro Met Pro Glu Cys Met Cys Gln
515 520 525

Gln Asp Gly Met Ile
    530

<210> 938
<211> 491
<212> PRT
<213> Oryza sativa Japonica Group

<400> 938

Met Thr Val Ala Ser Leu Arg Arg Arg Arg Ala Ala Ala Ala Ala Ala
1   5   10   15

Pro Gln Pro Gly Ser Val Tyr Arg Ser His Leu Val Phe Glu Arg Leu
            20   25   30

Trp Pro Asp Ile Arg Asp Asp Ala Ser Ser Ala Ser Ala Ala Ala Ser
        35   40   45

Ser Leu Ser Ser Thr Ser Trp Arg Arg Ser Met Leu Met Thr Ser His
    50   55   60

Tyr Gln Asn Pro Gly Glu Leu Trp Met Pro Cys Val Asn Arg Lys Leu
65   70   75   80

Ile Arg Pro Glu Leu Pro Pro Ser Asn Gly Tyr Leu Met Ile Glu Ala
                85   90   95

Asn Gly Gly Leu Asn Gln Gln Arg Leu Ser Ile Cys Asp Ala Val Ala
            100   105   110

Val Ala Ser Leu Leu Asn Ala Thr Leu Val Ile Pro Ala Phe His Phe
        115   120   125

Asn Ser Val Trp Arg Asp His Ser Lys Phe Gly Asp Ile Phe Asp Glu
    130   135   140

Asp His Phe Ile Glu Thr Leu Lys Glu His Val Arg Val Val Lys Glu
145   150   155   160

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

Pro Asn Met Arg Thr Lys Ala Tyr Ser Ser Pro Asn His Tyr Met Gln
180 185 190

Lys Val Leu Pro Lys Leu Leu Glu Leu Gly Ala Val Arg Ile Ala Pro
195 200 205

Phe Ser Asn Arg Leu Ala Gln Ser Val Pro Ser Asn Leu Gln Ala Leu
210 215 220

Arg Cys Phe Val Asn Tyr Gln Ala Leu Arg Phe Ala Glu Pro Ile Arg
225 230 235 240

Val Leu Ala Glu Asp Met Val Glu Arg Met Val Lys Arg Ser Thr Leu
245 250 255

Thr Gly Gly Lys Phe Val Ser Val His Leu Arg Phe Glu Glu Asp Met
260 265 270

Val Ala Phe Ser Cys Cys Thr Tyr Asp Gly Gly Leu Lys Glu Lys Thr
275 280 285

Glu Met Glu Asn Ala Arg Glu Arg Ser Trp Arg Gly Lys Phe His Arg
290 295 300

His Gly Arg Val Ile Asn Pro Glu Ala Asn Arg Arg Asp Gly Lys Cys
305 310 315 320

Pro Leu Thr Pro Leu Glu Val Gly Met Met Leu Arg Gly Met Gly Phe
325 330 335

Asp Asn Thr Thr Ser Leu Tyr Val Ala Ser Gly Lys Ile Tyr Asn Ala
340 345 350

Glu Lys Tyr Met Ala Pro Leu Arg Gln Met Phe Pro Leu Leu Ala Thr

355 360 365

Lys Asp Thr Leu Ala Leu Pro Glu Glu Leu Ala Glu Phe Glu Gly His
370 375 380

Ser Ser Arg Leu Ala Ala Leu Asp Tyr Ser Val Cys Leu Pro Ser Glu
385 390 395 400

Val Phe Val Thr Thr Gln Gly Gly Asn Phe Pro His Phe Leu Met Gly
405 410 415

His Arg Arg Tyr Leu Phe Gly Gly Asn Ala Arg Thr Ile Lys Pro Asp
420 425 430

Lys Arg Lys Leu Val Leu Ser Phe Asp Asp Pro Asn Ile Arg Trp Asn
435 440 445

Arg Phe Lys Arg His Met Gln Asp Ile Leu His His Ser Asp Met Arg
450 455 460

Gly Thr Ala Leu Arg Lys Pro Asn Asp Ser Ile Tyr Thr Phe Pro Met
465 470 475 480

Pro Glu Cys Met Cys Gln Gln Asp Gly Met Met
485 490

<210> 939
<211> 562
<212> PRT
<213> Oryza sativa Japonica Group

<400> 939

Met Ser Val Ala Leu Tyr Ala Arg Gly Gly Gly Cys Gly Ala Lys Ala
1 5 10 15

Ala Ala Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Arg Arg Arg Ala
20 25 30

Ala Val Val Leu Leu Leu Ala Leu Ala Tyr Val Ala Gly Leu Leu Val
35 40 45

Phe Val Leu Ala Gly Gly Gly Gly Val Gly Val Gly Gly Arg Val Glu
50 55 60

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

Arg Ala Ala Ala Ala Ala Ala Pro Gln Pro Gly Ser Val Tyr Arg Ser
85 90 95

His Leu Val Phe Glu Arg Leu Trp Pro Asp Ile Arg Asp Asp Ala Ser
100 105 110

Ser Ala Ser Ala Ala Ala Ser Ser Leu Ser Ser Thr Ser Trp Arg Arg
115 120 125

Ser Met Leu Met Thr Ser His Tyr Gln Asn Pro Gly Glu Leu Trp Met
130 135 140

Pro Cys Val Asn Arg Lys Leu Ile Arg Pro Glu Leu Pro Pro Ser Asn
145 150 155 160

Gly Tyr Leu Met Ile Glu Ala Asn Gly Gly Leu Asn Gln Gln Arg Leu
165 170 175

Ser Ile Cys Asp Ala Val Ala Val Ala Ser Leu Leu Asn Ala Thr Leu
180 185 190

Val Ile Pro Ala Phe His Phe Asn Ser Val Trp Arg Asp His Ser Lys
195 200 205

Phe Gly Asp Ile Phe Asp Glu Asp His Phe Ile Glu Thr Leu Lys Glu
210 215 220

His Val Arg Val Val Lys Glu Leu Pro Val Asp Val Leu Thr Arg Phe
225 230 235 240

Asp His Asn Ile Ser Ser Ile Pro Asn Met Arg Thr Lys Ala Tyr Ser
245 250 255

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

Gly Ala Val Arg Ile Ala Pro Phe Ser Asn Arg Leu Ala Gln Ser Val
275 280 285

Pro Ser Asn Leu Gln Ala Leu Arg Cys Phe Val Asn Tyr Gln Ala Leu
290 295 300

Arg Phe Ala Glu Pro Ile Arg Val Leu Ala Glu Asp Met Val Glu Arg
305 310 315 320

Met Val Lys Arg Ser Thr Leu Thr Gly Gly Lys Phe Val Ser Val His
325 330 335

Leu Arg Phe Glu Glu Asp Met Val Ala Phe Ser Cys Cys Thr Tyr Asp
340 345 350

Gly Gly Leu Lys Glu Lys Thr Glu Met Glu Asn Ala Arg Glu Arg Ser
355 360 365

Trp Arg Gly Lys Phe His Arg His Gly Arg Val Ile Asn Pro Glu Ala
370 375 380

Asn Arg Arg Asp Gly Lys Cys Pro Leu Thr Pro Leu Glu Val Gly Met
385 390 395 400

Met Leu Arg Gly Met Gly Phe Asp Asn Thr Thr Ser Leu Tyr Val Ala
405 410 415

Ser Gly Lys Ile Tyr Asn Ala Glu Lys Tyr Met Ala Pro Leu Arg Gln
420 425 430

Met Phe Pro Leu Leu Ala Thr Lys Asp Thr Leu Ala Leu Pro Glu Glu
435 440 445

Leu Ala Glu Phe Glu Gly His Ser Ser Arg Leu Ala Ala Leu Asp Tyr
450 455 460

Ser Val Cys Leu Pro Ser Glu Val Phe Val Thr Thr Gln Gly Gly Asn
465 470 475 480

Phe Pro His Phe Leu Met Gly His Arg Arg Tyr Leu Phe Gly Gly Asn
485 490 495

Ala Arg Thr Ile Lys Pro Asp Lys Arg Lys Leu Val Leu Ser Phe Asp
500 505 510

Asp Pro Asn Ile Arg Trp Asn Arg Phe Lys Arg His Met Gln Asp Ile
515 520 525

Leu His His Ser Asp Met Arg Gly Thr Ala Leu Arg Lys Pro Asn Asp
530 535 540

Ser Ile Tyr Thr Phe Pro Met Pro Glu Cys Met Cys Gln Gln Asp Gly
545 550 555 560

Met Met

<210> 940
<211> 566
<212> PRT
<213> Oryza sativa Indica Group

<400> 940

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

Lys Ala Ala Ala Ala Ala Arg Arg Pro Gly Arg Gly Gly Gly Gly Gly
20 25 30

Arg Arg Arg Ala Ala Ala Val Leu Leu Leu Leu Leu Ala Leu Ala Tyr
35 40 45

Val Ala Gly Leu Leu Val Phe Val Leu Ala Gly Val Ala Gly Val Gly
50 55 60

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

Leu Arg Arg Arg Arg Ala Ala Ala Ala Ala Ala Ala Gln Pro Gly Ser
85 90 95

Val Tyr Arg Ser His Leu Val Phe Glu Arg Leu Trp Pro Asp Ile Arg
100 105 110

Asp Asp Ala Ser Ser Ala Ser Ala Ala Ala Ser Ser Leu Ser Ser Thr
115 120 125

Ser Trp Arg Arg Ser Met Leu Met Thr Ser His Tyr Gln Asn Pro Gly
130 135 140

Glu Leu Trp Met Pro Cys Val Asn Arg Lys Leu Ile Arg Pro Glu Leu
145 150 155 160

Pro Pro Ser Asn Gly Tyr Leu Met Ile Glu Ala Asn Gly Gly Leu Asn
165 170 175

Gln Gln Arg Leu Ser Ile Cys Asp Ala Val Ala Val Ala Ser Leu Leu
180 185 190

Asn Ala Thr Leu Val Ile Pro Ala Phe His Phe Asn Ser Val Trp Arg
195 200 205

Asp His Ser Lys Phe Gly Asp Ile Phe Asp Glu Asp His Phe Ile Glu
210 215 220

Thr Leu Lys Gln His Val Arg Val Val Lys Glu Leu Pro Val Asp Val

225 230 235 240

Leu Thr Arg Phe Asp His Asn Ile Ser Ser Ile Pro Asn Met Arg Thr
245 250 255

Lys Ala Tyr Ser Ser Pro Asn His Tyr Met Gln Lys Val Leu Pro Glu
260 265 270

Leu Leu Glu Leu Gly Ala Val Arg Ile Ala Pro Phe Ser Asn Arg Leu
275 280 285

Ala Gln Ser Val Pro Ser Asn Leu Gln Ala Leu Arg Cys Phe Val Asn
290 295 300

Tyr Gln Ala Leu Arg Phe Ala Gly Pro Ile Arg Val Leu Ala Glu Asp
305 310 315 320

Met Val Glu Arg Met Val Lys Arg Ser Thr Leu Thr Gly Gly Lys Phe
325 330 335

Val Ser Val His Leu Arg Phe Glu Glu Asp Met Val Ala Phe Ser Cys
340 345 350

Cys Thr Tyr Asp Gly Gly Leu Lys Glu Lys Thr Glu Met Glu Asn Ala
355 360 365

Arg Glu Arg Ser Trp Arg Gly Lys Phe His Arg His Gly Arg Val Ile
370 375 380

Asn Pro Glu Ala Asn Arg Arg Asp Gly Lys Cys Pro Leu Thr Pro Leu
385 390 395 400

Glu Val Gly Met Met Leu Arg Gly Met Gly Phe Asp Asn Thr Thr Ser
405 410 415

Leu Tyr Val Ala Ser Gly Lys Ile Tyr Asn Ala Glu Lys Tyr Met Ala
420 425 430

Pro Leu Arg Gln Met Phe Pro Leu Leu Ala Thr Lys Asp Thr Leu Ala
435 440 445

Leu Pro Glu Glu Leu Ala Glu Phe Glu Gly His Ser Ser Arg Leu Ala
450 455 460

Ala Leu Asp Tyr Ser Val Cys Leu Pro Ser Glu Val Phe Val Thr Thr
465 470 475 480

Gln Gly Gly Asn Phe Pro His Phe Leu Met Gly His Arg Arg Tyr Leu
485 490 495

Phe Gly Gly Asn Ala Lys Thr Ile Lys Pro Asp Lys Arg Lys Leu Val
500 505 510

Leu Ser Phe Asp Asp Pro Asn Ile Arg Trp Asn Arg Phe Lys Arg His
515 520 525

Met Gln Asp Ile Leu His His Ser Asp Met Arg Gly Thr Ala Leu Arg
530 535 540

Lys Pro Asn Asp Ser Ile Tyr Thr Phe Pro Met Pro Glu Cys Met Cys
545 550 555 560

Gln Gln Asp Gly Met Met
565

<210> 941
<211> 489
<212> PRT
<213> Zea mays

<400> 941

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

Gln Pro Gly Arg Asp Arg Ala Val Ala Val Ala Val Ala Pro Ala Pro
20 25 30

Gly Pro Ala Arg Val Ala Val Ala Ala Val Gly Ser Ala Lys Leu Gly
35 40 45

Val Lys Ala Gly Thr Ser Arg Thr Ala Ala Val Ala Arg Leu Gly Val
50 55 60

Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp
65 70 75 80

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

Ala Ala Glu Leu Pro His Arg Leu Arg Leu Gly Arg Val Asp Lys Glu
100 105 110

Trp Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe
115 120 125

Met Arg Glu His Glu Phe Leu Gln Ala Leu His Phe Asn Ala Ile Arg
130 135 140

Gly Gln Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser
145 150 155 160

Val Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg
165 170 175

Val Ala Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp
180 185 190

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Val Ala Arg Thr Trp
195 200 205

Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
210 215 220

Ala Gly Asp Trp Leu Val Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
225 230 235 240

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

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
260 265 270

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
275 280 285

Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu
290 295 300

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp
305 310 315 320

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
325 330 335

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
340 345 350

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
355 360 365

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr
370 375 380

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
385 390 395 400

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
405 410 415

Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg
420 425 430

Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala
435 440 445

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp
450 455 460

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser
465 470 475 480

Ser Lys Leu Arg Glu Pro Val Ala Ala
485

<210> 942
<211> 489
<212> PRT
<213> Zea mays

<400> 942

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

Gln Pro Gly Arg Asp Arg Ala Val Ala Val Ala Val Ala Pro Ala Pro
20 25 30

Gly Pro Ala Arg Val Ala Val Ala Ala Val Gly Ser Ala Lys Leu Gly
35 40 45

Val Lys Ala Gly Thr Ser Arg Thr Ala Ala Val Ala Arg Leu Gly Val
50 55 60

Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp
65 70 75 80

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

Ala Ala Glu Leu Pro His Arg Leu Arg Leu Gly Arg Val Asp Lys Glu

100 105 110

Trp Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe
115 120 125

Met Arg Asp Asp Glu Phe Leu Gln Thr Leu His Phe Asn Ala Ile Arg
130 135 140

Gly Gln Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser
145 150 155 160

Val Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg
165 170 175

Val Ala Val Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp
180 185 190

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp
195 200 205

Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
210 215 220

Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
225 230 235 240

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

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
260 265 270

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
275 280 285

Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Pro
290 295 300

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp
305 310 315 320

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
325 330 335

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
340 345 350

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
355 360 365

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr
370 375 380

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
385 390 395 400

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
405 410 415

Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg
420 425 430

Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala
435 440 445

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp
450 455 460

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser
465 470 475 480

Ser Lys Leu Arg Glu Pro Ile Ala Ala
485

<210> 943

<211> 487
<212> PRT
<213> Zea mays

<400> 943

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

Gln Pro Ser Arg Asp Cys Ala Val Ala Val Ala Pro Thr Arg Val Ala
20 25 30

Val Ala Ala Val Gly Ser Ala Lys Val Gly Ala Arg Val Gly Leu Lys
35 40 45

Ala Gly Ile Ala Ala Pro Ala Pro Ala Ala Gly Arg Gly Val Arg Cys
50 55 60

Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Gln Leu Val Asp Leu Val
65 70 75 80

Ala Pro Glu Glu Gly Gly Arg Arg Ala Ala Leu Arg Arg Glu Ala Ala
85 90 95

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

His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe Met Arg
115 120 125

Glu His Glu Phe Leu Gln Thr Leu His Phe Asn Ala Ile Arg Gly Gln
130 135 140

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

Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg Val Ala
165 170 175

Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp Ile Glu
180 185 190

Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr
195 200 205

Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn Ala Gly
210 215 220

Asp Trp Leu Ile Gly Gly Asp Leu Glu Ile Ile Glu Pro Ile Lys Tyr
225 230 235 240

Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser Pro Ala Gln Leu Arg Glu
245 250 255

Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg
260 265 270

Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Lys
275 280 285

Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu His Pro
290 295 300

Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp Arg Met
305 310 315 320

Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro Glu Ser
325 330 335

Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr
340 345 350

Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe
355 360 365

Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr Glu Lys
370 375 380

Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala
385 390 395 400

Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala Ala Tyr
405 410 415

Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg Lys Asp
420 425 430

Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn
435 440 445

Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val
450 455 460

Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser Ser Lys
465 470 475 480

Leu Arg Glu Pro Ile Ala Ala
485

<210> 944
<211> 487
<212> PRT
<213> Zea mays

<400> 944

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

Gln Pro Ser Arg Asp Cys Ala Val Ala Val Ala Pro Thr Arg Val Ala
20 25 30

Val Ala Ala Val Gly Ser Ala Lys Val Gly Ala Arg Val Gly Leu Lys
35 40 45

Ala Gly Ile Ala Ala Pro Ala Pro Ala Ala Gly Arg Gly Val Arg Phe

50 55 60

Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Gln Leu Val Asp Leu Val
65 70 75 80

Ala Pro Glu Glu Gly Gly Arg Arg Ala Ala Leu Arg Arg Glu Ala Ala
85 90 95

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

His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe Met Arg
115 120 125

Glu His Glu Phe Leu Gln Thr Leu His Phe Asn Ala Ile Arg Gly Gln
130 135 140

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

Asp Ala Gln Arg Arg Ala Ile Leu Ala Asp Gly Ala Thr Arg Val Ala
165 170 175

Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp Ile Glu
180 185 190

Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr
195 200 205

Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn Ala Gly
210 215 220

Asp Trp Leu Ile Gly Gly Asp Leu Glu Ile Ile Glu Pro Ile Lys Tyr
225 230 235 240

Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser Pro Ala Gln Leu Arg Glu
245 250 255

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Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg
            260                 265                 270

Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Lys
        275                 280                 285

Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu His Pro
    290                 295                 300

Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp Arg Met
305                 310                 315                 320

Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro Glu Ser
                325                 330                 335

Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr
            340                 345                 350

Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe
        355                 360                 365

Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr Glu Lys
    370                 375                 380

Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala
385                 390                 395                 400

Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala Ala Tyr
                405                 410                 415

Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg Lys Asp
            420                 425                 430

Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn
        435                 440                 445

Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val
```

450 455 460

Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser Ser Lys
465 470 475 480

Leu Arg Glu Pro Ile Ala Ala
485

<210> 945
<211> 488
<212> PRT
<213> Sorghum bicolor

<400> 945

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

Gln Pro Gly Arg Asp Arg Ala Val Ala Pro Ala Arg Val Ala Val Ala
20 25 30

Ala Val Gly Val Gly Ser Ala Lys Val Gly Val Arg Val Gly Val Lys
35 40 45

Ala Gly Thr Ala Glu Ala Lys Ala Val Ala Gln Arg Arg Gly Val Arg
50 55 60

Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp Leu
65 70 75 80

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

Ala Glu Leu Pro His Arg Leu Arg Leu Ser Arg Val Asp Lys Glu Trp
100 105 110

Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe Met
115 120 125

Arg Glu His Glu Phe Leu Gln Ala Leu His Phe Asn Ala Ile Arg Gly
130 135 140

Ala Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser Leu
145 150 155 160

Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg Val
165 170 175

Ala Leu Val Asp Gln Arg Asp Arg Pro Ile Ala Val Leu Ser Asp Ile
180 185 190

Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly
195 200 205

Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn Ala
210 215 220

Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val Ile Glu Pro Ile Lys
225 230 235 240

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

Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu
260 265 270

Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg
275 280 285

Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu His
290 295 300

Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp Arg
305 310 315 320

Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro Glu
325 330 335

Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro
340 345 350

Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn
355 360 365

Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr Glu
370 375 380

Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met
385 390 395 400

Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala Ala
405 410 415

Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg Lys
420 425 430

Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys
435 440 445

Asn Arg Glu Asn Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys
450 455 460

Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser Ser
465 470 475 480

Lys Leu Arg Glu Pro Val Ala Ala
485

<210> 946
<211> 473
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 946

Met Ala Thr Gln Ala Ala Phe Ala Val Arg Phe Pro Gln Leu Ala Arg

1 5 10 15

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

Val Arg Gly Val Gly Arg Ala Ala Ala Ala Ala Ala Arg Gly Val Arg
35 40 45

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

Leu Val Ala Pro Glu Glu Gly Gly Arg Arg Ala Ala Leu Arg Arg Glu
65 70 75 80

Ala Ala Ala Leu Pro His Arg Val Arg Leu Gly Arg Val Asp Thr Glu
85 90 95

Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Arg Gly Phe
100 105 110

Met Arg Glu Thr Glu Phe Leu Gln Ala Leu His Phe Asn Ala Val Arg
115 120 125

Gly Ala Asp Gly Ser Leu Val Asn Met Ser Val Pro Ile Val Leu Ala
130 135 140

Leu Asp Asp Ala Gln Arg Arg Ala Ile Gln Ala Ser Ala Ala Thr Ser
145 150 155 160

Val Ala Leu Val Asp Ala His Asp Arg Pro Val Ala Val Leu Arg Asp
165 170 175

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile Ala Arg Thr Trp
180 185 190

Gly Thr Thr Ala Arg Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
195 200 205

Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
210 215 220

Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser Pro Ala Gln Leu
225 230 235 240

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
245 250 255

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
260 265 270

Arg Arg Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu
275 280 285

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Val
290 295 300

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
305 310 315 320

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
325 330 335

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
340 345 350

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Gly His Pro Thr
355 360 365

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
370 375 380

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
385 390 395 400

Ala Tyr Asp Thr Lys His Asn Lys Met Asn Phe Phe Asp Pro Ser Arg

405 410 415

Lys Glu Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Ser Leu Ala
420 425 430

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp
435 440 445

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Ala Pro Pro Glu Gly Ser
450 455 460

Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470

<210> 947
<211> 477
<212> PRT
<213> Oryza sativa Indica Group

<400> 947

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
20 25 30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Val Arg Leu Gly Arg
85 90 95

Val Glu Thr Glu Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro
100 105 110

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
115 120 125

Asn Ala Ile Arg Gly Gly Asp Gly Ala Met Val Asn Met Ser Val Pro
130 135 140

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

Gly Ala Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
165 170 175

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
180 185 190

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
195 200 205

Ala Ile Thr Asn Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val
210 215 220

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
225 230 235 240

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
245 250 255

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
260 265 270

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

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
290 295 300

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
305 310 315 320

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
325 330 335

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
340 345 350

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
355 360 365

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
370 375 380

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro
385 390 395 400

Phe Lys Val Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe
405 410 415

Asp Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met
420 425 430

Arg Thr Leu Ala Lys Asn Arg Gln Ser Pro Pro Asp Gly Phe Met Cys
435 440 445

Pro Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro
450 455 460

Ser Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470 475

<210> 948
<211> 477
<212> PRT
<213> Oryza sativa Japonica Group

<400> 948

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1   5   10   15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
            20   25   30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
    50   55   60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65   70   75   80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Val Arg Leu Gly Arg
                85   90   95

Val Glu Thr Glu Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro
            100   105   110

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
        115   120   125

Asn Ala Ile Arg Gly Gly Asp Gly Ala Met Val Asn Met Ser Val Pro
    130   135   140

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

Gly Ala Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
                165   170   175

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
            180   185   190

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
195 200 205

Ala Ile Thr Asn Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val
210 215 220

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
225 230 235 240

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
245 250 255

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
260 265 270

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

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
290 295 300

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
305 310 315 320

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
325 330 335

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
340 345 350

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
355 360 365

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
370 375 380

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro

385 390 395 400

Phe Lys Val Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe
405 410 415

Asp Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met
420 425 430

Arg Thr Leu Ala Lys Asn Cys Gln Ser Pro Pro Asp Gly Phe Met Cys
435 440 445

Pro Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro
450 455 460

Ser Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470 475

<210> 949
<211> 476
<212> PRT
<213> Oryza sativa Indica Group

<400> 949

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
20 25 30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Val Arg Leu Gly Arg
85 90 95

Val Glu Thr Glu Trp Leu His Val Leu Ser Glu Gly Trp Ala Ser Pro
100 105 110

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
115 120 125

Asn Ala Ile Arg Gly Gly Asp Gly Ala Met Val Asn Met Ser Val Pro
130 135 140

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

Gly Ala Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
165 170 175

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
180 185 190

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
195 200 205

Ala Ile Thr Asn Ala Gly Asp Trp Leu Ile Gly Gly Asp Leu Glu Val
210 215 220

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
225 230 235 240

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
245 250 255

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
260 265 270

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

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
290 295 300

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
305 310 315 320

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
325 330 335

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
340 345 350

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
355 360 365

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
370 375 380

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro
385 390 395 400

Phe Lys Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp
405 410 415

Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg
420 425 430

Thr Leu Ala Lys Asn Arg Gln Ser Pro Pro Asp Gly Phe Met Cys Pro
435 440 445

Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro Ser
450 455 460

Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
465 470 475

<210> 950
<211> 461
<212> PRT
<213> Oryza sativa Japonica Group

<400> 950

Met Ala Met Gln Ala Ala Phe Ala Ala Ser Met Phe Pro Gln Leu Ala
1 5 10 15

Gln Arg Arg Gly Ser Asp Arg Ala Val Val Val Ala Pro Pro Ala Pro
20 25 30

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

Ala Arg Gly Val Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly
50 55 60

Arg Leu Val Glu Leu Val Val Pro Glu Glu Gly Gly Arg Arg Glu Ala
65 70 75 80

Ala Arg Arg Glu Ala Ala Ala Leu Ala His Arg Gly Gly Ala Ser Pro
85 90 95

Leu Arg Gly Phe Met Arg Glu Ala Glu Phe Leu Gln Ala Leu His Phe
100 105 110

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

Ile Val Leu Pro Leu Gly Asp Ala Gln Arg Arg Ala Ile Glu Ala Ser
130 135 140

Gly Val Arg Arg Val Ala Leu Val Asp Ala Ala Asp Arg Pro Leu Ala
145 150 155 160

Val Leu Ser Asp Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Ile
165 170 175

Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
180 185 190

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

Ile Glu Pro Ile Lys Tyr Asn Asp Gly Leu Asp Gln Tyr Arg Leu Ser
210 215 220

Pro Ala Gln Leu Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val
225 230 235 240

Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
245 250 255

Met Thr Asp Thr Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro
260 265 270

Val Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
275 280 285

Pro Leu Ser Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly
290 295 300

Val Leu Asn Pro Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met
305 310 315 320

His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile
325 330 335

Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met
340 345 350

Gly His Pro Thr Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys
355 360 365

Lys Val Leu Ser Met Ala Pro Gly Leu Glu Lys Leu Asn Ile Leu Pro

370 375 380

Phe Lys Val Ala Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe
385 390 395 400

Asp Pro Ser Arg Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met
405 410 415

Arg Thr Leu Ala Lys Asn Cys Gln Ser Pro Pro Asp Gly Phe Met Cys
420 425 430

Pro Gly Gly Trp Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Thr Pro
435 440 445

Ser Ala Asp Ser Ser Lys Leu Arg Glu Ala Val Ala Ala
450 455 460

<210> 951
<211> 384
<212> PRT
<213> Sorghum bicolor

<400> 951

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

Ala Ala Glu Lys Gly Lys Arg Gly Gly Gly Val Leu Gly Arg Leu Trp
20 25 30

Arg Ala Leu Phe Gly Gly Arg Glu Asp Phe Glu Lys Arg Leu Gln Tyr
35 40 45

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

Gln Phe Ser Arg Arg Ala Val Arg Asn Leu Ile Val Leu Ser Val Leu
65 70 75 80

Ala Glu Val Leu Ala Val Val Tyr Ala Ile Met Met Thr Arg Asp Glu
85 90 95

Asp Leu Thr Trp Gln Met Arg Ala Ile Arg Val Leu Pro Met Phe Ile
100 105 110

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

Arg Met Leu Glu Arg Lys Asp Gln Lys Thr Leu Glu Lys Leu Arg Ala
130 135 140

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

Leu Thr Gln Gln Leu Ile Gln Lys Tyr Asp Leu Asp Pro Ala Ala Lys
165 170 175

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

Leu Lys Val His Val Gly Glu Glu Pro Lys Leu Asp Ala Ala Val Ala
195 200 205

Arg Ser Asn Asp Val Glu Ile Val Pro Ser Asp Gly Leu Arg Asn Arg
210 215 220

Lys His Pro Asn Ala Arg Gly Ser Arg Thr Gly Ser Pro Thr Ala His
225 230 235 240

Thr Glu Pro Ser Leu Pro Ala Asn Ala Gly Leu Glu Thr Ala Arg Ala
245 250 255

Pro Met Val Val Glu His His Gln Gly Ser Gly Ala Ser Asp Gly Gly
260 265 270

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

Gln Ser Tyr Ala Leu Ile Cys Gly Asn Cys His Met His Asn Gly Leu
290 295 300

Ala Arg Lys Glu Asp Tyr Pro His Val Thr Tyr Tyr Cys Pro His Cys
305 310 315 320

His Ala Leu Asn Thr Ser Lys Gln Ser Met Gly Gln Tyr Ser Gly Ser
325 330 335

Asp Ser Gly Gln Ser Thr Pro Val Val Leu Ala Asp Gly Leu Ser Thr
340 345 350

Ser Ser Ser Val Gln Glu Thr Glu Leu Ser Asn Leu Thr Thr Leu Gln
355 360 365

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

<210> 952
<211> 395
<212> PRT
<213> Zea mays

<400> 952

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

Glu Ala Ala Glu Ala Lys Glu Lys Gly Lys Gln Gly Gly Val Leu Gly
20 25 30

Arg Val Trp Arg Ala Leu Phe Gly Gly Arg Glu Asp Phe Glu Lys Arg
35 40 45

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

Arg Arg Thr Gln Phe Ser Arg Arg Ala Val Arg Asn Leu Ile Val Leu

65 70 75 80

Ser Val Leu Ala Glu Val Leu Ala Val Val Tyr Ala Ile Met Thr Thr
85 90 95

Arg Asn Glu Asp Leu Thr Trp Gln Met Arg Ala Ile Arg Val Leu Pro
100 105 110

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

Asn Phe Thr Arg Met Phe Glu Gln Lys Asp Gln Lys Thr Leu Glu Lys
130 135 140

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

Asn Tyr Tyr Leu Thr Gln Gln Leu Ile Gln Lys Tyr Asp Leu Asp Pro
165 170 175

Ala Ala Lys Ala Ala Ala Ala Ser Val Leu Ala Ser Lys Leu Gly Glu
180 185 190

Glu Thr Gly Leu Lys Val His Val Gly Glu Glu Pro Lys Leu Asp Ala
195 200 205

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

Arg Asn Arg Lys Gln Pro Ser Ala Arg Gly Ser Arg Thr Gly Ser Pro
225 230 235 240

Thr Ser His Thr Pro Ala Gln Gly Thr Glu Thr Asn Leu Pro Pro Ala
245 250 255

Pro Ala Ser Ala Gly Leu Glu Thr Ala Pro Ala Pro Val Val Val Glu
260 265 270

His His Gln Gly Ser Gly Ala Ser Asp Gly Gly Gly Trp Ile Ala Lys
275 280 285

Ile Ala Ala Leu Leu Val Gly Glu Asp Pro Ser Gln Ser Tyr Ala Leu
290 295 300

Ile Cys Gly Ser Cys His Met His Asn Gly Leu Ala Arg Lys Glu Asp
305 310 315 320

Tyr Pro His Val Thr Tyr Tyr Cys Pro His Cys His Ala Leu Asn Thr
325 330 335

Ser Lys Gln Ser Met Gly Gln Tyr Ser Gly Ser Asn Ser Gly Arg Ser
340 345 350

Thr Pro Val Val Leu Ala Asp Gly Leu Ser Thr Ser Ser Ser Val Gln
355 360 365

Glu Thr Glu Leu Ser Asn Leu Thr Thr Leu Gln Glu Leu Pro Glu Glu
370 375 380

Gly Lys Thr Asp Lys Gln Gln Val Glu Ala Ser
385 390 395

<210> 953
<211> 393
<212> PRT
<213> Zea mays

<400> 953

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

Glu Ala Ala Glu Ala Lys Glu Lys Gly Lys Gln Gly Gly Val Leu Gly
20 25 30

Arg Val Trp Arg Ala Leu Phe Gly Gly Arg Glu Asp Phe Glu Lys Arg
35 40 45

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

Arg Arg Thr Gln Phe Ser Arg Arg Ala Val Arg Asn Leu Ile Val Leu
65 70 75 80

Ser Val Leu Ala Glu Val Leu Ala Val Val Tyr Ala Ile Met Thr Thr
85 90 95

Arg Asn Glu Asp Leu Thr Trp Gln Met Arg Ala Ile Arg Val Leu Pro
100 105 110

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

Asn Phe Thr Arg Met Phe Glu Gln Lys Asp Gln Lys Thr Leu Glu Lys
130 135 140

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

Asn Tyr Tyr Leu Thr Gln Gln Leu Ile Gln Lys Tyr Asp Leu Asp Pro
165 170 175

Ala Ala Lys Ala Ala Ala Ala Ser Val Leu Ala Ser Lys Leu Gly Glu
180 185 190

Glu Thr Gly Leu Lys Val His Val Gly Glu Glu Pro Lys Leu Asp Ala
195 200 205

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

Arg Asn Arg Lys Gln Pro Asn Ala Arg Gly Ser Arg Thr Gly Ser Pro
225 230 235 240

Thr Ser His Thr Pro Ala Gln Gly Thr Glu Thr Asn Leu Pro Pro Ala
245 250 255

Ser Ala Val Leu Glu Thr Ala Pro Ala Pro Val Val Val Glu His His
260 265 270

Gln Gly Ser Gly Ala Ser Asp Gly Gly Gly Trp Ile Ala Lys Ile Ala
275 280 285

Ala Leu Leu Val Gly Glu Asp Pro Ser Gln Ser Tyr Ala Leu Ile Cys
290 295 300

Gly Ser Cys His Met His Asn Gly Leu Ser Arg Lys Glu Asp Tyr Pro
305 310 315 320

His Val Thr Tyr Tyr Cys Pro His Cys His Ala Leu Asn Thr Ser Lys
325 330 335

Gln Ser Met Gly Gln Tyr Ser Gly Ser Asn Ser Gly Arg Ser Thr Pro
340 345 350

Val Val Leu Ala Asp Gly Leu Ser Thr Ser Ser Ser Val Gln Glu Thr
355 360 365

Glu Leu Ser Asn Leu Thr Thr Leu Gln Glu Leu Pro Glu Glu Gly Lys
370 375 380

Thr Asp Lys Gln Gln Val Glu Ala Ser
385 390

<210> 954
<211> 377
<212> PRT
<213> Zea mays

<400> 954

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

Thr Glu Ala Lys Glu Lys Gly Lys Arg Gly Gly Val Leu Arg Arg Val
20 25 30

Trp Arg Ala Leu Phe Gly Gly Arg Glu Asp Phe Glu Lys Arg Leu Gln
35 40 45

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

Thr Gln Phe Ser Arg Arg Thr Val Arg Asn Leu Ile Val Leu Ser Val
65 70 75 80

Leu Ala Glu Val Leu Ala Val Val Tyr Ala Ile Met Met Thr Arg Asn
85 90 95

Glu Asp Leu Thr Trp Gln Met Arg Ala Ile Arg Val Leu Pro Met Phe
100 105 110

Val Leu Pro Val Val Ser Ser Val Ile Tyr Ser Thr Val Val Asn Phe
115 120 125

Thr Arg Met Leu Glu Arg Lys Asp Gln Lys Thr Leu Glu Lys Leu Arg
130 135 140

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

Tyr Leu Thr Gln Gln Leu Ile Gln Lys Tyr Asp Leu Asp Pro Ala Ala
165 170 175

Lys Ala Ala Ala Ala Ser Val Leu Ala Ser Lys Leu Gly Glu Asp Thr
180 185 190

Gly Leu Lys Val His Val Gly Glu Glu Pro Lys Leu Asp Ala Ala Val
195 200 205

Ala Arg Ser Asn Asp Val Glu Ile Val Pro Ser Asp Gly Leu Arg Asn

210 215 220

Arg Lys Gln Pro Asn Ala Arg Gly Ser Arg Thr Gly Ser Pro Thr Ala
225 230 235 240

Asp Thr Pro Ala Arg Gly Thr Glu Ser Ser Leu Thr Ala Gly Ala Asp
245 250 255

Leu Glu Thr Ala Pro Ala Pro Leu Val Val Glu His His Gln Gly Leu
260 265 270

Gly Ala Ser Asp Gly Gly Gly Trp Ile Ala Lys Ile Ala Ala Leu Leu
275 280 285

Val Ala Glu Asp Pro Ser Gln Ser Tyr Ala Leu Ile Cys Gly Asn Cys
290 295 300

His Met His Asn Gly Leu Ala Arg Lys Glu Asp Tyr Pro His Val Thr
305 310 315 320

Tyr Tyr Cys Pro His Cys His Ala Leu Asn Thr Ser Lys Gln Ser Met
325 330 335

Trp Gln Tyr Ser Gly Ser Asn Ser Gly Arg Ser Ser Pro Val Val Leu
340 345 350

Asp Asp Gly Leu Ser Thr Ser Ser Ser Val Gln Glu Thr Glu Leu Ser
355 360 365

Asn Leu Thr His Thr Ala Gly Ala Thr
370 375

<210> 955
<211> 389
<212> PRT
<213> Oryza sativa Japonica Group

<400> 955

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

Lys Gly Lys Lys Glu Glu Gly Arg Arg Gly Gly Gly Val Leu Gly Arg
20 25 30

Met Trp Arg Ala Leu Phe Gly Gly Arg Glu Asp Tyr Glu Lys Arg Leu
35 40 45

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

Arg Thr Gln Phe Ser Arg Thr Ala Val Arg Asn Leu Ile Val Leu Ser
65 70 75 80

Val Leu Ala Glu Val Val Ala Ile Val Tyr Ala Ile Met Thr Thr Arg
85 90 95

Asn Glu His Ile Thr Trp Glu Met Arg Ala Ile Arg Val Leu Pro Met
100 105 110

Phe Val Leu Pro Ala Val Ser Ser Val Ile Tyr Ser Thr Val Val Lys
115 120 125

Phe Thr Arg Met Leu Glu Arg Lys Asp Gln Lys Thr Leu Glu Lys Leu
130 135 140

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

Tyr Tyr Leu Thr Gln Gln Leu Ile Gln Lys Tyr Asp Leu Asp Pro Ala
165 170 175

Ala Lys Ala Ala Ala Ala Ser Val Leu Ala Ser Lys Leu Gly Glu Glu
180 185 190

Thr Gly Leu Lys Val His Val Gly Glu Glu Pro Lys Leu Asp Ser Ala
195 200 205

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

Asn Arg Lys Gln Ser Asn Ala Arg Gly Ser Arg Thr Gly Gly Thr Thr
225   230   235   240

Ala Ala Gln Asn Pro Ala Gln Gly Ala Glu Ser Ser Leu Thr Ser Ser
                245   250   255

Ser Gly Leu Glu Gln Pro Pro Met Val Val Glu His Phe Gln Gly Ser
            260   265   270

Gly Ala Ser Asp Gly Gly Trp Ile Ala Lys Ile Ala Ala Leu Leu Val
        275   280   285

Gly Glu Asp Pro Ser Gln Ser Tyr Ala Leu Ile Cys Gly Asn Cys His
    290   295   300

Met His Asn Gly Leu Ala Arg Lys Glu Asp Tyr Pro His Ile Thr Tyr
305   310   315   320

Tyr Cys Pro His Cys His Ala Leu Asn Thr Ser Lys Gln Ser Leu Gly
                325   330   335

Gln His Ser Gly Ser Asn Ser Gly Arg Ser Thr Pro Val Ala Pro Ala
            340   345   350

Asp Gly Ile Ser Ala Ser Ser Ser Val Val Glu Ser Glu Val Ser Asn
        355   360   365

Met Thr Thr Ile Gln Glu Leu Lys Asn Glu Glu Asn Thr Glu Lys Gln
    370   375   380

Glu Val Gln Ala Ser
385

<210> 956
<211> 393
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 956

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

Gly Lys Gly Lys Glu Glu Gly Glu Lys Lys Lys Ala Gly Gly Gly Val
20 25 30

Leu Gly Arg Met Trp Arg Gly Ile Phe Gly Gly Arg Glu Asp Tyr Glu
35 40 45

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

Met Arg Arg Arg Thr Gln Phe Ser Arg Arg Thr Val Arg Asn Ile Ile
65 70 75 80

Val Leu Ser Val Leu Ala Glu Ala Val Ala Val Gly Tyr Ala Ile Met
85 90 95

Met Thr Arg Asp Glu Asp Leu Thr Trp Gln Met Arg Ala Ile Arg Val
100 105 110

Leu Pro Ile Phe Val Leu Pro Ala Ile Ser Ser Val Val Tyr Ser Ala
115 120 125

Val Val Asn Phe Thr Arg Met Arg Glu Arg Lys Asp Glu Lys Thr Leu
130 135 140

Glu Lys Leu Arg Ala Glu Arg Lys Ala Lys Ile Asp Glu Leu Lys Glu
145 150 155 160

Arg Thr Asn Tyr Tyr Leu Thr Gln Gln Leu Ile Gln Lys Tyr Asp Leu
165 170 175

Asp Pro Ala Ala Lys Ala Ala Ala Ala Ser Val Leu Ala Ser Lys Leu
180 185 190

Gly Ala Asp Ser Gly Leu Lys Val His Leu Gly Glu Glu Pro Asn Phe
195 200 205

Asp Ala Ala Val Val Met Ser Asn Asn Ala Glu Ile Leu Pro Ser Asp
210 215 220

Gly Val Arg Asn Arg Lys Gln Pro Asn Ala Arg Gly Ser Arg Thr Gly
225 230 235 240

Ser Thr Thr Ala Ala His Thr Ser Val Gln Gly Ala Glu Ser Ser Ser
245 250 255

Thr Leu Asn Ala Gly Leu Glu Asn Val Gln Pro Thr Arg Val Val Glu
260 265 270

His Cys Gln Gly Ser Gly Ala Ser Asp Gly Gly Trp Ile Ala Lys Ile
275 280 285

Ala Ala Leu Leu Val Gly Glu Asp Pro Ser Gln Ser Tyr Ala Leu Ile
290 295 300

Cys Gly Asn Cys His Met His Asn Gly Leu Ala Arg Lys Glu Asp Tyr
305 310 315 320

Pro His Ile Thr Tyr Tyr Cys Pro His Cys His Ala Leu Asn Thr Ser
325 330 335

Lys Asn Ser Met Gly Gln Tyr Ser Gly Ser Ser Ser Gly Pro Ser Thr
340 345 350

Pro Val Ala Pro Ala Asp Gly Leu Ser Ala Thr Ser Ser Val Val Glu
355 360 365

Ser Glu Leu Ile Asn Met Ala Thr Val Glu Glu Leu Pro Asn Glu Glu

370 375 380

His Thr Glu Lys Lys Val Glu Ala Ser
385 390

<210> 957
<211> 455
<212> PRT
<213> Zea mays

<400> 957

Met Gln Leu Asp Leu Asn Val Ala Glu Ala Pro Pro Pro Val Glu Met
1 5 10 15

Glu Ala Ser Asp Ser Gly Ser Ser Val Leu Asn Ala Ser Glu Ala Ala
20 25 30

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

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

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

His Arg His Gln His Gln Gln Gln Leu Val Thr Arg Glu Leu Phe Pro
85 90 95

Ala Gly Ala Gly Pro Pro Ala Pro Thr Pro Arg His Trp Ala Glu Leu
100 105 110

Gly Phe Phe Arg Ala Asp Leu Gln Gln Gln Gln Ala Pro Gly Pro Arg
115 120 125

Ile Val Pro His Pro His Ala Ala Pro Pro Pro Ala Lys Lys Ser Arg
130 135 140

Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr
145 150 155 160

Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys Gln
165 170 175

Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr
180 185 190

Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile Asn Phe
195 200 205

Asn Leu Ser Asp Tyr Glu Asp Asp Met Lys Gln Met Gly Ser Leu Ser
210 215 220

Lys Glu Glu Phe Val His Val Leu Arg Arg Gln Ser Thr Gly Phe Ser
225 230 235 240

Arg Gly Ser Ser Arg Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg
245 250 255

Trp Glu Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys
260 265 270

Ala Ala Ile Lys Cys Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Pro
275 280 285

Ser Thr Tyr His Gly Glu Leu Pro Thr Glu Val Ala Asp Val Asp Leu
290 295 300

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

Leu Gly Leu Gln Leu His His Gly Pro Phe Glu Gly Ser Glu Leu Lys
325 330 335

Lys Thr Lys Ile Asp Asp Ala Pro Ser Glu Leu Pro Gly Arg Pro Arg
340 345 350

Gln Leu Ser Pro Leu Val Ala Glu His Pro Pro Ala Trp Pro Ala Gln
355 360 365

Pro Pro His Pro Phe Phe Val Phe Thr Asn His Glu Met Ser Ala Ser
370 375 380

Gly Asp Leu His Arg Arg Pro Ala Gly Ala Val Pro Ser Trp Ala Trp
385 390 395 400

Gln Val Ala Ala Ala Ala Pro Pro Pro Ala Ala Leu Pro Ser Ser Ala
405 410 415

Ala Ala Ser Ser Gly Phe Ser Asn Thr Ala Thr Thr Ala Ala Thr Thr
420 425 430

Ala Pro Ser Ala Ser Ser Leu Arg Tyr Cys Pro Pro Pro Pro Pro Pro
435 440 445

Ser Ser His His His Pro Arg
450 455

<210> 958
<211> 456
<212> PRT
<213> Zea mays

<400> 958

Met Gln Leu Asp Leu Asn Val Ala Glu Ala Pro Pro Pro Val Glu Met
1 5 10 15

Glu Ala Ser Asp Ser Gly Ser Ser Val Leu Asn Ala Ser Glu Ala Ala
20 25 30

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

Pro Ala Ala Leu Glu Phe Ser Ile Leu Ile Arg Ser Asp Ser Asp Ala

50 55 60

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

His Arg His Gln His Gln Gln Gln Leu Val Thr Arg Glu Leu Phe Pro
85 90 95

Ala Gly Ala Gly Pro Pro Ala Pro Ala Pro Arg His Trp Ala Glu Leu
100 105 110

Gly Phe Phe Arg Ala Asp Leu Gln Gln Gln Gln Ala Pro Gly Pro Arg
115 120 125

Ile Val Pro His Pro His Ala Ala Pro Pro Pro Ala Lys Lys Ser Arg
130 135 140

Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr
145 150 155 160

Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys Gln
165 170 175

Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr
180 185 190

Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile Asn Phe
195 200 205

Asn Leu Ser Asp Tyr Glu Asp Asp Met Lys Gln Met Gly Ser Leu Ser
210 215 220

Lys Glu Glu Phe Val His Val Leu Arg Arg Gln Ser Thr Gly Phe Ser
225 230 235 240

Arg Gly Ser Ser Arg Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg
245 250 255

Trp Glu Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys
260 265 270

Ala Ala Ile Lys Cys Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Pro
275 280 285

Ser Thr Tyr His Gly Glu Leu Pro Thr Glu Val Ala Asp Val Asp Leu
290 295 300

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

Leu Gly Leu Gln Leu His His Gly Pro Phe Glu Gly Ser Glu Leu Lys
325 330 335

Lys Thr Lys Ile Asp Asp Ala Pro Ser Asp Leu Pro Gly Arg Pro Arg
340 345 350

Arg Leu Ser Pro Leu Val Ala Glu His Pro Pro Ala Trp Pro Ala Gln
355 360 365

Pro Pro His Pro Phe Phe Val Phe Thr Asn His Glu Met Ser Ala Ser
370 375 380

Gly Asp Leu His Arg Arg Pro Ala Gly Ala Val Pro Ser Trp Ala Trp
385 390 395 400

Gln Val Ala Ala Ala Ala Pro Pro Pro Ala Ala Leu Pro Ser Ser Ala
405 410 415

Ala Ala Ser Ser Gly Phe Ser Asn Thr Ala Thr Thr Ala Ala Thr Ala
420 425 430

Ala Pro Ser Ala Ser Ser Leu Arg Tyr Cys Pro Pro Pro Pro Pro Pro
435 440 445

Pro Ser Ser His His His Arg Arg

450 455

<210> 959
<211> 539
<212> PRT
<213> Sorghum bicolor

<400> 959

Met Ala Ser Pro Ala Ile Pro Phe Ala Pro Leu Thr Ser His Arg Ala
1 5 10 15

Val Pro Phe Val Leu Gly Cys Pro Pro Pro Trp Pro Pro Arg Pro Pro
20 25 30

Pro Ala Ala Pro Gly Arg Pro Pro Arg Pro Asp Ala Ala Ala Ala Ala
35 40 45

Arg Leu Leu Glu Glu Glu Ala Arg Ala Gly Ser Ser Arg Ala Arg Ser
50 55 60

Pro Ala Gly Arg Pro Glu Leu Glu Ser Met Val Leu Asp Leu Asn Ala
65 70 75 80

Glu Ser Pro Thr Ala Gly Ser Ala Ser Ala Thr Ser Ser Ser Ser Gly
85 90 95

Val Phe Arg Phe Asp Leu Leu Gly Gly Thr Pro Asp Glu Glu Gly Cys
100 105 110

Ser Pro Ser Pro Pro Val Val Thr Arg Gln Leu Phe Pro Leu Pro Ser
115 120 125

Tyr Pro Asp Ala Ala Ala Ala Pro Thr Ala Ala Ser Asn Gly Ser Pro
130 135 140

Pro Pro Pro Gln Ala Ala Gly Pro Trp Ala Arg Arg Ala Ala Asp Leu
145 150 155 160

Val Ala Pro Ala Leu Gly Gln Gly Gln Gly Gln Gly Ala Val Val Met
165 170 175

Pro Ala Pro Ser Ser Pro Pro Ala Ala Val Ser Pro Ala Ala Gly Lys
180 185 190

Lys Ser Arg Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val
195 200 205

Thr Phe Tyr Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys
210 215 220

Gly Lys Gln Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala
225 230 235 240

Arg Ala Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Leu Asp Ala Asp
245 250 255

Ile Asn Phe Gln Leu Lys Asp Tyr Glu Asp Asp Leu Lys Gln Met Lys
260 265 270

Asn Trp Thr Lys Glu Glu Phe Val His Ile Leu Arg Arg Gln Ser Thr
275 280 285

Gly Phe Ala Arg Gly Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys
290 295 300

Cys Gly Arg Trp Glu Ala Arg Met Gly Gln Leu Leu Gly Lys Lys Tyr
305 310 315 320

Ile Tyr Leu Gly Leu Phe Asp Ser Glu Ile Glu Ala Ala Arg Ala Tyr
325 330 335

Asp Arg Ala Ala Ile Arg Phe Asn Gly Pro Asp Ala Val Thr Asn Phe
340 345 350

Asp Ser Ser Ser Tyr Asp Gly Asp Val Pro Leu Pro Thr Ala Ile Glu
355 360 365

Lys Asp Val Val Asp Gly Asp Ile Leu Asp Leu Asn Leu Arg Ile Ser
370 375 380

Gln Pro Asn Val His Asp Leu Lys Ser Asp Gly Thr Leu Thr Gly Phe
385 390 395 400

Gly Leu Gly Cys Asn Ser Pro Glu Ala Ser Ser Ser Ile Val Ser Gln
405 410 415

Pro Ile Ser Pro Gln Trp Pro Val His Pro His Ser Thr Pro Met Gln
420 425 430

Leu Gln His Pro His Leu Tyr Ala Ser Pro Cys Pro Gly Phe Phe Val
435 440 445

Asn Leu Arg Glu Ala Pro Met Glu Glu Glu Lys Arg Ala Glu Arg Ala
450 455 460

Gly Pro Glu Pro Ala Phe Pro Ser Trp Ala Trp Gln Thr Gln Gly Ser
465 470 475 480

Pro Ala Pro Phe Leu Pro Ala Thr Ala Thr Ala Ala Ser Ser Gly Phe
485 490 495

Ser Thr Ala Ala Thr Thr Thr Gly Val Asp Ala Ala Thr Ala Ala Arg
500 505 510

Ser Val Pro Pro Ser Leu Ser Gly Gly Pro Arg Gln Leu Phe Ser Gly
515 520 525

Tyr Gln Leu Gln Leu Arg Phe Pro Pro Thr Ala
530 535

<210> 960
<211> 535
<212> PRT
<213> Zea mays

<400> 960

Met Ala Ser Pro Ala Ile Pro Phe Ala Pro Leu Thr Ser His Arg Ala
1 5 10 15

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

Pro Ala Ala Arg Pro Arg Pro Pro Pro Pro Arg Pro Asp Ala Ala Ala
35 40 45

Ala Ala Arg Leu Leu Glu Glu Glu Ala Gly Ala Gly Ser Ser Arg Ala
50 55 60

Arg Ser Pro Gly Gly Pro Glu Leu Glu Ser Met Val Leu Asp Leu Asn
65 70 75 80

Ala Glu Ser Pro Thr Pro Gly Ser Ala Ser Ala Ala Ser Ser Ser Ser
85 90 95

Val Val Val Gly Gly Gly Phe Phe Arg Phe Asp Leu Leu Gly Gly Thr
100 105 110

Pro Asp Glu Glu Gly Cys Ser Pro Ser Pro Pro Ile Val Thr Arg Gln
115 120 125

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

Thr Ala Ser Asn Gly Ser Pro Pro Pro Glu Val Ala Gly Ala Trp Ala
145 150 155 160

Arg Arg Pro Ala Asp Leu Gly Ala Pro Ala Leu Ala Gln Gly Lys Val
165 170 175

Met Ser Ala Pro Ser Ser Pro Ala Val Leu Ser Pro Ala Ala Gly Lys
180 185 190

Lys Ser Arg Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val
195 200 205

Thr Phe Tyr Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys
210 215 220

Gly Lys Gln Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala
225 230 235 240

Arg Ala Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Leu Asp Ala Asp
245 250 255

Ile Asn Phe Gln Leu Lys Asp Tyr Glu Asp Asp Leu Lys Gln Met Arg
260 265 270

Asn Trp Thr Lys Glu Glu Phe Val His Ile Leu Arg Arg Gln Ser Thr
275 280 285

Gly Phe Ala Arg Gly Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys
290 295 300

Cys Gly Arg Trp Glu Ala Arg Met Gly Gln Leu Leu Gly Lys Lys Tyr
305 310 315 320

Ile Tyr Leu Gly Leu Phe Asp Ser Glu Ile Glu Ala Ala Arg Ala Tyr
325 330 335

Asp Arg Ala Ala Ile Arg Phe Asn Gly Pro Asp Ala Val Arg Asn Phe
340 345 350

Asp Ser Val Ser Tyr Asp Gly Asp Val Pro Leu Pro Pro Ala Ile Glu
355 360 365

Lys Asp Ala Val Val Asp Gly Asp Ile Leu Asp Leu Asn Leu Arg Ile
370 375 380

Ser Gln Pro Asn Val His Asp Leu Arg Ser Asp Gly Thr Leu Thr Gly

385 390 395 400

Phe Gly Leu Ser Cys Asn Ser Pro Glu Ala Ser Ser Ser Ile Val Ser
405 410 415

Gln Pro Met Gly Pro Gln Trp Pro Val His Pro His Ser Arg Ser Met
420 425 430

Arg Pro Gln His Pro His Leu Tyr Ala Ser Pro Cys Pro Gly Phe Phe
435 440 445

Val Asn Leu Arg Glu Ala Pro Met Gln Glu Glu Glu Asn Arg Ser Glu
450 455 460

Pro Ala Cys Pro Gln Pro Phe Pro Ser Trp Ala Trp Gln Thr Gln Gly
465 470 475 480

Ser Arg Ala Pro Val Leu Pro Ala Thr Thr Ala Ala Ser Ser Gly Phe
485 490 495

Ser Thr Ala Ala Ala Thr Gly Val Asp Ala Ala Thr Ala Gly His Ser
500 505 510

Val Pro Pro Pro Ser Gly Ser Leu Arg Gln Phe Ser Gly Tyr His Gln
515 520 525

Leu Arg Phe Pro Pro Thr Ala
530 535

<210> 961
<211> 528
<212> PRT
<213> Zea mays

<400> 961

Pro Phe Ala Pro Leu Thr Ser His Arg Ala Ala Pro Phe Val Leu Gly
1 5 10 15

Cys Pro Pro Pro Trp Pro Pro Pro Pro Pro Pro Ala Ala Arg Pro Arg
20 25 30

Pro Pro Pro Pro Arg Pro Asp Ala Ala Ala Ala Ala Arg Leu Leu Glu
35 40 45

Glu Glu Ala Gly Ala Gly Ser Ser Arg Ala Arg Ser Pro Gly Gly Pro
50 55 60

Glu Leu Glu Ser Met Val Leu Asp Leu Asn Ala Glu Ser Pro Thr Pro
65 70 75 80

Gly Ser Ala Ser Ala Ala Ser Ser Ser Ser Val Val Val Gly Gly Gly
85 90 95

Phe Phe Arg Phe Asp Leu Leu Gly Gly Thr Pro Asp Glu Glu Gly Cys
100 105 110

Ser Pro Ser Pro Pro Ile Val Thr Arg Gln Leu Phe Pro Leu Pro Tyr
115 120 125

Pro Asp Ala Ala Gly Ser Thr Ala Ala Ser Thr Ala Ser Asn Gly Ser
130 135 140

Pro Pro Pro Glu Val Ala Gly Ala Trp Ala Arg Arg Pro Ala Asp Leu
145 150 155 160

Gly Ala Pro Ala Leu Ala Gln Gly Lys Val Met Ser Ala Pro Ser Ser
165 170 175

Pro Ala Val Leu Ser Pro Ala Ala Gly Lys Lys Ser Arg Arg Gly Pro
180 185 190

Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr
195 200 205

Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu
210 215 220

Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala
225 230 235 240

Ala Ile Lys Phe Arg Gly Leu Asp Ala Asp Ile Asn Phe Gln Leu Lys
245 250 255

Asp Tyr Glu Asp Asp Leu Lys Gln Met Arg Asn Trp Thr Lys Glu Glu
260 265 270

Phe Val His Ile Leu Arg Arg Gln Ser Thr Gly Phe Ala Arg Gly Ser
275 280 285

Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu Ala
290 295 300

Arg Met Gly Gln Leu Leu Gly Lys Lys Tyr Ile Tyr Leu Gly Leu Phe
305 310 315 320

Asp Ser Glu Ile Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Arg
325 330 335

Phe Asn Gly Pro Asp Ala Val Arg Asn Phe Asp Ser Val Ser Tyr Asp
340 345 350

Gly Asp Val Pro Leu Pro Pro Ala Ile Glu Lys Asp Val Val Asp Gly
355 360 365

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

Leu Arg Ser Asp Gly Thr Leu Thr Gly Phe Gly Leu Ser Cys Asn Ser
385 390 395 400

Pro Glu Ala Ser Ser Ser Ile Val Ser Gln Pro Met Gly Pro Gln Trp
405 410 415

Pro Val His Pro His Ser Arg Ser Met Arg Pro Gln His Pro His Leu
420 425 430

Tyr Ala Ser Pro Cys Pro Gly Phe Phe Val Asn Leu Arg Glu Ala Pro
435 440 445

Met Gln Glu Glu Glu Asn Arg Ser Glu Pro Ala Cys Pro Gln Pro Phe
450 455 460

Pro Ser Trp Ala Trp Gln Thr Gln Gly Ser Arg Ala Pro Val Leu Pro
465 470 475 480

Ala Thr Thr Ala Ala Ser Ser Gly Phe Ser Thr Ala Ala Ala Thr Gly
485 490 495

Val Asp Ala Ala Thr Ala Gly His Ser Val Pro Pro Pro Ser Gly Ser
500 505 510

Leu Arg Gln Phe Ser Gly Tyr His Gln Leu Arg Phe Pro Pro Thr Ala
515 520 525

<210> 962
<211> 460
<212> PRT
<213> Zea mays

<400> 962

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

Ala Ala Ser Ser Ser Ser Val Val Val Gly Gly Gly Phe Phe Arg Phe
20 25 30

Asp Leu Leu Gly Gly Thr Pro Asp Glu Glu Gly Cys Ser Pro Ser Pro
35 40 45

Pro Ile Val Thr Arg Gln Leu Phe Pro Leu Pro Tyr Pro Asp Ala Ala
50 55 60

Gly Ser Thr Ala Ala Ser Thr Ala Ser Asn Gly Ser Pro Pro Pro Glu
65 70 75 80

Val Ala Gly Ala Trp Ala Arg Arg Pro Ala Asp Leu Gly Ala Pro Ala
85 90 95

Leu Ala Gln Gly Lys Val Met Ser Ala Pro Ser Ser Pro Ala Val Leu
100 105 110

Ser Pro Ala Ala Gly Lys Lys Ser Arg Arg Gly Pro Arg Ser Arg Ser
115 120 125

Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp Glu
130 135 140

Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe Asp
145 150 155 160

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

Arg Gly Leu Asp Ala Asp Ile Asn Phe Gln Leu Lys Asp Tyr Glu Asp
180 185 190

Asp Leu Lys Gln Met Arg Asn Trp Thr Lys Glu Glu Phe Val His Ile
195 200 205

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

Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu Ala Arg Met Gly Gln
225 230 235 240

Leu Leu Gly Lys Lys Tyr Ile Tyr Leu Gly Leu Phe Asp Ser Glu Ile
245 250 255

Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Arg Phe Asn Gly Pro

260 265 270

Asp Ala Val Arg Asn Phe Asp Ser Val Ser Tyr Asp Gly Asp Val Pro
275 280 285

Leu Pro Pro Ala Ile Glu Lys Asp Val Val Asp Gly Asp Ile Leu Asp
290 295 300

Leu Asn Leu Arg Ile Ser Gln Pro Asn Val His Asp Leu Arg Ser Asp
305 310 315 320

Gly Thr Leu Thr Gly Phe Gly Leu Ser Cys Asn Ser Pro Glu Ala Ser
325 330 335

Ser Ser Ile Val Ser Gln Pro Met Gly Pro Gln Trp Pro Val His Pro
340 345 350

His Ser Arg Ser Met Arg Pro Gln His Pro His Leu Tyr Ala Ser Pro
355 360 365

Cys Pro Gly Phe Phe Val Asn Leu Arg Glu Ala Pro Met Gln Glu Glu
370 375 380

Glu Asn Arg Ser Glu Pro Ala Cys Pro Gln Pro Phe Pro Ser Trp Ala
385 390 395 400

Trp Gln Thr Gln Gly Ser Arg Ala Pro Val Leu Pro Ala Thr Thr Ala
405 410 415

Ala Ser Ser Gly Phe Ser Thr Ala Ala Ala Thr Gly Val Asp Ala Ala
420 425 430

Thr Ala Gly His Ser Val Pro Pro Pro Ser Gly Ser Leu Arg Gln Phe
435 440 445

Ser Gly Tyr His Gln Leu Arg Phe Pro Pro Thr Ala
450 455 460

<210> 963
<211> 142
<212> PRT
<213> Oryza sativa Japonica Group

<400> 963

Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His
1   5   10   15

Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
            20   25   30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
        35   40   45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
    50   55   60

Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
65   70   75   80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Ile Glu Glu Asn
                85   90   95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
            100   105   110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
        115   120   125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
    130   135   140

<210> 964
<211> 142
<212> PRT
<213> Zea mays

<400> 964

Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His
1 5 10 15

Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
20 25 30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60

Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
65 70 75 80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

<210> 965
<211> 142
<212> PRT
<213> Zea mays

<400> 965

Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His
1 5 10 15

Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
20 25 30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Val Ser Ser His Ala Lys Gly
35 40 45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60

Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
65 70 75 80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

<210> 966
<211> 142
<212> PRT
<213> Elaeis guineensis

<400> 966

Met Gly Lys Thr Arg Gly Met Gly Ala Ala Arg Lys Leu Lys Thr His
1 5 10 15

Arg Arg Arg Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
20 25 30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala

50 55 60

Ile Arg Lys Cys Ala Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile
65 70 75 80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Ile Glu Glu Asn
85 90 95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

<210> 967
<211> 142
<212> PRT
<213> Elaeis guineensis

<400> 967

Met Gly Lys Thr Arg Gly Met Gly Ala Ala Arg Lys Leu Lys Thr His
1 5 10 15

Arg Arg Arg Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
20 25 30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60

Ile Arg Lys Cys Ala Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile
65 70 75 80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

<210> 968
<211> 142
<212> PRT
<213> Solanum tuberosum

<400> 968

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

Arg Arg Arg Gln Arg Trp Ala Asp Lys Ser Tyr Lys Lys Ser His Leu
20 25 30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60

Ile Arg Lys Cys Ala Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile
65 70 75 80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

<210> 969
<211> 142
<212> PRT
<213> Ricinus communis

<400> 969

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

Arg Arg Arg Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
20 25 30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60

Ile Arg Lys Cys Ala Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile
65 70 75 80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

<210> 970
<211> 142
<212> PRT
<213> Vitis vinifera

<400> 970

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

Arg Arg Arg Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser Asn Leu
            20                  25                  30

Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
        35                  40                  45

Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
    50                  55                  60

Ile Arg Lys Cys Ala Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile
65                  70                  75                  80

Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
                85                  90                  95

Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
            100                 105                 110

Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
        115                 120                 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
    130                 135                 140
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<210> 971
<211> 325
<212> PRT
<213> Zea mays

<400> 971

Met Asp Trp Ala Ala Ala Ser Gly Ser Pro Ser Trp Gly Ala Ala Ala
1 5 10 15

Thr Asp Pro Gly Pro Thr Met Leu Ser Phe Ala Gly Pro Ser Ser Ser
20 25 30

Ala Ala Asp Ala Glu Val Arg Leu Gln Asp Phe Ala Ala Gly Leu Ala
35 40 45

Gln Ser Ser Arg Pro Thr Gly Ala Ala Pro Gly Ala Gly Arg Arg Ser
50 55 60

Arg Ala Ala Val Gly Gly Ala Gly Ala Glu Ala Cys Ser Val Asp Gly
65 70 75 80

Cys Arg Ser Asp Leu Ser Arg Cys Arg Glu Tyr His Arg Arg His Lys
85 90 95

Val Cys Glu Ala His Ser Lys Ala Pro Val Val Val Val Gly Gly Gln
100 105 110

Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Met Leu Ser Glu
115 120 125

Phe Asp Glu Glu Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly His Asn
130 135 140

Arg Arg Arg Arg Lys Pro Gln His Asp Leu Thr Asn Leu Gly Gly Phe
145 150 155 160

Phe Pro Tyr His Gln Val Asn Gln Phe Glu Phe Tyr Pro Gln Thr Ile
165 170 175

Pro Thr Val Gly Gln Asn Ser Asp Ala Val His Leu Val Gly Arg Gln
180 185 190

Gln Pro Phe Ser Ile Ser Phe Ser Arg Thr Pro Asp Glu Phe Pro Phe
195 200 205

Pro Gln Gly Gly Gly Ser Ser Val Leu His His Leu His Ala Ala Arg
210 215 220

Pro Gly His His Ala Glu Gly Ser Ser His Thr Gly Ser Ser Thr Arg
225 230 235 240

Asp Asn Ala Leu Ser Gly Thr Leu Gly Pro Glu Cys Ala Leu Ser Leu
245 250 255

Leu Ser Ser Ser Leu Arg Arg Pro Ser Thr Ala Gly Val Pro Ala Val
260 265 270

Gly Gln Pro Gln Val Thr Ala Ser Ser Thr Thr Ala Val Ser Gln Ala
275 280 285

Ala Thr Ala Ala Val Ala Thr Ala Ala Phe Ala Ala Ser Ala Gly His
290 295 300

His Val Phe Val Pro Asp Ala Met Phe Glu Asp Pro Ser Gln Ala Leu
305 310 315 320

Pro Phe Ser Trp Gln
325

<210> 972
<211> 331
<212> PRT
<213> Zea mays

<400> 972

Met Asp Trp Ala Ala Ala Ser Gly Ser Pro Ser Trp Gly Ala Ala Ala
1 5 10 15

Thr Asp Pro Gly Pro Thr Met Leu Ser Phe Ala Gly Pro Ser Ser Ala
20 25 30

```
Ala Ala Asp Ala Glu Val Arg Leu Gln Asp Phe Ala Ala Gly Leu Ala
        35                  40                  45

Gln Ser Ser Arg Pro Thr Gly Ala Ala Pro Gly Ala Gly Arg Arg Ser
    50                  55                  60

Arg Ala Ala Gly Gly Gly Ala Gly Ala Glu Ala Cys Ser Val Asp Val
65                  70                  75                  80

Cys Arg Ser Asp Leu Ser Arg Cys Arg Glu Tyr His Arg Arg His Lys
                85                  90                  95

Val Cys Glu Ala His Ser Lys Ala Pro Val Val Val Val Gly Gly Gln
            100                 105                 110

Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Met Leu Ser Glu
        115                 120                 125

Phe Asp Glu Glu Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly His Asn
    130                 135                 140

Arg Arg Arg Arg Lys Pro Gln His Asp Leu Thr Asn Leu Gly Gly Phe
145                 150                 155                 160

Phe Pro Tyr His Gln Val Asn Gln Phe Glu Phe Tyr Pro Gln Thr Ile
                165                 170                 175

Pro Thr Val Gly Gln Asn Ser Asp Ala Val His Leu Val Gly Arg Gln
            180                 185                 190

Gln Pro Phe Ser Ile Ser Phe Ser Arg Thr Pro Pro Asp Glu Phe Pro
        195                 200                 205

Phe Pro Gln Gly Gln Gly Gly Gly Ser Ser Val Leu His His Leu His
    210                 215                 220

Ala Ala Arg Pro Gly His His Ala Glu Gly Ser Ser Ser His Thr Gly
```

225 230 235 240

Ser Ser Thr Arg Asp Asn Ala Leu Ser Val Ser Gly Thr Leu Gly Pro
245 250 255

Glu Cys Ala Leu Ser Leu Leu Ser Ser Ser Leu Arg Arg Pro Ser Thr
260 265 270

Ala Gly Val Pro Ala Val Gly Gln Pro Gln Val Thr Ala Ser Ser Thr
275 280 285

Thr Ala Val Ser Gln Ala Ala Thr Ala Ala Val Ala Thr Ala Ala Phe
290 295 300

Ala Ala Ser Ala Gly His Arg Val Phe Val Pro Asp Ala Met Phe Glu
305 310 315 320

Asp Pro Ser Gln Ala Leu Pro Phe Ser Trp Gln
325 330

<210> 973
<211> 325
<212> PRT
<213> Sorghum bicolor

<400> 973

Met Asp Trp Ala Ala Ala Ser Gly Ala Pro Ser Trp Gly Ala Ala Ala
1 5 10 15

Thr Asp Pro Gly Pro Thr Met Leu Ser Phe Ala Gly Pro Ser Ser Ser
20 25 30

Thr Thr Pro Ala Ala Asp Ala Glu Ala Arg Leu Gln Asp Phe Ala Ala
35 40 45

Gly Leu Ala Gln Ser Ala Arg Pro Ala Gly Ala Ala Gly Ala Gly Arg
50 55 60

Arg Ser Arg Ala Ala Gly Gly Gly Ala Gly Val Glu Ala Cys Ser Val
65 70 75 80

Asp Gly Cys Arg Ser Asp Leu Ser Arg Cys Arg Glu Tyr His Arg Arg
85 90 95

His Lys Val Cys Glu Ala His Ser Lys Thr Pro Val Val Val Val Ala
100 105 110

Gly Gln Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Met Leu
115 120 125

Ser Glu Phe Asp Glu Gly Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly
130 135 140

His Asn Arg Arg Arg Arg Lys Pro Gln His Asp Leu Thr Asn Leu Gly
145 150 155 160

Gly Phe Phe Pro Tyr His Gln Val Asn Gln Phe Glu Val Tyr Pro Arg
165 170 175

Thr Ile Pro Thr Val Gly Gln Asn Ser Asp Ala Met His Leu Val Gly
180 185 190

Arg Gln Gln Pro Phe Ser Ile Ser Phe Ser Arg Thr Pro Asn Gln Phe
195 200 205

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

His Leu Leu Ala Glu Gly Ser Ser His Thr Gly Ser Ser Thr Cys Ser
225 230 235 240

Asn Pro Leu Ser Gly Thr Leu Gly Pro Glu Cys Ala Leu Ser Leu Leu
245 250 255

Ser Ser Ser Leu His His Pro Ser Ala Ala Gly Ile Pro Thr Ala Gly
260 265 270

Gln Pro Gln Val Ala Ser Ser Leu Ser Arg Ile Ala Ala Val Ser Gln
        275   280   285

Ala Ala Thr Thr Ala Met Ala Thr Ala Phe Ala Ala Gly Val Gly His
    290   295   300

His Val Phe Val Pro Asp Ala Met Phe Glu Asp Pro Ser Gln Ala Leu
305   310   315   320

Pro Phe Ser Trp Gln
                325

<210> 974
<211> 264
<212> PRT
<213> Sorghum bicolor

<400> 974

Met Gly Gly Gly Glu Cys Ala Leu Gly Asp Ala Ala Ile Gly Glu Glu
1   5   10   15

Thr Leu Asn Tyr Asp Gly Asp Asp Val Glu Met Ala Asp Ala Asp Ser
            20   25   30

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

Ala Ala Gly Gly Gly Gly His Ala Glu Lys Asp Gly Pro Glu Gly Lys
    50   55   60

Lys Lys Lys Lys Lys Lys Arg Asn Lys Gly Lys Lys Asn Lys Gly Arg
65   70   75   80

Gln Asp Ala Ala Pro Thr Thr Ile Ala Gly Ile Asn Arg Phe Val Leu
                85   90   95

Glu Thr Cys Lys Arg Leu Lys Glu Lys Lys Ser Tyr Leu Val Trp Asn

100 105 110

Ala Val Gly Cys Leu Gly Val Thr Ala Val Thr Asp Leu Val Arg Glu
115 120 125

Val Glu Ala Ile Gln Lys Cys Gly Gly Gln Thr Ile Ala Asp Gly Ser
130 135 140

Arg Phe Arg Thr Gly Gly Gly Ile Leu Trp Asn Ile Leu Lys Ser Arg
145 150 155 160

Glu Pro Lys Ala Tyr Lys Glu Ile Met Ala Lys Gly Lys Glu Leu Glu
165 170 175

Lys Gln Phe Arg Tyr Thr Lys Arg Pro Gln Ile Ser Arg Asn Glu Asp
180 185 190

Ala Ser Ser Gln Gly Ser Ala Leu Ile Asp Asp Glu Ile Glu Ala Gln
195 200 205

Glu Gln Lys Glu Met Leu Asp Asp Pro Glu Gln Leu Asp Asp Val Gly
210 215 220

Glu Pro Pro Ala Ser Asp Asn Arg Thr Gln Arg Lys Pro Leu Ala Asp
225 230 235 240

Arg Ile Arg Ala Pro Val Ala Tyr Asp Asp Leu Phe Glu Glu Gly Glu
245 250 255

Ile His Glu Gly Glu Pro Gln Ser
260

<210> 975
<211> 263
<212> PRT
<213> Zea mays

<400> 975

Met Gly Gly Ser Glu Cys Ala Leu Gly Asp Ala Ala Ile Gly Glu Glu
1 5 10 15

Thr Leu Asn Tyr Asp Gly Asp Asp Val Glu Met Ala Asp Ala Asp Ser
20 25 30

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

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

Lys Lys Arg Lys Lys Arg Arg Asn Lys Gly Lys Lys Asn Lys Gly Arg
65 70 75 80

Gln Asp Gly Ala Pro Thr Asn Ile Ala Asp Ile Asn Arg Phe Val Leu
85 90 95

Asn Thr Cys Lys Arg Leu Lys Glu Lys Lys Ser Tyr Leu Val Trp Asn
100 105 110

Ala Val Gly Cys Leu Gly Val Thr Ala Val Asn Asp Leu Val Arg Glu
115 120 125

Val Glu Ala Ile Gln Lys Cys Gly Gly Gln Thr Ile Ala Asp Gly Ser
130 135 140

Arg Phe Arg Thr Gly Gly Gly Ile Leu Trp Asn Ile Leu Lys Ser Arg
145 150 155 160

Glu Pro Lys Ala Tyr Lys Glu Ile Met Ala Lys Gly Lys Glu Leu Glu
165 170 175

Lys Gln Phe Arg Cys Thr Lys Arg Pro Gln Ile Ser Arg Asn Glu Asp
180 185 190

Ala Ser Ser Gln Gly Ser Ala Leu Ile Asp Asp Glu Ile Glu Ala Arg
195 200 205

Asp Gln Lys Glu Thr Leu Asp Asp Pro Lys Gln Leu Asp Asp Val Glu
210 215 220

Ile His Val Ser Asp Asn Lys Ala Gln Arg Lys Pro Leu Ala Asp Arg
225 230 235 240

Ile Arg Ala Pro Val Ala Tyr Asp Asp Leu Phe Glu Glu Gly Glu Ile
245 250 255

His Asp Gly Glu Pro Arg Ser
260

<210> 976
<211> 263
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<222> (94)..(94)
<223> Xaa can be any naturally occurring amino acid

<400> 976

Met Gly Gly Ser Glu Cys Ala Leu Gly Asp Ala Ala Ile Gly Glu Glu
1 5 10 15

Thr Leu Asn Tyr Asp Gly Asp Asp Val Glu Met Ala Asp Ala Asp Ser
20 25 30

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

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

Lys Lys Arg Lys Lys Arg Arg Asn Lys Gly Lys Lys Asn Lys Gly Arg
65 70 75 80

Gln Asp Gly Ala Pro Thr Asn Ile Ala Asp Ile Asn Arg Xaa Val Leu
85 90 95

Asn Thr Cys Lys Arg Leu Lys Glu Lys Lys Ser Tyr Leu Val Trp Asn
100 105 110

Ala Val Gly Cys Leu Gly Val Thr Ala Val Asn Asp Leu Val Arg Glu
115 120 125

Val Glu Ala Ile Gln Lys Cys Gly Gly Gln Thr Ile Ala Asp Gly Ser
130 135 140

Arg Phe Arg Thr Gly Gly Gly Ile Leu Trp Asn Ile Leu Lys Ser Arg
145 150 155 160

Glu Pro Lys Ala Tyr Lys Glu Ile Met Ala Lys Gly Lys Glu Leu Glu
165 170 175

Lys Gln Phe Arg Cys Thr Lys Arg Pro Gln Ile Ser Arg Asn Glu Asp
180 185 190

Ala Ser Ser Gln Gly Ser Ala Leu Ile Asp Asp Glu Ile Glu Ala Arg
195 200 205

Asp Gln Lys Glu Thr Leu Asp Asp Pro Lys Gln Leu Asp Asp Val Glu
210 215 220

Ile His Val Ser Asp Asn Lys Ala Gln Arg Lys Pro Leu Ala Asp Arg
225 230 235 240

Ile Arg Ala Pro Val Ala Tyr Asp Asp Leu Phe Glu Glu Gly Glu Ile
245 250 255

His Asp Gly Glu Pro Arg Ser
260

<210> 977

<211> 378
<212> PRT
<213> Zea mays

<400> 977

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

Lys Phe Gly Lys Lys Ile Tyr Phe Glu Gln Asp Gly Gly Ser Gly Ser
20 25 30

Gly Ala Gly Ala Val Gly Gly Arg Lys Gly Lys Gly Val Ala Thr Gly
35 40 45

Gly Ala Arg Pro Ala Ser Ala Ala Ser Ala Ala Gln Pro Pro Arg Cys
50 55 60

Gln Val Asp Gly Cys Gly Val Asp Leu Ser Ala Val Lys Gln Tyr Tyr
65 70 75 80

Cys Arg His Lys Val Cys Asn Met His Ser Lys Glu Pro Arg Val Phe
85 90 95

Val Ala Gly Ile Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His
100 105 110

Gln Leu His Glu Phe Asp Gln Gly Lys Arg Ser Cys Arg Arg Arg Leu
115 120 125

Ile Gly His Asn Glu Arg Arg Arg Lys Pro Pro Pro Gly Pro Leu Thr
130 135 140

Ser Arg Tyr Gly Arg Leu Ala Ala Ser Leu Gln Glu Pro Gly Arg Phe
145 150 155 160

Arg Ser Phe Leu Leu Asp Phe Ser Tyr Pro Arg Val Pro Ser Ser Val
165 170 175

Arg Asp Ala Trp Pro Gly Ile Gln His Gly Gly Asp Arg Met Leu Gly
180 185 190

Thr Val Gln Trp His Gly His Gln Glu Pro Pro His Pro His Arg Ser
195 200 205

Ala Ala Ala Gly Tyr Gly Asn His Ala Ala Tyr Asn Cys His Gly Gly
210 215 220

Leu Val Ala Gly Gly Ala Pro Met Leu Ser Ser Ala Ala Phe Glu Leu
225 230 235 240

Pro Pro Gly Gly Cys Val Ala Gly Val Ala Ala Asp Ser Ser Cys Ala
245 250 255

Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr Ser His Asp His
260 265 270

Arg Ser Pro Ala Met Pro Ala Ala Gly Ala Phe Asp Gly Thr Pro Val
275 280 285

Ala Pro Ser Val Met Ala Ser Ser Tyr Ala Ala Ser Ser Ala Trp Thr
290 295 300

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

Asp Asp Ala Leu His Leu Val His Pro Gly Ser Ala Ala Val His Phe
325 330 335

Ser Gly Glu Leu Glu Leu Ala Leu Gln Gly Ser Gly Gly Pro Pro His
340 345 350

Leu Pro Arg Val Asp His Gly Gly Ser Gly Gly Gly Thr Phe Asn His
355 360 365

Ser Thr Thr Ser Ala Met Asn Trp Ser Leu
370 375

<210> 978
<211> 378
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<222> (151)..(151)
<223> Xaa can be any naturally occurring amino acid

<400> 978

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

Lys Phe Gly Lys Lys Ile Tyr Phe Glu Gln Asp Gly Gly Ser Gly Ser
            20   25   30

Gly Ala Gly Ala Val Gly Gly Arg Lys Gly Lys Gly Val Ala Thr Gly
        35   40   45

Gly Ala Arg Pro Ala Ser Ala Ala Ser Ala Ala Gln Pro Pro Arg Cys
    50   55   60

Gln Val Asp Gly Cys Gly Val Asp Leu Ser Ala Val Lys Gln Tyr Tyr
65   70   75   80

Cys Arg His Lys Val Cys Asn Met His Ser Lys Glu Pro Arg Val Phe
                85   90   95

Val Ala Gly Ile Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His
            100   105   110

Gln Leu His Glu Phe Asp Gln Gly Lys Arg Ser Cys Arg Arg Arg Leu
        115   120   125

Ile Gly His Asn Glu Arg Arg Arg Lys Pro Pro Pro Gly Pro Leu Thr
    130   135   140

Ser Arg Tyr Gly Arg Leu Xaa Ala Ser Leu Gln Glu Pro Gly Arg Phe
145 150 155 160

Arg Ser Phe Leu Leu Asp Phe Ser Tyr Pro Arg Val Pro Ser Ser Val
165 170 175

Arg Asp Ala Trp Pro Gly Ile Gln His Gly Gly Asp Arg Met Leu Gly
180 185 190

Thr Val Gln Trp His Gly His Gln Glu Pro Pro His Pro His Arg Ser
195 200 205

Ala Ala Ala Gly Tyr Gly Asn His Ala Ala Tyr Asn Cys His Gly Gly
210 215 220

Leu Val Ala Gly Gly Ala Pro Met Leu Ser Ser Ala Ala Phe Glu Leu
225 230 235 240

Pro Pro Gly Gly Cys Val Ala Gly Val Ala Ala Asp Ser Ser Cys Ala
245 250 255

Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr Ser His Asp His
260 265 270

Arg Ser Pro Ala Met Pro Ala Ala Gly Ala Phe Asp Gly Thr Pro Val
275 280 285

Ala Pro Ser Val Met Ala Ser Ser Tyr Ala Ala Ser Ser Ala Trp Thr
290 295 300

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

Asp Asp Ala Leu His Leu Val His Pro Gly Ser Ala Ala Val His Phe
325 330 335

Ser Gly Glu Leu Glu Leu Ala Leu Gln Gly Ser Gly Gly Pro Pro His

340 345 350

Leu Pro Arg Val Asp His Gly Gly Ser Gly Gly Gly Thr Phe Asn His
355 360 365

Ser Thr Thr Ser Ala Met Asn Trp Ser Leu
370 375

<210> 979
<211> 388
<212> PRT
<213> Sorghum bicolor

<400> 979

Met Ala Thr Gly Gly Ser Gly Ser Asp Asp Val His Gly Leu Thr Phe
1 5 10 15

Gly Lys Lys Ile Tyr Phe Glu Gln Asp Ala Ala Val Ala Ala Ala Gly
20 25 30

Gly Ser Gly Ser Gly Ser Ala Thr Ala Ala Ala Gly Gly Arg Lys Gly
35 40 45

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

Ser Ala Thr Gln Pro Pro Arg Cys Gln Val Asp Gly Cys Gly Val Asp
65 70 75 80

Leu Ser Ala Val Lys Gln Tyr Tyr Cys Arg His Lys Val Cys Tyr Met
85 90 95

His Ser Lys Glu Pro Arg Val Val Val Ala Gly Ile Glu Gln Arg Phe
100 105 110

Cys Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe Asp Gln Gly
115 120 125

Lys Arg Ser Cys Arg Arg Arg Leu Ile Gly His Asn Glu Arg Arg Arg
130 135 140

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

Ser Phe Gln Glu Pro Gly Arg Phe Arg Ser Phe Leu Leu Asp Phe Ser
165 170 175

Tyr Pro Arg Val Pro Ser Ser Val Arg Asp Ala Trp Gln Gly Val Gln
180 185 190

Pro Gly Gly Asp Arg Met Leu Gly Thr Ile Gln Trp His Gly Asn Gln
195 200 205

Glu Pro His Pro His Arg Ser Ala Ala Ala Gly Tyr Gly Asn His Ala
210 215 220

Tyr Asn Cys His Gly Gly Leu Val Ala Gly Ala Ser Met Leu Pro Ser
225 230 235 240

Ala Phe Glu Leu Pro Pro Gly Gly Cys Val Ala Gly Val Thr Thr Asp
245 250 255

Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr
260 265 270

Pro Gln Ser Gly Ser His Asn Arg Ser Pro Ala Met Ser Ala Ala Ala
275 280 285

Ser Ala Phe Glu Gly Thr Pro Val Ala Pro Ser Val Met Ala Ser Ser
290 295 300

Tyr Thr Ala Ser Ser Thr Trp Thr Ala Ser Arg Asp Pro Ala Asp Gly
305 310 315 320

Ala Arg Asn Ala Gln Gln His His Asp Asp Ala Leu His Leu Val His
325 330 335

Pro Gly Pro Val His His Gly His Phe Ser Gly Glu Leu Glu Leu Ala
340 345 350

Leu Gln Gly Ser Gly Pro Pro Pro Pro Pro Asn Met Pro His Val Asp
355 360 365

His Gly Ser Ser Ser Gly Thr Phe Ser His Ser Thr Thr Asn Ala Met
370 375 380

Asn Trp Ser Leu
385

<210> 980
<211> 383
<212> PRT
<213> Zea mays

<400> 980

Met Ala Thr Gly Gly Gly Gly Gly Ser Asp Asp Phe His Gly Leu Thr
1 5 10 15

Phe Gly Gln Lys Ile Tyr Phe Glu Gln Asp Ala Gly Ala Ala Gly Gly
20 25 30

Ser Ala Thr Gly Gly Arg Lys Gly Lys Gly Ala Ala Ala Ser Ala Ser
35 40 45

Ala Ala Gln Pro Pro Arg Cys Arg Val Asp Gly Cys Gly Val Asp Leu
50 55 60

Ser Ala Val Lys Gln Tyr Tyr Cys Arg His Lys Val Cys Tyr Met His
65 70 75 80

Ser Lys Glu Pro Arg Val Phe Val Ala Gly Ile Glu Gln Arg Phe Cys
85 90 95

Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe Asp Gln Gly Lys

100 105 110

Arg Ser Cys Arg Arg Arg Leu Ile Gly His Asn Glu Arg Arg Arg Lys
115 120 125

Pro Pro Pro Gly Pro Leu Thr Ser Arg Tyr Gly Pro Leu Ala Ala Ser
130 135 140

Leu Val Gln Glu Pro Gly Arg Phe Arg Ser Phe Leu Leu Asp Phe Ser
145 150 155 160

Tyr Pro Arg Val Pro Ser Ser Val Arg Asp Asp Ala Trp Gln Trp Gln
165 170 175

Gly Met Gln His Gly Gly Asp Arg Met Leu Leu Gly Thr Ala Ser Ala
180 185 190

Ile Gln Trp His Gly Asn Gln Glu Pro His Pro Pro His Arg Ser Ala
195 200 205

Ala Ala Gly Tyr Gly Asn His Ala Tyr Asn Asn Cys His Gly Gly Gly
210 215 220

Gly Leu Val Ala Ala Ala Ala Gly Ala Ser Met Leu Ser Ser Ala Phe
225 230 235 240

Glu Pro Pro Pro Gly Gly Gly Gly Cys Val Ala Gly Ala Thr Ala Ala
245 250 255

Asp Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr
260 265 270

Pro Thr Gln Ser Gly Ser Ser His His Asn Arg Ser Pro Ala Met Ser
275 280 285

Ala Ala Ala Gly Ala Phe Glu Val Ala Pro Ser Ser Val Val Ala Ser
290 295 300

Ser Tyr Thr Ala Ser Ser Ser Trp Ser Gly Ser Arg Asp Pro Ala Asp
305 310 315 320

Gly Ala Arg Lys Asn Ala Gln Arg His Asp Asp Gly Leu His Leu Val
325 330 335

His Pro Pro Gly Pro Val His His Gly His Phe Ser Gly Glu Leu Glu
340 345 350

Leu Ala Leu Gln Gly Ser Gly Pro Pro His Val Asp His Gly Gly Gly
355 360 365

Thr Cys Phe Ser His Ser Asp Thr Asn Ala Met Asn Trp Ser Leu
370 375 380

<210> 981
<211> 439
<212> PRT
<213> Zea mays

<400> 981

Met Gly Ser Phe Gly Met Asn Trp Asn Gln Lys Asp Pro Met Val Trp
1 5 10 15

Asp Trp Glu His Leu Val Pro Ser Val Ser Asn Ala Val Thr Arg His
20 25 30

Gly Ser Ala Asn Ser Ser Gly Gly Thr Leu Thr Ser Asn Ser Glu Leu
35 40 45

Gly His Gly Ser Ser Lys Ser Ser Ile Ser Ala Ser Ile Asp Ser Pro
50 55 60

Ser Gly Val Gly Asn Ser Leu Glu Phe Asn Phe Ala Ala Val Glu Arg
65 70 75 80

His Val Lys Asn Thr Gly Thr Asn Gly Arg Val Asp Asp Ser Gly Asn
85 90 95

Ser Pro Ser Ser Met Ile Ala Phe Asn Gln Gly Glu Pro Leu Ile Ser
100 105 110

Leu Lys Leu Gly Lys Arg Ala Tyr Phe Glu Asn Ala Cys Gly Gly Gln
115 120 125

Asp Ala Lys Val Ser Ala Ala Ser Asp Val Thr Ser Ala Ala Ser Val
130 135 140

Val Lys Lys Thr Lys Val Ser Gln Gln Asn Ala Lys Asn Trp Tyr Cys
145 150 155 160

Gln Val Glu Gly Cys Lys Val Asp Leu Ser Ser Ala Lys Asp Tyr Asn
165 170 175

Arg Lys His Lys Val Cys Val Val His Ser Lys Ala Thr Lys Val Val
180 185 190

Val Ala Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His
195 200 205

Gly Leu Ala Glu Phe Asp Gln Asn Lys Arg Ser Cys Arg Arg Arg Leu
210 215 220

Met His His Asn Ala Arg Arg Arg Lys Pro Gln Ala Asp Thr Ile Ser
225 230 235 240

Phe Asn Ser Ser Thr Met Phe Tyr Asp Thr Arg Gln Arg Thr Asn Leu
245 250 255

Phe Phe Ser Gln Pro Leu Tyr Gly Gln Val Arg Ser Asn Ala Gly Ser
260 265 270

Ser Trp Asp Asn Leu Gly Gly Leu Lys Phe Met Glu Thr Lys His Pro
275 280 285

Pro Val His Pro Thr Lys Thr Ala Ser Pro Asp Glu Leu His Phe Ser
290 295 300

Ala Leu Gln Ile Thr Ser Ala Ala Ala His Thr Gly His His His Asp
305 310 315 320

Leu Asp Gly Phe Met Ala Phe Lys Gly Thr Ser Thr Lys Val Leu Asn
325 330 335

Gln Gly Val Glu Ala Trp Ala Ala Ala Ser Ser Ser Asn Asn Gly Gly
340 345 350

Pro Glu Gly Gly Arg Ala Leu Ser Leu Leu Ser Asp Gly Ser Trp Gly
355 360 365

Ser Ser Ser Ala Val Ile Gln Gln Pro Thr Ser His Ala Asp Ala Gly
370 375 380

Ala Leu Leu Pro Pro Leu Ala Thr Val Ala Val Ser Asn Ala Ala Ala
385 390 395 400

Ala Ala Gly His Pro Leu Asp Pro Ser Pro Gly Arg Phe Trp Pro Gln
405 410 415

Asp Asp His Pro Pro Leu Val Asp Gly Pro Ala Thr Gln Ile Pro Glu
420 425 430

Leu Ala His Leu Arg Ile Trp
435

<210> 982
<211> 440
<212> PRT
<213> Sorghum bicolor

<400> 982

Met Gly Ser Phe Gly Met Asn Trp Asn Gln Lys Asn Ser Met Val Trp
1 5 10 15

Asp Trp Glu His Leu Val Pro Ser Val Ser Asn Ala Val Thr Arg His
20 25 30

Gly Ser Ala Asn Ser Ser Gly Gly Thr Leu Thr Ser Ser Ser Glu Leu
35 40 45

Gly His Gly Ser Ser Lys Ser Ser Ile Ser Ala Ser Ile Asp Ser Pro
50 55 60

Ser Gly Val Gly Asn Ser Leu Glu Phe Asn Phe Ala Ala Val Gln Arg
65 70 75 80

His Val Lys Asn Thr Gly Thr Asn Gly Arg Val Asp Asp Ser Gly Asn
85 90 95

Ser Pro Ser Ser Met Ile Ala Phe Ser Gln Gly Glu Pro Leu Ile Ser
100 105 110

Leu Lys Leu Gly Lys Arg Ala Tyr Phe Glu Asn Val Cys Gly Gly Gln
115 120 125

Glu Ala Lys Val Ser Ala Pro Ser Asp Val Thr Ser Ala Val Thr Val
130 135 140

Val Lys Lys Thr Lys Val Ser Gln Gln Asn Ala Lys Asn Trp Tyr Cys
145 150 155 160

Gln Val Glu Gly Cys Lys Val Asp Leu Ser Ser Ala Lys Asp Tyr Asn
165 170 175

Arg Lys His Lys Val Cys Val Ala His Ser Lys Ala Pro Lys Val Val
180 185 190

Val Ala Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His
195 200 205

Gly Leu Ala Glu Phe Asp Gln Asn Lys Arg Ser Cys Arg Arg Arg Leu

210 215 220

Thr His His Asn Ala Arg Arg Arg Lys Pro Gln Ala Asp Ala Ile Ser
225 230 235 240

Phe Asn Ser Ser Arg Leu Ser Ser Met Phe Tyr Asp Thr Ser His Arg
245 250 255

Thr Asn Leu Phe Phe Ser Gln Pro Leu Tyr Gly Gln Val Arg Ser Asn
260 265 270

Ala Val Ser Pro Trp Asp Asn Ser Gly Gly Phe Lys Phe Met Glu Thr
275 280 285

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

His Phe Ser Thr Pro Gln Ile Ser Thr Ser Val Val Ala His Thr Gly
305 310 315 320

His His His Asn Phe Asp Arg Phe Met Pro Phe Lys Gly Thr Asn Thr
325 330 335

Lys Val Leu Asn Gln Val Ser Gly Val Glu Ala Ser Ala Thr Ala Ser
340 345 350

Asn Ser Asn Asn Gly Ala Pro Glu Pro Gly Arg Ala Leu Ser Leu Leu
355 360 365

Ser Asp Gly Ser Trp Gly Ser Asn Ser Ala Val Ile Gln Gln Pro Pro
370 375 380

Ser His Ala Asp Ala Gly Ala Leu Pro Pro Leu Ala Thr Val Ala Val
385 390 395 400

Ser Asn Thr Ala Ala Arg His Pro Leu Asp Pro Ser Leu Gly Arg Phe
405 410 415

Trp Gln Asp Asp His Pro Pro Leu Asp Gly Pro Ala Pro Gln Ile Gln
420 425 430

Glu Leu Ala His Leu Arg Thr Trp
435 440

<210> 983
<211> 383
<212> PRT
<213> Zea mays

<400> 983

Met Ala Thr Gly Gly Gly Gly Gly Ser Asp Asp Phe His Gly Leu Thr
1 5 10 15

Phe Gly Gln Lys Ile Tyr Phe Glu Gln Asp Ala Gly Ala Ala Gly Gly
20 25 30

Ser Ala Thr Gly Gly Arg Lys Gly Lys Gly Ala Ala Ala Ser Ala Ser
35 40 45

Ala Ala Gln Pro Pro Arg Cys Arg Val Asp Gly Cys Gly Val Asp Leu
50 55 60

Ser Ala Val Lys Gln Tyr Tyr Cys Arg His Lys Val Cys Tyr Met His
65 70 75 80

Ser Lys Glu Pro Arg Val Phe Val Ala Gly Ile Glu Gln Arg Phe Cys
85 90 95

Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe Asp Gln Gly Lys
100 105 110

Arg Ser Cys Arg Arg Arg Leu Ile Gly His Asn Glu Arg Arg Arg Lys
115 120 125

Pro Pro Pro Gly Pro Leu Thr Ser Arg Tyr Gly Pro Leu Ala Ala Ser
130 135 140

Leu Val Gln Glu Pro Gly Arg Phe Arg Ser Phe Leu Leu Asp Phe Ser
145 150 155 160

Tyr Pro Arg Val Pro Ser Ser Val Arg Asp Asp Ala Trp Gln Trp Gln
165 170 175

Gly Met Gln His Gly Gly Asp Arg Met Leu Leu Gly Thr Ala Ser Ala
180 185 190

Ile Gln Trp His Gly Asn Gln Glu Pro His Pro Pro His Arg Ser Ala
195 200 205

Ala Ala Gly Tyr Gly Asn His Ala Tyr Asn Asn Cys His Gly Gly Gly
210 215 220

Gly Leu Val Ala Ala Ala Ala Gly Ala Ser Met Leu Ser Ser Ala Phe
225 230 235 240

Glu Pro Pro Pro Gly Gly Gly Gly Cys Val Ala Gly Ala Thr Ala Ala
245 250 255

Asp Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr
260 265 270

Pro Thr Gln Ser Gly Ser Ser His His Asn Arg Ser Pro Ala Met Ser
275 280 285

Ala Ala Ala Gly Ala Phe Glu Val Ala Pro Ser Ser Val Val Ala Ser
290 295 300

Ser Tyr Thr Ala Ser Ser Ser Trp Ser Gly Ser Arg Asp Pro Ala Asp
305 310 315 320

Gly Ala Arg Lys Asn Ala Gln Arg His Asp Asp Gly Leu His Leu Val
325 330 335

His Pro Pro Gly Pro Val His His Gly His Phe Ser Gly Glu Leu Glu
340 345 350

Leu Ala Leu Gln Gly Ser Gly Pro Pro His Val Asp His Gly Gly Gly
355 360 365

Thr Cys Phe Ser His Ser Asp Thr Asn Ala Met Asn Trp Ser Leu
370 375 380

<210> 984
<211> 388
<212> PRT
<213> Sorghum bicolor

<400> 984

Met Ala Thr Gly Gly Ser Gly Ser Asp Asp Val His Gly Leu Thr Phe
1 5 10 15

Gly Lys Lys Ile Tyr Phe Glu Gln Asp Ala Ala Val Ala Ala Ala Gly
20 25 30

Gly Ser Gly Ser Gly Ser Ala Thr Ala Ala Ala Gly Gly Arg Lys Gly
35 40 45

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

Ser Ala Thr Gln Pro Pro Arg Cys Gln Val Asp Gly Cys Gly Val Asp
65 70 75 80

Leu Ser Ala Val Lys Gln Tyr Tyr Cys Arg His Lys Val Cys Tyr Met
85 90 95

His Ser Lys Glu Pro Arg Val Val Val Ala Gly Ile Glu Gln Arg Phe
100 105 110

Cys Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe Asp Gln Gly
115 120 125

Lys Arg Ser Cys Arg Arg Arg Leu Ile Gly His Asn Glu Arg Arg Arg
130 135 140

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

Ser Phe Gln Glu Pro Gly Arg Phe Arg Ser Phe Leu Leu Asp Phe Ser
165 170 175

Tyr Pro Arg Val Pro Ser Ser Val Arg Asp Ala Trp Gln Gly Val Gln
180 185 190

Pro Gly Gly Asp Arg Met Leu Gly Thr Ile Gln Trp His Gly Asn Gln
195 200 205

Glu Pro His Pro His Arg Ser Ala Ala Ala Gly Tyr Gly Asn His Ala
210 215 220

Tyr Asn Cys His Gly Gly Leu Val Ala Gly Ala Ser Met Leu Pro Ser
225 230 235 240

Ala Phe Glu Leu Pro Pro Gly Gly Cys Val Ala Gly Val Thr Thr Asp
245 250 255

Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr
260 265 270

Pro Gln Ser Gly Ser His Asn Arg Ser Pro Ala Met Ser Ala Ala Ala
275 280 285

Ser Ala Phe Glu Gly Thr Pro Val Ala Pro Ser Val Met Ala Ser Ser
290 295 300

Tyr Thr Ala Ser Ser Thr Trp Thr Ala Ser Arg Asp Pro Ala Asp Gly
305 310 315 320

Ala Arg Asn Ala Gln Gln His His Asp Asp Ala Leu His Leu Val His

325 330 335

Pro Gly Pro Val His His Gly His Phe Ser Gly Glu Leu Glu Leu Ala
340 345 350

Leu Gln Gly Ser Gly Pro Pro Pro Pro Pro Asn Met Pro His Val Asp
355 360 365

His Gly Ser Ser Ser Gly Thr Phe Ser His Ser Thr Thr Asn Ala Met
370 375 380

Asn Trp Ser Leu
385

<210> 985
<211> 378
<212> PRT
<213> Zea mays

<400> 985

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

Lys Phe Gly Lys Lys Ile Tyr Phe Glu Gln Asp Gly Gly Ser Gly Ser
20 25 30

Gly Ala Gly Ala Val Gly Gly Arg Lys Gly Lys Gly Val Ala Thr Gly
35 40 45

Gly Ala Arg Pro Ala Ser Ala Ala Ser Ala Ala Gln Pro Pro Arg Cys
50 55 60

Gln Val Asp Gly Cys Gly Val Asp Leu Ser Ala Val Lys Gln Tyr Tyr
65 70 75 80

Cys Arg His Lys Val Cys Asn Met His Ser Lys Glu Pro Arg Val Phe
85 90 95

Val Ala Gly Ile Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His
100 105 110

Gln Leu His Glu Phe Asp Gln Gly Lys Arg Ser Cys Arg Arg Arg Leu
115 120 125

Ile Gly His Asn Glu Arg Arg Arg Lys Pro Pro Pro Gly Pro Leu Thr
130 135 140

Ser Arg Tyr Gly Arg Leu Ala Ala Ser Leu Gln Glu Pro Gly Arg Phe
145 150 155 160

Arg Ser Phe Leu Leu Asp Phe Ser Tyr Pro Arg Val Pro Ser Ser Val
165 170 175

Arg Asp Ala Trp Pro Gly Ile Gln His Gly Gly Asp Arg Met Leu Gly
180 185 190

Thr Val Gln Trp His Gly His Gln Glu Pro Pro His Pro His Arg Ser
195 200 205

Ala Ala Ala Gly Tyr Gly Asn His Ala Ala Tyr Asn Cys His Gly Gly
210 215 220

Leu Val Ala Gly Gly Ala Pro Met Leu Ser Ser Ala Ala Phe Glu Leu
225 230 235 240

Pro Pro Gly Gly Cys Val Ala Gly Val Ala Ala Asp Ser Ser Cys Ala
245 250 255

Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr Ser His Asp His
260 265 270

Arg Ser Pro Ala Met Pro Ala Ala Gly Ala Phe Asp Gly Thr Pro Val
275 280 285

Ala Pro Ser Val Met Ala Ser Ser Tyr Ala Ala Ser Ser Ala Trp Thr
290 295 300

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

Asp Asp Ala Leu His Leu Val His Pro Gly Ser Ala Ala Val His Phe
325 330 335

Ser Gly Glu Leu Glu Leu Ala Leu Gln Gly Ser Gly Gly Pro Pro His
340 345 350

Leu Pro Arg Val Asp His Gly Gly Ser Gly Gly Gly Thr Phe Asn His
355 360 365

Ser Thr Thr Ser Ala Met Asn Trp Ser Leu
370 375

<210> 986
<211> 378
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<222> (151)..(151)
<223> Xaa can be any naturally occurring amino acid

<400> 986

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

Lys Phe Gly Lys Lys Ile Tyr Phe Glu Gln Asp Gly Gly Ser Gly Ser
20 25 30

Gly Ala Gly Ala Val Gly Gly Arg Lys Gly Lys Gly Val Ala Thr Gly
35 40 45

Gly Ala Arg Pro Ala Ser Ala Ala Ser Ala Ala Gln Pro Pro Arg Cys
50 55 60

Gln Val Asp Gly Cys Gly Val Asp Leu Ser Ala Val Lys Gln Tyr Tyr
65 70 75 80

Cys Arg His Lys Val Cys Asn Met His Ser Lys Glu Pro Arg Val Phe
85 90 95

Val Ala Gly Ile Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His
100 105 110

Gln Leu His Glu Phe Asp Gln Gly Lys Arg Ser Cys Arg Arg Arg Leu
115 120 125

Ile Gly His Asn Glu Arg Arg Arg Lys Pro Pro Pro Gly Pro Leu Thr
130 135 140

Ser Arg Tyr Gly Arg Leu Xaa Ala Ser Leu Gln Glu Pro Gly Arg Phe
145 150 155 160

Arg Ser Phe Leu Leu Asp Phe Ser Tyr Pro Arg Val Pro Ser Ser Val
165 170 175

Arg Asp Ala Trp Pro Gly Ile Gln His Gly Gly Asp Arg Met Leu Gly
180 185 190

Thr Val Gln Trp His Gly His Gln Glu Pro Pro His Pro His Arg Ser
195 200 205

Ala Ala Ala Gly Tyr Gly Asn His Ala Ala Tyr Asn Cys His Gly Gly
210 215 220

Leu Val Ala Gly Gly Ala Pro Met Leu Ser Ser Ala Ala Phe Glu Leu
225 230 235 240

Pro Pro Gly Gly Cys Val Ala Gly Val Ala Ala Asp Ser Ser Cys Ala
245 250 255

Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr Ser His Asp His

260 265 270

Arg Ser Pro Ala Met Pro Ala Ala Gly Ala Phe Asp Gly Thr Pro Val
275 280 285

Ala Pro Ser Val Met Ala Ser Ser Tyr Ala Ala Ser Ser Ala Trp Thr
290 295 300

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

Asp Asp Ala Leu His Leu Val His Pro Gly Ser Ala Ala Val His Phe
325 330 335

Ser Gly Glu Leu Glu Leu Ala Leu Gln Gly Ser Gly Gly Pro Pro His
340 345 350

Leu Pro Arg Val Asp His Gly Gly Ser Gly Gly Gly Thr Phe Asn His
355 360 365

Ser Thr Thr Ser Ala Met Asn Trp Ser Leu
370 375

<210> 987
<211> 329
<212> PRT
<213> Zea mays

<400> 987

Pro Ser Thr Ala Pro Ala Pro Ala Arg Cys Gln Val Asp Gly Cys Asn
1 5 10 15

Val Asp Leu Thr Asp Val Lys Pro Ala Tyr Tyr Cys Arg His Lys Val
20 25 30

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

Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe
    50   55   60

Asp Gln Leu Lys Lys Ser Cys Arg Lys Arg Leu Ala Gly His Asn Glu
65   70   75   80

Arg Arg Arg Arg Pro Pro Pro Gly Pro Leu Ala Ser Arg Tyr Gly Arg
                85   90   95

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

Asp Phe Ser Tyr Pro Arg Val Ser Ser Ala Met Arg Gly Gly Phe Pro
        115   120   125

Ala Val Arg Pro Gly Gly Glu Arg Val Pro Gly Gly Ile Gln Trp Gln
    130   135   140

Ala Gly Leu Asp Pro Arg His His Gln Gly Ala Val Ala Gly Tyr Gly
145   150   155   160

Ala His Tyr Gly Ser Glu Gly Gly Ser Ser Ser Ser Ala Arg Pro Pro
                165   170   175

Val Phe Pro Gly Pro Glu Leu Pro Pro Gly Gly Cys Leu Ala Gly Val
            180   185   190

Pro Ala Asp Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp
        195   200   205

Asp Ala Ala His Ser His Ser His Ser His Ala Ala Pro Thr Ala Gly
    210   215   220

Phe Asp Gly Gly Ser Pro Val Ala Pro Ser Leu Met Ala Ala Ser Ser
225   230   235   240

Tyr Ile Ala Pro Ser Pro Trp Thr Glu Thr Asp Ser Trp Gly His Glu
                245   250   255

Gly Gly Arg Ser Val Pro Gln Leu Pro Pro Asp Asp Val Pro Leu Gly
260 265 270

Glu Val His Ser Gly Ser Ser Ser His His Gly Gln Phe Ser Gly Glu
275 280 285

Leu Glu Leu Ala Leu Gln Gly Asn Arg Pro Ala Pro Gly Ser Ala Ala
290 295 300

Pro Pro Ala Pro Arg Asn Asn Gln Gly Ser Ala Gly Thr Phe Asp Gln
305 310 315 320

Ala Gly Asn Thr Met Asp Trp Ser Leu
325

<210> 988
<211> 409
<212> PRT
<213> Sorghum bicolor

<400> 988

Met Glu Ser Gly Gly Ala Ser Gly Gly Gly Gly Gly Gly Gly Gly Asp
1 5 10 15

Asp Gln Leu His Gly Leu Lys Phe Gly Lys Lys Ile Tyr Phe Glu Asp
20 25 30

Ala Ala Ala Ala Gly Ser Ser Ser Gly Gly Gly Gly Gly Gly Ser Gly
35 40 45

Asn Ala Ser Ala Thr Thr Ala Ala Pro Ala Thr Gln Gln Pro Ser Pro
50 55 60

Pro Gln Ala Ala Ser Pro Arg Ala Ala Ser Gly Gly Gly Gly Arg Arg
65 70 75 80

Gly Arg Ala Ala Gly Gly Pro Ser Pro Ala Pro Ala Pro Ala Arg Cys

85 90 95

Gln Val Asp Gly Cys Asn Val Asp Leu Thr Asp Val Lys Pro Tyr Tyr
100 105 110

Cys Arg His Lys Val Cys Lys Met His Ser Lys Glu Pro Arg Val Val
115 120 125

Val Asn Gly Leu Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His
130 135 140

Gln Leu Pro Glu Phe Asp Gln Leu Lys Lys Ser Cys Arg Arg Arg Leu
145 150 155 160

Ala Gly His Asn Glu Arg Arg Arg Arg Pro Pro Pro Gly Pro Leu Ala
165 170 175

Thr Arg Tyr Gly Arg Leu Ala Ala Ser Phe Gly Glu Glu Pro Gly Arg
180 185 190

Phe Arg Ser Phe Met Leu Asp Phe Ser Tyr Pro Arg Val Pro Thr Ala
195 200 205

Met Arg Asp Gly Phe Pro Ala Val Arg Pro Gly Glu Arg Ala Pro Gly
210 215 220

Ser Ile Gln Trp Gln Ala Ser Leu Asp Pro His His His Gln Ser Ala
225 230 235 240

Val Ala Gly Tyr Ser Ala His Ser Tyr Gly Ser Gln Gly Ser Ser Ser
245 250 255

Ser Arg Pro Pro Val Phe Pro Gly Pro Glu Ile Pro Pro Gly Gly Cys
260 265 270

Leu Ala Gly Val Pro Ser Asp Ser Ser Cys Ala Leu Ser Leu Leu Ser
275 280 285

Thr Gln Pro Trp Asp Thr Thr His Ser Ser Gly His Ser His Ala Ala
290 295 300

Ser Met Pro Ala Thr Ala Gly Phe Asp Gly Asn Pro Val Ala Pro Ser
305 310 315 320

Leu Met Ala Ser Ser Tyr Ile Ala Pro Ser Pro Trp Thr Asp Ser Arg
325 330 335

Gly His Glu Gly Gly Arg Asn Val Pro Gln Leu Pro Pro Asp Val Pro
340 345 350

Leu Ser Glu Val His Ser Gly Ser Ser Ser His His Gly Gln Phe Ser
355 360 365

Gly Glu Leu Glu Leu Ala Leu Gln Gly Asn Arg Pro Ala Pro Gly Ser
370 375 380

Ala Pro Ala Pro Arg Asn Asp Gln Gly Ser Thr Gly Ala Phe Asp Gln
385 390 395 400

Ser Gly Asn Thr Met Asp Trp Ser Leu
405

<210> 989
<211> 408
<212> PRT
<213> Zea mays

<400> 989

Met Glu Ala Gly Gly Ala Ser Gly Gly Asp Asp Gly Asp Gly Gln Leu
1 5 10 15

His Gly Leu Lys Phe Gly Lys Lys Ile Tyr Phe Glu Asp Ala Gly Gly
20 25 30

Ser Ser Ser Ser Gly Gly Ser Gly Ser Ala Ser Ala Thr Ala Pro Pro
35 40 45

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

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

Leu Pro Pro Ala Pro Pro Arg Cys Leu Val Asp Gly Cys Asn Ala Asp
85 90 95

Leu Thr Asp Ala Lys Thr Tyr Tyr Cys Arg His Lys Val Cys Glu Met
100 105 110

His Ser Lys Glu Pro Arg Val Val Val Asn Gly Leu Glu Leu Arg Phe
115 120 125

Cys Gln Gln Cys Ser Arg Phe His Asn Leu Ala Glu Phe Asp Gln Gln
130 135 140

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

Arg Pro Pro Pro Gly Pro Leu Ala Ser Arg Tyr Gly Arg Leu Ala Ala
165 170 175

Pro Leu Gly Glu Glu Pro Gly Gly Arg Phe Arg Ser Phe Met Leu Asp
180 185 190

Phe Ser Tyr Pro Arg Val Pro Ser Ala Met Arg Asp Gly Phe Pro Ala
195 200 205

Val Arg Pro Gly Gly Glu Arg Val Pro Gly Ser Asn Ile Gln Trp Gln
210 215 220

Ala Ala Ser Leu Asp Pro Pro Pro Pro His His Gln Ser Ala Ala Ala
225 230 235 240

Gly Tyr Gly Ala His Ser Tyr Gly Ser Pro Gly Ser Ser Ser Ser Ser
245 250 255

Arg Pro Pro Val Phe Pro Ala Gly Pro Glu Leu Pro Pro Gly Gly Gly
260 265 270

Cys Leu Ala Gly Val Pro Thr Asp Ser Ser Cys Ala Leu Ser Leu Leu
275 280 285

Ser Thr Gln Pro Trp Asp Ala Ala Gly His Ser Ala Gly His Gly His
290 295 300

Gly His Ala Ala Ser Leu Pro Ala Thr Ala Gly Phe Asp Gly Asn Pro
305 310 315 320

Val Ala Met Ala Ser Ser Tyr Ile Ala Pro Pro Ser Pro Trp Thr Asp
325 330 335

Ser Arg Ala His Glu Gly Gly Arg Arg Asn Val Pro Gln Leu Pro Pro
340 345 350

Asp Val Pro Leu Gly Asp Val His Ser Gly Pro Gly Thr His His Gly
355 360 365

Gln Phe Ser Gly Glu Leu Glu Leu Ala Leu Gln Gly Asn Arg Pro Ala
370 375 380

Pro Ala Pro Arg Asn Gly Gln Gly Ser Ala Gly Ala Phe Asp Gln Ala
385 390 395 400

Gly Ser Thr Thr Glu Trp Ser Leu
405

<210> 990
<211> 251
<212> PRT
<213> Zea mays

<400> 990

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

Met Gln Lys Glu Ala Thr Pro Leu Val His Lys Phe Asn Leu Val Glu
20 25 30

Ala Pro Ala His Gln Ser Thr Phe Pro Lys Gly Ala Pro Trp Val Trp
35 40 45

Tyr His Gly Ser Tyr Lys Gly Leu His Ile Asp Leu Val Leu Pro Gly
50 55 60

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

Val Val Thr Ser Phe Ser Ile Gln Thr Leu Lys Pro Asp Leu Ile Ile
85 90 95

Asn Ala Gly Thr Ala Gly Gly Phe Lys Ala Lys Gly Ala Ser Ile Thr
100 105 110

Asp Val Phe Leu Ala Ser Asp Val Ala Phe His Asp Arg Arg Ile Pro
115 120 125

Ile Pro Ile Phe Asp Met Tyr Gly Thr Gly Ala Arg Lys Thr Phe Ala
130 135 140

Ala Pro Asn Ile Leu Lys Glu Leu Asn Leu Lys Val Gly Lys Leu Ser
145 150 155 160

Thr Gly Asp Ser Leu Asp Met Cys Pro Gln Asp Lys Glu Leu Ile Leu
165 170 175

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

Val Ala Asp Met Phe Ser Thr Pro Ala Ile Phe Val Lys Ala Val Thr

195 200 205

Asp Ile Val Asp Gly Val Lys Pro Thr Tyr Glu Glu Phe Leu Gln Asn
210 215 220

Leu Ile Ala Val Thr Thr Ala Leu Glu Leu Ala Val Thr Lys Val Val
225 230 235 240

Asp Phe Ile Ser Gly Lys Arg Ile Ser Asp Leu
245 250

<210> 991
<211> 251
<212> PRT
<213> Zea mays

<400> 991

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

Met Gln Thr Glu Ala Met Pro Leu Val His Lys Phe Lys Leu Val Glu
20 25 30

Ala Pro Ala His Glu Ser Thr Phe Pro Lys Gly Ala Pro Trp Val Arg
35 40 45

Tyr His Gly Asn Tyr Lys Gly Leu His Ile Asp Leu Val Leu Pro Gly
50 55 60

Lys Asp Ala Val Leu Gly Val Asp Ser Val Gly Thr Val Ser Ala Ala
65 70 75 80

Leu Leu Thr Ser Phe Ser Ile Gln Thr Leu Lys Pro Asp Leu Ile Ile
85 90 95

Asn Ala Gly Thr Ala Gly Gly Phe Lys Ala Lys Gly Ala Ser Ile Gly
100 105 110

Asp Val Phe Leu Ala Ser Asp Val Ser Phe His Asp Arg Arg Ile Pro
115 120 125

Ile Pro Val Phe Asp Met Tyr Gly Ile Gly Ala Arg Lys Thr Ser Ala
130 135 140

Val Pro Asn Ile Leu Lys Glu Leu Asn Leu Lys Ile Gly Lys Leu Ser
145 150 155 160

Thr Gly Asp Ser Leu Asp Met Ser Pro Gln Asp Glu Lys Val Ile Leu
165 170 175

Ser Asn Asp Ala Thr Val Lys Asp Met Glu Gly Ala Ala Val Ala Tyr
180 185 190

Val Ala Asp Met Phe Ser Thr Pro Ala Ile Phe Val Lys Ala Val Thr
195 200 205

Asp Ile Val Asp Gly Glu Lys Pro Thr Ser Glu Glu Phe Leu Gln Asn
210 215 220

Leu Ile Ala Val Thr Ala Ala Leu Asp Leu Ala Val Thr Lys Val Val
225 230 235 240

Asp Phe Ile Ser Gly Lys Arg Ile Ser Asp Leu
245 250

<210> 992
<211> 251
<212> PRT
<213> Zea mays

<400> 992

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

Met Gln Thr Glu Ala Met Pro Leu Val His Lys Phe Lys Leu Val Glu
20 25 30

Ala Pro Ala His Glu Ser Thr Phe Pro Lys Gly Ala Pro Trp Val Arg
35 40 45

Tyr His Gly Asn Tyr Lys Gly Leu His Ile Asp Leu Val Leu Pro Gly
50 55 60

Lys Asp Ala Val Leu Gly Val Asp Ser Val Gly Thr Val Ser Ala Ala
65 70 75 80

Leu Leu Thr Ser Phe Ser Ile Gln Thr Leu Lys Pro Asp Leu Ile Ile
85 90 95

Asn Ala Gly Thr Ala Gly Gly Phe Lys Ala Lys Gly Ala Ser Ile Gly
100 105 110

Asp Val Phe Leu Ala Ser Asp Val Ser Phe His Asp Arg Arg Ile Pro
115 120 125

Ile Pro Val Phe Asp Met Tyr Gly Ile Gly Ala Arg Lys Thr Ser Ala
130 135 140

Val Pro Asn Ile Leu Lys Glu Leu Asn Leu Lys Ile Gly Lys Leu Ser
145 150 155 160

Thr Gly Asp Ser Leu Asp Met Ser Pro Gln Asp Glu Lys Val Ile Leu
165 170 175

Ser Asn Asp Ala Thr Val Lys Asp Met Glu Gly Ala Ala Val Ala Tyr
180 185 190

Val Ala Asp Met Phe Ser Thr Pro Ala Ile Phe Val Lys Ala Val Thr
195 200 205

Asp Ile Val Asp Gly Asp Lys Pro Thr Ser Glu Glu Phe Leu Gln Asn
210 215 220

Leu Leu Ile Ala Val Thr Ala Ala Leu Asp Leu Ala Val Thr Lys Val Val

225 230 235 240

Asp Phe Ile Ser Gly Lys Arg Ile Ser Asp Leu
245 250

<210> 993
<211> 251
<212> PRT
<213> Sorghum bicolor

<400> 993

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

Met Gln Thr Glu Ala Met Pro Leu Val Asn Lys Phe Lys Leu Val Glu
20 25 30

Ala Pro Ala His Glu Ser Thr Phe Pro Lys Gly Ala Pro Trp Val Arg
35 40 45

Tyr His Gly Asn Tyr Lys Asp Leu His Ile Asp Leu Val Leu Pro Gly
50 55 60

Lys Asp Ala Ala Phe Gly Val Asp Ser Val Gly Thr Val Ser Val Ala
65 70 75 80

Leu Val Thr Ser Phe Ser Ile Gln Thr Leu Lys Pro Asp Leu Ile Ile
85 90 95

Asn Ala Gly Thr Ala Gly Gly Phe Lys Ala Lys Gly Ala Ser Ile Gly
100 105 110

Asp Val Phe Leu Ala Ser Asp Val Ala Phe His Asp Arg Arg Ile Pro
115 120 125

Ile Pro Val Phe Asp Met Tyr Gly Ile Gly Ala Arg Lys Thr Phe Ala
130 135 140

Ala Pro Asn Ile Leu Lys Glu Leu Asn Leu Lys Val Gly Lys Leu Ser
145 150 155 160

Thr Gly Asp Ser Leu Asp Met Ser Pro His Asp Glu Glu Val Ile Leu
165 170 175

Ser Asn Asp Ala Thr Val Lys Asp Met Glu Gly Ala Ala Val Ala Tyr
180 185 190

Val Ala Asp Met Phe Ser Thr Pro Ala Ile Phe Leu Lys Ala Val Thr
195 200 205

Asp Ile Val Asp Gly Glu Lys Pro Thr Thr Glu Glu Phe Leu Gln Asn
210 215 220

Leu Ile Ala Val Thr Ala Ala Leu Asp Leu Ala Val Thr Lys Val Val
225 230 235 240

Asp Phe Ile Ser Gly Lys Arg Ile Ser Asp Leu
245 250

<210> 994
<211> 226
<212> PRT
<213> Zea mays

<400> 994

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

Met Gln Lys Glu Ala Thr Pro Leu Val His Lys Phe Asn Leu Val Glu
20 25 30

Ala Pro Ala His Gln Ser Thr Phe Pro Lys Gly Ala Pro Trp Val Trp
35 40 45

Tyr His Gly Ser Tyr Lys Gly Leu His Ile Asp Leu Val Leu Pro Gly
50 55 60

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

Val Val Thr Ser Phe Ser Ile Gln Thr Leu Lys Pro Asp Leu Ile Ile
85 90 95

Asn Ala Gly Thr Ala Gly Gly Phe Lys Ala Lys Gly Ala Ser Ile Thr
100 105 110

Asp Val Phe Leu Ala Ser Asp Val Ala Phe His Asp Arg Arg Ile Pro
115 120 125

Ile Pro Val Gly Lys Leu Ser Thr Gly Asp Ser Leu Asp Met Cys Pro
130 135 140

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

Glu Gly Ala Ala Val Ala Tyr Val Ala Asp Met Phe Ser Thr Pro Ala
165 170 175

Ile Phe Val Lys Ala Val Thr Asp Ile Val Asp Gly Val Lys Pro Thr
180 185 190

Tyr Glu Glu Phe Leu Gln Asn Leu Ile Ala Val Thr Thr Ala Leu Glu
195 200 205

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

Asp Leu
225

<210> 995
<211> 259
<212> PRT
<213> Oryza sativa Japonica Group

<400> 995

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

Ala Ile Ser Lys Leu Leu Ile Val Ile Ala Met Gln Thr Glu Ala Leu
            20   25   30

Pro Leu Val Asn Lys Phe His Leu Val Glu Ala Glu Glu Ser Ile Phe
        35   40   45

Pro Lys Gly Ala Pro Trp Ile Arg Tyr His Gly Asn Tyr Lys Gly Leu
    50   55   60

His Val Asp Leu Val Trp Pro Gly Lys Asp Pro Val Leu Gly Val Asp
65   70   75   80

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

Ser Leu Lys Pro Asp Leu Ile Ile Asn Ala Gly Thr Ala Gly Gly Phe
            100   105   110

Lys Ala Lys Gly Ala Asp Ile Gly Asp Val Tyr Leu Ala Ser Asp Val
        115   120   125

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

Ile Gly Thr Arg Lys Thr Phe Ala Thr Pro Asn Ile Leu Lys Glu Leu
145   150   155   160

Asn Leu Lys Val Gly Lys Leu Ser Thr Gly Asp Ser Leu Asp Met Ser
                165   170   175

Pro His Asp Glu Ser Ala Ile Leu Asn Asn Asp Ala Thr Val Lys Asp
            180   185   190

Met Glu Gly Ala Ala Val Ala Tyr Val Ala Asp Met Phe Ser Thr Pro
195 200 205

Ala Ile Phe Val Lys Ala Val Thr Asp Ile Val Asp Gly Glu Lys Pro
210 215 220

Thr Ala Glu Glu Phe Leu Gln Asn Leu Val Ala Val Thr Ala Ala Leu
225 230 235 240

Asp Lys Ala Val Thr Glu Val Val Asp Phe Ile Ser Gly Lys Cys Ile
245 250 255

Ser Asp Leu

<210> 996
<211> 259
<212> PRT
<213> Oryza sativa

<400> 996

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

Ala Ile Ser Lys Leu Leu Ile Val Ile Ala Met Gln Thr Glu Ala Leu
20 25 30

Pro Leu Val Asn Glu Phe His Leu Val Glu Ala Glu Glu Ser Ile Phe
35 40 45

Pro Lys Gly Ala Pro Trp Ile Arg Tyr His Gly Asn Tyr Lys Gly Leu
50 55 60

His Val Asp Leu Val Trp Pro Gly Lys Asp Pro Val Leu Gly Val Asp
65 70 75 80

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

Ser Leu Lys Pro Asp Leu Ile Ile Asn Ala Gly Thr Ala Gly Gly Phe
100 105 110

Lys Ala Lys Gly Ala Asp Ile Gly Asp Val Tyr Leu Ala Ser Asp Val
115 120 125

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

Ile Gly Thr Arg Lys Thr Phe Ala Thr Pro Asn Ile Leu Lys Glu Leu
145 150 155 160

Asn Leu Lys Val Gly Lys Leu Ser Thr Gly Asp Ser Leu Asp Met Ser
165 170 175

Pro His Asp Glu Ser Ala Ile Leu Asn Asn Asp Ala Thr Val Lys Asp
180 185 190

Met Glu Gly Ala Ala Val Ala Tyr Val Ala Asp Met Phe Ser Thr Pro
195 200 205

Ala Ile Phe Val Lys Ala Val Thr Asp Ile Val Asp Gly Glu Lys Pro
210 215 220

Thr Ala Glu Glu Phe Leu Gln Asn Leu Val Ala Val Thr Ala Ala Leu
225 230 235 240

Asp Lys Ala Val Thr Glu Val Val Asp Phe Ile Ser Gly Lys Cys Ile
245 250 255

Ser Asp Leu

<210> 997
<211> 256
<212> PRT
<213> Oryza sativa Indica Group

<400> 997

Pro Ser Asp Ser Asp Asp Ser Ala Pro Ile Pro Ala Gly Ala Ile Ser
1   5   10   15

Lys Leu Leu Ile Val Ile Ala Met Gln Thr Glu Ala Leu Pro Leu Val
            20   25   30

Asn Lys Phe His Leu Val Glu Ala Glu Glu Ser Ile Phe Pro Thr Gly
        35   40   45

Ala Pro Trp Ile Arg Tyr His Gly Asn Tyr Lys Gly Leu His Val Asp
    50   55   60

Leu Val Trp Pro Gly Lys Asp Pro Val Leu Gly Val Asp Cys Val Gly
65   70   75   80

Thr Val Ser Ala Ala Leu Val Thr Tyr Ala Ser Ile Gln Ser Leu Lys
                85   90   95

Pro Asp Leu Ile Ile Asn Ala Gly Thr Ala Gly Gly Phe Lys Ala Lys
            100   105   110

Gly Ala Asp Ile Gly Asp Val Tyr Leu Ala Ser Asp Val Ala Phe His
        115   120   125

Asp Arg Arg Ile Pro Ile Pro Val Phe Asp Met Tyr Gly Ile Gly Thr
    130   135   140

Arg Lys Thr Phe Ala Thr Pro Asn Ile Leu Lys Glu Leu Asn Leu Lys
145   150   155   160

Val Gly Lys Leu Ser Thr Gly Asp Ser Leu Asp Met Ser Pro His Asp
                165   170   175

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

Ala Ala Val Ala Tyr Val Ala Asp Met Phe Ser Thr Pro Ala Ile Phe
195 200 205

Val Lys Ala Val Thr Asp Ile Val Asp Gly Glu Lys Pro Thr Ala Glu
210 215 220

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

Val Thr Glu Val Val Asp Phe Ile Ser Gly Lys Cys Ile Ser Asp Leu
245 250 255

<210> 998
<211> 265
<212> PRT
<213> Hordeum vulgare subsp. vulgare

<400> 998

Met Ala Pro Pro Ser Ser Glu Glu Pro Ala Ala Ala Ser Ala Glu Ala
1 5 10 15

Ser Ala Ala Gly Ala Ile Ser Lys Val Leu Val Val Ile Ala Met Gln
20 25 30

Thr Glu Ala Leu Pro Leu Val Thr Arg Phe Gln Leu Val Glu Ala Ala
35 40 45

Ala Asp Glu Ser Ile Phe Pro Lys Gly Ala Pro Trp Thr Arg Tyr His
50 55 60

Gly Glu Tyr Lys Gly Leu His Ile Asp Leu Val Trp Pro Gly Lys Asp
65 70 75 80

Pro Leu Leu Gly Val Asp Ser Val Gly Thr Val Ser Ala Ala Leu Val
85 90 95

Thr Tyr Ala Ser Ile Gln Leu Leu Lys Pro Asp Leu Ile Ile Asn Ala
100 105 110

Gly Thr Ala Gly Gly Phe Lys Ala Lys Gly Ala Gly Ile Gly Asp Val
115 120 125

Phe Leu Ala Ser Asp Val Ala Phe His Asp Arg Arg Ile Pro Ile Pro
130 135 140

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

Asn Ile Val Lys Glu Leu Asn Leu Lys Val Gly Lys Leu Ser Thr Gly
165 170 175

Asp Ser Leu Asp Met Ser Pro His Asp Glu Ser Ala Ile Leu Ser Asn
180 185 190

Glu Ala Thr Val Lys Asp Met Glu Gly Ala Ala Val Ala Tyr Val Ala
195 200 205

Asp Leu Phe Ser Thr Pro Ala Ile Phe Val Lys Ala Val Thr Asp Ile
210 215 220

Val Asp Gly Glu Lys Pro Thr Ala Glu Glu Phe Leu Gln Asn Leu Ile
225 230 235 240

Ser Val Thr Met Ala Leu Asp Gln Ala Val Leu Gln Val Val Asp Phe
245 250 255

Ile Ser Gly Lys Cys Ile Ser Asp Leu
260 265

<210> 999
<211> 275
<212> PRT
<213> Oryza sativa Indica Group

<400> 999

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

Ala Ile Ser Lys Leu Leu Ile Val Ile Ala Met Gln Thr Glu Ala Leu
20 25 30

Pro Leu Val Asn Lys Phe His Leu Val Glu Ala Glu Glu Ser Ile Phe
35 40 45

Pro Lys Gly Ala Pro Trp Ile Arg Tyr His Gly Asn Tyr Lys Gly Leu
50 55 60

His Val Asp Leu Val Trp Pro Gly Lys Asp Pro Val Leu Gly Val Asp
65 70 75 80

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

Ser Leu Lys Pro Asp Leu Ile Ile Asn Ala Gly Thr Ala Gly Gly Phe
100 105 110

Lys Ala Lys Gly Ala Asp Ile Gly Asp Val Tyr Leu Ala Ser Asp Val
115 120 125

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

Ile Gly Thr Arg Lys Thr Phe Ala Thr Pro Asn Ile Leu Lys Glu Leu
145 150 155 160

Asn Leu Lys Val Gly Lys Leu Ser Thr Gly Asp Ser Leu Asp Met Ser
165 170 175

Pro His Asp Glu Ser Ala Ile Leu Asn Asn Asp Ala Thr Val Lys Gly
180 185 190

Tyr Gly Val Val Ile Cys Arg Leu Lys Leu Ala Ser Leu Phe Leu Phe
195 200 205

Phe Gln Gly Ala Ala Val Ala Tyr Val Ala Asp Met Phe Ser Thr Pro
210 215 220

Ala Ile Phe Val Lys Ala Val Thr Asp Ile Val Asp Gly Glu Lys Pro
225 230 235 240

Thr Ala Glu Glu Phe Leu Gln Asn Leu Val Ala Val Thr Ala Ala Leu
245 250 255

Asp Lys Ala Val Thr Glu Val Val Asp Phe Ile Ser Gly Lys Cys Ile
260 265 270

Ser Asp Leu
275

<210> 1000
<211> 432
<212> PRT
<213> Zea mays subsp. mays

<400> 1000

Met Asp Trp Asp Leu Asn Ala Ala Gly Ala Trp Asp Leu Ala Glu Leu
1 5 10 15

Glu Arg Asp His Ala Ala Ala Ala Pro Ser Ser Gly Gly His Ala Ala
20 25 30

Asn Ala Ala Ala Ala Gly Thr Gly Thr Glu Ser Arg Pro Pro Ala Pro
35 40 45

Gly Ala Ala Gly Ala Pro Ala Glu Cys Ser Val Asp Leu Lys Leu Gly
50 55 60

Gly Met Gly Glu Cys Glu Pro Gly Ala Ala Arg Arg Glu Arg Glu Ala
65 70 75 80

Ala Ala Gly Ala Ala Lys Arg Pro Arg Pro Ala Gly Pro Gly Gly Gln
85 90 95

Gln Gln Gln Gln Gln Cys Pro Ser Cys Ala Val Asp Gly Cys Arg Ala
100 105 110

Asp Leu Gly Lys Cys Arg Asp Tyr His Arg Arg His Lys Val Cys Glu
115 120 125

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

Phe Cys Gln Gln Cys Ser Arg Phe His Leu Leu Ala Glu Phe Asp Ala
145 150 155 160

Asp Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly His Asn Arg Arg Arg
165 170 175

Arg Lys Pro Gln Pro Asp Thr Met Ala Ser Ala Ser Phe Ile Ala Ser
180 185 190

Gln Gln Gly Thr Arg Phe Ser Pro Phe Ala His Pro Arg Leu Glu Ala
195 200 205

Ser Trp Pro Pro Gly Val Met Lys Thr Glu Glu Ser Pro Tyr His Ile
210 215 220

Thr His Gln Ile Pro Leu Gly Ser Ser Ser Ser Ser Arg Gln Gln His
225 230 235 240

Phe Val Ala Leu Gly Ala Ala Thr Pro Ala Tyr Ala Lys Glu Gly Arg
245 250 255

Arg Phe Pro Phe Leu Gln Glu Gly Glu Ile Ser Phe Ala Thr Gly Val
260 265 270

Val Leu Glu Pro Pro Ala Ala Ala Pro Ala Cys Gln Pro Leu Leu Arg
275 280 285

Thr Gly Ala Pro Ser Glu Ser Ser Gly Ala Gly Gly Ser Lys Met Phe

290 295 300

Ser Asp Gln Gly Leu Ala Arg Val Leu Asp Ser Asp Cys Ala Leu Ser
305 310 315 320

Leu Leu Ser Ala Pro Ala Asn Ser Ser Gly Ile Asp Val Ser Arg Met
325 330 335

Val Arg Pro Thr Glu His Val Pro Met Ala Gln Gln Pro Val Val Pro
340 345 350

Gly Leu Gln Phe Gly Ser Ala Ser Trp Phe Pro Arg Pro Gln Ala Ser
355 360 365

Thr Gly Gly Ser Phe Val Pro Ser Cys Pro Ala Ala Val Glu Gly Glu
370 375 380

Gln Gln Leu Asn Ala Val Leu Gly Pro Asn Asp Ser Glu Val Ser Met
385 390 395 400

Asn Tyr Gly Gly Met Phe His Val Gly Gly Gly Ser Gly Gly Gly Glu
405 410 415

Gly Ser Ser Asp Gly Gly Thr Ser Ser Ser Met Pro Phe Ser Trp Gln
420 425 430

<210> 1001
<211> 432
<212> PRT
<213> Zea mays subsp. mays

<400> 1001

Met Asp Trp Asp Leu Lys Ala Ala Gly Ala Trp Asp Leu Ala Glu Leu
1 5 10 15

Glu Gln Asp His Ala Ala Ala Ala Pro Ser Ser Gly Gly His Ala Ala
20 25 30

Asn Ala Ala Ala Ala Gly Thr Gly Thr Glu Ser Arg Pro Pro Ala Pro
35 40 45

Gly Ala Ala Gly Ala Pro Ala Glu Cys Ser Val Asp Leu Lys Leu Gly
50 55 60

Gly Met Gly Glu Cys Glu Pro Gly Ala Ala Arg Arg Glu Arg Glu Ala
65 70 75 80

Ala Ala Gly Ala Ala Lys Arg Pro Arg Pro Ala Gly Pro Gly Gly Gln
85 90 95

Gln Gln Gln Gln Cys Pro Ser Cys Ala Val Asp Gly Cys Arg Ala Asp
100 105 110

Leu Gly Lys Cys Arg Asp Tyr His Arg Arg His Lys Val Cys Glu Ala
115 120 125

His Ser Lys Thr Pro Val Val Val Val Ala Gly Arg Glu Met Arg Phe
130 135 140

Cys Gln Gln Cys Ser Arg Phe His Leu Leu Ala Glu Phe Asp Ala Asp
145 150 155 160

Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly His Asn Arg Arg Arg Arg
165 170 175

Lys Pro Gln Pro Asp Thr Met Ala Ser Ala Ser Phe Ile Ala Ser Gln
180 185 190

Gln Gly Thr Arg Phe Ser Pro Phe Ala His Pro Arg Leu Glu Ala Ser
195 200 205

Trp Pro Pro Gly Val Met Lys Asn Glu Glu Ser Pro Tyr His Ile Thr
210 215 220

His Gln Ile Pro Leu Gly Ser Ser Ser Ser Gly Asn Arg Gln Gln His
225 230 235 240

Phe Val Ala Leu Gly Ala Ala Thr Pro Ala Tyr Ala Lys Glu Gly Arg
245 250 255

Arg Phe Pro Phe Leu Gln Glu Gly Glu Ile Ser Phe Ala Thr Gly Val
260 265 270

Val Leu Glu Pro Pro Ala Ser Ala Pro Ala Cys Gln Pro Leu Leu Arg
275 280 285

Thr Gly Ala Pro Ser Glu Ser Ser Gly Ala Gly Gly Ser Lys Met Phe
290 295 300

Ser Asp Gln Gly Leu Ala Arg Val Leu Asp Ser Asp Cys Ala Leu Ser
305 310 315 320

Leu Leu Ser Ala Pro Ala Asn Ser Ser Gly Ile Asp Val Ser Arg Met
325 330 335

Val Arg Pro Thr Glu His Val Pro Met Ala Gln Gln Pro Val Val Pro
340 345 350

Gly Leu Gln Phe Gly Ser Ala Ser Trp Phe Pro Arg Pro Gln Ala Ser
355 360 365

Thr Gly Gly Ser Phe Val Pro Ser Cys Pro Ala Ala Val Glu Gly Glu
370 375 380

Gln Gln Leu Asn Ala Val Leu Gly Pro Asn Asp Ser Glu Val Ser Met
385 390 395 400

Asn Tyr Gly Gly Met Phe His Val Gly Gly Gly Ser Gly Gly Gly Glu
405 410 415

Gly Ser Ser Asp Gly Gly Thr Ser Ser Ser Met Pro Phe Ser Trp Gln
420 425 430

<210> 1002
<211> 431
<212> PRT
<213> Zea mays subsp. mays

<400> 1002

Met Asp Trp Asp Leu Asn Ala Ala Gly Ala Trp Asp Leu Ala Glu Leu
1 5 10 15

Glu Gln Asp His Ala Ala Ala Ala Pro Ser Ser Gly Gly His Ala Ala
20 25 30

Asn Ala Ala Ala Ala Gly Thr Gly Thr Glu Ser Arg Pro Pro Ala Pro
35 40 45

Gly Ala Ala Gly Ala Pro Ala Glu Cys Ser Val Asp Leu Lys Leu Gly
50 55 60

Gly Met Gly Glu Cys Glu Pro Gly Ala Ala Arg Arg Glu Arg Glu Ala
65 70 75 80

Ala Ala Gly Ala Ala Lys Arg Pro Arg Pro Ala Gly Pro Gly Gly Gln
85 90 95

Gln Gln Gln Gln Cys Pro Ser Cys Ala Val Asp Gly Cys Arg Ala Asp
100 105 110

Leu Gly Lys Cys Arg Asp Tyr His Arg Arg His Lys Val Cys Glu Ala
115 120 125

His Ser Lys Thr Pro Val Val Val Val Ala Gly Arg Glu Met Arg Phe
130 135 140

Cys Gln Gln Cys Ser Arg Phe His Leu Leu Ala Glu Phe Asp Ala Asp
145 150 155 160

Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly His Asn Arg Arg Arg Arg
165 170 175

Lys Pro Gln Pro Asp Thr Met Ala Ser Ala Ser Phe Ile Ala Ser Gln
180 185 190

Gln Gly Thr Arg Phe Ser Pro Phe Ala His Pro Arg Leu Glu Ala Ser
195 200 205

Trp Pro Pro Gly Val Met Lys Thr Glu Glu Ser Pro Tyr His Ile Thr
210 215 220

His Gln Ile Pro Leu Gly Ser Ser Ser Ser Ser Arg Gln Gln His Phe
225 230 235 240

Val Ala Leu Gly Ala Ala Thr Pro Ala Tyr Ala Lys Glu Gly Arg Arg
245 250 255

Phe Pro Phe Leu Gln Glu Gly Glu Ile Ser Phe Ala Thr Gly Val Val
260 265 270

Leu Glu Pro Pro Ala Ala Ala Pro Ala Cys Gln Pro Leu Leu Arg Thr
275 280 285

Gly Ala Pro Ser Glu Ser Ser Gly Ala Gly Gly Ser Lys Met Phe Ser
290 295 300

Asp Gln Gly Leu Ala Arg Val Leu Asp Ser Asp Cys Ala Leu Ser Leu
305 310 315 320

Leu Ser Ala Pro Ala Asn Ser Ser Gly Ile Asp Val Ser Arg Met Val
325 330 335

Arg Pro Thr Glu His Val Pro Met Ala Gln Gln Pro Val Val Pro Gly
340 345 350

Leu Gln Phe Gly Ser Ala Ser Trp Phe Pro Arg Pro Gln Ala Ser Thr
355 360 365

Gly Gly Ser Phe Val Pro Phe Cys Pro Ala Ala Val Glu Gly Glu Gln

370 375 380

Gln Leu Asn Ala Val Leu Gly Pro Asn Asp Ser Glu Val Ser Met Asn
385 390 395 400

Tyr Gly Gly Met Phe His Val Gly Gly Gly Ser Gly Gly Gly Glu Gly
405 410 415

Ser Ser Asp Gly Gly Thr Ser Ser Ser Met Pro Phe Ser Trp Gln
420 425 430

<210> 1003
<211> 435
<212> PRT
<213> Sorghum bicolor

<400> 1003

Met Asp Trp Asp Leu Lys Ala Pro Gly Ala Trp Asp Leu Ala Glu Leu
1 5 10 15

Glu His Glu Gln His Ala Ala Ala Thr Ala Ala Ala Ala Gly Pro Ser
20 25 30

Gly Gly His Ala Asn Ala Gly Val Ala Gly Thr Gly Thr Gly Cys Arg
35 40 45

Pro Pro Pro Gly Ala Gly Gly Ala Pro Ala Glu Cys Ser Val Asp Leu
50 55 60

Lys Leu Gly Gly Leu Gly Glu Pro Gly Ala Ala Pro Pro Ala Arg Arg
65 70 75 80

Glu Arg Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala Glu His Gln Gln
85 90 95

Gly Gln Gly Gln His Gln Gln Gln Gln Cys Pro Ser Cys Ala Val Glu
100 105 110

Gly Cys Lys Ala Asp Leu Ser Lys Cys Arg Asp Tyr His Arg Arg His
115 120 125

Lys Val Cys Glu Ala His Ser Lys Thr Pro Val Val Val Val Ala Gly
130 135 140

Arg Glu Met Arg Phe Cys Gln Gln Cys Ser Arg Phe His Leu Leu Ala
145 150 155 160

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

Asn Arg Arg Arg Arg Lys Pro Gln Pro Asp Thr Met Ala Ser Ala Ser
180 185 190

Phe Ile Thr Ser Gln Gln Gly Thr Arg Phe Ser Pro Phe Ala Pro Pro
195 200 205

Arg Leu Glu Ala Ser Trp Pro Gly Val Ile Lys Thr Glu Glu Ser Pro
210 215 220

Tyr Tyr Thr His Gln Ile Pro Leu Gly Ser Ser Ser Asn Arg Gln Gln
225 230 235 240

His Phe Val Gly Ser Thr Thr Pro Ala Tyr Ala Lys Glu Gly Arg Arg
245 250 255

Phe Pro Phe Leu Gln Glu Gly Glu Ile Ser Phe Ala Thr Gly Val Val
260 265 270

Leu Glu Pro Pro Ala Cys Gln Pro Leu Leu Lys Thr Val Ala Val Ala
275 280 285

Pro Pro Glu Ser Ser Ser Ser Ser Ser Ala Gly Gly Gly Asn Lys Met
290 295 300

Phe Ser Asp Gly Leu Thr Arg Val Leu Asp Ser Glu Cys Ala Leu Ser
305 310 315 320

Leu Leu Ser Ala Pro Ala Asn Ser Ser Gly Ile Asp Val Ser Arg Met
325 330 335

Val Arg Pro Thr Glu His Val Pro Met Ala Gln Pro Val Val Ser Gly
340 345 350

Leu Gln Phe Gly Ser Ser Ser Trp Phe Ser Pro Arg Pro Gln Ala Ser
355 360 365

Thr Gly Val Thr Ala Gly Ser Gly Phe Pro Ser Cys Pro Ala Val Val
370 375 380

Glu Gly Glu Gln Gln Gln Leu Asn Thr Val Leu Ser Pro His Asp Asn
385 390 395 400

Glu Val Asn Tyr Gly Gly Met Phe His Val Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Glu Gly Ser Ser Asp Gly Gly Thr Ser Ser Ser Met Pro Phe
420 425 430

Ser Trp Gln
435

<210> 1004
<211> 301
<212> PRT
<213> Sorghum bicolor

<400> 1004

Met Pro Val Leu Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly Lys Lys Val Cys Asp Lys Asp Ser Ser Ser Glu Ser Asp

35 40 45

Gln Ser His Gln Glu Ala Ser Ala Val Ser Glu Ser Ser Pro Ala Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu Asp Tyr Ser Pro Ser Phe Ala Tyr Ile Pro
100 105 110

Tyr Thr Ala Asp Ala Cys Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr
115 120 125

Ala Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser
130 135 140

Pro Gly Ile Leu Pro Val Glu Pro Thr Glu Glu Glu Pro Ile Tyr Val
145 150 155 160

Asn Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala
165 170 175

Lys Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu
180 185 190

His Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly
195 200 205

Gly Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Leu Ser Ser Ser Met Cys Ser Lys Ile Ile Gly Asn Ser Leu
225 230 235 240

Ile Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Asp Thr Ala Gly
245 250 255

Ala Ser Thr Ala Ser Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Met Thr Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1005
<211> 300
<212> PRT
<213> Zea mays

<400> 1005

Met Pro Val Ile Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly His Lys Val Cys Asp Arg His Ser Ser Ser Glu Ser Asp
35 40 45

Arg Ser His Gln Glu Ala Ser Ala Ala Ser Glu Ser Ser Pro Asn Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu His Tyr Ser Pro Ser Phe Ala Cys Ile Pro
100 105 110

Tyr Thr Val Asp Ala Tyr Tyr Ser Gly Val Gly Val Leu Thr Gly Tyr
115 120 125

Ala Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Thr
130 135 140

Pro Gly Met Leu Pro Val Glu Pro Ala Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Asn Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr Gln
210 215 220

Ala Ser Ser Gly Ser Leu Cys Ser Lys Ile Ile Gly Asn Ser Ile Ile
225 230 235 240

Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Gly Thr Ala Gly Ala
245 250 255

Ser Thr Ala Cys Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe Arg
260 265 270

Pro Thr Thr Asn Phe Ser Asp Gln Gly Arg Gly Gly Leu Lys Leu Ala
275 280 285

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

<210> 1006
<211> 300
<212> PRT
<213> Zea mays

<400> 1006

Met Pro Val Ile Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly His Lys Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp
35 40 45

Arg Ser His Gln Glu Ala Ser Ala Ala Ser Glu Ser Ser Pro Asn Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu His Tyr Ser Pro Ser Phe Ala Cys Ile Pro
100 105 110

Tyr Thr Ser Asp Ala Tyr Tyr Ser Ala Val Gly Val Leu Thr Gly Tyr
115 120 125

Pro Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Thr
130 135 140

Pro Gly Met Leu Pro Val Glu Pro Ala Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Asn Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr Gln
210 215 220

Ala Ser Ser Gly Ser Leu Cys Ser Lys Ile Ile Ala Asn Ser Ile Ile
225 230 235 240

Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Gly Thr Ala Gly Ala
245 250 255

Ser Thr Ala Gly Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe Arg
260 265 270

Pro Thr Thr Asn Phe Ser Asp Gln Gly Arg Gly Gly Leu Lys Leu Ala
275 280 285

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

<210> 1007
<211> 300
<212> PRT
<213> Zea mays

<400> 1007

Met Pro Val Ile Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly His Lys Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp
35 40 45

Arg Ser His Gln Glu Ala Ser Ala Ala Ser Glu Ser Ser Pro Asn Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu His Tyr Ser Pro Ser Phe Ala Cys Ile Pro
100 105 110

Tyr Thr Ser Asp Ala Tyr Tyr Ser Ala Val Gly Val Leu Thr Gly Tyr
115 120 125

Pro Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Thr
130 135 140

Pro Gly Met Leu Pro Val Glu Pro Ala Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Asn Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Glu Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr Gln
210 215 220

Ala Ser Ser Gly Ser Leu Cys Ser Lys Ile Ile Ala Asn Ser Ile Ile
225 230 235 240

Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Gly Thr Ala Gly Ala
245 250 255

Ser Thr Ala Gly Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe Arg
260 265 270

Pro Thr Thr Asn Phe Ser Asp Gln Gly Arg Gly Gly Leu Lys Leu Ala
275 280 285

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

<210> 1008
<211> 301
<212> PRT
<213> Zea mays

<400> 1008

Met Cys Leu Leu Arg Glu Met Glu Asp His Tyr Val His Pro Lys Ser
1 5 10 15

Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
20 25 30

Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
35 40 45

Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His
50 55 60

Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
65 70 75 80

Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
85 90 95

Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Ala Tyr Ile Pro Tyr
100 105 110

Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
115 120 125

Pro His Thr Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
130 135 140

Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Gln Pro Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asn Ser Val
225 230 235 240

Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly
245 250 255

Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1009

<211> 301
<212> PRT
<213> Zea mays

<400> 1009

Met Cys Leu Leu Arg Glu Met Glu Asp His Ser Val His Pro Lys Ser
1 5 10 15

Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
20 25 30

Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
35 40 45

Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His
50 55 60

Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
65 70 75 80

Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
85 90 95

Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Pro Tyr Ile Pro Tyr
100 105 110

Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
115 120 125

Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
130 135 140

Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Gln Leu Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asp Ser Val
225 230 235 240

Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly
245 250 255

Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1010
<211> 301
<212> PRT
<213> Zea mays

<400> 1010

Met Cys Leu Leu Arg Glu Met Glu Asp His Ser Val His Pro Lys Ser
1 5 10 15

Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
20 25 30

Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
35 40 45

Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His
50 55 60

Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
65 70 75 80

Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
85 90 95

Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Pro Tyr Ile Pro Tyr
100 105 110

Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
115 120 125

Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
130 135 140

Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu Arg
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Gln Leu Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asp Ser Val
225 230 235 240

Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly

245 250 255

Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1011
<211> 300
<212> PRT
<213> Zea mays

<400> 1011

Met Pro Val Ile Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly His Lys Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp
35 40 45

Arg Ser His Gln Glu Ala Ser Ala Ala Ser Glu Ser Ser Pro Asn Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu His Tyr Ser Pro Ser Phe Ala Cys Ile Pro
100 105 110

Tyr Thr Ser Asp Ala Tyr Tyr Ser Ala Val Gly Val Leu Thr Gly Tyr
115 120 125

Pro Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Thr
130 135 140

Pro Gly Met Leu Pro Val Glu Pro Ala Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Asn Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr Gln
210 215 220

Ala Ser Ser Gly Ser Leu Cys Ser Lys Ile Ile Ala Asn Ser Ile Ile
225 230 235 240

Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Gly Thr Ala Gly Ala
245 250 255

Ser Thr Ala Gly Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe Arg
260 265 270

Pro Thr Thr Asn Phe Ser Asp Gln Gly Arg Gly Gly Leu Lys Leu Ala
275 280 285

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

<210> 1012
<211> 300

<212> PRT
<213> Zea mays

<400> 1012

Met Pro Val Ile Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly His Lys Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp
35 40 45

Arg Ser His Gln Glu Ala Ser Ala Ala Ser Glu Ser Ser Pro Asn Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu His Tyr Ser Pro Ser Phe Ala Cys Ile Pro
100 105 110

Tyr Thr Ser Asp Ala Tyr Tyr Ser Ala Val Gly Val Leu Thr Gly Tyr
115 120 125

Pro Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Thr
130 135 140

Pro Gly Met Leu Pro Val Glu Pro Ala Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Asn Arg Lys Pro Tyr Leu His

180 185 190

Glu Ser Arg His Arg His Ala Met Glu Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr Gln
210 215 220

Ala Ser Ser Gly Ser Leu Cys Ser Lys Ile Ile Ala Asn Ser Ile Ile
225 230 235 240

Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Gly Thr Ala Gly Ala
245 250 255

Ser Thr Ala Gly Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe Arg
260 265 270

Pro Thr Thr Asn Phe Ser Asp Gln Gly Arg Gly Gly Leu Lys Leu Ala
275 280 285

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

<210> 1013
<211> 300
<212> PRT
<213> Zea mays

<400> 1013

Met Pro Val Ile Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly His Lys Val Cys Asp Arg His Ser Ser Ser Glu Ser Asp
35 40 45

Arg Ser His Gln Glu Ala Ser Ala Ala Ser Glu Ser Ser Pro Asn Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu His Tyr Ser Pro Ser Phe Ala Cys Ile Pro
100 105 110

Tyr Thr Val Asp Ala Tyr Tyr Ser Gly Val Gly Val Leu Thr Gly Tyr
115 120 125

Ala Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Thr
130 135 140

Pro Gly Met Leu Pro Val Glu Pro Ala Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Asn Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr Gln
210 215 220

Ala Ser Ser Gly Ser Leu Cys Ser Lys Ile Ile Gly Asn Ser Ile Ile
225 230 235 240

Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Gly Thr Ala Gly Ala
245 250 255

Ser Thr Ala Cys Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe Arg
260 265 270

Pro Thr Thr Asn Phe Ser Asp Gln Gly Arg Gly Gly Leu Lys Leu Ala
275 280 285

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

<210> 1014
<211> 301
<212> PRT
<213> Sorghum bicolor

<400> 1014

Met Pro Val Leu Leu Arg Glu Met Glu Asp His Ser Val His Pro Met
1 5 10 15

Ser Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys
20 25 30

His Ser Gly Lys Lys Val Cys Asp Lys Asp Ser Ser Ser Glu Ser Asp
35 40 45

Gln Ser His Gln Glu Ala Ser Ala Val Ser Glu Ser Ser Pro Ala Glu
50 55 60

His Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn
65 70 75 80

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

Phe Leu Ala Pro Lys Leu Asp Tyr Ser Pro Ser Phe Ala Tyr Ile Pro
100 105 110

Tyr Thr Ala Asp Ala Cys Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr

115 120 125

Ala Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser
130 135 140

Pro Gly Ile Leu Pro Val Glu Pro Thr Glu Glu Glu Pro Ile Tyr Val
145 150 155 160

Asn Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala
165 170 175

Lys Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu
180 185 190

His Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly
195 200 205

Gly Arg Phe Leu Asn Thr Lys Gln Leu Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Leu Ser Ser Ser Met Cys Ser Lys Ile Ile Gly Asn Ser Leu
225 230 235 240

Ile Ser Gln Ser Gly Pro Thr Cys Thr Pro Ser Ser Asp Thr Ala Gly
245 250 255

Ala Ser Thr Ala Ser Gln Asp Arg Ser Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Met Thr Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1015
<211> 301
<212> PRT

<213> Zea mays

<400> 1015

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Met Cys Leu Leu Arg Glu Met Glu Asp His Tyr Val His Pro Lys Ser
1               5                   10                  15


Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
            20                  25                  30


Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
        35                  40                  45


Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His
    50                  55                  60


Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
65                  70                  75                  80


Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
                85                  90                  95


Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Ala Tyr Ile Pro Tyr
            100                 105                 110


Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
        115                 120                 125


Pro His Thr Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
    130                 135                 140


Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
145                 150                 155                 160


Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
                165                 170                 175


Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu His
            180                 185                 190
```

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Gln Pro Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asn Ser Val
225 230 235 240

Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly
245 250 255

Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1016
<211> 301
<212> PRT
<213> Zea mays

<400> 1016

Met Cys Leu Leu Arg Glu Met Glu Asp His Ser Val His Pro Lys Ser
1 5 10 15

Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
20 25 30

Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
35 40 45

Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His

50 55 60

Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
65 70 75 80

Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
85 90 95

Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Pro Tyr Ile Pro Tyr
100 105 110

Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
115 120 125

Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
130 135 140

Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu His
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Gln Leu Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asp Ser Val
225 230 235 240

Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly
245 250 255

Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1017
<211> 301
<212> PRT
<213> Zea mays

<400> 1017

Met Cys Leu Leu Arg Glu Met Glu Asp His Ser Val His Pro Lys Ser
1 5 10 15

Lys Ser Asn His Gly Ser Leu Ser Gly Asn Gly Tyr Glu Met Lys Asn
20 25 30

Pro Gly His Glu Val Cys Asp Arg Asp Ser Ser Ser Glu Ser Asp Arg
35 40 45

Ser His Pro Glu Ala Ser Ala Val Ser Glu Ser Ser Leu Asp Glu His
50 55 60

Thr Ser Thr Gln Ser Asp Asn Asp Glu Asp His Gly Lys Asp Asn Gln
65 70 75 80

Asp Thr Leu Lys Pro Val Leu Ser Leu Gly Lys Glu Gly Ser Ala Phe
85 90 95

Leu Ala Pro Lys Ile Asp Tyr Asn Pro Ser Phe Pro Tyr Ile Pro Tyr
100 105 110

Thr Ala Asp Ala Tyr Tyr Gly Gly Val Gly Val Leu Thr Gly Tyr Ala
115 120 125

Pro His Ala Ile Val His Pro Gln Gln Asn Asp Thr Thr Asn Ser Pro
130 135 140

Val Met Leu Pro Ala Glu Pro Ala Glu Glu Glu Pro Ile Tyr Val Asn
145 150 155 160

Ala Lys Gln Tyr His Ala Ile Leu Arg Arg Arg Gln Thr Arg Ala Lys
165 170 175

Leu Glu Ala Gln Asn Lys Met Val Lys Gly Arg Lys Pro Tyr Leu Arg
180 185 190

Glu Ser Arg His Arg His Ala Met Lys Arg Ala Arg Gly Ser Gly Gly
195 200 205

Arg Phe Leu Asn Thr Lys Gln Gln Leu Gln Glu Gln Asn Gln Gln Tyr
210 215 220

Gln Ala Ser Ser Gly Ser Met Cys Ser Lys Thr Ile Gly Asp Ser Val
225 230 235 240

Ile Ser Gln Ser Gly Pro Ile Cys Thr Pro Ser Ser Asp Ala Ala Gly
245 250 255

Ala Ser Ala Ala Ser Gln Asp Arg Gly Cys Leu Pro Ser Val Gly Phe
260 265 270

Arg Pro Thr Ala Asn Phe Ser Glu Gln Gly Gly Gly Gly Ser Lys Leu
275 280 285

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

<210> 1018
<211> 275
<212> PRT
<213> Zea mays

<400> 1018

Met Leu Leu Pro Ser Ser Ser Ser Ala Ser Ala Ser Ala Ser Ala Ser
1   5   10   15

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

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

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

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

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

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

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

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

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

Arg Phe Leu Asn Thr Lys Gln Leu Gln Gln Ser His Thr Ala Leu Thr
                165   170   175

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

Arg Leu Gly Gly Gly Ala Ala Ala Ala Gly Asp Arg Ser Val Leu Ala
195 200 205

Pro Lys Thr Met Ala Ser Gln Asp Ser Ser Lys Lys Ala Val Ser Ser
210 215 220

Ala Leu Ala Phe Thr Val Thr Pro Met Leu Arg Arg Asp Asp Gly Phe
225 230 235 240

Leu Gln His Pro Ser His Leu Phe Ser Phe Ser Gly His Phe Gly Gln
245 250 255

Ala Ser Ala Gln Ala Gly Val His Asn Gly Ser Gln His Arg Val Pro
260 265 270

Val Met Arg
275

<210> 1019
<211> 264
<212> PRT
<213> Sorghum bicolor

<400> 1019

Met Phe Leu Phe Leu Ser Ile Ser Leu Leu Cys Asn Ser Phe Gly Asn
1 5 10 15

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

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

Ile Ser Tyr Pro Tyr Asn His Ser Gly Ser Gly Gly Val Trp Ala Ala
50 55 60

Tyr Glu Ser Gly Thr Thr Ala Thr Thr Val Phe His Ser Gln Ile Ser
65 70 75 80

Gly Gly Gly Ala Arg Ile Pro Leu Pro Leu Glu Leu Ala Glu Asn Glu
85 90 95

Pro Ile Tyr Val Asn Pro Lys Gln Tyr His Gly Ile Leu Arg Arg Arg
100 105 110

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

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

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

Gln Gln Ser His Thr Ala Ser Thr Arg Ser Thr Thr Asn Gly Thr Ser
165 170 175

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

Arg Ser Met Leu Ala Pro Lys Thr Met Ala Ser Gln Asp Ser Ser Lys
195 200 205

Lys Ala Val Ser Ser Ala Leu Ala Phe Thr Val Thr Pro Met Leu His
210 215 220

Arg Asp Asp Ala Phe Leu Gln His Pro Ser His Tyr Leu Ser Phe Ser
225 230 235 240

Gly His Phe Gly Gln Ala Ser Val Gln Ala Gly Met His Asn Gly Ser
245 250 255

Gln His Arg Val Pro Phe Met Arg
260

<210> 1020
<211> 202
<212> PRT
<213> Sorghum bicolor

<400> 1020

Met Ile Thr Gly Leu Asn Tyr Asn Asp Tyr Gln Ile Ser Arg Gly Lys
1 5 10 15

Glu Leu Val Phe Ser Ala Gly Leu Asn Glu Gln Cys Ser Phe Leu Lys
20 25 30

Gln Gly Val Tyr Ser Glu Ile Tyr Arg Val Leu Lys Pro Gly Gln Tyr
35 40 45

Phe Ala Leu Asp Glu Trp Cys Leu Thr Asp Arg Phe Asp Pro Asn Asn
50 55 60

Gly Lys His Leu Ala Ile Lys Ala Glu Ile Glu Leu Gly Asp Gly Leu
65 70 75 80

Pro Asp Ile Arg Thr Thr Arg Gln Cys Val Gln Ala Met Lys Asp Ala
85 90 95

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

Pro Trp Tyr Gln Met Met Asp Pro Asn Asn Phe Ser Trp Thr Ser Phe
115 120 125

Gln Cys Thr Arg Pro Gly Arg Ile Ile Thr Arg Ala Ile Val Asn Ala
130 135 140

Leu Glu Phe Leu Arg Ile Ala Pro Ala Gly Ser Ala Gly Ile Tyr Ser
145 150 155 160

Phe Leu Thr Ser Ala Ser Asp Gly Leu Leu Lys Gly Gly Arg Glu Gly
165 170 175

Ile Phe Thr Ala Thr Phe Phe Val Leu Ala Arg Lys Pro Leu Asn Lys
180 185 190

Glu Thr Glu Ile Val Asn Asp Gly Asn Leu
195 200

<210> 1021
<211> 254
<212> PRT
<213> Zea mays

<400> 1021

Met Lys Val Leu Asp Val Gly Cys Gly Ile Gly Gly Pro Leu Ile Glu
1 5 10 15

Ile Ala Arg Phe Ser Ser Thr Ser Ile Thr Gly Leu Asn Asn Asn Asp
20 25 30

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

Glu Gln Cys Cys Phe Leu Lys Gly Asp Phe Met Asp Met Pro Ile Ser
50 55 60

Asp Asn Thr Phe Asp Ala Ala Tyr Ala Ile Gln Ala Thr Cys His Ala
65 70 75 80

Pro Asp Ala Gln Gly Val Tyr Ser Glu Val Tyr Arg Val Leu Lys Pro
85 90 95

Gly Gln Tyr Phe Ala Leu Asp Glu Trp Cys Leu Thr Asp Arg Phe Asp
100 105 110

Pro Asn Asn Ala Lys His Leu Ala Ile Lys Ala Glu Ile Glu Leu Gly
115 120 125

Asp Gly Leu Pro Asp Ile Arg Thr Thr Arg Gln Cys Val Gln Ala Met
130 135 140

Lys Asp Ala Gly Phe Glu Val Val Phe Ala Lys Asp Leu Ala Gln Val
145 150 155 160

Phe Pro Cys Pro Trp Tyr Arg Val Met Asp Pro Thr Tyr Phe Ser Trp
165 170 175

Ala His Phe Gln Cys Thr Arg Pro Gly Arg Ile Val Thr Arg Ala Ile
180 185 190

Val Asn Thr Leu Glu Phe Leu Arg Ile Ala Pro Ala Gly Ser Met Gly
195 200 205

Ala Tyr Asn Val Leu Met Ser Ala Ser Asp Gly Leu Leu Lys Gly Gly
210 215 220

Arg Glu Gly Ile Phe Thr Ala Thr Phe Phe Val Leu Gly Arg Lys Pro
225 230 235 240

Leu Lys Glu Val Asp Ile Val Ser Leu Ser Arg Lys Leu Ile
245 250

<210> 1022
<211> 1824
<212> DNA
<213> Zea mays

<400> 1022
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gagagagtcc cccagatggt tttatgtgcc cgggtggctg gaaggtactc gttgaatact 1440

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atctggaaaa tccttcatat aaggaatgct actatatctt agcaagcggt tctttgcgac 1560

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tcggatgtta atgtgtgctt tgtacccggt gtaccttctc tgctggcagt gttgcacatg 1680

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tgtacatata tacattgtgg tgatatataa ttataaagct gacctctgcc gtccgggctc 1800

gtagtgatga acagttttat cact 1824

<210> 1023

<211> 1878
<212> DNA
<213> Zea mays

<400> 1023
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ataaaaaccc tgttcttctg ctccatccac tgggaggatt cacaaaagca gatgatgtgc 1080

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aaggacagac tatgtatcat ctgccagatt gttgtacata tacattgtgg tgatataaac 1860

atgaagctgt cttctgct 1878

<210> 1024
<211> 1795
<212> DNA
<213> Zea mays

<400> 1024
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<210> 1025
<211> 1790
<212> DNA
<213> Zea mays

<400> 1025
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<212> DNA
<213> Oryza sativa Japonica Group

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gcctaaacat ttgggtttga ttggaagcgc 1590

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<211> 1721
<212> DNA
<213> Hordeum vulgare subsp. vulgare

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Ala Leu Tyr Cys Lys Pro Val Glu Leu Tyr Asn Ile Ile Gln Arg Arg
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Ala Met Lys Asn Pro Leu Phe Ile Gln Arg Cys Leu Leu Tyr Asn Ile
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His Ala Arg Arg Lys Lys Arg Ile Gln Ile Thr Ile Ser Leu Ser Gly
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Ser Thr Asn Thr Glu Leu Gln Thr His Tyr Val Phe Pro Leu Tyr Val
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Leu Leu Ala Arg Pro Thr Ser Asn Leu Ser Leu Glu Gly His Ser Pro
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Ile Tyr Arg Phe Ser Arg Val Cys Leu Leu Thr Ser Phe Ser Glu His
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Gly Asn Lys Asp Asn Ser Glu Ala Thr Phe Ile Ile Pro Asp Val Lys
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Ser Leu Ser Thr Ser Arg Ala Cys Asn His Asp Ile Ile Phe Ile Ser
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Cys Gly Gln Val Gly Gln Ser Asn Gly Glu Asp Asn Cys Ser Gly Asn
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His Val Glu Asp Ser Ser Leu Gln Met Leu Glu Gly Lys Cys Ser Trp
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Phe His Ser His Arg Ala Gln Pro Met Gln Leu Glu Gln Val Phe Ser
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Asp Arg Arg Met Leu Asp Asp Phe Val Asp Val Thr Lys Asp Glu Lys
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Phe Met Ile Lys Leu Trp Asn His Asn Ile Leu Asp Ala Arg Thr Met
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cgtttcttca tgattaaact ttggaaccat aacattttag atgcccgcac tatgaacaca 1980

tgcaatacag tccttcaaat tttacaagaa gaaagcacag gactaaagta attttgatgc 2040

ttctgatgaa aattcaaggg aagaagattt ctttaccatt tccaagaaga aagcatagaa 2100 ttggagtaac ttttattga taatttcatt catatctatt gtcaattgta ttaatggttt 2160

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<400> 1103
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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

attcaacggc gagccatgaa aaatcccctt tttattcaaa gatgccttct ttataatata 240

catgcgagga ggaaaaagag gattcagata accatatcac tttctggaag tacaaatact 300

gagttgcaaa cacattatgt ctttcctctt tatgttctgt tagctagacc cactagtaac 360

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tttagtgaac atggaaataa ggacaacagt gaagctacat tcatcattcc tgacgtgaag 480

agtttgtcaa cctcccgtgc ttgcaaccat gatattatct ttattagctg tgggcaagtt 540

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gagagttgtg tcaatttaag tttgggacat attgtggagt tggcatctaa agttacaatg 720

agaccaagct tcttagagcc aaaatttctg gagcaagaca gttgcttgac attttgctct 780

cataaggttg atgctgtggg ttcatataaa ctacaactat gcatgtccgc acaagaggct 840

ggtgcaagag atatgtcttt gtctccatat agtagttact catataatga tgtcccacct 900

tcgtcattat cagatatcat aaggttaaga tctggcaatg tactttttaa ttacaagtac 960

tacaataata caatgcaaga gactgaagtc actgaagatt tctcttgtcc attttgctat 1020

gtacgatgtg gaagcttcaa gggtctagga tgccatttaa actcatcaca tgatctattc 1080

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gatgatgata ttgctgactt cgaggataga agaatgcttg atgattttgt tgatgttacg 1620

aaagatgaaa aacttattat gcatatgtgg aattcatttg ttcgaaaaca aagagtgtta 1680

gctgatggtc atataccttg ggcctgcgag gcattctccc agttgcatgg acgacaactt 1740

atacaaaatc ctgctctgct gtggggttgg cgtttcttca tgattaaact ttggaaccat 1800

aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

gaaagcacag gactaaag 1878

<210> 1104
<211> 1878
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1104
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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

attcaacggc gagccatgaa aaatcccctt tttattcaaa gatgccttct ttataatata 240

catgcgagga ggaaaaagag gattcagata accatatcac tttctggaag tacaaatact 300

gagttgcaaa cacattatgt ctttcctctt tatgttctgt tagctagacc cactagtaac 360

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tttagtgaac atggaaataa ggacaacagt gaagctacat tcatcattcc tgacgtgaag 480 agtttgtcaa cctcccgtgc ttgcaaccat gatattatct ttattagctg tgggcaagtt 540

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gagagttgtg tcaatttaag tttgggacat attgtggagt tggcatctaa agttacaatg 720

agaccaagct tcttagagcc aaaatttctg gagcaagaca gttgcttgac attttgctct 780

cataaggttg atgctgtggg ttcatataaa ctacaactat gcatgtccgc acaagaggct 840

ggtgcaagag atatgtcttt gtctccatat agtagttact catataatga tgtcccacct 900

tcgtcattat cagatatcat aaggttaaga tctggcaatg tactttttaa ttacaagtac 960

tacaataata caatgcaaga gactgaagtc actgaagatt tctcttgtcc attttgctat 1020

gtacgatgtg gaagcttcaa gggtctagga tgccatttaa actcatcaca tgatctattc 1080

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gatgatgata ttgctgactt cgaggataga agaatgcttg atgattttgt tgatgttacg 1620

aaagatgaaa aacttattat gcatatgtgg aattcatttg ttcgaaaaca aagagtactc 1680

gcagacggac acatcccatg ggcctgcgag gcattctccc agttgcatgg acgacaactt 1740

atacaaaatc ctgctctgct gtggggttgg cgtttcttca tgattaaact ttggaaccat 1800

aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

gaaagcacag gactaaag 1878

<210> 1105
<211> 1878
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

attcaacggc gagccatgaa aaatcccctt tttattcaaa gatgccttct ttataatata 240

catgcgagga ggaaaaagag gattcagata accatatcac tttctggaag tacaaatact 300

gagttgcaaa cacattatgt ctttcctctt tatgttctgt tagctagacc cactagtaac 360

ctttcacttg aagggcattc tccaatttat cgattcagtc gggtttgctt gcttacttcc 420

tttagtgaac atggaaataa ggacaacagt gaagctacat tcatcattcc tgacgtgaag 480

agtttgtcaa cctcccgtgc ttgcaaccat gatattatct ttattagctg tgggcaagtt 540

ggacaaagta atggtgaaga taactgctct gggaaccatg tggaagattc ttctctccaa 600

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gagagttgtg tcaatttaag tttgggacat attgtggagt tggcatctaa agttacaatg 720

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cataaggttg atgctgtggg ttcatataaa ctacaactat gcatgtccgc acaagaggct 840

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tcgtcattat cagatatcat aaggttaaga tctggcaatg tactttttaa ttacaagtac 960

tacaataata caatgcaaga gactgaagtc actgaagatt tctcttgtcc attttgctat 1020

gtacgatgtg gaagcttcaa gggtctagga tgccatttaa actcatcaca tgatctattc 1080

cactatgagt tttggatatc tgaagagtac caggttgtta atgttagtct gaaggctgat 1140

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gatgatgata ttgctgactt cgaggataga agaatgcttg atgattttgt tgatgttacg 1620

aaagatgaaa aacttattat gcatatgtgg aattcatttg ttcgaaaaca aagagtgctc 1680

gcagacggac acatcccatg ggcctgcgag gcattctccc agttgcatgg acgacaactt 1740

atacaaaatc ctgctctgct gtggggttgg cgtttcttca tgattaaact ttggaaccat 1800

aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

gaaagcacag gactaaag 1878

<210> 1106
<211> 1878
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

attcaacggc gagccatgaa aaatcccctt tttattcaaa gatgccttct ttataatata 240

catgcgagga ggaaaaagag gattcagata accatatcac tttctggaag tacaaatact 300

gagttgcaaa cacattatgt ctttcctctt tatgttctgt tagctagacc cactagtaac 360

ctttcacttg aagggcattc tccaatttat cgattcagtc gggtttgctt gcttacttcc 420

tttagtgaac atggaaataa ggacaacagt gaagctacat tcatcattcc tgacgtgaag 480

agtttgtcaa cctcccgtgc ttgcaaccat gatattatct ttattagctg tgggcaagtt 540 ggacaaagta atggtgaaga taactgctct gggaaccatg tggaagattc ttctctccaa 600

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gagagttgtg tcaatttaag tttgggacat attgtggagt tggcatctaa agttacaatg 720

agaccaagct tcttagagcc aaaatttctg gagcaagaca gttgcttgac attttgctct 780

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cgctcaaggt ttaagaagcg tagacgatca aagaacacaa tggagaaaat caggcatgta 1260

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gatgatgata ttgctgactt cgaggataga agaatgcttg atgattttgt tgatgttacg 1620

aaagatgaaa aacttattat gcatatgtgg aattcatttg ttcgaaaaca aagagtgctc 1680

gcagacggac acatcccatg ggcctgcgag gcattctccc agttgcatgg acgacaactt 1740

atacaaaatc ctgctctgct gtggggttgg cgtttcttca tgattaaact ttggaaccat 1800

aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

gaaagcacag gactaaag 1878

<210> 1107
<211> 1878

<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

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gagttgcaaa cacattatgt ctttcctctt tatgttctgt tagctagacc cactagtaac 360

ctttcacttg aagggcattc tccaatttat cgattcagtc gggtttgctt gcttacttcc 420

tttagtgaac atggaaataa ggacaacagt gaagctacat tcatcattcc tgacgtgaag 480

agtttgtcaa cctcccgtgc ttgcaaccat gatattatct ttattagctg tgggcaagtt 540

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gagagttgtg tcaatttaag tttgggacat attgtggagt tggcatctaa agttacaatg 720

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aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

gaaagcacag gactaaag 1878

<210> 1108
<211> 1878
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<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

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ctttcacttg aagggcattc tccaatttat cgattcagtc gggtttgctt gcttacttcc 420

tttagtgaac atggaaataa ggacaacagt gaagctacat tcatcattcc tgacgtgaag 480

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gcagacggac acatcccatg ggcctgcgag gcattctccc agttgcatgg acgacaactt 1740

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aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

gaaagcacag gactaaag 1878

<210> 1109
<211> 1878
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<213> Artificial sequence

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<223> MiR ressistant mutated nucleic acid sequence

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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

attcaacggc gagccatgaa aaatcccctt tttattcaaa gatgccttct ttataatata 240

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aacattttag atgcccgcac tatgaacaca tgcaatacag tccttcaaat tttacaagaa 1860

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aaacttaccg ctgaaaaaga tttggctctg tattgcaagc cagtcgagct ctacaatatt 180

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gagttgcaaa cacattatgt ctttcctctt tatgttctgt tagctagacc cactagtaac 360

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gcagacggac acatcccatg ggcctgcgag gcattctccc agttgcatgg acgacaactt 1740

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gaaagcacag gactaaag 1878

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agtttgtcaa cctcccgtgc ttgcaaccat gatattatct ttattagctg tgggcaagtt   540

ggacaaagta atggtgaaga taactgctct gggaaccatg tggaagattc ttctctccaa   600

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gaaagcacag gactaaag 1878

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gaaagcacag gactaaag 1878

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<211> 507
<212> PRT
<213> Zea mays

<400> 1114

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Asp His Asp Ile Arg Leu Gly Gln Val Pro Glu Lys Cys Ser Phe Arg
35 40 45

Thr Leu Arg Glu Phe Val Ala Lys Arg Phe Pro Ser Ser Lys Ala Val
50 55 60

Leu Ile Lys Tyr Lys Asp Ala Asp Gly Asp Leu Val Thr Ile Thr Ser
65 70 75 80

Thr Glu Glu Leu Arg Leu Ala Glu Leu Phe Ile Asp Lys Val Gly His
85 90 95

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

Arg Leu His Leu Val Glu Val Ser Pro Glu Gln Glu Pro Thr Leu Pro
115 120 125

Leu Glu Glu Glu Lys Leu Glu Glu Asp Glu Glu Leu Leu Ile Asn Gly
130 135 140

Glu Asp Ser Thr Leu His Ala Leu Ala Val Val Thr Asp Ala Glu Val
145 150 155 160

Val Lys Gln Asp Val Glu Asn Arg Ser Ala Asp Gln Ser Val Glu Thr
165 170 175

Gly Lys Asn Asp Cys Gly His Ala Glu Cys Lys Glu Ala Glu Ile Asp
180 185 190

Asp Trp Leu Leu Gln Phe Ala Asp Leu Phe Arg Asn Gln Val Gly Ile
195 200 205

Asp Ala Asp Ala His Leu Asp Leu His Glu Leu Gly Met Glu Leu Cys
210 215 220

Ser Glu Ala Leu Glu Glu Thr Val Thr Ser Met Glu Ala Gln Val Leu
225 230 235 240

Phe Glu Leu Ala Ala Ser Lys Phe Gln Glu Val Ala Ala Leu Ala Leu
245 250 255

Phe Asn Trp Gly Asn Val His Met Cys Glu Ala Arg Lys Arg Ile Pro
260 265 270

Leu Asp Glu Ser Ala Pro Lys Glu Val Met Ala Ala Gln Leu Arg Thr
275 280 285

Ala Tyr Tyr Trp Val Lys Glu Arg Tyr Ala Leu Ala Gly His Lys Tyr
290 295 300

Glu Glu Ala Leu Lys Ile Lys Pro Asp Phe His Glu Gly Leu Leu Ala

305 310 315 320

Leu Gly Gln Gln His Phe Glu Thr Ala Lys Leu His Trp Ser Tyr Ala
325 330 335

Leu Ala Asp Lys Ala Asp Leu Ser Thr Trp Asp Ser Leu Glu Thr Phe
340 345 350

Lys Leu Phe Asp Ser Ala Glu Gln Asn Met Arg Ala Ala Thr Glu Met
355 360 365

Trp Glu Lys Val Glu Glu Gln Arg Met Ala Glu Leu Lys Glu Pro Gly
370 375 380

Ala Cys Asp Lys Asp Gly Val Leu Arg Lys Arg Gln His Gly Ala Gly
385 390 395 400

Gly Gln Pro Glu Leu Thr Pro Glu Glu Ala Ala Glu Gln Ala Ala Val
405 410 415

Met Arg Gln Gln Ile His Leu Phe Trp Gly Asn Met Leu Phe Glu Arg
420 425 430

Ser Gln Val Glu Phe Lys Leu Ser Val Gly Asp Trp Lys Thr Asn Leu
435 440 445

Asp Ala Ser Val Glu Arg Phe Lys Leu Ala Gly Ala Ser Glu Ser Asp
450 455 460

Ile Leu Thr Val Leu Lys Asn His Phe Ser Asn Val Ala Ser Glu Cys
465 470 475 480

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gataagtgtg tggttgaaac c 1521

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<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1117
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gttgtgacga gatggaggcc tctcaagctg gtgtatgacc acgacattag gcttgggcag 120

gttccagaga aatgcagctt ccgaacactt cgtgagtttg tagctaagag gttcccatca 180

tccaaggcag tgttgattaa atataaagac gcagacggag acttggtaac catcacatca 240

acagaagagc tccggttagc tgaattattc attgataaag ttggccacga ggttgtagaa 300

aatgggaggg aggatgacaa taagctcccg gtgttgaggc tgcaccttgt tgaagttagc 360

ccagaacagg aaccaacttt gccattggaa gaagagaagt tggaggagga tgaggaattg 420

ttgatcaatg gtgaagatag cactttacat gctttagcag tggtaaccga cgcagaggtg 480

gtgaagcaag atgttgagaa cagatctgct gatcaaagtg tggagacagg gaagaatgat 540

tgtggccatg ccgagtgcaa ggaagctgag attgatgatt ggttgcttca gtttgcagat 600

ttgttccgga accaggttgg gattgatgca gatgcacatt tagacctgca tgagttgggc 660

atggagctgt gctccgaggc tctcgaggaa actgtgacaa gcatggaggc tcaggtcctt 720

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aatgtgcaca tgtgtgaagc aaggaagcgc atccctctcg atgaatctgc tccaaaggaa 840

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ttaggccagc aacacttcga gactgcaaag cttcattggt catatgcact ggcagataag 1020

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aaagaaccag gcgcatgtga taaggatggg gtactgagga aaaggcagca cggtgcaggt 1200

ggtcaaccgg agttgacacc agaagaagca gctgagcagg cagcagtaat gaggcaacag 1260

attcacctct tctggggtaa tatgcttttc gagcgttccc aagtggagtt taagctcagt 1320

gttggtgact ggaagacaaa tcttgatgca tctgttgaaa ggtttaagtt ggctggagct 1380

tcagaatcag atattttgac agtgttgaaa aatcactttt ctaatgtagc ctctgagtgt 1440

gaagagaaga aagtcatgac ttcaggcaca gaaatttccc aaacaaatga caatgttgag 1500

gataagtgtg tggttgaaac c 1521

<210> 1118
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1118
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gttgtgacga gatggaggcc tctcaagctg gtgtatgacc acgacattag gcttgggcag 120

gttccagaga aatgcagctt ccgaacactt cgtgagtttg tagctaagag gttcccatca 180

tccaaggcag tgttgattaa atataaggac gcagacggag acttggtaac catcacatca 240

acagaagagc tccggttagc tgaattattc attgataaag ttggccacga ggttgtagaa 300

aatgggaggg aggatgacaa taagctcccg gtgttgaggc tgcaccttgt tgaagttagc 360

ccagaacagg aaccaacttt gccattggaa gaagagaagt tggaggagga tgaggaattg 420

ttgatcaatg gtgaagatag cactttacat gctttagcag tggtaaccga cgcagaggtg 480

gtgaagcaag atgttgagaa cagatctgct gatcaaagtg tggagacagg gaagaatgat 540

tgtggccatg ccgagtgcaa ggaagctgag attgatgatt ggttgcttca gtttgcagat 600

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atggagctgt gctccgaggc tctcgaggaa actgtgacaa gcatggaggc tcaggtcctt 720 tttgagttgg ctgcttctaa atttcaggag gttgctgctt tggccttatt caattgggga 780

aatgtgcaca tgtgtgaagc aaggaagcgc atccctctcg atgaatctgc tccaaaggaa 840

gtcatggctg ctcagctccg cacagcttat tattgggtga aggagaggta tgctcttgca 900

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ttaggccagc aacacttcga gactgcaaag cttcattggt catatgcact ggcagataag 1020

gctgacctat ctacctggga ttctttggaa acattcaagc tttttgatag cgctgagcag 1080

aacatgaggg ctgcaacaga gatgtgggag aaggtggaag aacagagaat ggcagagtta 1140

aaagaaccag gcgcatgtga taaggatggg gtactgagga aaaggcagca cggtgcaggt 1200

ggtcaaccgg agttgacacc agaagaagca gctgagcagg cagcagtaat gaggcaacag 1260

attcacctct tctggggtaa tatgcttttc gagcgttccc aagtggagtt taagctcagt 1320

gttggtgact ggaagacaaa tcttgatgca tctgttgaaa ggtttaagtt ggctggagct 1380

tcagaatcag atattttgac agtgttgaaa aatcactttt ctaatgtagc ctctgagtgt 1440

gaagagaaga aagtcatgac ttcaggcaca gaaatttccc aaacaaatga caatgttgag 1500

gataagtgtg tggttgaaac c 1521

<210> 1119
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1119
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gttgtgacga gatggaggcc tctcaagctg gtgtatgacc acgacattag gcttgggcag 120

gttccagaga aatgcagctt ccgaacactt cgtgagtttg tagctaagag gttcccatca 180

tccaaggcag tgttgattaa atataaagat gcagatggag atttggtaac catcacatca 240

acagaagagc tccggttagc tgaattattc attgataaag ttggccacga ggttgtagaa 300

aatgggaggg aggatgacaa taagctcccg gtgttgaggc tgcaccttgt tgaagttagc 360 ccagaacagg aaccaacttt gccattggaa gaagagaagt tggaggagga tgaggaattg 420

ttgatcaatg gtgaagatag cactttacat gctttagcag tggtaaccga cgcagaggtg 480

gtgaagcaag atgttgagaa cagatctgct gatcaaagtg tggagacagg gaagaatgat 540

tgtggccatg ccgagtgcaa ggaagctgag attgatgatt ggttgcttca gtttgcagat 600

ttgttccgga accaggttgg gattgatgca gatgcacatt tagacctgca tgagttgggc 660

atggagctgt gctccgaggc tctcgaggaa actgtgacaa gcatggaggc tcaggtcctt 720

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aatgtgcaca tgtgtgaagc aaggaagcgc atccctctcg atgaatctgc tccaaaggaa 840

gtcatggctg ctcagctccg cacagcttat tattgggtga aggagaggta tgctcttgca 900

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ttaggccagc aacacttcga gactgcaaag cttcattggt catatgcact ggcagataag 1020

gctgacctat ctacctggga ttctttggaa acattcaagc tttttgatag cgctgagcag 1080

aacatgaggg ctgcaacaga gatgtgggag aaggtggaag aacagagaat ggcagagtta 1140

aaagaaccag gcgcatgtga taaggatggg gtactgagga aaaggcagca cggtgcaggt 1200

ggtcaaccgg agttgacacc agaagaagca gctgagcagg cagcagtaat gaggcaacag 1260

attcacctct tctggggtaa tatgcttttc gagcgttccc aagtggagtt taagctcagt 1320

gttggtgact ggaagacaaa tcttgatgca tctgttgaaa ggtttaagtt ggctggagct 1380

tcagaatcag atattttgac agtgttgaaa aatcactttt ctaatgtagc ctctgagtgt 1440

gaagagaaga aagtcatgac ttcaggcaca gaaatttccc aaacaaatga caatgttgag 1500

gataagtgtg tggttgaaac c 1521

<210> 1120
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1120

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gttgtgacga gatggaggcc tctcaagctg gtgtatgacc acgacattag gcttgggcag 120

gttccagaga aatgcagctt ccgaacactt cgtgagtttg tagctaagag gttcccatca 180

tccaaggcag tgttgattaa atataaagac gctgacggag acttggtaac catcacatca 240

acagaagagc tccggttagc tgaattattc attgataaag ttggccacga ggttgtagaa 300

aatgggaggg aggatgacaa taagctcccg gtgttgaggc tgcaccttgt tgaagttagc 360

ccagaacagg aaccaacttt gccattggaa gaagagaagt tggaggagga tgaggaattg 420

ttgatcaatg gtgaagatag cactttacat gctttagcag tggtaaccga cgcagaggtg 480

gtgaagcaag atgttgagaa cagatctgct gatcaaagtg tggagacagg gaagaatgat 540

tgtggccatg ccgagtgcaa ggaagctgag attgatgatt ggttgcttca gtttgcagat 600

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gttggtgact ggaagacaaa tcttgatgca tctgttgaaa ggtttaagtt ggctggagct 1380

tcagaatcag atattttgac agtgttgaaa aatcactttt ctaatgtagc ctctgagtgt 1440

gaagagaaga aagtcatgac ttcaggcaca gaaatttccc aaacaaatga caatgttgag 1500 gataagtgtg tggttgaaac c 1521

<210> 1121
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1121
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gttgtgacga gatggaggcc tctcaagctg gtgtatgacc acgacattag gcttgggcag 120

gttccagaga aatgcagctt ccgaacactt cgtgagtttg tagctaagag gttcccatca 180

tccaaggcag tgttgattaa atataaagat gcagatggag atttggtaac catcacatca 240

acagaagagc tccggttagc tgaattattc attgataaag ttggccacga ggttgtagaa 300

aatgggaggg aggatgacaa taagctcccg gtgttgaggc tgcaccttgt tgaagttagc 360

ccagaacagg aaccaacttt gccattggaa gaagagaagt tggaggagga tgaggaattg 420

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gtgaagcaag atgttgagaa cagatctgct gatcaaagtg tggagacagg gaagaatgat 540

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atggagctgt gctccgaggc tctcgaggaa actgtgacaa gcatggaggc tcaggtcctt 720

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gaagagaaga aagtcatgac ttcaggcaca gaaatttccc aaacaaatga caatgttgag 1500

gataagtgtg tggttgaaac c 1521

<210> 1122
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1122
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gttgtgacga gatggaggcc tctcaagctg gtgtatgacc acgacattag gcttgggcag 120

gttccagaga aatgcagctt ccgaacactt cgtgagtttg tagctaagag gttcccatca 180

tccaaggcag tgttgattaa atataaagac gcagacggtg acttggtaac catcacatca 240

acagaagagc tccggttagc tgaattattc attgataaag ttggccacga ggttgtagaa 300

aatgggaggg aggatgacaa taagctcccg gtgttgaggc tgcaccttgt tgaagttagc 360

ccagaacagg aaccaacttt gccattggaa gaagagaagt tggaggagga tgaggaattg 420

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<210> 1123
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1123
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gataagtgtg tggttgaaac c 1521

<210> 1124
<211> 1521
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1124
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gaagagaaga aagtcatgac ttcaggcaca gaaatttccc aaacaaatga caatgttgag 1500

gataagtgtg tggttgaaac c 1521

<210> 1125
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<212> PRT
<213> Zea mays

<400> 1125

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Gly Pro Ala Arg Val Ala Val Ala Ala Val Gly Ser Ala Lys Leu Gly
35 40 45

Val Lys Ala Gly Thr Ser Arg Thr Ala Ala Val Ala Arg Leu Gly Val
50 55 60

Arg Cys Arg Ala Ser Leu Ile Glu Pro Asp Gly Gly Arg Leu Val Asp
65 70 75 80

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

Ala Ala Glu Leu Pro His Arg Leu Arg Leu Gly Arg Val Asp Lys Glu
100 105 110

Trp Val His Val Leu Ser Glu Gly Trp Ala Ser Pro Leu Gln Gly Phe
115 120 125

Met Arg Glu His Glu Phe Leu Gln Ala Leu His Phe Asn Ala Ile Arg
130 135 140

Gly Gln Asp Gly Arg Met Val Asn Met Ser Val Pro Ile Val Leu Ser
145 150 155 160

Val Gly Asp Ala Gln Arg Arg Ala Ile Gln Ala Asp Gly Ala Thr Arg
165 170 175

Val Ala Leu Val Asp Glu Arg Asp Arg Pro Ile Ala Val Leu Ser Asp
180 185 190

Ile Glu Ile Tyr Lys His Asn Lys Glu Glu Arg Val Ala Arg Thr Trp
195 200 205

Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Glu Glu Ala Ile Thr Asn
210 215 220

Ala Gly Asp Trp Leu Val Gly Gly Asp Leu Glu Val Ile Glu Pro Ile
225 230 235 240

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

Arg Glu Glu Phe Ala Arg Arg Asn Ala Asp Ala Val Phe Ala Phe Gln
260 265 270

Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr
275 280 285

Arg Lys Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro Val Leu Leu Leu
290 295 300

His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Ser Trp
305 310 315 320

Arg Met Lys Gln His Glu Lys Val Leu Glu Glu Gly Val Leu Asn Pro
325 330 335

Glu Ser Thr Val Val Ala Ile Phe Pro Ser Pro Met His Tyr Ala Gly
340 345 350

Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala
355 360 365

Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Ser His Pro Thr
370 375 380

Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser
385 390 395 400

Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Lys Val Ala
405 410 415

Ala Tyr Asp Thr Lys Gln Lys Lys Met Asp Phe Phe Asp Pro Ser Arg
420 425 430

Lys Asp Asp Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala
435 440 445

Lys Asn Arg Glu Ser Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp
450 455 460

Lys Val Leu Val Glu Tyr Tyr Asp Ser Leu Val Pro Ser Glu Gly Ser
465 470 475 480

Ser Lys Leu Arg Glu Pro Val Ala Ala
485

<210> 1126
<211> 1878
<212> DNA
<213> Zea mays

<400> 1126
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accaccttgg catggcgaca caggccgctt tcctcgcagg gttctcgcag ctcgccgcgc 180

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cggcggagct gccgcaccgg ctgcgcttgg gccgcgtcga caaggaatgg gtccacgtcc 480

tcagcgaagg gtgggcgagc ccgctgcaag ggttcatgcg cgagcatgag ttcctccaag 540

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tcgcgctcgt tgacgagcgc gaccgcccca tcgccgtcct cagcgacatt gagatctata 720

agcataataa ggaagaaagg gtagcacgga catgggggac aactgcacct ggattacctt 780

atgtcgagga ggcaattacc aatgctggtg actggttggt tggtggggac ttggaggtta 840

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gtgaagagtt tgccaggcgc aatgctgatg cagtatttgc ctttcagctt cgcaatcctg 960

tacacaatgg gcatgctctt cttatgaccg acacacgcaa acgtctcctt gagatgggtt 1020

ataaaaaccc tgttcttctg ctccatccac tgggaggatt cacaaaagca gatgatgtgc 1080

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aaggacagac tatgtatcat ctgccagatt gttgtacata tacattgtgg tgatataaac 1860 atgaagctgt cttctgct 1878

<210> 1127
<211> 1467
<212> DNA
<213> Zea mays

<400> 1127
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

gcggtgggta gcgccaagtt gggcgtgaag gcggggacgt ccaggaccgc ggcggtggcg 180

cgcctcgggg tgcggtgccg ggccagcctg atcgagcccg acggcgggcg gctggtggac 240

ctggtggcgc ccgaggaggg cgggcggcgc gcggcgctgc ggcgggaggc ggcggagctg 300

ccgcaccggc tgcgcttggg ccgcgtcgac aaggaatggg tccacgtcct cagcgaaggg 360

tgggcgagcc cgctgcaagg gttcatgcgc gagcatgagt tcctccaagc acttcatttc 420

aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

gtcggggacg cacagcgaag ggccatccag gccgacggcg ccacgcgcgt cgcgctcgtt 540

gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

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aagtacaacg atggtctaga tcagtatcgc ctgtctccag cacagctgcg tgaagagttt 780

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gttcttctgc tccatccact gggaggattc acaaaagcag atgatgtgcc tcttagttgg 960

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agcaagctgc gcgagccagt tgcagcc 1467

<210> 1128
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1128
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

gcggtgggta gcgccaagtt gggcgtgaag gcgggggacgt ccaggaccgc ggcggtggcg 180

cgcctcgggg tgcggtgccg ggccagcctg atcgagcccg acggcgggcg gctggtggac 240

ctggtggcgc ccgaggaggg cgggcggcgc gcggcgctgc ggcgggaggc ggcggagctg 300

ccgcaccggc tgcgcttggg ccgcgtcgac aaggaatggg tccacgtcct cagcgaaggg 360

tgggcgagcc cgctgcaagg gttcatgcgc gagcatgaat ttttacaggc cttacacttc 420

aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

gtcggggacg cacagcgaag ggccatccag gccgacggcg ccacgcgcgt cgcgctcgtt 540

gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

gaagaaaggg tagcacggac atgggggaca actgcacctg gattacctta tgtcgaggag 660

gcaattacca atgctggtga ctggttggtt ggtggggact tggaggttat agaaccaatc 720

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ccgggtggct ggaaagtgct cgttgaatac tatgacagct tggtgccatc cgagggcagc 1440

agcaagctgc gcgagccagt tgcagcc 1467

<210> 1129
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1129
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

gcggtgggta gcgccaagtt gggcgtgaag gcggggacgt ccaggaccgc ggcggtggcg 180

cgcctcgggg tgcggtgccg ggccagcctg atcgagcccg acggcgggcg gctggtggac 240

ctggtggcgc ccgaggaggg cgggcggcgc gcggcgctgc ggcgggaggc ggcggagctg 300

ccgcaccggc tgcgcttggg ccgcgtcgac aaggaatggg tccacgtcct cagcgaaggg 360

tgggcgagcc cgctgcaagg gttcatgcgc gagcatgagt ttttacaggc cttacacttc 420

aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

gtcggggacg cacagcgaag ggccatccag gccgacggcg ccacgcgcgt cgcgctcgtt 540

gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

gaagaaaggg tagcacggac atgggggaca actgcacctg gattacctta tgtcgaggag 660 gcaattacca atgctggtga ctggttggtt ggtggggact tggaggttat agaaccaatc 720

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gttcttctgc tccatccact gggaggattc acaaaagcag atgatgtgcc tcttagttgg 960

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ccgggtggct ggaaagtgct cgttgaatac tatgacagct tggtgccatc cgagggcagc 1440

agcaagctgc gcgagccagt tgcagcc 1467

<210> 1130
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1130
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

gcggtgggta gcgccaagtt gggcgtgaag gcggggacgt ccaggaccgc ggcggtggcg 180

cgcctcgggg tgcggtgccg ggccagcctg atcgagcccg acggcgggcg gctggtggac 240

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aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

gtcggggacg cacagcgaag ggccatccag gccgacggcg ccacgcgcgt cgcgctcgtt 540

gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

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aagtacaacg atggtctaga tcagtatcgc ctgtctccag cacagctgcg tgaagagttt 780

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agccatccca cggagaaaag ggacctctat gatgctgacc acgggaagaa ggttttgagc 1200

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ccgggtggct ggaaagtgct cgttgaatac tatgacagct tggtgccatc cgagggcagc 1440

agcaagctgc gcgagccagt tgcagcc 1467

<210> 1131
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1131
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

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ctggtggcgc ccgaggaggg cgggcggcgc gcggcgctgc ggcgggaggc ggcggagctg 300

ccgcaccggc tgcgcttggg ccgcgtcgac aaggaatggg tccacgtcct cagcgaaggg 360

tgggcgagcc cgctgcaagg gttcatgcgc gagcatgaat ttctccaggc cctccacttc 420

aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

gtcggggacg cacagcgaag ggccatccag gccgacggcg ccacgcgcgt cgcgctcgtt 540

gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

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gcaattacca atgctggtga ctggttggtt ggtggggact tggaggttat agaaccaatc 720

aagtacaacg atggtctaga tcagtatcgc ctgtctccag cacagctgcg tgaagagttt 780

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ccgggtggct ggaaagtgct cgttgaatac tatgacagct tggtgccatc cgagggcagc 1440

agcaagctgc gcgagccagt tgcagcc 1467

<210> 1132
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1132
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

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cgcctcgggg tgcggtgccg ggccagcctg atcgagcccg acggcgggcg gctggtggac 240

ctggtggcgc ccgaggaggg cgggcggcgc gcggcgctgc ggcgggaggc ggcggagctg 300

ccgcaccggc tgcgcttggg ccgcgtcgac aaggaatggg tccacgtcct cagcgaaggg 360

tgggcgagcc cgctgcaagg gttcatgcgc gagcatgaat ttttacaagc cttacacttc 420

aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

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gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

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gcaattacca atgctggtga ctggttggtt ggtggggact tggaggttat agaaccaatc 720

aagtacaacg atggtctaga tcagtatcgc ctgtctccag cacagctgcg tgaagagttt 780

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ccgggtggct ggaaagtgct cgttgaatac tatgacagct tggtgccatc cgagggcagc 1440

agcaagctgc gcgagccagt tgcagcc 1467

<210> 1133
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1133
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggcccgggt ggccgttgcg 120

gcggtgggta gcgccaagtt gggcgtgaag gcggggacgt ccaggaccgc ggcggtggcg 180

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ctggtggcgc ccgaggaggg cgggcggcgc gcggcgctgc ggcgggaggc ggcggagctg 300

ccgcaccggc tgcgcttggg ccgcgtcgac aaggaatggg tccacgtcct cagcgaaggg 360

tgggcgagcc cgctgcaagg gttcatgcgc gagcatgaat ttttacaggc attacacttc 420

aatgccatcc gcggccagga tggcaggatg gtcaacatgt ccgtccccat cgtgctctct 480

gtcggggacg cacagcgaag ggccatccag gccgacggcg ccacgcgcgt cgcgctcgtt 540

gacgagcgcg accgccccat cgccgtcctc agcgacattg agatctataa gcataataag 600

gaagaaaggg tagcacggac atgggggaca actgcacctg gattacctta tgtcgaggag 660

gcaattacca atgctggtga ctggttggtt ggtggggact tggaggttat agaaccaatc 720

aagtacaacg atggtctaga tcagtatcgc ctgtctccag cacagctgcg tgaagagttt 780

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aaggctcgta ttaatgctgg tgcaaatttc tatattgttg gaagggatcc tgctggtatg 1140

agccatccca cggagaaaag ggacctctat gatgctgacc acgggaagaa ggttttgagc 1200

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agcaagctgc gcgagccagt tgcagcc 1467

<210> 1134
<211> 1467
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1134
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gaccgcgccg tggcggtggc ggtggcgccg gcgccgggcc cggccccgggt ggccgttgcg 120

gcggtgggta gcgccaagtt gggcgtgaag gcggggacgt ccaggaccgc ggcggtggcg 180

cgcctcgggg tgcggtgccg ggccagcctg atcgagcccg acggcgggcg gctggtggac 240

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<210> 1135
<211> 325
<212> PRT
<213> Zea mays

<400> 1135

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Ala Ala Asp Ala Glu Val Arg Leu Gln Asp Phe Ala Ala Gly Leu Ala
35 40 45

Gln Ser Ser Arg Pro Thr Gly Ala Ala Pro Gly Ala Gly Arg Arg Ser

50 55 60

Arg Ala Ala Val Gly Gly Ala Gly Ala Glu Ala Cys Ser Val Asp Gly
65 70 75 80

Cys Arg Ser Asp Leu Ser Arg Cys Arg Glu Tyr His Arg Arg His Lys
85 90 95

Val Cys Glu Ala His Ser Lys Ala Pro Val Val Val Val Gly Gly Gln
100 105 110

Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Met Leu Ser Glu
115 120 125

Phe Asp Glu Glu Lys Arg Ser Cys Arg Lys Arg Leu Asp Gly His Asn
130 135 140

Arg Arg Arg Arg Lys Pro Gln His Asp Leu Thr Asn Leu Gly Gly Phe
145 150 155 160

Phe Pro Tyr His Gln Val Asn Gln Phe Glu Phe Tyr Pro Gln Thr Ile
165 170 175

Pro Thr Val Gly Gln Asn Ser Asp Ala Val His Leu Val Gly Arg Gln
180 185 190

Gln Pro Phe Ser Ile Ser Phe Ser Arg Thr Pro Asp Glu Phe Pro Phe
195 200 205

Pro Gln Gly Gly Gly Ser Ser Val Leu His His Leu His Ala Ala Arg
210 215 220

Pro Gly His His Ala Glu Gly Ser Ser His Thr Gly Ser Ser Thr Arg
225 230 235 240

Asp Asn Ala Leu Ser Gly Thr Leu Gly Pro Glu Cys Ala Leu Ser Leu
245 250 255

Leu Ser Ser Ser Leu Arg Arg Pro Ser Thr Ala Gly Val Pro Ala Val
260 265 270

Gly Gln Pro Gln Val Thr Ala Ser Ser Thr Thr Ala Val Ser Gln Ala
275 280 285

Ala Thr Ala Ala Val Ala Thr Ala Ala Phe Ala Ala Ser Ala Gly His
290 295 300

His Val Phe Val Pro Asp Ala Met Phe Glu Asp Pro Ser Gln Ala Leu
305 310 315 320

Pro Phe Ser Trp Gln
325

<210> 1136
<211> 1283
<212> DNA
<213> Zea mays

<400> 1136
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ggcataaggt ctgtgaggca cactccaagg cgccggtggt ggtcgtcggc ggacaggagc 480

ggcgcttctg ccagcaatgc agccggtttc acatgctgtc cgagtttgac gaggaaaaaa 540

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tctctcttct gtcatcgtcg ctgcgtcgcc cctcaactgc tggcgtcccc gccgttggcc 960

aaccccaggt tactgcctct tcgaccactg ccgtgtcgca ggctgcaacg gcagctgtgg 1020

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gactagtgct ggcatctgaa agg 1283

<210> 1137
<211> 975
<212> DNA
<213> Zea mays

<400> 1137
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agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1138
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1138
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caggatttcg ccgcgggtct tgcccagagc tcgcggccga ctggggcggc gccgggagcc 180

gggaggaggt cccgcgcggc cgtgggaggt gccggcgcgg aggcgtgctc cgtcgacggc 240

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agccggtttc acatgctgtc cgagtttgac gaggaaaaaa gaagttgccg gaagcgtctg 420

gatggccata ataggcgtcg aagaaagcca cagcatgatc tgacaaatct agggggtttc 480

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cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600

agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

catgcagccc gccctggcca tcacgctgaa ggcagcagcc acactggaag cagcacacgc 720

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ccattctctt ggcag 975

<210> 1139
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1139
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gggaggaggt cccgcgcggc cgtgggaggt gccggcgcgg aggcgtgctc cgtcgacggc 240

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cactccaagg cgccggtggt ggtcgtcggc ggacaggagc ggcgcttctg ccagcaatgc 360

agccggtttc acatgctgtc cgagtttgac gaggaaaaaa gaagttgccg gaagcgtctg 420

gatggccata ataggcgtcg aagaaagcca cagcatgatc tgacaaatct agggggtttc 480

tttccatacc accaagtgaa tcagtttgag ttctacccac aaacaattcc aacagttggc 540

cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600

agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

catgcagccc gccctggcca tcacgctgaa ggcagcagcc acactggaag cagcacacgc 720

gacaacgctc tctccggcac actgggcccc gaatgcgcat taagcttatt atcatcgtcg 780

ctgcgtcgcc cctcaactgc tggcgtcccc gccgttggcc aaccccaggt tactgcctct 840

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agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1140
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1140
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

caggatttcg ccgcgggtct tgcccagagc tcgcggccga ctggggcggc gccgggagcc 180

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agccggtttc acatgctgtc cgagtttgac gaggaaaaaa gaagttgccg gaagcgtctg 420

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tttccatacc accaagtgaa tcagtttgag ttctacccac aaacaattcc aacagttggc 540

cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600

agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

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agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1141
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1141
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

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agccggtttc acatgctgtc cgagtttgac gaggaaaaaa gaagttgccg gaagcgtctg 420

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agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1142
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1142
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

caggatttcg ccgcgggtct tgcccagagc tcgcggccga ctggggcggc gccgggagcc 180

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gatggccata ataggcgtcg aagaaagcca cagcatgatc tgacaaatct agggggtttc 480

tttccatacc accaagtgaa tcagtttgag ttctacccac aaacaattcc aacagttggc 540

cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600

agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

catgcagccc gccctggcca tcacgctgaa ggcagcagcc acactggaag cagcacacgc 720

gacaacgctc tctccggcac actgggccca gagtgcgcat taagcttatt atcatcgtcg 780

ctgcgtcgcc cctcaactgc tggcgtcccc gccgttggcc aaccccaggt tactgcctct 840

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agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1143
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1143
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

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tttccatacc accaagtgaa tcagtttgag ttctacccac aaacaattcc aacagttggc 540

cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600

agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

catgcagccc gccctggcca tcacgctgaa ggcagcagcc acactggaag cagcacacgc 720

gacaacgctc tctccggcac actgggccca gagtgcgcat taagcttatt atcatcgtcg 780

ctgcgtcgcc cctcaactgc tggcgtcccc gccgttggcc aaccccaggt tactgcctct 840

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agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1144
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1144
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

caggatttcg ccgcgggtct tgcccagagc tcgcggccga ctggggcggc gccgggagcc 180

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tttccatacc accaagtgaa tcagtttgag ttctacccac aaacaattcc aacagttggc 540

cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600

agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

catgcagccc gccctggcca tcacgctgaa ggcagcagcc acactggaag cagcacacgc 720

gacaacgctc tctccggcac actgggccca gagtgcgcat taagcttatt atcatcgtcg 780

ctgcgtcgcc cctcaactgc tggcgtcccc gccgttggcc aaccccaggt tactgcctct 840

tcgaccactg ccgtgtcgca ggctgcaacg gcagctgtgg ccactgctgc attcgcggcc 900

agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1145
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1145
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

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cactccaagg cgccggtggt ggtcgtcggc ggacaggagc ggcgcttctg ccagcaatgc 360

agccggtttc acatgctgtc cgagtttgac gaggaaaaaa gaagttgccg gaagcgtctg 420

gatggccata ataggcgtcg aagaaagcca cagcatgatc tgacaaatct agggggtttc 480

tttccatacc accaagtgaa tcagtttgag ttctacccac aaacaattcc aacagttggc 540

cagaattcgg acgccgtgca cttggtgggc cgtcagcagc ctttctccat atcgttctca 600 agaacaccag acgagttccc tttcccacag ggtggcggta gcagtgtgct gcaccacctc 660

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gacaacgctc tctccggcac actgggccca gaatgtgcat taagcttatt atcatcgtcg 780

ctgcgtcgcc cctcaactgc tggcgtcccc gccgttggcc aaccccaggt tactgcctct 840

tcgaccactg ccgtgtcgca ggctgcaacg gcagctgtgg ccactgctgc attcgcggcc 900

agtgctggcc accatgtgtt tgttcctgat gctatgtttg aggatccatc acaggcactg 960

ccattctctt ggcag 975

<210> 1146
<211> 975
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1146
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ccgaccatgc tgtccttcgc aggcccgtcc tcctccgccg ccgacgccga ggtgcggctc 120

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<211> 378
<212> PRT
<213> Zea mays

<400> 1148

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35 40 45

Gly Ala Arg Pro Ala Ser Ala Ala Ser Ala Ala Gln Pro Pro Arg Cys
50 55 60

Gln Val Asp Gly Cys Gly Val Asp Leu Ser Ala Val Lys Gln Tyr Tyr
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Cys Arg His Lys Val Cys Asn Met His Ser Lys Glu Pro Arg Val Phe
85 90 95

Val Ala Gly Ile Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His
100 105 110

Gln Leu His Glu Phe Asp Gln Gly Lys Arg Ser Cys Arg Arg Arg Leu
115 120 125

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

Arg Ser Phe Leu Leu Asp Phe Ser Tyr Pro Arg Val Pro Ser Ser Val
165 170 175

Arg Asp Ala Trp Pro Gly Ile Gln His Gly Gly Asp Arg Met Leu Gly
180 185 190

Thr Val Gln Trp His Gly His Gln Glu Pro Pro His Pro His Arg Ser
195 200 205

Ala Ala Ala Gly Tyr Gly Asn His Ala Ala Tyr Asn Cys His Gly Gly
210 215 220

Leu Val Ala Gly Gly Ala Pro Met Leu Ser Ser Ala Ala Phe Glu Leu
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Pro Pro Gly Gly Cys Val Ala Gly Val Ala Ala Asp Ser Ser Cys Ala
245 250 255

Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr Thr Ser His Asp His
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Arg Ser Pro Ala Met Pro Ala Ala Gly Ala Phe Asp Gly Thr Pro Val
275 280 285

Ala Pro Ser Val Met Ala Ser Ser Tyr Ala Ala Ser Ser Ala Trp Thr
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Gly Ser Arg Asp Pro Ala Ala Asp Gly Ala Arg Asn Ala Gln Arg Leu
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Asp Asp Ala Leu His Leu Val His Pro Gly Ser Ala Ala Val His Phe
325 330 335

Ser Gly Glu Leu Glu Leu Ala Leu Gln Gly Ser Gly Gly Pro Pro His
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<213> Zea mays

<400> 1150
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<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1151
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<211> 1134
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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<212> DNA
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<220>
<223> MiR ressistant mutated nucleic acid sequence

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<223> MiR ressistant mutated nucleic acid sequence

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<211> 1134
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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<220>
<223> MiR ressistant mutated nucleic acid sequence

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tgccggcaca aggtgtgcaa catgcactcc aaggagccgc gcgtcttcgt cgccggcatc 300

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<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1157
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ccgccgaggt gccaggtgga cgggtgcggc gtggatctga gcgccgtcaa gcagtactac   240

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gagcagcgct tctgccaaca gtgcagcagg ttccaccagc tacatgaatt tgaccaaggg   360

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ccgccgaggt gccaggtgga cgggtgcggc gtggatctga gcgccgtcaa gcagtactac 240

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<223> MiR ressistant mutated nucleic acid sequence

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aaggggaagg gcgtggccac cggtggcgcg aggccggcgt ccgccgcctc cgcagcccag 180

ccgccgaggt gccaggtgga cgggtgcggc gtggatctga gcgccgtcaa gcagtactac 240

tgccggcaca aggtgtgcaa catgcactcc aaggagccgc gcgtcttcgt cgccggcatc 300

gagcagcgct tctgccaaca gtgcagcagg ttccaccagc tacatgaatt tgaccaaggg 360

aaacgtagct gccgccgccg cctcatcggt cacaacgagc gccggaggaa gccaccacct 420

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tccggcggcg gcaccttcaa ccattccacc accagcgcga tgaactggtc cctg 1134

<210> 1161
<211> 439
<212> PRT
<213> Zea mays

<400> 1161

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Asp Trp Glu His Leu Val Pro Ser Val Ser Asn Ala Val Thr Arg His
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Gly Ser Ala Asn Ser Ser Gly Gly Thr Leu Thr Ser Asn Ser Glu Leu
35 40 45

Gly His Gly Ser Ser Lys Ser Ser Ile Ser Ala Ser Ile Asp Ser Pro
50 55 60

Ser Gly Val Gly Asn Ser Leu Glu Phe Asn Phe Ala Ala Val Glu Arg
65 70 75 80

His Val Lys Asn Thr Gly Thr Asn Gly Arg Val Asp Asp Ser Gly Asn
85 90 95

Ser Pro Ser Ser Met Ile Ala Phe Asn Gln Gly Glu Pro Leu Ile Ser
100 105 110

Leu Lys Leu Gly Lys Arg Ala Tyr Phe Glu Asn Ala Cys Gly Gly Gln
115 120 125

Asp Ala Lys Val Ser Ala Ala Ser Asp Val Thr Ser Ala Ala Ser Val
130 135 140

Val Lys Lys Thr Lys Val Ser Gln Gln Asn Ala Lys Asn Trp Tyr Cys
145 150 155 160

Gln Val Glu Gly Cys Lys Val Asp Leu Ser Ser Ala Lys Asp Tyr Asn
165 170 175

Arg Lys His Lys Val Cys Val Val His Ser Lys Ala Thr Lys Val Val
180 185 190

Val Ala Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His
195 200 205

Gly Leu Ala Glu Phe Asp Gln Asn Lys Arg Ser Cys Arg Arg Arg Leu
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Met His His Asn Ala Arg Arg Arg Lys Pro Gln Ala Asp Thr Ile Ser
225   230   235   240

Phe Asn Ser Ser Thr Met Phe Tyr Asp Thr Arg Gln Arg Thr Asn Leu
                245   250   255

Phe Phe Ser Gln Pro Leu Tyr Gly Gln Val Arg Ser Asn Ala Gly Ser
            260   265   270

Ser Trp Asp Asn Leu Gly Gly Leu Lys Phe Met Glu Thr Lys His Pro
        275   280   285

Pro Val His Pro Thr Lys Thr Ala Ser Pro Asp Glu Leu His Phe Ser
    290   295   300

Ala Leu Gln Ile Thr Ser Ala Ala Ala His Thr Gly His His His Asp
305   310   315   320

Leu Asp Gly Phe Met Ala Phe Lys Gly Thr Ser Thr Lys Val Leu Asn
                325   330   335

Gln Gly Val Glu Ala Trp Ala Ala Ala Ser Ser Ser Asn Asn Gly Gly
            340   345   350

Pro Glu Gly Gly Arg Ala Leu Ser Leu Leu Ser Asp Gly Ser Trp Gly
        355   360   365

Ser Ser Ser Ala Val Ile Gln Gln Pro Thr Ser His Ala Asp Ala Gly
    370   375   380

Ala Leu Leu Pro Pro Leu Ala Thr Val Ala Val Ser Asn Ala Ala Ala
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Ala Ala Gly His Pro Leu Asp Pro Ser Pro Gly Arg Phe Trp Pro Gln

405 410 415

Asp Asp His Pro Pro Leu Val Asp Gly Pro Ala Thr Gln Ile Pro Glu
420 425 430

Leu Ala His Leu Arg Ile Trp
435

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<211> 1827
<212> DNA
<213> Zea mays

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caaggcacgg atctgctaat tcatctggtg gtactcttac ttctaactca gagctagggc 480

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<213> Zea mays

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<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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<220>
<223> MiR ressistant mutated nucleic acid sequence

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<220>
<223> MiR ressistant mutated nucleic acid sequence

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<210> 1167
<211> 1317
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actcttactt ctaactcaga gctagggcat ggttcatcca agagctctat ttcagcgtcc 180

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gcagccagcg tggtcaagaa gactaaggtg tctcagcaga atgcaaagaa ctggtactgt 480

caggttgaag ggtgcaaagt tgacctgtct tctgctaaag attacaatcg caagcacaag 540

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ttattatcag acggctcgtg gggctcgagt tcagccgtca tccagcagcc cacatctcac 1140

gcggacgccg gtgcattgct gccgcccctc gccaccgttg ccgtctccaa cgccgccgcc 1200

gccgccgggc atcctctgga cccgtccccg ggaaggttct ggccgcaaga cgatcatccc 1260

ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1168
<211> 1317
<212> DNA

<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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actcttactt ctaactcaga gctagggcat ggttcatcca agagctctat ttcagcgtcc 180

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gcagccagcg tggtcaagaa gactaaggtg tctcagcaga atgcaaagaa ctggtactgt 480

caggttgaag ggtgcaaagt tgacctgtct tctgctaaag attacaatcg caagcacaag 540

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ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1169
<211> 1317
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1169
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actcttactt ctaactcaga gctagggcat ggttcatcca agagctctat ttcagcgtcc 180

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atgatagctt tcaaccaagg agagccatta atcagcctga aacttgggaa gagggcttac 360

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gcagccagcg tggtcaagaa gactaaggtg tctcagcaga atgcaaagaa ctggtactgt 480

caggttgaag ggtgcaaagt tgacctgtct tctgctaaag attacaatcg caagcacaag 540

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gcttgggcgg ccgcttccag ctcgaacaac ggaggcccag aagggggggag agcattaagc 1080

ttattatcag acggctcgtg ggctcgagt tcagccgtca tccagcagcc cacatctcac 1140

gcggacgccg gtgcattgct gccgcccctc gccaccgttg ccgtctccaa cgccgccgcc 1200 gccgccgggc atcctctgga cccgtccccg ggaaggttct ggccgcaaga cgatcatccc 1260

ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1170
<211> 1317
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1171
<211> 1317
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1171
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ctagtaccgt ctgtctcaaa tgcagttaca aggcacggat ctgctaattc atctggtggt 120

actcttactt ctaactcaga gctagggcat ggttcatcca agagctctat ttcagcgtcc 180

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gcagccagcg tggtcaagaa gactaaggtg tctcagcaga atgcaaagaa ctggtactgt 480

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ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1172
<211> 1317
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1172
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actcttactt ctaactcaga gctagggcat ggttcatcca agagctctat ttcagcgtcc 180

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ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1173
<211> 1317
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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ctagtaccgt ctgtctcaaa tgcagttaca aggcacggat ctgctaattc atctggtggt 120

actcttactt ctaactcaga gctagggcat ggttcatcca agagctctat ttcagcgtcc 180

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atgatagctt tcaaccaagg agagccatta atcagcctga aacttgggaa gagggcttac 360

ttcgaaaacg cctgcggagg acaggatgcc aaggtttctg cagcttcaga cgttacttct 420

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ccgctcgtcg acggacccgc cacgcagatt ccggagctgg cgcacctccg gatatgg 1317

<210> 1174
<211> 383
<212> PRT
<213> Zea mays

<400> 1174

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Phe Gly Gln Lys Ile Tyr Phe Glu Gln Asp Ala Gly Ala Ala Gly Gly
20 25 30

Ser Ala Thr Gly Gly Arg Lys Gly Lys Gly Ala Ala Ala Ser Ala Ser
35 40 45

Ala Ala Gln Pro Pro Arg Cys Arg Val Asp Gly Cys Gly Val Asp Leu
50 55 60

Ser Ala Val Lys Gln Tyr Tyr Cys Arg His Lys Val Cys Tyr Met His
65 70 75 80

Ser Lys Glu Pro Arg Val Phe Val Ala Gly Ile Glu Gln Arg Phe Cys
85 90 95

Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe Asp Gln Gly Lys
100 105 110

Arg Ser Cys Arg Arg Arg Leu Ile Gly His Asn Glu Arg Arg Arg Lys
115 120 125

Pro Pro Pro Gly Pro Leu Thr Ser Arg Tyr Gly Pro Leu Ala Ala Ser
130 135 140

Leu Val Gln Glu Pro Gly Arg Phe Arg Ser Phe Leu Leu Asp Phe Ser
145 150 155 160

Tyr Pro Arg Val Pro Ser Ser Val Arg Asp Asp Ala Trp Gln Trp Gln
165 170 175

Gly Met Gln His Gly Gly Asp Arg Met Leu Leu Gly Thr Ala Ser Ala
180 185 190

Ile Gln Trp His Gly Asn Gln Glu Pro His Pro Pro His Arg Ser Ala
195 200 205

Ala Ala Gly Tyr Gly Asn His Ala Tyr Asn Asn Cys His Gly Gly Gly
210 215 220

Gly Leu Val Ala Ala Ala Ala Gly Ala Ser Met Leu Ser Ser Ala Phe
225 230 235 240

Glu Pro Pro Pro Gly Gly Gly Gly Cys Val Ala Gly Ala Thr Ala Ala
245 250 255

Asp Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp Asp Thr
260 265 270

Pro Thr Gln Ser Gly Ser Ser His His Asn Arg Ser Pro Ala Met Ser
275 280 285

Ala Ala Ala Gly Ala Phe Glu Val Ala Pro Ser Ser Val Val Ala Ser
290 295 300

Ser Tyr Thr Ala Ser Ser Ser Trp Ser Gly Ser Arg Asp Pro Ala Asp
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Gly Ala Arg Lys Asn Ala Gln Arg His Asp Asp Gly Leu His Leu Val
325 330 335

His Pro Pro Gly Pro Val His His Gly His Phe Ser Gly Glu Leu Glu
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<210> 1175
<211> 1616
<212> DNA
<213> Zea mays

<400> 1175
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<212> DNA
<213> Zea mays

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<210> 1177
<211> 1149
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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tacccgaggg ttccaagcag cgtgagagat gatgcgtggc aatggcaagg gatgcagcat 540

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cctcacccac cacatcgcag cgcagctgcg ggctatggca accatgcgta caacaactgc 660

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tggtccctg 1149

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aagggcgccg cggcgtccgc gagcgccgcc cagccgccgc ggtgccgggt ggacgggtgc 180

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aggttccacc agttacctga atttgaccaa gggaaacgaa gctgccgccg ccgcctcatt 360

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tggtccctg 1149

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aagggcgccg cggcgtccgc gagcgccgcc cagccgccgc ggtgccgggt ggacgggtgc 180

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tggtccctg 1149

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<212> DNA
<213> Artificial sequence

<220>
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aagggcgccg cggcgtccgc gagcgccgcc cagccgccgc ggtgccgggt ggacgggtgc 180

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aggttccacc agttacctga atttgaccaa gggaaacgaa gctgccgccg ccgcctcatt 360

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cttgctgcat cactagttca agagcctggt aggttcagga gcttcctgct cgacttctcg 480

tacccgaggg ttccaagcag cgtgagagat gatgcgtggc aatggcaagg gatgcagcat 540

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ggcgccagga aaaacgcgca gcgtcacgat gatggcctgc acctggtcca tccaccaggc 1020

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ccgcatgtcg accatggcgg cggcacctgc ttcagccatt ctgacaccaa cgcgatgaat 1140

tggtccctg 1149

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<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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tggtccctg 1149

<210> 1182
<211> 1149
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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atctacttcg agcaggacgc gggcgccgcc ggggggagcg cgacgggcgg caggaagggg 120

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<210> 1183
<211> 1149
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1183
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<210> 1184
<211> 1149
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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<210> 1185
<211> 1149
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<220>
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<211> 1149
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

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<210> 1187
<211> 329
<212> PRT
<213> Zea mays

<400> 1187

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

Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Gln Leu Pro Glu Phe
50 55 60

Asp Gln Leu Lys Lys Ser Cys Arg Lys Arg Leu Ala Gly His Asn Glu
65 70 75 80

Arg Arg Arg Arg Pro Pro Pro Gly Pro Leu Ala Ser Arg Tyr Gly Arg
85 90 95

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

Asp Phe Ser Tyr Pro Arg Val Ser Ser Ala Met Arg Gly Gly Phe Pro
115 120 125

Ala Val Arg Pro Gly Gly Glu Arg Val Pro Gly Gly Ile Gln Trp Gln
130 135 140

Ala Gly Leu Asp Pro Arg His His Gln Gly Ala Val Ala Gly Tyr Gly
145 150 155 160

Ala His Tyr Gly Ser Glu Gly Gly Ser Ser Ser Ser Ala Arg Pro Pro
165 170 175

Val Phe Pro Gly Pro Glu Leu Pro Pro Gly Gly Cys Leu Ala Gly Val
180 185 190

Pro Ala Asp Ser Ser Cys Ala Leu Ser Leu Leu Ser Thr Gln Pro Trp
195 200 205

Asp Ala Ala His Ser His Ser His Ser His Ala Ala Pro Thr Ala Gly
210 215 220

Phe Asp Gly Gly Ser Pro Val Ala Pro Ser Leu Met Ala Ala Ser Ser
225 230 235 240

Tyr Ile Ala Pro Ser Pro Trp Thr Glu Thr Asp Ser Trp Gly His Glu

245 250 255

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

Leu Glu Leu Ala Leu Gln Gly Asn Arg Pro Ala Pro Gly Ser Ala Ala
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agctgcctga attcgaccag ctaaagaaga gctgccgcaa acgcctcgca ggccacaacg 240

agcgccggag gaggccgccg cctggacccc ttgcgtcacg atacggccgt cacgctgcgt 300

cgctcggcga gcccggcagg ctcagaagct tcatgctgga tttctcgtac ccgagggtct 360

caagcgccat gaggggtggg tttccggcgg tgaggcccgg tggtgaaagg gtgcctggcg 420

gtatccagtg gcaagcgggc ttggatcctc gtcaccacca aggcgcggtc gcgggatacg 480

gcgcccacta tgggagcgag ggtggtagct cgtcgtcggc gaggccgccg gtgttccctg 540

gcccggagct gcccccaggt ggatgccttg caggagtccc cgcggactcc agctgtgctc 600

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cagggtcggc ggcaccgcca gcgccgcgca ataatcaggg ctccgcgggc acgttcgacc 960

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tcctagccgc gcagggagat ggaggaggct gaaagtctga tgctgcacgc tgcttgctta 1080

gcttagagca tccagcatga taagagtgat gaactgatgc ggtgtcagga gactagttta 1140

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ctcattgttc accatccaga aaaaaaaaaa aaaaaaaaaa aaaa 1304

<210> 1189
<211> 987
<212> DNA
<213> Zea mays

<400> 1189
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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca 360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggactccag ctgtgctctc 600 tctcttctgt caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1190
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1190
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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca 360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggacagttc atgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

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caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1191
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1191
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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca 360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc cccaggtgg atgccttgca ggagtccccg cggactcctc atgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960 gctggcaaca cgatggactg gtcgctc 987

<210> 1192
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1192
ccctcgacgg cgcccgcgcc cgcccgctgc caggtcgacg gctgcaacgt tgacctcacc 60

gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca 360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggactcctc atgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1193
<211> 987
<212> DNA

<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1193
ccctcgacgg cgcccgcgcc cgcccgctgc caggtcgacg gctgcaacgt tgacctcacc   60

gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc   120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag   180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag   240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg   300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca   360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt   420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc   480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc   540

ccggagctgc cccaggtgg atgccttgca ggagtccccg cggactcctc atgcgcatta   600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg   660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc   720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc   780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc   840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca   900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag   960

gctggcaaca cgatggactg gtcgctc   987

<210> 1194
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1194

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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca 360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggactcctc atgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1195
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1195
ccctcgacgg cgcccgcgcc cgcccgctgc caggtcgacg gctgcaacgt tgacctcacc 60

gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180 ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

ctcggcgagc ccggcaggct cagaagcttc atgctggatt tctcgtaccc gagggtctca 360

agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggactcctc atgcgcatta 600

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ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1196
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1196
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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

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atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc cccaggtgg atgccttgca ggagtccccg cggacagtag ctgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1197
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1197
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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

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agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540 ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggacagtag ctgcgcatta 600

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ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1198
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1198
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gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

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agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc ccccaggtgg atgccttgca ggagtccccg cggacagtag ctgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720 tacatcgcgc cgagcccctg gaccgagacc gactcctggg gccacgaagg cgggcggagc 780

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caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900

gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1199
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> MiR ressistant mutated nucleic acid sequence

<400> 1199
ccctcgacgg cgcccgcgcc cgcccgctgc caggtcgacg gctgcaacgt tgacctcacc 60

gacgtcaagc ccgcctacta ctgccgccac aaggtgtgca aaatgcactc caaggagccc 120

cgcgtcctcg tcaacggcct cgagcagcgc ttctgccagc agtgcagcag gttccaccag 180

ctgcctgaat tcgaccagct aaagaagagc tgccgcaaac gcctcgcagg ccacaacgag 240

cgccggagga ggccgccgcc tggacccctt gcgtcacgat acggccgtca cgctgcgtcg 300

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agcgccatga ggggtgggtt tccggcggtg aggcccggtg gtgaaagggt gcctggcggt 420

atccagtggc aagcgggctt ggatcctcgt caccaccaag gcgcggtcgc gggatacggc 480

gcccactatg ggagcgaggg tggtagctcg tcgtcggcga ggccgccggt gttccctggc 540

ccggagctgc cccaggtgg atgccttgca ggagtccccg cggacagtag ctgcgcatta 600

agcttattat caactcagcc atgggatgct gcccacagcc acagccacag ccacgctgcg 660

ccaacagcgg gtttcgacgg cggcagccct gtggcgccct ccctcatggc ggcgagtagc 720

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gtgcctcagc tgccacctga cgacgtcccc ctcggcgagg tgcactccgg ctcgagcagc 840

caccacggcc agttctcagg tgagctcgag ctcgccctgc agggaaacag gccagcgcca 900 gggtcggcgg caccgccagc gccgcgcaat aatcagggct ccgcgggcac gttcgaccag 960

gctggcaaca cgatggactg gtcgctc 987

<210> 1200
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Bulge Reverse Complement miR

<400> 1200
gagttccccc actaaacact tcac 24

<210> 1201
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Bulge Reverse Complement miR

<400> 1201
atgcagcatc actatcaaga ttcc 24

<210> 1202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Bulge Reverse Complement miR

<400> 1202
aggctgtact cctatctctc ttct 24

<210> 1203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Bulge Reverse Complement miR

<400> 1203

caggcaaatc actatccctg gcta 24

<210> 1204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Bulge in Target Binding Sequence

<400> 1204
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<210> 1211

<211> 139
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<211> 368
<212> DNA
<213> Zea mays

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