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(54) **Title:** PLANTS HAVING IMPROVED GROWTH CHARACTERISTICS AND A METHOD FOR MAKING THE SAME

(57) **Abstract:** The present invention relates generally to the field of molecular biology and concerns a method for improving plant growth characteristics relative to corresponding wild type plants. More specifically, the present invention concerns a method for improving plant growth characteristics comprising modulating expression in a plant of a nucleic acid encoding a class I homeodomain leucine zipper (HDZip) hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a nitrate transporter protein (NRT) or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a polypeptide denoted Yield Enhancing Protein 16 (referred to as YEP16); or comprising modulating expression in a plant of a Group I glycogen synthase kinase (Group I shaggy-like kinase) or a homologue thereof. The present invention also concerns plants having modulated expression of a nucleic acid encoding a class I homeodomain leucine zipper (HDZip) hox5 polypeptide or a homologue thereof; or having modulated expression of a nucleic acid encoding a nitrate transporter protein (NRT) or a homologue thereof; or having modulated expression of a nucleic acid encoding a polypeptide denoted Yield Enhancing Protein 16 (hereinafter referred to as YEP16); or having modulated expression of a Group I glycogen synthase kinase (Group I shaggy-like kinase) or a homologue thereof, which plants have improved growth characteristics relative to corresponding wild type plants. The invention also provides constructs useful in the methods of the invention.

WO 2007/051866 A2

Plants having improved growth characteristics and a method for making the same

The present invention relates generally to the field of molecular biology and concerns a method for improving plant growth characteristics relative to corresponding wild type plants or other control plants. More specifically, the present invention concerns a method for improving plant growth characteristics comprising modulating expression in a plant of a nucleic acid encoding a class I homeodomain leucine zipper (HDZip) hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a nitrate transporter protein (NRT) or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a polypeptide denoted Yield Enhancing Protein 16 (hereinafter referred to as YEP16) or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a Group I glycogen synthase kinase (Group I shaggy-like kinase) or a homologue thereof. The present invention also concerns plants having modulated expression of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or having modulated expression of a nucleic acid encoding an NRT polypeptide or a homologue thereof; or having modulated expression of a nucleic acid encoding a YEP16; or having modulated expression of a nucleic acid encoding a Group I shaggy-like kinase) or a homologue thereof, which plants have improved growth characteristics relative to corresponding wild type or other control plants. The invention also provides constructs useful in the methods of the invention.

The ever-increasing world population and the dwindling supply of arable land available for agriculture fuels research towards increasing the efficiency of agriculture. Conventional means for crop and horticultural improvements utilise selective breeding techniques to identify plants having desirable characteristics. However, such selective breeding techniques have several drawbacks, namely that these techniques are typically labour intensive and result in plants that often contain heterogeneous genetic components that may not always result in the desirable trait being passed on from parent plants. Advances in molecular biology have allowed mankind to modify the germplasm of animals and plants. Genetic engineering of plants entails the isolation and manipulation of genetic material (typically in the form of DNA or RNA) and the subsequent introduction of that genetic material into a plant. Such technology has the capacity to deliver crops or plants having various improved economic, agronomic or horticultural traits.

A trait of particular economic interest is yield. Yield is normally defined as the measurable produce of economic value from a crop. This may be defined in terms of quantity and/or quality. Yield is directly dependent on several factors, for example, the number and size of the

organs, plant architecture (for example, the number of branches), seed production leaf senescence and more. Root development, nutrient uptake and stress tolerance and early vigour may also be important factors in determining yield. Optimizing one of the abovementioned factors may therefore contribute to increasing crop yield.

Seed yield is a particularly important trait, since the seeds of many plants are important for human and animal nutrition. Crops such as, corn, rice, wheat, canola and soybean account for over half the total human caloric intake, whether through direct consumption of the seeds themselves or through consumption of meat products raised on processed seeds. They are also a source of sugars, oils and many kinds of metabolites used in industrial processes. Seeds contain an embryo (the source of new shoots and roots) and an endosperm (the source of nutrients for embryo growth during germination and during early growth of seedlings). The development of a seed involves many genes, and requires the transfer of metabolites from the roots, leaves and stems into the growing seed. The endosperm, in particular, assimilates the metabolic precursors of carbohydrates, oils and proteins and synthesizes them into storage macromolecules to fill out the grain.

Another trait of particular economic interest is that of improved abiotic stress tolerance. Abiotic stress is a primary cause of crop loss worldwide, reducing average yields for most major crop plants by more than 50% (Wang *et al.*, *Planta* (2003) 218: 1-14). Abiotic stresses may be caused by drought, salinity, extremes of temperature, chemical toxicity and oxidative stress. The ability to improve plant tolerance to abiotic stress would be of great economic advantage to farmers worldwide and would allow for the cultivation of crops during adverse conditions and in territories where cultivation of crops may not otherwise be possible.

The ability to increase plant yield would have many applications in areas such as agriculture, including in the production of ornamental plants, arboriculture, horticulture and forestry. Increasing yield may also find use in the production of algae for use in bioreactors (for the biotechnological production of substances such as pharmaceuticals, antibodies or vaccines, or for the bioconversion of organic waste) and other such areas.

BACKGROUND

Homeodomain leucine zipper (HDZm) proteins

Homeodomain leucine zipper (HDZip) proteins constitute a family of transcription factors characterized by the presence of a DNA-binding domain (HD) and an adjacent leucine zipper (Zip) motif. The homeodomain usually consists of 60 conserved amino acid residues that form a helix1-loop-helix2-turn-helix3 that binds DNA. This DNA binding site is usually

pseudopalindromic. The leucine zipper, adjacent to the C-terminal end of the homeodomain, consists of several heptad repeats (at least four) in which usually a leucine (occasionally a valine or an isoleucine) appears every seventh amino acid. The leucine zipper is important for protein dimerisation. This dimerisation is a prerequisite for DNA binding (Sessa *et al.* (1993) EMBO J 12(9): 3507-3517), and may proceed between two identical HDZip proteins (homodimer) or between two different HDZip proteins (heterodimer).

Homeodomain genes are present in all eucaryotes, and constitute a gene family of at least 89 members in *Arabidopsis thaliana*. The leucine zipper is also found by itself in eukaryotes other than plants. However, the presence of both a homeodomain and a leucine zipper is plant-specific (found in at least 47 out of the 89 proteins in *Arabidopsis*), and has been encountered in moss in addition to vascular plants (Sakakibara *et al.* (2001) Mol Biol Evol 18(4): 491-502). The leucine zipper is then located at the C-terminal end of the homeodomain, these two features overlapping by three amino acids.

The *Arabidopsis* HDZip genes have been classified into four different classes, HDZip I to IV, based on sequence similarity criteria (Sessa *et al.* (1994) In Plant Molec Biol, pp412-426). Like the HD-Zip proteins from the three other classes, class I HDZip proteins are quite divergent in their primary amino structure outside of the homeodomain and the leucine zipper. Within both the homeodomain and the leucine zipper, class I HDZip proteins are further characterized by two specific features:

- 1) in the homeodomain, in addition to the invariant amino acids Leu₆Trp₄₈Phe₄₉Asn₅₁Arg₅₃, position 46 is occupied by an Ala (A) and position 56 by a Try (W) (or occasionally by a Phe (F)) (Sessa *et al.* (1997) J Mol Biol 274(3):303-309; see Figure 1), referred to as a class I homeodomain, and
- 2) the leucine zipper comprises six heptads, except for the fern *Ceratopteris richardii* which presents seven heptads (within each heptad, positions are named a, b, c, d, e, f and g, the conserved leucine being at position d; Sakakibara *et al.* (2001) Mol Biol Evol 18(4): 491-502; see Figure 2). HDZip II, III and IV present a leucine zipper with five heptads only.

Concerning their DNA binding properties, class I HDZip proteins preferably bind to 5 bp half-sites that overlap at a central position, CAA(A/T)ATTG (Sessa *et al.* (1993) EMBO J 12(9): 3507-3517).

Different HDZip proteins have been shown to either activate or repress transcription. In *Arabidopsis*, the class I HDZip ATHB1, -5, -6, and -16 were shown to act as transcriptional activators in transient expression assays on *Arabidopsis* leaves using a reporter gene (luciferase; Henriksson *et al.* (2005) *Plant Phys* 139: 509-518). Two rice class I HDZip proteins, Oshox4 and Oshox5, acted as activators in transient expression assays on rice cell suspension cultures using another reporter gene (glucuronidase; Meijer *et al.* (2000) *Mol Gen Genet* 263:12-21). In contrast, two rice class II HDZip proteins, Oshox1 and Oshox3, acted as transcriptional repressors in the same experiments (Meijer *et al.* (1997) *Plant J* 11: 263-276; Meijer *et al.* (2000) *supra*).

Several class I HDZip proteins have been shown to be involved in light response and in abscisic acid (ABA)/ water deficit related response (Hjellström *et al.* (2003) *Plant Cell Environ* 26: 1127-1136). Transgenic *Arabidopsis* overexpressing class I HDZip ATHB1, -3, -13, -20, and -23 suggest that these genes are involved in the regulation of cotyledon and leaf development (Aoyama *et al.* (1995) *Plant Cell* 7: 1773-1785; Hanson (2000) *In Comprehensive summaries of Uppsala Dissertations from the Faculty of Science and Technology, Uppsala*). The ATHB3, -13, -20, and -23 genes are similar and form a distinct subclass within the class I HDZip. Since these genes cause similar alterations in cotyledon shape when expressed constitutively, they are referred to as the *pointed cotyledon* (POC) HDZip genes. Hanson concludes that class I HDZip proteins that are closely related phylogenetically are also functionally related, in most cases.

Nitrate transporter proteins (NRT)

Plants lead a sessile life and have to rely on resources in the soil for their nutrition. Nitrogen in soil is mainly present as ammonium or nitrate. Nitrate uptake by the plants may occur via three NO_3^- uptake systems: a low affinity transport system that is active when the NO_3^- concentration is more than 1 mM, a constitutive and an inducible high affinity transport system, both for NO_3^- concentrations between 1 μM and 1 mM. The three uptake systems are regulated in a complex way. Once taken up, nitrate is transported into the vacuole or reduced to nitrite, which on its turn is further metabolised in the chloroplast. Nitrate may also be secreted again in the apoplasm or into the xylem for transport to the shoot. Proteins for uptake of nitrate in root cells (NRT, NitRate Transporter proteins) belong to the so-called Major Facilitator Superfamily, which encompasses proteins involved in transport of small solutes and which are generally 450 to 600 amino acids in length with 12 transmembrane domains. NRT proteins fall into two families, NRT1 and NRT2 (Crawford & Glass, *Trends Plant Sci.* 3, 389-395, 1998) and are encoded by a multigene family. NRT proteins are highly conserved in their sequence, for example, NRT2 proteins from mosses share 60% sequence identity with NRT2

protein from dicotyledonous plants, within the group of dicotyledonous plants the sequence identity among NRT2 proteins is around 81%, which may amount up to 89% for monocotyledonous NRT2 proteins. The NRT2 family of proteins in *Arabidopsis* was extensively studied by Orsel et al. (Plant Physiol. 129, 886-896, 2002). The family comprises 7 members, distributed over three chromosomes. The protein structure is conserved and five of the seven NRT2 proteins are preferentially expressed in the roots of young plants. Structurally, NRT2 proteins comprise a MFS_1 domain that spans about 90% of the protein and a C-terminal transmembrane domain. The MFS_1 domain itself is predicted to comprise 10 or 11 transmembrane domains.

NRT2 proteins are proposed to be mainly involved in the high affinity transport system. In higher plants, this high affinity uptake system is postulated to be controlled by a two-protein complex, consisting of NRT2 and NAR, a protein with an unclear function (Zhou et al. FEBS Letters 466, 225-227; Tong et al. Plant J. 41, 442-450, 2005). Overexpression of NRT2 increased the capacity of the high affinity uptake system (Fraisier et al. Plant J. 23, 489-496). NRT2 possibly also functions as a nitrate sensor (Little et al., Proc. Natl. Acad. Sci. USA 102, 13693-13698, 2005).

Mori et al. studied transgenic rice plants overexpressing the rice *NRT2* gene and showed that nitrate starved seedlings had a better NO_3^- uptake compared to wild type plants. Good et al. (US 20050044585) discloses transgenic plants with elevated levels of nitrogen utilisation proteins, and in particular aminotransferases, under control of a root specific promoter that may or may not be stress inducible. These plants showed improved nitrogen uptake efficiency, but no effects on seed yield were reported. In addition, this document also discloses that overexpression of nitrate transporter proteins in plants did not result in advantageous growth properties for these plants. Furthermore, NRT proteins have not been studied yet in normal growth conditions or for a complete plant life cycle.

Yield Enhancing Protein 16 (YEP16)

A YEP16 polypeptide shares some similarity with the N-terminal domain of the delta subunit of the F_1FO -ATP synthase ATPase delta domain (see InterPro IPR000711 for details of the delta subunit).

Shaggy-like kinases

Plant shaggy-like kinases are encoded by a multigene family. The *Arabidopsis* genome has been found to contain ten shaggy-like kinase-encoding genes which fall into four distinct subfamilies. The protein sequences of distinct family members are highly conserved

throughout the kinase domain, however the N- and C- terminal regions differ considerably indicating that the various plant shaggy-like kinases are involved in diverse biological processes, such as hormone signalling, development and stress responses. Based on protein sequence homology, the plant shaggy-like kinases can be classed into four groups (I-IV), with each of the four groups being involved in different processes (see Figure 13). In addition to the full-length cDNA sequences available for *Arabidopsis thaliana* shaggy-like kinases, full-length cDNA sequences are also available in public databases for shaggy-like kinases from *Brassica napus*, *Medicago sativa*, *Nicotiana tabacum*, *Oryza sativa* and *Petunia hybrida* and *Zea mays*, among others. *AtGSK1*, a gene encoding a group II *Arabidopsis* shaggy-like kinase, has been reported to complement the salt sensitive phenotype of yeast calcineurin mutants. In seedlings, the production of the same shaggy-like kinase has been shown to be induced by NaCl and abscisic acid. Overproduction of the *AtGSK1* gene has been reported to induce salt-stress-responsive genes and anthocyanin accumulation and to alter intracellular cation levels, which result in enhanced salt and drought tolerance.

Given that shaggy-like kinases from different groups are known to be involved in diverse biological processes, it was surprising to find shaggy-like kinases from two different groups to be involved in the same biological process, i.e. in stress responses. It was unexpected to find that a shaggy-like kinase from a group other than Group II was able to confer increased tolerance in plants to abiotic stress.

It has now been found that modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or modulating expression in a plant of a nucleic acid encoding a nitrate transporter protein (NRT) or a homologue thereof; or modulating expression in a plant of a nucleic acid encoding a YEP16 polypeptide; or modulating expression in a plant of a Group I shaggy-like kinase or a homologue thereof gives plants having improved growth characteristics relative to corresponding wild type plants or other control plants.

The present invention therefore provides a method for improving plant growth characteristics comprising modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding an NRT or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a YEP16 polypeptide; or comprising modulating expression in a plant of a Group I shaggy-like kinase or a homologue thereof.

The choice of suitable control plants is a routine part of an experimental setup and may include corresponding wild type plants or corresponding plants without the gene of interest. The control plant is typically of the same plant species or even of the same variety as the plant to be assessed. The control plant may also be a nullizygote of the plant to be assessed. A "control plant" as used herein refers not only to whole plants, but also to plant parts, including seeds and seed parts.

Advantageously, performance of the methods according to the present invention results in plants having improved growth characteristics, particularly one or more of increased yield, improved growth, improved biomass, improved architecture, improved cell division and improved tolerance to abiotic stress relative to corresponding wild type or other control plants.

The term "increased yield" as defined herein is taken to mean an increase in any one or more of the following, each relative to corresponding wild type or other control plants: (i) increased biomass (weight) of one or more parts of a plant, particularly aboveground (harvestable) parts, or increased root biomass, increased root volume, increased root number, increased root diameter or increased root length (of thick or thin roots), or increased biomass of any other harvestable part; (ii) increased total seed yield, which includes an increase in seed biomass (seed weight) and which may be an increase in the seed weight per plant or on an individual seed basis and/or per hectare or acre; (iii) increased number of flowers (florets) per panicle, which is expressed as a ratio of number of filled seeds over number of primary panicles; (iv) increased seed fill rate (expressed in percentage terms as the proportion of the number of filled seeds over the number of florets); (v) increased number of (filled) seeds; (vi) increased seed size, which may also influence the composition of seeds; (vii) increased seed volume, which may also influence the composition of seeds (including oil, protein and carbohydrate total content and composition); (viii) increased (individual or average) seed area; (ix) increased (individual or average) seed length; (x) increased (individual or average) seed width; (xi) increased (individual or average) seed perimeter; (xii) increased harvest index (HI), which is expressed as a ratio of the yield of harvestable parts, such as seeds, over the total biomass; and (xiii) increased thousand kernel weight (TKW), which is extrapolated from the number of filled seeds counted and their total weight. An increased TKW may result from an increased seed size and/or seed weight. An increased TKW may result from an increase in embryo size and/or endosperm size.

Taking corn as an example, a yield increase may be manifested as one or more of the following: increase in the number of plants established per hectare or acre, an increase in the number of ears per plant, an increase in the number of rows, number of kernels per row, kernel

weight, thousand kernel weight, ear length/diameter, increase in the seed filling rate (which is the number of filled seeds divided by the total number of seeds and multiplied by 100), among others. Taking rice as an example, a yield increase may manifest itself as an increase in one or more of the following: number of plants per hectare or acre, number of panicles per plant, number of spikelets per panicle, number of flowers (florets) per panicle (which is expressed as a ratio of the number of filled seeds over the number of primary panicles), increase in the seed filling rate (which is the number of filled seeds divided by the total number of seeds and multiplied by 100), increase in thousand kernel weight, among others.

Since the transgenic plants according to the present invention have increased yield, it is likely that these plants exhibit an increased growth rate (during at least part of their life cycle), relative to the growth rate of control plants at a corresponding stage in their life cycle. The increased growth rate may be specific to one or more parts of a plant (including seeds), or may be throughout substantially the whole plant. Plants having an increased growth rate may have a shorter life cycle. The life cycle of a plant may be taken to mean the time needed to grow from a dry mature seed up to the stage where the plant has produced dry mature seeds, similar to the starting material. This life cycle may be influenced by factors such as early vigour, growth rate, greenness index, flowering time and speed of seed maturation. The increase in growth rate may take place at one or more stages in the life cycle of a plant or during substantially the whole plant life cycle. Increased growth rate during the early stages in the life cycle of a plant may reflect enhanced vigour. The increase in growth rate may alter the harvest cycle of a plant allowing plants to be sown later and/or harvested sooner than would otherwise be possible (a similar effect may be obtained with earlier flowering time). If the growth rate is sufficiently increased, it may allow for the further sowing of seeds of the same plant species (for example sowing and harvesting of rice plants followed by sowing and harvesting of further rice plants all within one conventional growing period). Similarly, if the growth rate is sufficiently increased, it may allow for the further sowing of seeds of different plants species (for example the sowing and harvesting of rice plants followed by, for example, the sowing and optional harvesting of soybean, potato or any other suitable plant). Harvesting additional times from the same rootstock in the case of some crop plants may also be possible. Altering the harvest cycle of a plant may lead to an increase in annual biomass production per acre (due to an increase in the number of times (say in a year) that any particular plant may be grown and harvested). An increase in growth rate may also allow for the cultivation of transgenic plants in a wider geographical area than their wild-type counterparts, since the territorial limitations for growing a crop are often determined by adverse environmental conditions either at the time of planting (early season) or at the time of harvesting (late season). Such adverse conditions may be avoided if the harvest cycle is shortened. The

growth rate may be determined by deriving various parameters from growth curves, such parameters may be: T-Mid (the time taken for plants to reach 50% of their maximal size) and T-90 (time taken for plants to reach 90% of their maximal size), amongst others.

Performance of the methods of the invention gives plants having an increased growth rate. Therefore, according to the present invention, there is provided a method for increasing the growth rate of plants which method comprises modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding an NRT or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid encoding a YEP16 polypeptide; or comprising modulating expression in a plant of a Group I shaggy-like kinase or a homologue thereof.

An increase in yield and/or growth rate occurs whether the plant is under non-stress conditions or whether the plant is exposed to various stresses compared to control plants. Plants typically respond to exposure to stress by growing more slowly. In conditions of severe stress, the plant may even stop growing altogether. Mild stress on the other hand is defined herein as being any stress to which a plant is exposed which does not result in the plant ceasing to grow altogether without the capacity to resume growth. Mild stress in the sense of the invention leads to a reduction in the growth of the stressed plants of less than 40%, 35% or 30%, preferably less than 25%, 20% or 15%, more preferably less than 14%, 13%, 12%, 11% or 10% or less in comparison to the control plant under non-stress conditions. Due to advances in agricultural practices (irrigation, fertilization, pesticide treatments) severe stresses are not often encountered in cultivated crop plants. As a consequence, the compromised growth induced by mild stress is often an undesirable feature for agriculture. Mild stresses are the everyday biotic and/or abiotic (environmental) stresses to which a plant is exposed. Abiotic stresses may be due to drought or excess water, anaerobic stress, salt stress, chemical toxicity, oxidative stress and hot, cold or freezing temperatures. The abiotic stress may be an osmotic stress caused by a water stress (particularly due to drought), salt stress, oxidative stress or an ionic stress. Biotic stresses are typically those stresses caused by pathogens, such as bacteria, viruses, fungi and insects.

Performance of the methods according to the present invention results in plants having increased tolerance to abiotic stress. As reported in Wang *et al.* (Planta (2003) 218: 1-14), abiotic stress leads to a series of morphological, physiological, biochemical and molecular changes that adversely affect plant growth and productivity. Drought, salinity, extreme temperatures and oxidative stress are known to be interconnected and may induce growth and

cellular damage through similar mechanisms. For example, drought and/or salinisation are manifested primarily as osmotic stress, resulting in the disruption of homeostasis and ion distribution in the cell. Oxidative stress, which frequently accompanies high or low temperature, salinity or drought stress may cause denaturation of functional and structural proteins. As a consequence, these diverse environmental stresses often activate similar cell signaling pathways and cellular responses, such as the production of stress proteins, up-regulation of anti-oxidants, accumulation of compatible solutes and growth arrest.

Since diverse environmental stresses activate similar pathways, the exemplification of the present invention with drought stress (insofar as the invention concerns the use of class I HDZip hox5 polypeptides and their encoding nucleic acids) should not be seen as a limitation to drought stress, but more as a screen to indicate the involvement of class I HDZip hox5 polypeptides or a homologues thereof in abiotic stresses in general. Furthermore, the methods of the present invention may be performed under non-stress conditions or under conditions of mild drought to give plants having improved growth characteristics (particularly increased yield) relative to corresponding wild type or other control plants. The term "non-stress" conditions as used herein are preferably those environmental conditions that do not significantly go beyond the everyday climatic and other abiotic conditions that plants may encounter most preferably those conditions that allow optimal growth of plants. Persons skilled in the art are aware of normal soil conditions and climatic conditions for a given location.

A particularly high degree of "cross talk" is reported between drought stress and high-salinity stress (Rabbani *et al.* (2003) Plant Physiol 133: 1755-1767). Therefore, it would be apparent that a class I HDZip hox5 polypeptide or a homologue thereof would, along with its usefulness in conferring drought-tolerance in plants, also find use in protecting the plant against various other abiotic stresses. Similarly, it would be apparent that a Group I shaggy-like kinase (as defined herein) would, along with its usefulness in conferring salt-tolerance in plants, also find use in protecting the plant against various other abiotic stresses. Furthermore, Rabbani *et al.* (2003, Plant Physiol 133: 1755-1767) report that similar molecular mechanisms of stress tolerance and responses exist between dicots and monocots. The methods of the invention are therefore advantageously applicable to any plant.

The term "abiotic stress" as defined herein is taken to mean any one or more of: water stress (due to drought or excess water), anaerobic stress, salt stress, temperature stress (due to hot, cold or freezing temperatures), chemical toxicity stress and oxidative stress. According to one aspect of the invention, the abiotic stress is an osmotic stress, selected from water stress, salt stress, oxidative stress and ionic stress. Preferably, the water stress is drought stress. The

term salt stress is not restricted to common salt (NaCl), but may be any one or more of: NaCl, KCl, LiCl, $MgCl_2$, $CaCl_2$, amongst others.

Increased tolerance to abiotic stress is manifested by increased plant yield in abiotic stress conditions. Particularly insofar as the invention concerns the use of class I HDZip hox5 polypeptides and their encoding nucleic acids, such increased yield may include one or more of the following: increased number of filled seeds, increased total seed yield, increased number of flowers per panicle, increased seed fill rate, increased HI, increased TKW, increased root length or increased root diameter, each relative to corresponding wild type plants.

Performance of the methods of the invention gives plants having increased tolerance to abiotic stress. Performance of the methods of the invention gives plants grown under non-stress conditions or under mild drought conditions improved growth characteristics (particularly increased yield) relative to corresponding wild type plants or other control plants grown under comparable conditions.

According to the present invention, there is provided a method for increasing abiotic stress tolerance in plants which method comprises modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof. According to one aspect of the invention, the abiotic stress is an osmotic stress, selected from one or more of the following: water stress, salt stress, oxidative stress and ionic stress. Preferably, the water stress is drought stress.

The present invention also provides a method for improving abiotic stress tolerance in plants, comprising increasing activity in a plant of a Group I shaggy-like kinase or a homologue thereof, which Group I shaggy-like kinase has: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid.

The present invention also provides a method for improving plant growth characteristics (particularly increasing yield) in plants grown under non-stress conditions or under mild drought conditions, which method comprises modulating expression (preferably increasing expression) in a plant of a nucleic acid encoding a NRT polypeptide or a homologue thereof. In a preferred embodiment of the invention, the increase in yield and/or growth rate occurs according to the methods of the present invention under non-stress conditions.

Particularly insofar as the invention concerns the use of class I HDZip hox5 polypeptides and their encoding nucleic acids, performance of the methods of the invention gives an increased greenness index relative to corresponding wild type plants. The greenness index as defined herein is the proportion (expressed as %) of yellow pixels in plant images recorded by a digital camera. An increased greenness index may indicate reduced or delayed senescence which in turn allows prolongation of the photosynthetic activity of a plant, which in turn leads to various beneficial effects well known in the art.

The invention therefore provides a method for increasing greenness index in plants which method comprises modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof. Preferably, the greenness index is increased in abiotic stress conditions, more preferably in water stress conditions, further preferably in drought stress conditions.

Preferably, where the method of the invention comprises modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof, the increased yield includes one or more of the following: increased number of filled seeds, increased total seed yield, increased number of flowers per panicle, increased seed fill rate, increased HI, increased TKW, increased root length or increased root diameter, each relative to corresponding wild type or other control plants.

According to a preferred feature of the present invention, there is provided a method for increasing plant yield relative to corresponding wild type or other control plants, which method comprises modulating expression in a plant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof.

Preferably, where the method of the invention comprises modulating expression in a plant of a nucleic acid encoding an NRT or a homologue thereof, the resultant plants have increased yield and more particularly, increased biomass and/or increased seed yield. Preferably, the increased seed yield comprises an increase in one or more of number of (filled) seeds, total seed weight, seed size, thousand kernel weight and harvest index, each relative to corresponding wild type or other control plants.

According to another preferred feature of the present invention, there is provided a method for increasing plant yield, which method comprises modulating expression (preferably increasing activity and/or expression) in a plant of a nucleic acid encoding an NRT polypeptide or a homologue thereof.

Preferably, where the method of the invention comprises modulating expression in a plant of a nucleic acid encoding a YEP16 polypeptide, the increased or improved yield is improved seed yield relative to the seed yield of corresponding wild type plants.

Therefore, according to another preferred feature of the present invention, there is provided a method for increasing seed yield in a plant relative to corresponding wild type or other control plants, comprising modulating expression in a plant of a nucleic acid encoding a YEP16 polypeptide or a homologue thereof.

Preferably, where the method of the invention comprises modulating expression in a plant of a nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof, the improved growth characteristic is improved tolerance to abiotic stress.

According to the another preferred feature of the present invention, there is provided a method for improving abiotic stress tolerance in plants, comprising modulating expression (preferably increasing activity and/or expression) in a plant of a Group I shaggy-like kinase or a homologue thereof, which Group I shaggy-like kinase has: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid.

The methods of the invention are therefore advantageously applicable to any plant.

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, leaves, roots (including tubers), flowers, and tissues and organs, wherein each of the aforementioned comprise the gene/nucleic acid of interest. The term "plant" also encompasses plant cells, suspension cultures, callus tissue, embryos, meristematic regions, gametophytes, sporophytes, pollen and microspores, again wherein each of the aforementioned comprises the gene/nucleic acid of interest.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs 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 deer*, *Baikiaea plurijuga*, *Betula spp.*, *Brassica spp.*, *Bruguiera gymnorhiza*, *Burkea africana*, *Butea frondosa*, *Cadaba farinosa*, *Calliandra spp.*, *Camellia*

sinensis, *Canna indica*, *Capsicum* spp., *Cassia* spp., *Centroema pubescens*, *Chaenomeles* 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*, *Diheteropogon amplexans*, *Dioclea* spp., *Dolichos* spp., *Dorycnium rectum*, *Echinochloa pyramidalis*, *Ehrartia* spp., *Eleusine coracana*, *Eragrostis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperii*, *Eulalia villosa*, *Fagopyrum* spp., *Feijoa sellowiana*, *Fragaria* spp., *Flemingia* spp., *Freycinetia banksii*, *Geranium thunbergii*, *Ginkgo biloba*, *Glycine javanica*, *Gliricidia* spp., *Gossypium hirsutum*, *Grevillea* spp., *Guibourtia coleosperma*, *Hedysarum* spp., *Hemarthia altissima*, *Heteropogon contortus*, *Hordeum vulgare*, *Hyparrhenia rufa*, *Hypericum erectum*, *Hyperthelia dissoluta*, *Indigo incarnata*, *Iris* spp., *Leptarrhena pyrolifolia*, *Lespedeza* spp., *Lettuca* spp., *Leucaena leucocephala*, *Loudetia simplex*, *Lotonus bainesii*, *Lotus* spp., *Macrotyloma axillare*, *Malus* spp., *Manihot esculenta*, *Medicago sativa*, *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 sativum*, *Podocarpus totara*, *Pogonarthria fleckii*, *Pogonarthria squarrosa*, *Populus* spp., *Prosopis cineraria*, *Pseudotsuga menziesii*, *Pterolobium stellatum*, *Pyrus communis*, *Quercus* spp., *Rhaphiolepis umbellata*, *Rhopalostylis sapida*, *Rhus natalensis*, *Ribes grossularia*, *Ribes* spp., *Robinia pseudoacacia*, *Rosa* spp., *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum*, *Sciadopitys verticillata*, *Sequoia sempervirens*, *Sequoiadendron giganteum*, *Sorghum bicolor*, *Spinacia* spp., *Sporobolus fimbriatus*, *Stiburus alopecuroides*, *Stylosanthes 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, strawberry, sugar beet, sugar cane, sunflower, tomato, squash, tea and algae, amongst others.

According to a preferred embodiment of the present invention, the plant is a crop plant such as soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco. Further preferably, the plant is a monocotyledonous plant, such as sugarcane. More preferably the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum or oats.

Class I HDZip hox δ polypeptides and homologues thereof, and class I HDZip hox δ nucleic acids/genes useful in the methods of the invention

The term "class I HDZip hox5 polypeptide or homologue thereof" as defined herein refers to a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads.

Additionally, the class I HDZip hox5 polypeptide or a homologue thereof may comprise any one or both of the following: (a) a Trp tail; and (b) the RPFF amino acid motif, where R is Arg, P Pro and F Phe. Within this motif, are allowed one or more conservative change(s) at any position, and/or one or two non-conservative change(s) at any position. The motif of (b) precedes the acidic box, when examining the protein from N-terminal to C-terminal.

An example of a class I HDZip hox5 polypeptide as defined hereinabove comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads; and additionally comprising: (a) a Trp tail; and (b) the RPFF amino acid motif, where R is Arg, P Pro and F Phe, is represented as in SEQ ID NO: 2. Further such examples are given in Table A of Example 1 herein.

A class I HDZip hox5 polypeptide or homologue thereof is encoded by a class I HDZip hox5 nucleic acid/gene. Therefore the term "class I HDZip hox5 nucleic acid/gene" as defined herein is any nucleic acid/gene encoding a class I HDZip hox5 polypeptide or a homologue thereof as defined hereinabove.

Class I HDZip hox5 polypeptides or homologues thereof may readily be identified using routine techniques well known in the art, such as by sequence alignment. Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch ((1970) J Mol Biol 48: 443-453) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. The BLAST algorithm (Altschul *et al.* (1990) J Mol Biol 215: 403-10) calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information. Homologues of class I HDZip hox5 comprising a class I homeodomain and a leucine zipper with more than 5 heptads may readily be identified using, for example, the ClustalW multiple sequence alignment algorithm (version 1.83) available at <http://clustalw.genome.jp/sit-bin/nph->

ClustalW, with the default pairwise alignment parameters, and a scoring method in percentage. Minor manual editing may be performed to optimise alignment between conserved motifs, as would be apparent to a person skilled in the art.

The various structural domains in a class I HDZip hox5 protein, such as the homeodomain and the leucine zipper, may be identified using specialised databases e.g. SMART (Schultz *et al.* (1998) Proc. Natl. Acad. Sci. USA 95, 5857-5864; Letunic *et al.* (2002) Nucleic Acids Res 30, 242-244; <http://smart.embl-heidelberg.de/>), InterPro (Mulder *et al.*, (2003) Nucl. Acids. Res. 31, 315-318; <http://www.ebi.ac.uk/interpro/>), Prosite (Bucher and Bairoch (1994), A generalized profile syntax for biomolecular sequences motifs and its function in automatic sequence interpretation. (In) ISMB-94; Proceedings 2nd International Conference on Intelligent Systems for Molecular Biology. Altman R., Brutlag D., Karp P., Lathrop R., Searls D., Eds., pp53-61, AAAIPress, Menlo Park; Hulo *et al.*, Nucl. Acids. Res. 32:D134-D137, (2004), <http://www.expasy.org/prosite/>) or Pfam (Bateman *et al.*, Nucleic Acids Research 30(1):276-280 (2002), <http://www.sanger.ac.uk/Software/Pfam/>). Leucine zipper prediction and heptad identification may be done using specialised software such as 2ZIP, which combines a standard coiled coil prediction algorithm with an approximate search for the characteristic leucine repeat (Bornberg-Bauer *et al.* (1998) Computational Approaches to Identify Leucine Zippers, Nucleic Acids Res., 26(11): 2740-2746, <http://2zip.molgen.mpg.de>).

Furthermore, the presence of an acidic box may also readily be identified. Primary amino acid composition (in %) to determine if a polypeptide domain is rich in specific amino acids may be calculated using software programs from the ExPASy server, in particular the ProtParam tool (Gasteiger E *et al.* (2003) ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Res 31:3784-3788). The composition of the protein of interest may then be compared to the average amino acid composition (in %) in the Swiss-Prot Protein Sequence data bank. Within this databank, the average Asp (D) and Glu (E) content are of 5.3 % and of 6.6 % respectively, the combined average being of 11.9 %. As an example, the acidic box of SEQ ID NO: 2 contains 9.1 % of D and 54.5 % of E, the combined average being of 63.6 %. As defined herein, an acidic rich box has a combined Asp (D) and Glu (E) content (in % terms) above that found in the average amino acid composition (in % terms) of the proteins in the Swiss-Prot Protein Sequence database. An acidic box may be part of a transcription activation domain. Eukaryotic transcription activation domains have been classified according to their amino acid content, and major categories include acidic, glutamine-rich and proline-rich activation domains (Rutherford *etal.* (2005) Plant J. 43(5):769-88, and references therein).

A selected number of proteins amongst the class I HDZip hox5 polypeptides or homologues thereof further comprise the RPFF amino acid motif, where R is Arg, P Pro and F Phe. Within this motif, are allowed one or more conservative change(s) at any position, and/or one or two non-conservative change(s) at any position. This motif precedes the acidic box, when examining the protein from N-terminal to C-terminal (see Figure 2). The presence of the RPFF may be identified using methods for the alignment of sequences for comparison as described hereinabove. In some instances, the default parameters may be adjusted to modify the stringency of the search. For example using BLAST, the statistical significance threshold (called "expect" value) for reporting matches against database sequences may be increased to show less stringent matches. This way, short nearly exact matches may be identified.

A selected number of proteins amongst the class I HDZip hox5 polypeptides or homologues thereof may further comprise a Trp tail. A Trp tail as defined herein is the last 10 amino acids of the C-terminal of the protein comprising at least one Trp residue (see Figure 2).

Examples of class I HDZip hox5 polypeptides or homologues thereof (encoded by polynucleotide sequence accession number in parenthesis) are given in Table A.

It is to be understood that sequences falling under the definition of "class I HDZip hox5 polypeptide or homologue thereof" are not to be limited to the sequences given in Table A, but that any polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads, may be suitable for use in performance of the methods of the invention.

Class I HDZip hox5 polypeptides or homologues thereof have DNA binding activity, preferably to 5 bp half-sites that overlap at a central position, CAA(A/T)ATTG, as detected in yeast one-hybrid assays (Meijer *et al.* (2000) *Mol Gen Genet* 263:12-21). In transient assays on rice cell suspensions, co-bombardement of a class I HDZip hox5 polypeptide with the GUS reporter gene resulted in an increase number of stained spots, which were also more intense in color (Meijer *et al.*, *supra*). This assay is useful to demonstrate the activator function of class I HDZip hox5 polypeptides or homologues.

NRT polypeptides and homologues thereof and their encoding nucleic acids useful in the methods of the invention

The term "NRT or homologue thereof" as defined herein refers to a polypeptide comprising (i) an MFS_1 domain (Pfam accession PF07690, InterPro accession **IPR01 1701**) followed by (ii) a transmembrane domain. An example is given in Figure 6. Preferably, the NRT protein or

homologue thereof has NRT activity such as high affinity nitrate transport, and does not comprise a PTR2 domain (Pfam accession PF00854, InterPro accession IPR000109).

Preferably, the NRT protein or homologue thereof comprises a signature sequence 1 (SEQ ID NO: 57):

(NZS)(YZP)(TZGZSZA)W(IZVZL)(FZLZT)(VZAZFZL)(LMMZI)(LZTZIZAZN)YG(YZF)(SZCZT)(MZFZY)G(VZI)EL(TZS)(TZIZV)(DZGZN)N(VZIZN)(IZV)(AZSZHZV)(EZQZG)Y.

Further preferably, the NRT protein or homologue thereof comprises one or more of: signature sequence 2 (SEQ ID NO: 58):

LG(PZA)RYG(CZT)AF(LZS);

signature sequence 3 (SEQ ID NO: 59):

STFAA(AZR)PL(VZI)(PZV)(IZLZV) IR(DZE)NL(NZD)(LZP) ;

signature sequence 4 (SEQ ID NO: 60):

VRF(LZM)IGF(SZC)LA;

signature sequence 5 (SEQ ID NO: 61):

FVSC(QZR)YW(MZT)S(TZV)(MZS)(FZM).

More preferably, the NRT protein or homologue thereof comprises one or more of:

signature sequence 6 (SEQ ID NO: 62):

K(AZQZSZMZHZT)D(IZV)GNAGVASV(SZT)G(SZA) I(FZL)SR(LZG) ;

signature sequence 7 (SEQ ID NO: 63):

NG(LZTZC)A(AZG)GWG;

signature sequence 8 (SEQ ID NO: 64):

G(AZS)G(LZVZQ)TQ(LZP)(LZVZI)(FZE)F(TZSZD)(SZT)(SZAZT).

Most preferably, the NRT protein is as represented in SEQ ID NO: 53.

Transmembrane domains are about 15 to 30 amino acids long and are usually composed of hydrophobic residues that form an alpha helix. They are usually predicted on the basis of hydrophobicity (for example Klein et al., *Biochim. Biophys. Acta* 815, 468, 1985; or Sonnhammer et al., In J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen, editors, *Proceedings of the Sixth International Conference on Intelligent Systems for Molecular Biology*, pages 175-182, Menlo Park, CA, 1998. AAAI Press.).

Alternatively, the homologue of an NRT protein has in increasing order of preference 50%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% overall sequence identity to the amino acid represented by SEQ ID NO: 53. The overall sequence identity is

determined using a global alignment algorithm, such as the Needleman Wunsch algorithm in the program GAP (GCG Wisconsin Package, Accelrys), preferably with default parameters.

The various structural domains in an NRT protein may be identified using specialised databases e.g. SMART (Schultz *et al.* (1998) Proc. Natl. Acad. Sci. USA 95, 5857-5864; Letunic *et al.* (2002) Nucleic Acids Res 30, 242-244; <http://smart.embl-heidelberg.de/>), InterPro (Mulder *et al.*, (2003) Nucl. Acids. Res. 31, 315-318; <http://www.ebi.ac.uk/interpro/>), Prosite (Bucher and Bairoch (1994), A generalized profile syntax for biomolecular sequences motifs and its function in automatic sequence interpretation. (In) ISMB-94; Proceedings 2nd International Conference on Intelligent Systems for Molecular Biology. Altman R., Brutlag D., Karp P., Lathrop R., Searls D., Eds., pp53-61, AAAIPress, Menlo Park; Hulo *et al.*, Nucl. Acids. Res. 32:D134-D137, (2004), <http://www.expasy.org/prosite/>) or Pfam (Bateman *et al.*, Nucleic Acids Research 30(1):276-280 (2002), <http://www.sanger.ac.uk/Software/Pfam/>).

Methods for the search and identification of NRT homologues would be well within the realm of persons skilled in the art. Such methods comprise comparison of the sequences represented by SEQ ID NO: 1 or 2, in a computer readable format, with sequences that are available in public databases such as MIPS (<http://mips.gsf.de/>), GenBank (<http://www.ncbi.nlm.nih.gov/Genbank/index.html>) or EMBL Nucleotide Sequence Database (<http://www.ebi.ac.uk/embl/index.html>), using algorithms well known in the art for the alignment or comparison of sequences, such as GAP (Needleman and Wunsch, J. Mol. Biol. 48; 443-453 (1970)), BESTFIT (using the local homology algorithm of Smith and Waterman (Advances in Applied Mathematics 2; 482-489 (1981))), BLAST (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J., J. Mol. Biol. 215:403-410 (1990)), FASTA and TFASTA (W. R. Pearson and D. J. Lipman Proc.Natl.Acad.Sci. USA 85:2444- 2448 (1988)). The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information (NCBI).

Examples of proteins falling under the definition of "NRT polypeptide or a homologue thereof" include rice proteins and proteins from other species such as *Zea mays*, *Phragmites australis*, *Hordeum vulgare*, *Triticum aestivum*, *Brassica napus*, *Lycopersicon esculentum*, *Nicotiana tabacum*, *Daucus carota*, *Populus tremulus*, *Lotus japonica*, *Prunus persica*, *Glycine max* and *Arabidopsis thaliana*, among others. A non-limiting list of examples of NRT proteins is given in Table I of Example 14 herein.

It is however envisaged that NRT proteins from other plant taxa, such as mosses or ferns, may equally be useful in the methods of the present invention. For example, the moss

Physcomitrella patens possesses at least 5 NRT proteins (GenBank accession numbers BAD00097, BAD00098, BAD00099, BAD00100, BAD00101).

It is to be understood that the term "NRT polypeptide or a homologue thereof" is not to be limited to the sequence represented by SEQ ID NO: 53 or to the sequences given in Table 1, but that any polypeptide meeting the criteria of comprising a functional MFS_1 domain, and one or more of the conserved signature sequences of SEQ ID NO: 57 to 64, and a transmembrane domain located C-terminally of the MFS_1 domain as defined above; or having at least 50% sequence identity to the sequence of SEQ ID NO: 53, may be suitable for use in the methods of the invention.

To determine the transporter activity of NRT, the nitrate uptake assay as described by Tong et al. (Plant J. 41, 442-450, 2005). Briefly, the NRT protein of interest is expressed in *Xenopus* oocytes, and the uptake of ¹⁵N-enriched nitrate is measured. If required, a *nar2* gene may be co-expressed to increase nitrate transport.

Alternatively, the activity of an NRT protein or homologue thereof may be assayed by expressing the NRT protein or homologue thereof under control of a GOS2 promoter in the *Oryza sativa* cultivar Nipponbare, which results in plants with increased aboveground biomass and/or increased seed yield compared to corresponding wild type plants. This increase in seed yield may be measured in several ways, for example as an increase of total seed weight, number of filled seeds or total number of seeds, as an increase of harvest index or as an increase of flowers per panicle.

An NRT protein or homologue thereof is encoded by an *NRT* nucleic acid/gene. Therefore the term "*NRT* nucleic acid/gene" as defined herein is any nucleic acid/gene encoding an NRT protein or a homologue thereof as defined above.

YEP16 polypeptides and homologues and their encoding nucleic acids useful in the methods of the invention

The term "YEP16 polypeptide" refers to the sequence of SEQ ID NO: 128. A homologue of a YEP16 polypeptide refers to any amino acid sequence sharing, in increasing order of preference, at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128. Reference herein to "a nucleic acid encoding a YEP16 polypeptide or a homologue thereof" therefore refers to any nucleic acid sequence encoding a YEP16 polypeptide as defined hereinabove or any nucleic acid encoding a homologue of a YEP16 polypeptide as defined hereinabove.

Group I shaggy-like kinases and homologues thereof and their encoding nucleic acids useful in the methods of the invention

The term "Group I shaggy-like kinase or homologue thereof" as defined herein refers to a polypeptide having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid. A polypeptide meeting the aforementioned requirements allows a Group I shaggy-like kinase to be distinguished from those of other groups.

A "Group I shaggy-like kinase or a homologue thereof" falling within the above definition may readily be identified using routine techniques well known to persons skilled in the art. For example, a polypeptide having at least 77% identity to the amino acid represented by SEQ ID NO: 147 may readily be established by sequence alignment. Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453, 1970) to find the alignment of two complete sequences that maximises the number of matches and minimises the number of gaps. The BLAST algorithm calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information. A shaggy-like kinase or a homologue thereof having at least 77% identity to the amino acid represented by SEQ ID NO: 147 may readily be identified by aligning a query amino acid sequence with known Group I shaggy-like kinase sequences (see for example the alignment shown in Figure 14) using, for example, the VNTI AlignX multiple alignment program, based on a modified clustal W algorithm (InforMax, Bethesda, MD, <http://www.informaxinc.com>), with default settings for gap opening penalty of 10 and a gap extension of 0.05.

A person skilled in the art will also readily be able to identify sequences having motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid. This may be achieved by making an alignment and searching for homologous regions.

Table 1 below shows motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S (where X may be any amino acid) as found in the sequence of SEQ ID NO: 147 and the corresponding motifs in homologous sequences. The overall percentage identity shown in Table 1 is when comparing SEQ ID NO: 147 with the accession numbers shown in the Table (full-length sequence to full-length sequence).

Table 1: Conserved motifs found in Group I shaggy-like kinases and in homologues thereof

Accession number: Group I shaggy-like kinase	Gene name	Motif 1	Motif 2	% overall identity with SEQ ID NO: 147 (EMBOSS)
BAB40983.1 (SEQ ID NO: 147)	Rice OSK gamma	HELKG	KQCSYAG	-
AY103545	Corn	HELKG	KQCSYVG	94.4%
AY108486	Corn	HELKN	KQCAFVG	84.4%
AAM77397.1	Triticum	HELKG	KNCAFVG	80.9%
CAA48538.1, At5g26750	Ara ASK Alpha	HELKG	KQCPWLG	85.6%
CAA48474.1	Medicago MSK-1	HELKG	KQCPFLG	83.5%
CAA04265	Ara Ask alpha	HGLKG	KQCPWLG	84.6%
CAA54803.1	Tobacco NtK1	HELKG	KQCPSLG	85.3%
CAA48472.1	Medicago MSK3	NELKG	KQCALFG	85.0%
CAA48473.1	Medicago MSK2	VELKG	KQCSLFA	82.0%
CAA58594.1	Petunia Shaggy 4	QELKG	KQCTFLG	81.5%
At5g14640	Ara ASK epsilon	QELKG	KQCSFLA	83.9%
At3g05840	Ara ASK gamma	HELKG	KQCPWLS	84.6%
CAA04265	Rice shaggy alpha	HGLKG	KQCPWLG	84.6%
AK058276	Rice shaggy	HELKG	KQCAFVG	83.2%
AK099599	Rice Shaggy	RELKG	KQCAFLG	78.5%
Other shaggy-like groups				
At4g18710	Ara Ask eta	No	No	70.0%
At2g30980	Ara Ask dzeta	No	No	72.9%
At4g00720	Ara Ask theta	No	No	64.1%
At1g57870	Ara Ask delta	No	No	73.4%
At1g09840	Ara Ask kappa	No	No	72.4%
At1g06390	Ara Ask iota	No	No	71.6%
At3g61160	Ara Ask beta	No	No	61.3%

Examples of polypeptides falling under the definition of a "shaggy-like kinase or a homologue thereof" include the following sequences: SEQ ID NO: 147, a gamma shaggy-like kinase from rice (NCBI Accession number AB059621); SEQ ID NO: 149 (NCBI Accession number

AK058276) a shaggy-like kinase from rice; SEQ ID NO: 151 (NCBI Accession number AK099599) a shaggy like kinase from rice; SEQ ID NO: 153, an alpha shaggy-like kinase from *Arabidopsis thaliana* (NCBI Accession number At5g26750); SEQ ID NO: 155, a gamma shaggy-like kinase from *Arabidopsis thaliana* (NCBI Accession number At3g05840); SEQ ID NO: 157, an alpha shaggy-like kinase from *Arabidopsis thaliana* (NCBI Accession number CAA48538.1); SEQ ID NO: 159, an epsilon shaggy-like kinase from *Arabidopsis thaliana* (NCBI Accession number At5g14640); SEQ ID NO: 161, a gamma shaggy-like kinase from *Arabidopsis thaliana* (NCBI Accession number CAA73247.1); SEQ ID NO: 163 from maize (NCBI Accession number AY103545); SEQ ID NO: 165 from maize (NCBI Accession number AY108486.1); SEQ ID NO: 167 from Medicago (NCBI Accession number CAA48472.1); SEQ ID NO: 169 from Medicago (NCBI Accession number CAA48474.1); SEQ ID NO: 171 from Medicago (NCBI Accession number CAA48473.1); SEQ ID NO: 173 from tobacco (NCBI Accession number CAA54803.1); SEQ ID NO: 175 a protein prediction of a shaggy-like kinase from *Triticum aestivum* (NCBI Accession number AAM77397.1); SEQ ID NO: 177 from *Petunia hybrida* (NCBI Accession number CAA58594.1).

The "term shaggy-like kinase or a homologue thereof" is not to be limited to the sequences represented by the SEQ ID NOs mentioned in the aforementioned paragraph, but that any polypeptide meeting the criteria of having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid, would be suitable for use in the methods of the invention.

Shaggy-like kinases, as the name suggests, have kinase activity. An assay for glycogen synthase kinase-3 (GSK-3), the animal homologue, is reported in The Biochemical Journal, Vol. 303 (Pt3), Nov. 1, 1994, pp701-704 (Stambolic and Woodgett).

Sequences useful in the methods of the invention are not limited to the aforementioned class I homeodomain leucine zipper (HDZip) hox5 nucleic acids and polypeptides; or to the aforementioned NRT polypeptides and their encoding nucleic acids; or to the aforementioned YEP16 polypeptides and their encoding nucleic acids; or to the aforementioned Group I shaggy-like kinases and their encoding polypeptides. The methods according to the present invention may also be performed using variants of nucleic acids encoding class I homeodomain leucine zipper (HDZip) hox5 polypeptides or homologues thereof; or using variants of nucleic acids encoding NRT polypeptides or homologues thereof; or using variants of nucleic acids encoding YEP16 polypeptides and homologues thereof; or using variants of nucleic acids encoding Group I shaggy-like kinases and homologues thereof.

Examples of such variants include portions, hybridizing sequences, allelic variants, splice variants and variants obtained by gene shuffling.

A portion may be prepared, for example, by making one or more deletions to a nucleic acid. The portions may be used in isolated form or they may be fused to other coding (or non coding) sequences in order to, for example, produce a protein that combines several activities. When fused to other coding sequences, the resulting polypeptide produced upon translation may be bigger than that predicted for the portion.

Where the sequence useful in the methods of the invention is a class I HDZip hox5, the portion encodes a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads. Preferably, the portion is a portion of one of the nucleic acids given in Table A. Most preferably the portion is a portion of a nucleic acid as represented by SEQ ID NO: 1.

Where the sequence useful in the methods of the invention is a nucleic acid encoding an NRT, the portion refers to a piece of DNA encoding a polypeptide comprising a MFS_1 domain and a transmembrane domain located C-terminally of the MFS_1 domain. Preferably, the portion comprises one or more of the signature sequences defined above. Preferably, the portion is a portion of one of the nucleic acids given in Table 1. Most preferably the portion of a nucleic acid is as represented by SEQ ID NO: 52.

Where the sequence useful in the methods of the invention is a YEP1 6-encoding nucleic acid, the portion refers to a piece of DNA encoding a YEP1 6 polypeptide or a homologue thereof having, in increasing order of preference, at least 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575 consecutive nucleotides of the nucleic acid sequence represented by SEQ ID NO: 127 or SEQ ID NO: 129, or wherein a portion has in increasing order of preference, at least 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575 consecutive nucleotides of a nucleic acid sequence encoding a YEP1 6 polypeptide or a homologue thereof. Preferably, the portion is a portion of a nucleic acid as represented by SEQ ID NO: 127 or SEQ ID NO: 129.

Where the sequence useful in the methods of the invention is a Group I shaggy-like kinase, the portion refers to a shaggy-like kinase-encoding piece of DNA of at least 1,200 nucleotides in length, and which portion encodes a polypeptide having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) having motif 1: R/H/V/N/Q

E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid. Preferably, the portion is a portion of a nucleic acid as represented by any one of SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174 and SEQ ID NO: 176.

The invention therefore provides a method for improving plant growth characteristics comprising modulating expression in a plant of a portion of a nucleic acid encoding a class I liomeoddomain leucine zip_{per} (HDZip) hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of a portion of a nucleic acid encoding an NRT polypeptide or a homologue thereof; or comprising modulating expression in a plant of a portion of a nucleic acid encoding a YEP16 polypeptide or homologue thereof; or comprising modulating expression in a plant of a portion of a nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof.

Another nucleic acid variant is a nucleic acid capable of hybridising under reduced stringency conditions, preferably under stringent conditions, with a nucleic acid encoding a class I HDZip hox5 nucleic acid/gene or homologue thereof; or with a nucleic acid encoding an NRT polypeptide or homologue thereof; or with a nucleic acid encoding a YEP16 polypeptide or homologue thereof; or with a nucleic acid encoding a Group I shaggy-like kinase or homologue thereof.

The term "hybridisation" as defined herein is a process wherein substantially homologous complementary nucleotide sequences anneal to each other. The hybridisation process can occur entirely in solution, i.e. both complementary nucleic acids are in solution. The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitro-cellulose or nylon membrane or immobilised by e.g. photolithography to, for example, a siliceous glass support (the latter known as nucleic acid arrays or microarrays or as nucleic acid chips). In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration, ionic strength and hybridisation buffer composition.

"Stringent hybridisation conditions" and "stringent hybridisation wash conditions" in the context of nucleic acid hybridisation experiments such as Southern and Northern hybridisations are sequence dependent and are different under different environmental parameters. The skilled artisan is aware of various parameters which may be altered during hybridisation and washing and which will either maintain or change the stringency conditions.

The T_m is the temperature under defined ionic strength and pH, at which 50% of the target sequence hybridises to a perfectly matched probe. The T_m is dependent upon the solution conditions and the base composition and length of the probe. For example, longer sequences hybridise specifically at higher temperatures. The maximum rate of hybridisation is obtained from about 16°C up to 32°C below T_m . The presence of monovalent cations in the hybridisation solution reduce the electrostatic repulsion between the two nucleic acid strands thereby promoting hybrid formation; this effect is visible for sodium concentrations of up to 0.4M. Formamide reduces the melting temperature of DNA-DNA and DNA-RNA duplexes with 0.6 to 0.7°C for each percent formamide, and addition of 50% formamide allows hybridisation to be performed at 30 to 45°C, though the rate of hybridisation will be lowered. Base pair mismatches reduce the hybridisation rate and the thermal stability of the duplexes. On average and for large probes, the T_m decreases about 1°C per % base mismatch. The T_m may be calculated using the following equations, depending on the types of hybrids:

1. DNA-DNA hybrids (Meinkoth and Wahl, Anal. Biochem., 138: 267-284, 1984):

$$T_m = 81.5^\circ\text{C} + 16.6 \times \log[\text{Na}^+]^a + 0.41 \times \%[\text{G/C}]^b - 500 \times [\text{L}]^{-1} - 0.61 \times \% \text{ formamide}$$

2. DNA-RNA or RNA-RNA hybrids:

$$T_m = 79.8 + 18.5 (\log[\text{Na}^+]^a) + 0.58 (\% \text{G/C})^b + 11.8 (\% \text{G/C})^b - 820/\text{L}^c$$

3. oligo-DNA or oligo-RNA^d hybrids:

$$\text{For } <20 \text{ nucleotides: } T_m = 2 (I_n)$$

$$\text{For } 20-35 \text{ nucleotides: } T_m = 22 + 1.46 (I_n)$$

^a or for other monovalent cation, but only accurate in the 0.01-0.4 M range.

^b only accurate for %GC in the 30% to 75% range.

^c L = length of duplex in base pairs.

^d Oligo, oligonucleotide; I_n , effective length of primer = $2 \chi(\text{no. of G/C}) + (\text{no. of A/T})$.

[Note; for each 1% formamide, the T_m is reduced by about 0.6 to 0.7°C, while the presence of 6 M urea reduces the T_m by about 30°C]

Specificity of hybridisation is typically the function of post-hybridisation washes. To remove background resulting from non-specific hybridisation, samples are washed with dilute salt solutions. Critical factors of such washes include the ionic strength and temperature of the final wash solution: the lower the salt concentration and the higher the wash temperature, the higher the stringency of the wash. Wash conditions are typically performed at or below hybridisation stringency. Generally, suitable stringent conditions for nucleic acid hybridisation assays or gene amplification detection procedures are as set forth above. Conditions of greater or less stringency may also be selected. Generally, low stringency conditions are selected to be about 50°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. Medium stringency conditions are when the temperature is 20°C below T_m , and high stringency conditions are when the temperature is 10°C below T_m . For example, stringent conditions are those that are at least as stringent as, for example, conditions A-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R. Non-specific binding may be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein containing solutions, additions of heterologous RNA, DNA, and SDS to the hybridisation buffer, and treatment with RNase. Examples of hybridisation and wash conditions are listed in Table 2 below.

Table 2: Examples of hybridisation and wash conditions

Stringency Condition	Polynucleotide Hybrid ⁺	Hybrid Length (bp) [*]	Hybridisation Temperature and Buffer ⁺	Wash Temperature and Buffer [†]
A	DNA :DNA	> or equal to 50	65°C 1xSSC; or 42°C, 1xSSC and 50% formamide	65°C; 0.3xSSC
B	DNA :DNA	<50	Tb* ; 1xSSC	Tb* ; 1xSSC
C	DNA :RNA	> or equal to 50	67°C 1xSSC; or 45°C, 1xSSC and 50% formamide	67°C; 0.3xSSC
D	DNA :RNA	<50	Td* ; 1xSSC	Td* ; 1xSSC
E	RNA :RNA	> or equal to 50	70°C 1xSSC; or 50°C, 1xSSC and 50% formamide	70°C ; 0.3xSSC
F	RNA :RNA	<50	Tf* ; 1xSSC	Tf* ; 1xSSC
G	DNA :DNA	> or equal to 50	65°C 4xSSC; or 45°C, 4xSSC and 50% formamide	65°C; 1xSSC

H	DNA :DNA	<50	Th* ; 4 xSSC	Th*, 4xS SC
I	DNA :RNA	> or equal to 50	67°C 4xSSC; or 45°C, 4xSSC and 50% formamide	67°C ; 1xSSC
J	DNA :RNA	<50	T ₃ * ; 4 xSSC	T _J *, 4 xSSC
K	RNA :RNA	> or equal to 50	70°C 4xSSC; or 40°C, 6xSSC and 50% formamide	67°C ; 1xSSC
L	RNA :RNA	<50	Tl* ; 2 xSSC	Tl*, 2xS SC
M	DNA :DNA	> or equal to 50	50°C 4xSSC; or 40°C, 6xSSC and 50% formamide	50°C ; 2xSSC
N	DNA :DNA	<50	Tn* ; 6 xSSC	Tn*, 6xS SC
O	DNA :RNA	> or equal to 50	55°C 4xSSC; or 42°C, 6xSSC and 50% formamide	55°C ; 2xSSC
P	DNA :RNA	<50	Tp* ; 6 xSSC	Tp*, 6xS SC
Q	RNA :RNA	> or equal to 50	60°C 4xSSC; or 45°C, 6xSSC and 50% formamide	60°C ; 2xSSC
R	RNA :RNA	<50	Tr* ; 4 xSSC	Tr*, 4xS SC

* The "hybrid length" is the anticipated length for the hybridising nucleic acid. When nucleic acids of known sequence are hybridised, the hybrid length may be determined by aligning the sequences and identifying the conserved regions described herein.

+ SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) may be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridisation and wash buffers; washes are performed for 15 minutes after hybridisation is complete. The hybridisations and washes may additionally include 5 x Denhardt's reagent, 0.5-1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.5% sodium pyrophosphate, and up to 50% formamide.

* Tb-Tr: The hybridisation temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature T_m of the hybrids; the T_m is determined according to the above-mentioned equations.

[±] The present invention also encompasses the substitution of any one, or more DNA or RNA hybrid partners with either a PNA, or a modified nucleic acid.

For the purposes of defining the level of stringency, reference can be made to Sambrook *et al.* (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York or to Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989).

Where the sequence useful in the methods of the invention is a class I HDZip hox5, the hybridizing sequence encodes a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads. Preferably, the hybridising sequence is capable of hybridizing under reduced stringency conditions, preferably under stringent conditions, with one of the nucleic acids given in Table A or a portion thereof as defined herein. Most preferably the portion is a portion of a nucleic acid as represented by SEQ ID NO: 1.

Where the sequence useful in the methods of the invention is a nucleic acid encoding an NRT polypeptide or homologue thereof, the hybridising sequence is a nucleic acid/gene capable of hybridising under reduced stringency conditions, preferably under stringent conditions, with an NRT nucleic acid/gene encodes a polypeptide comprising an MFS_1 domain and a transmembrane domain located C-terminally of the MFS_1 domain, and preferably also one or more of the signature sequences defined above. Preferably, the hybridising sequence is one that is capable of hybridising to a nucleic acid given in Table I of Example 14 or to a portion of any of the nucleic acids given in Table I, a portion being as defined above. Most preferably the hybridising sequence is capable of hybridising to SEQ ID NO: 52.

Where the sequence useful in the methods of the invention is a nucleic acid encoding a YEP16 polypeptide or homologue thereof, the hybridising sequence is a nucleic acid sequence capable of hybridising under reduced stringency conditions, preferably under stringent conditions, with a nucleic acid sequence encoding a YEP16 polypeptide or a homologue thereof. Preferably, the hybridizing sequence is capable of hybridizing under reduced stringency conditions to a nucleic acid as represented by SEQ ID NO: 127 or SEQ ID NO: 129.

Where the nucleic acid useful in the methods of the invention is a nucleic acid encoding a Group I shaggy-like kinase, the hybridising sequence is a nucleic acid capable of hybridising under reduced stringency conditions, preferably under stringent conditions, with a Group I

shaggy-like kinase-encoding nucleic acid/gene as hereinbefore defined, which hybridising sequence encodes a polypeptide having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid. The hybridising sequence is at least 1,200 nucleotides in length. Preferably, the hybridising sequence is capable of hybridising to a nucleic acid as represented by any one of SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174 and SEQ ID NO: 176.

The invention therefore provides a method for improving plant growth characteristics comprising modulating expression in a plant of a nucleic acid capable of hybridising under reduced stringency, preferably under stringent conditions to a nucleic acid encoding a class I homeodomain leucine zip_{per} (HDZip) hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid capable of hybridising under reduced stringency, preferably under stringent conditions to a nucleic acid encoding an NRT polypeptide or a homologue thereof; or comprising modulating expression in a plant of a nucleic acid capable of hybridising under reduced stringency, preferably under stringent conditions to a nucleic acid encoding a YEP16 polypeptide or homologue thereof; or comprising modulating expression in a plant of a nucleic acid capable of hybridising under reduced stringency, preferably under stringent conditions to a nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof.

The nucleic acids or variant thereof may be derived from any natural or artificial source. The nucleic acid/gene or variant thereof may be isolated from a microbial source, such as yeast or fungi, or from a plant, algae or animal (including human) source. This nucleic acid may be modified from its native form in composition and/or genomic environment through deliberate human manipulation. The nucleic acid is preferably of plant origin, whether from the same plant species (for example to the one in which it is to be introduced) or whether from a different plant species. The nucleic acid may be isolated from a monocotyledonous species, preferably from the family Poaceae, further preferably from *Oryza* genus, most preferably from *Oryza sativa*. The nucleic acid may be isolated from a dicotyledonous species, preferably from the family Brassicaceae, further preferably from *Arabidopsis thaliana*.

The expression of a nucleic acid may be modulated by introducing a genetic modification (preferably in the locus of the gene in question). The locus of a gene as defined herein is

taken to mean a genomic region, which includes the gene of interest and 10 kb up- or downstream of the coding region.

The genetic modification may be introduced, for example, by any one (or more) of the following methods: T-DNA activation, TILLING, site-directed mutagenesis, directed evolution and homologous recombination or by introducing and expressing in a plant a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or by introducing and expressing in a plant a nucleic acid encoding an NRT or a homologue thereof; or by introducing and expressing in a plant a nucleic acid encoding a YEP16 or homologue thereof; or by introducing and expressing in a plant a nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof. Following introduction of the genetic modification, there follows a step of selecting for modulated expression of the nucleic acid, which modulation in expression gives plants having improved growth characteristics, particularly increased yield.

T-DNA activation tagging (Hayashi *et al.* Science (1992) 1350-1353) involves insertion of T-DNA, usually containing a promoter (may also be a translation enhancer or an intron), in the genomic region of the gene of interest or 10 kb up- or downstream of the coding region of a gene in a configuration such that the promoter directs expression of the targeted gene. Typically, regulation of expression of the targeted gene by its natural promoter is disrupted and the gene falls under the control of the newly introduced promoter. The promoter is typically embedded in a T-DNA. This T-DNA is randomly inserted into the plant genome, for example, through *Agrobacterium* infection and leads to overexpression of genes near the inserted T-DNA. The resulting transgenic plants show dominant phenotypes due to overexpression of genes close to the introduced promoter. The promoter to be introduced may be any promoter capable of directing expression of a gene in the desired organism, in this case a plant. For example, constitutive, tissue-preferred, cell type-preferred and inducible promoters are all suitable for use in T-DNA activation.

A genetic modification may also be introduced in the locus of the gene in question using the technique of TILLING (Targeted Induced Local Lesions in Genomes). This is a mutagenesis technology useful to generate and/or identify and isolate mutagenised variants. TILLING also allows selection of plants carrying such mutant variants. These mutant variants may even exhibit higher activity than that exhibited by the gene in its natural form. TILLING combines high-density mutagenesis with high-throughput screening methods. The steps typically followed in TILLING are: (a) EMS mutagenesis (Redei GP and Koncz C (1992) *In Methods in Arabidopsis Research*, Koncz C, Chua NH, Schell J, eds. Singapore, World Scientific Publishing Co, pp. 16-82; Feldmann *et al.*, (1994) *In Meyerowitz EM, Somerville CR, eds,*

Arabidopsis. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp 137-172; Lightner J and Caspar T (1998) In J Martinez-Zapater, J Salinas, eds, *Methods on Molecular Biology*, Vol. 82. Humana Press, Totowa, NJ, pp 91-104); (b) DNA preparation and pooling of individuals; (c) PCR amplification of a region of interest; (d) denaturation and annealing to allow formation of heteroduplexes; (e) DHPLC, where the presence of a heteroduplex in a pool is detected as an extra peak in the chromatogram; (f) identification of the mutant individual; and (g) sequencing of the mutant PCR product. Methods for TILLING are well known in the art (McCallum *et al.*, (2000) *Nat Biotechnol* 18: 455-457; reviewed by Stemple (2004) *Nat Rev Genet* 5(2): 145-50).

Site-directed mutagenesis may be used to generate variant nucleic acids. Several methods are available to achieve site-directed mutagenesis, the most common being PCR based methods (Current Protocols in Molecular Biology, Wiley Eds <http://www.4ulr.com/products/currentprotocols/index.html>).

Directed evolution or gene shuffling may also be used to generate nucleic acid variants. This consists of iterations of DNA shuffling followed by appropriate screening and/or selection to generate variants having a modified biological activity (Castle *et al.*, (2004) *Science* 304(5674): 1151-4; US patents 5,811,238 and 6,395,547).

T-DNA activation, TILLING, site-directed mutagenesis and directed evolution are examples of technologies that enable the generation of novel alleles and variants.

Homologous recombination allows introduction in a genome of a selected nucleic acid at a defined selected position. Homologous recombination is a standard technology used routinely in biological sciences for lower organisms such as yeast or the moss *Physcomitrella*. Methods for performing homologous recombination in plants have been described not only for model plants (Offringa *et al.* (1990) *EMBO J* 9(10): 3077-84) but also for crop plants, for example rice (Terada *et al.* (2002) *Nat Biotech* 20(10): 1030-4; Iida and Terada (2004) *Curr Opin Biotech* 15(2): 132-8). The nucleic acid to be targeted need not be targeted to the locus of the gene in question, but may be introduced in, for example, regions of high expression. The nucleic acid to be targeted may be an improved allele used to replace the endogenous gene or may be introduced in addition to the endogenous gene.

A preferred method for introducing a genetic modification is to introduce and express in a plant a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or to introduce and express in a plant a nucleic acid encoding an NRT or a homologue thereof; or to

introduce and express in a plant a nucleic acid encoding a YEP16 or homologue thereof; or to introduce and express in a plant a nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof. The nucleic acid to be introduced into a plant may be a full-length nucleic acid or may be a portion or a hybridising sequence as hereinbefore defined.

Where the sequence useful in the methods of the invention is a YEP16 polypeptide or homologue thereof, targeting to a plastid is preferred; methods for such targeting of proteins to plastids are well known in the art, as is the use of transit peptides for such targeting. Table 3 below shows examples of transit peptides suitable for targeting any YEP16 polypeptide or homologue thereof to a plastid, preferably to a chloroplast. Preferred is the use of the transit peptide native to the YEP16 polypeptide sequence of SEQ ID NO: 128, which native transit peptide is shown in SEQ ID NO: 131. SEQ ID NO: 130 represents the YEP16 polypeptide together with its native transit peptide for targeting to the chloroplast (SEQ ID NO: 129 represents the nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 130). Most preferred is the use of the native transit peptide as shown in SEQ ID NO: 131 to target a YEP16 polypeptide as represented by SEQ ID NO: 128, although any transit peptide may be used with any YEP16 polypeptide or homologue thereof.

Table 3: Examples of transit peptide sequences useful in targeting amino acids to plastids

NCBI Accession Number/SEQ ID NO	Source Organism	Protein Function	Transit Peptide Sequence
SEQ ID NO: 131			MDTLSASVSSLNLPSPPPPQPPLRSI SSRFKSTVNATTSASSTNLSKPTSSSP SSS
SEQ ID NO: 132 - P07839	<i>Chlamydomonas</i>	Ferredoxin	MAMAMRSTFAARVGAKPAVRGARPA SRMSCMA
SEQ ID NO: 133 - AR23425	<i>Chlamydomonas</i>	Rubisco activase	MQVTMKSSAVSGQRVGGARVATRSV RRAQLQV
SEQ ID NO: 134 - AA56932	<i>Arabidopsis thaliana</i>	asp Amino transferase	MASLMLSLGSTSLLPREINKDKLKLGT SASNPFLLKAKSFSRVTMTVAVKPSR
SEQ ID NO: 135- CAA31991	<i>Arabidopsis thaliana</i>	Acyl carrier protein1	MATQFSASVSLQTSCLATTRISFQKPA LISNHGKTNLSFNLRRSIPSRRLSVSC
SEQ ID NO: 136- CAB63798	<i>Arabidopsis thaliana</i>	Acyl carrier protein2	MASIAASASISLQARPRQLAIAASQVK SFSNGRRSSLSFNLRLPTRLTVSCA AKPETVDKVCVVVRKQL

SEQ ID NO: 137- CAB63799	<i>Arabidopsis thaliana</i>	Acyl carrier protein3	MASIATSASTSLQARPRQLVIGAKQVK SFSYGSRSNLSFNLRQLPTRLTVYCA AKPETVDKVCVVVRKQLSLKE
SEQ ID NO: 138-NP_199191	<i>Arabidopsis thaliana</i>	ATP sulfurylase	MASSAAAIVSGSPFRSSPLIHNHHASR YAPGSISVVSLPRQVSRRLSVKS
SEQ ID NO: 139- CAA81736	<i>Brassica napus</i>	RuBisCO subunit binding-protein alpha subunit	MATANALSSPSVLCSSRQGKLSSGGS QQKGQRVSYRKANRRFSLRANVKEIA FDQSSRAALQAGIDKLADAVGLTLGP RGRNVVLDEFGSPKVVNDGVTIA
SEQ ID NO: 140- AAA87039	<i>Hordeum vulgare</i>	ribulose-1,5- bisphosphate carboxylase small subunit	MAPTVMASSATSVAPFQGLKSTAGLP VSRRSNASSASVSNGGRIRCMQVWPI EGIKKFETLSYLPPLSTEALLKQVDYLI RSKWVPCLEFSKVGFIFREH
SEQ ID NO: 141- AAC82334	<i>Medicago truncatula</i>	Gamma- glutamylcysteine synthetase	MTTIFRLASSSSPSLRHDATPHNFHIR KTSISNTFSFSSKNSLSFKRILTSGGS RRFIVAASPPTEDAVVATEPLTKQDLI DYLASGCKTKDKWRIGTEH
SEQ ID NO: 142- AAB81104	<i>Spinacia oleracea</i>	Sedoheptulose-1,7- bisphosphatase	METSMACCSRSIVLPRVSPQHSSALV PSSINLKSLKSSSLFGESLRMTTKSSV RVNKAKNSSLVTKCELGDSLEEFLAK ATTDKGLIRLMMCMGEALRTI

"Homologues" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived. To produce such homologues, amino acids of the protein may be replaced by other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α -helical structures or β -sheet structures). Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company and Table 4 below). The homologues useful in the methods according to the invention are preferably polypeptides having in increasing order of preference at least 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% or more sequence identity or similarity (functional identity) to the sequences mentioned herein as being useful in the methods of the invention, for example the sequences given in Table A and I herein

Also encompassed by the term "homologues" are two special forms of homology, which include orthologous sequences and paralogous sequences, which encompass evolutionary concepts used to describe ancestral relationships of genes. 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 speciation.

Orthologues in, for example, monocot plant species may easily be found by performing a so-called reciprocal blast search. Taking the example of finding an orthologue or pralogue of a class I HDZip hox5 nucleic acid or class I HDZip hox5 polypeptide, this may be done by a first blast involving blasting the sequence in question (for example, SEQ ID NO: 1 or SEQ ID NO: 2) against any sequence database, such as the publicly available NCBI database which may be found at: <http://www.ncbi.nlm.nih.gov>. BLASTN or TBLASTX may be used when starting from nucleotide sequence, or BLASTP or TBLASTN when starting from the protein, with standard default values. 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 in question is derived. The results of the first and second BLASTs are then compared. When the results of the second BLAST give as hits with the highest similarity a class I HDZip hox5 nucleic acid or class I HDZip hox5 polypeptide, then a paralogue has been found, if it originates from the same organism as for the sequence used in the first BLAST. In case it originates from an organism other than that of the sequence used in the first BLAST, then an orthologue has been found. In the case of large families, ClustalW may be used, followed by a neighbour joining tree, to help visualize the clustering.

The same procedure may also be used to find orthologues and paralogues of nucleic acids encoding an NRT and NRT polypeptides; and for finding orthologues and paralogues of YEP16-encoding nucleic acids and YEP16 polypeptides; and for finding orthologues and paralogues of nucleic acids encoding Group I shaggy-like kinases and Group I shaggy-like kinase polypeptides.

A homologue may be in the form of a "substitutional variant" of a protein, i.e. where at least one residue in an amino acid sequence has been removed and a different residue inserted in its place. Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide; insertions will usually be of the order of about 1 to 10 amino acid residues. Preferably, amino acid substitutions comprise conservative amino acid substitutions. Conservative substitution tables are readily available in the art. The table below gives examples of conserved amino acid substitutions.

Table 4: Examples of conserved amino acid substitutions

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

A homologue may also be in the form of an "insertional variant" of a protein, i.e. where one or more amino acid residues are introduced into a predetermined site in a protein. Insertions may comprise N-terminal and/or C-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than N- or C-terminal fusions, of the order of about 1 to 10 residues. Examples of N- or C-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, (histidine)-6-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag-100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

Homologues in the form of "deletion variants" of a protein are characterised by the removal of one or more amino acids from a protein.

Amino acid variants of a protein may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulations. Methods for the manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art. For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen *in vitro* mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

The class I HDZip hox5 polypeptide or homologue thereof; the nucleic acid encoding a nitrate transporter protein (NRT) or a homologue thereof; the nucleic acid encoding a YEP16 polypeptide; and the nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof may be a derivative. "Derivatives" include peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise substitutions, deletions or additions of naturally and non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the protein. The Derivatives may comprise naturally occurring altered, glycosylated, acylated, prenylated or non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents compared to the amino acid sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence, such as a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein.

The class I HDZip hox5 polypeptide or homologue thereof may be encoded by an alternative splice variant; the NRT polypeptide or homologue thereof may be encoded by an alternative splice variant; the YEP16 polypeptide or homologue thereof may be encoded by an alternative splice variant; and the Group I shaggy-like kinase or a homologue thereof may be encoded by an alternative splice variant.

Where the sequence useful in the methods of the invention is a nucleic acid encoding a class I HDZip hox5 polypeptide or homologue thereof, the splice variant encodes a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads. Additionally, the class I HDZip hox5 polypeptide or a homologue thereof may comprise one or both of the following: (a) a Trp tail; and (b) the RPFF amino acid motif, where R is Arg, P Pro and F Phe. Within this motif, are allowed one or more conservative change(s) at any position, and/or one or two non-conservative change(s) at any position. The motif of (b) precedes the acidic box, when examining the protein from N-terminal to C-terminal. Further preferred are splice variants of nucleic acid sequences given in Table A. Most preferred is a splice variant of a nucleic acid sequence as represented by SEQ ID NCM .

Where the sequence useful in the methods of the invention is an NRT polypeptide or homologue thereof or nucleic acid encoding the same, the splice variant encodes a polypeptide comprising the MFS_1 domain and a transmembrane domain located C-terminally of the MFS_1 domain, and preferably also one or more of the conserved signature sequences

of SEQ ID NO: 57 to SEQ ID NO: 64 as defined above. Further preferred are splice variants of any of the nucleic acids given in Table B. Most preferred is a splice variant of the nucleic acid of SEQ ID NO: 52.

Where the sequence useful in the methods of the invention is a YEP16-encoding nucleic acid, the splice variant is of a nucleic acid sequence represented by SEQ ID NO: 127 or SEQ ID NO: 129.

Where the sequence useful in the methods of the invention is a nucleic acid encoding a Group I shaggy-like kinase or homologue thereof, the alternative splice variants are splice variants of the nucleic acid represented by any one of SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174 and SEQ ID NO: 176. Further preferred are splice variants encoding a polypeptide having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid.

The present invention therefore provides a method for improving plant growth characteristics comprising modulating expression in a plant of an alternative splice variant of a nucleic acid encoding a class I liomeodomain leucine zip_{per} (HDZip) hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of an alternative splice variant of a nucleic acid encoding an NRT polypeptide or a homologue thereof; or comprising modulating expression in a plant of an alternative splice variant of a nucleic acid encoding a YEP16 polypeptide or homologue thereof; or comprising modulating expression in a plant of an alternative splice variant of a nucleic acid encoding an Group I glycogen synthase kinase (Group I shaggy-like kinase) or a homologue thereof.

The term "alternative splice variant" as used herein encompasses variants of a nucleic acid sequence in which selected introns and/or exons have been excised, replaced or added, or in which introns have been shortened or lengthened. Such variants will be ones in which the biological activity of the protein is retained, which may be achieved by selectively retaining functional segments of the protein. Such splice variants may be found in nature or may be manmade. Methods for making such splice variants are well known in the art.

The homologue may also be encoded by an allelic variant of a nucleic acid encoding a class I HDZip hox5 polypeptide or a homologue thereof; or encoded by an allelic variant of a nucleic

acid encoding a nitrate transporter protein (NRT) or a homologue thereof; or encoded by an allelic variant of a nucleic acid encoding a YEP16 polypeptide; or encoded by an allelic variant of a nucleic acid encoding a Group I shaggy-like kinase or a homologue thereof.

Where the sequence useful in the methods of the invention is a nucleic acid encoding a class I HDZip hox5 polypeptide or homologue thereof, the allelic variant encodes a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads. Additionally, the class I HDZip hox5 polypeptide or a homologue thereof may comprise one or both of the following: (a) a Trp tail; and (b) the RPFF amino acid motif, where R is Arg, P Pro and F Phe. Within this motif, are allowed one or more conservative change(s) at any position, and/or one or two non-conservative change(s) at any position. The motif of (b) precedes the acidic box, when examining the protein from N-terminal to C-terminal. Further preferred are allelic variants of nucleic acid sequences given in Table A. Most preferred is an allelic variant of a nucleic acid sequence as represented by SEQ ID NO: 1.

Where the sequence useful in the methods of the invention is an NRT polypeptide or homologue thereof or nucleic acid encoding the same, the allelic variant encodes a polypeptide comprising the MFS_1 domain and a transmembrane domain located C-terminally of the MFS_1 domain, and preferably also one or more of the conserved signature sequences of SEQ ID NO: 57 to SEQ ID NO: 64 as defined above. Further preferred are allelic variants of any of the nucleic acids given in Table 1. Most preferred is an allelic variant of the nucleic acid of SEQ ID NO: 52.

Where the sequence useful in the methods of the invention is a YEP16-encoding nucleic acid, the allelic variant is of a nucleic acid sequence represented by SEQ ID NO: 127 or SEQ ID NO: 129.

Where the sequence useful in the methods of the invention is a nucleic acid encoding a Group I shaggy-like kinase or homologue thereof, the allelic variants are allelic variants of the nucleic acid represented by any one of SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174 and SEQ ID NO: 176. Further preferred are allelic variants encoding a polypeptide having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid.

The present invention therefore provides a method for improving plant growth characteristics comprising modulating expression in a plant of an allelic variant of a nucleic acid encoding a class I liomeodomain leucine zip_per (HDZip) hox5 polypeptide or a homologue thereof; or comprising modulating expression in a plant of an allelic variant of a nucleic acid encoding an NRT polypeptide or a homologue thereof; or comprising modulating expression in a plant of an allelic variant of a nucleic acid encoding a YEP16 polypeptide or homologue thereof; or comprising modulating expression in a plant of an allelic variant of a nucleic acid encoding an Group I glycogen synthase kinase (Group I shaggy-like kinase) or a homologue thereof.

Allelic variants exist in nature, and encompassed within the methods of the present invention is the use of these natural alleles. Allelic variants encompass Single Nucleotide Polymorphisms (SNPs), as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms.

According to the present invention, modulated expression of the nucleic acid or variant thereof is envisaged. Methods for modulating expression of genes or gene products are well documented in the art and include, for example, overexpression driven by appropriate promoters, the use of transcription enhancers or translation enhancers. Isolated nucleic acids which serve as promoter or enhancer elements may be introduced in an appropriate position (typically upstream) of a non-heterologous form of a polynucleotide so as to upregulate expression of the nucleic acid or variant thereof. For example, endogenous promoters may be altered *in vivo* by mutation, deletion, and/or substitution (see, Kmiec, U.S. Pat. No. 5,565,350; Zarling *et al.*, PCT/US93/03868), or isolated promoters may be introduced into a plant cell in the proper orientation and distance from a gene of the present invention so as to control the expression of the gene.

Methods for reducing the expression of genes or gene products are well documented in the art.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or from any other eukaryotic gene.

An intron sequence may also be added to the 5' untranslated region or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold (Buchman and Berg (1988) *Mol. Cell Biol.* 8:4395-4405; CalMs *et al.* (1987) *Genes Dev* 1:1183-1200). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of the maize introns Adh1 - S intron 1, 2, and 6, the Bronze-1 intron are known in the art. See generally, *The Maize Handbook*, Chapter 116, Freeling and Walbot, Eds., Springer, N.Y. (1994).

The invention also provides genetic constructs and vectors to facilitate introduction and/or expression of the nucleotide sequences useful in the methods according to the invention.

Therefore, there is provided a gene construct comprising:

- (i) A class I HDZip hox5 nucleic acid or variant thereof; or an NRT-encoding nucleic acid or variant thereof; or a YEP16-encoding nucleic acid or variant thereof; or a Group I shaggy-like kinase-encoding nucleic acid or variant thereof;
- (ii) One or more control sequences capable of driving expression of the nucleic acid sequence of (i); and optionally
- (iii) A transcription termination sequence.

Constructs useful in the methods according to the present invention may be constructed using recombinant DNA technology well known to persons skilled in the art. The gene constructs may be inserted into vectors, which may be commercially available, suitable for transforming into plants and suitable for expression of the gene of interest in the transformed cells. The invention therefore provides use of a gene construct as defined hereinabove in the methods of the invention.

Plants are transformed with a vector comprising the sequence of interest. The sequence of interest is operably linked to one or more control sequences (at least to a promoter). The terms "regulatory element", "control sequence" and "promoter" are all used interchangeably herein and are to be taken in a broad context to refer to regulatory nucleic acid sequences capable of effecting expression of the sequences to which they are ligated. Encompassed by the aforementioned terms are transcriptional regulatory sequences derived from a classical eukaryotic genomic gene (including the TATA box which is required for accurate transcription

initiation, with or without a CCAAT box sequence) and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or external stimuli, or in a tissue-specific manner. Also included within the term is a transcriptional regulatory sequence of a classical prokaryotic gene, in which case it may include a -35 box sequence and/or -10 box transcriptional regulatory sequences. The term "regulatory element" also encompasses a synthetic fusion molecule or derivative that confers, activates or enhances expression of a nucleic acid molecule in a cell, tissue or organ. The term "operably linked" as used herein refers to a functional linkage between the promoter sequence and the gene of interest, such that the promoter sequence is able to initiate transcription of the gene of interest.

Advantageously, any type of promoter may be used to drive expression of the nucleic acid sequence. The promoter may be an inducible promoter, i.e. having induced or increased transcription initiation in response to a developmental, chemical, environmental or physical stimulus. An example of an inducible promoter being a stress-inducible promoter, i.e. a promoter activated when a plant is exposed to various stress conditions. Additionally or alternatively, the promoter may be a tissue-preferred promoter, i.e. one that is capable of preferentially initiating transcription in certain tissues, such as the leaves, roots, seed tissue etc. Promoters able to initiate transcription in certain tissues only are referred to herein as "tissue-specific".

Preferably, the class I HDZip hox5 nucleic acid or variant thereof; the NRT-encoding nucleic acid or variant thereof; the Group I shaggy-like kinase-encoding nucleic acid or variant thereof is operably linked to a constitutive promoter. A constitutive promoter is transcriptionally active during most but not necessarily all phases of growth and development and is substantially ubiquitously expressed. The constitutive promoter is preferably a GOS2 promoter, more preferably the constitutive promoter is a rice GOS2 promoter, further preferably the constitutive promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 33 or SEQ ID NO: 178, most preferably the constitutive promoter is as represented by SEQ ID NO: 33 or SEQ ID NO: 178, . It should be clear that the applicability of the present invention is not restricted to the class I HDZip hox5 nucleic acid or variant thereof; the NRT-encoding nucleic acid or variant thereof; or Group I shaggy-like kinase-encoding nucleic acid or variant thereof when driven by a GOS2 promoter. Examples of other constitutive promoters which may also be used perform the methods of the invention are shown in Table 5 below.

Table 5: Examples of constitutive promoters

Gene Source	Reference
Actin	McElroy et al, Plant Cell, 2: 163-171, 1990
CAMV 35S	Odell et al, Nature, 313: 810-812, 1985
CaMV 19S	Nilsson et al., Physiol. Plant. 100:456-462, 1997
GOS2	de Pater et al, Plant J Nov;2(6):837-44, 1992, WO 2004/065596
Ubiquitin	Christensen et al, Plant Mol. Biol. 18: 675-689, 1992
Rice cyclophilin	Buchholz et al, Plant Mol Biol. 25(5): 837-43, 1994
Maize H3 histone	Lepetit et al, Mol. Gen. Genet. 231:276-285, 1992
Alfalfa H3 histone	Wu et al. Plant Mol. Biol. 11:641-649, 1988
Actin 2	An et al, Plant J. 10(1); 107-121, 1996
34S FMV	Sanger et al., Plant. Mol. Biol., 14, 1990: 433-443
Rubisco small subunit	US 4,962,028
OCS	Leisner (1988) Proc Natl Acad Sci USA 85(5): 2553
SAD1	Jain et al., Crop Science, 39 (6), 1999: 1696
SAD2	Jain et al., Crop Science, 39 (6), 1999: 1696
Nos	Shaw et al. (1984) Nucleic Acids Res. 12(20):7831-7846
V-ATPase	WO 01/14572
Super promoter	WO 95/14098
G-box proteins	WO 94/12015

Preferably, the nucleic acid sequence encoding a YEP1 6 polypeptide or homologue thereof is operably linked to a seed-specific promoter. A seed-specific promoter is one that is transcriptionally active predominantly in seed tissue. A seed-specific promoter may also have some residual activity in other parts. Preferably, the seed-specific promoter is an endosperm-specific and/or an aleurone-specific promoter meaning that the promoter is transcriptionally active predominantly in endosperm tissue and/or in the aleurone layers of a seed, although there may be some residual activity or leaky expression elsewhere. Preferably, the promoter is an oleosin promoter, such as from rice (SEQ ID NO: 143). It should be clear that the applicability of the present invention is not restricted to a YEP1 6-encoding nucleic acid represented by SEQ ID NO: 127 or SEQ ID NO: 129, nor is the applicability of the invention restricted to expression of a YEP1 6-encoding nucleic acid when driven by an oleosin promoter. Examples of other seed-specific promoters which may also be used to drive expression of a nucleic acid encoding a YEP1 6 polypeptide or homologue thereof are shown in Table 6 below.

Table 6: Examples of seed-specific promoters

Gene source	Expression pattern	Reference
seed-specific genes	seed	Simon, <i>et al.</i> , <i>Plant Mol. Biol.</i> 5: 191, 1985; Scofield, <i>et al.</i> , <i>J. Biol. Chem.</i> 262: 12202, 1987.; Baszczynski, <i>et al.</i> , <i>Plant Mol. Biol.</i> 14: 633, 1990.
Brazil Nut albumin	seed	Pearson, <i>et al.</i> , <i>Plant Mol. Biol.</i> 18: 235-245, 1992.
Legumin	seed	Ellis, <i>et al.</i> , <i>Plant Mol. Biol.</i> 10: 203-214, 1988.
Glutelin (rice)	seed	Takaiwa, <i>et al.</i> , <i>Mol. Gen. Genet.</i> 208: 15-22, 1986; Takaiwa, <i>et al.</i> , <i>FEBS Letts.</i> 221: 43-47, 1987.
Zein	seed	Matzke <i>et al</i> <i>Plant Mol Biol</i> , 14(3):323-32 1990
napA	seed	Stalberg, <i>et al</i> , <i>Planta</i> 199: 515-519, 1996.
wheat LMW and HMW glutenin-1	endosperm	<i>Mol Gen Genet</i> 216:81-90, 1989; <i>NAR</i> 17:461-2, 1989
wheat SPA	seed	Albani <i>et al</i> , <i>Plant Cell</i> , 9: 171-184, 1997
wheat α , β , γ -gliadins	endosperm	<i>EMBO</i> 3:1409-15, 1984
barley <i>ltr1</i> promoter	endosperm	
barley B1, C, D, hordein	endosperm	<i>Theor Appl Gen</i> 98:1253-62, 1999; <i>Plant J</i> 4:343-55, 1993; <i>Mol Gen Genet</i> 250:750-60, 1996
barley DOF	endosperm	Mena <i>et al</i> , <i>The Plant Journal</i> , 116(1): 53-62, 1998
<i>blz2</i>	endosperm	EP99106056.7
synthetic promoter	endosperm	Vicente-Carbajosa <i>et al.</i> , <i>Plant J.</i> 13: 629-640, 1998.
rice prolamin NRP33	endosperm	Wu <i>et al</i> , <i>Plant Cell Physiology</i> 39(8) 885-889, 1998
rice α -globulin Glb-1	endosperm	Wu <i>et al</i> , <i>Plant Cell Physiology</i>

		39(8) 885-889, 1998
rice OSH1	embryo	Sato <i>et al</i> , Proc. Natl. Acad. Sci. USA, 93: 8117-8122, 1996
rice α -globulin REB/OHP-1	endosperm	Nakase <i>et al</i> . Plant Mol. Biol. 33: 513-522, 1997
rice ADP-glucose PP	endosperm	Trans Res 6:157-68, 1997
maize ESR gene family	endosperm	Plant J 12:235-46, 1997
Sorgum α -kafirin	endosperm	PMB 32:1029-35, 1996
KNOX	embryo	Postma-Haarsma <i>et al</i> , Plant Mol. Biol. 39:257-71, 1999
rice oleosin	embryo and aleuron	Wu <i>et at</i> , J. Biochem., 123:386, 1998
sunflower oleosin	seed (embryo and dry seed)	Cummins, <i>et al.</i> , Plant Mol. Biol. 19: 873-876, 1992
putative rice 40S ribosomal protein	weak in endosperm	
rice alpha-globulin	strong in endosperm	
rice alanine aminotransferase	weak in endosperm	
trypsin inhibitor ITR1 (barley)	weak in endosperm	
rice WSI18	embryo + stress	
rice RAB21	embryo + stress	
rice oleosin 18kd	aleurone + embryo	

For the identification of functionally equivalent promoters, the promoter strength and/or expression pattern of a candidate promoter may be analysed for example by operably linking the promoter to a reporter gene and assay the expression level and pattern of the reporter gene in various tissues of the plant. Suitable well-known reporter genes include for example beta-glucuronidase or beta galactosidase. The promoter activity is assayed by measuring the enzymatic activity of the beta-glucuronidase or beta-galactosidase. The promoter strength and/or expression pattern may then be compared to that of a reference promoter (such as the one used in the methods of the present invention). Alternatively, promoter strength may be assayed by quantifying mRNA levels or by comparing mRNA levels of the nucleic acid used in the methods of the present invention, with mRNA levels of housekeeping genes such as 18S rRNA, using methods known in the art, such as Northern blotting with densitometric analysis of

autoradiograms, quantitative real-time PCR or RT-PCR (Heid et al., 1996 Genome Methods 6: 986-994). Generally by "weak promoter" is intended a promoter that drives expression of a coding sequence at a low level. By "low level" is intended at levels of about 1/10,000 transcripts to about 1/100,000 transcripts, to about 1/500,000 transcripts per cell. Conversely, a "strong promoter" drives expression of a coding sequence at high level, or at about 1/10 transcripts to about 1/100 transcripts to about 1/1,000 transcripts per cell.

Optionally, one or more terminator sequences may also be used in the construct introduced into a plant. The term "terminator" encompasses a control sequence which is a DNA sequence at the end of a transcriptional unit which signals 3' processing and polyadenylation of a primary transcript and termination of transcription. Additional regulatory elements may include transcriptional as well as translational enhancers. Those skilled in the art will be aware of terminator and enhancer sequences that may be suitable for use in performing the invention. Such sequences would be known or may readily be obtained by a person skilled in the art.

The genetic constructs of the invention may further include an origin of replication sequence that is required for maintenance and/or replication in a specific cell type. One example is when a genetic construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule). Preferred origins of replication include, but are not limited to, the f1-ori and colE1.

The genetic construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene that confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells that are transfected or transformed with a nucleic acid construct of the invention.

For the detection of the successful transfer of the nucleic acid sequences as used in the methods of the invention and/or selection of transgenic plants comprising these nucleic acids, it is advantageous to use marker genes (or reporter genes). Therefore, the genetic construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker", "selectable marker gene" or "reporter gene" includes any gene that confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells that are transfected or transformed with a nucleic acid construct of the invention. These marker genes enable the identification of a successful transfer of the nucleic acid molecules via a series of different principles. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance, that introduce a new metabolic trait or that allow visual

selection. Examples of selectable marker genes include genes conferring resistance to antibiotics (such as *nptII* that phosphorylates neomycin and kanamycin, or *hpt*, phosphorylating hygromycin, or genes conferring resistance to, for example, bleomycin, streptomycin, tetracyclin, chloramphenicol, ampicillin, gentamycin, geneticin (G418), spectinomycin or blasticidin), to herbicides (for example *bar* which provides resistance to Basta; *aroA* or *gox* providing resistance against glyphosate, or the genes conferring resistance to, for example, imidazolinone, phosphinothricin or sulfonylurea), or genes that provide a metabolic trait (such as *manA* that allows plants to use mannose as sole carbon source or xlose isomerase for the utilisation of xylose, or antinutritive markers such as the resistance to 2-deoxyglucose). Expression of visual marker genes results in the formation of colour (for example β -glucuronidase, GUS or β -galactosidase with its coloured substrates, for example X-Gal), luminescence (such as the luciferin/luciferase system) or fluorescence (Green Fluorescent Protein, GFP, and derivatives thereof). This list represents only a small number of possible markers. The skilled worker is familiar with such markers. Different markers are preferred, depending on the organism and the selection method.

It is known that upon stable or transient integration of nucleic acids into plant cells, only a minority of the cells takes up the foreign DNA and, if desired, integrates it into its genome, depending on the expression vector used and the transfection technique used. To identify and select these integrants, a gene coding for a selectable marker (such as the ones described above) is usually introduced into the host cells together with the gene of interest. These markers can for example be used in mutants in which these genes are not functional by, for example, deletion by conventional methods. Furthermore, nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector that comprises the sequence encoding the polypeptides of the invention or used in the methods of the invention, or else in a separate vector. Cells which have been stably transfected with the introduced nucleic acid can be identified for example by selection (for example, cells which have integrated the selectable marker survive whereas the other cells die).

Since the marker genes, particularly genes for resistance to antibiotics and herbicides, are no longer required or are undesired in the transgenic host cell once the nucleic acids have been introduced successfully, the process according to the invention for introducing the nucleic acids advantageously employs techniques which enable the removal or excision of these marker genes. One such a method is what is known as co-transformation. The co-transformation method employs two vectors simultaneously for the transformation, one vector bearing the nucleic acid according to the invention and a second bearing the marker gene(s). A large proportion of transformants receives or, in the case of plants, comprises (up to 40% or

more of the transformants), both vectors. In case of transformation with *Agrobacteria*, the transformants usually receive only a part of the vector, i.e. the sequence flanked by the T-DNA, which usually represents the expression cassette. The marker genes can subsequently be removed from the transformed plant by performing crosses. In another method, marker genes integrated into a transposon are used for the transformation together with desired nucleic acid (known as the Ac/Ds technology). The transformants can be crossed with a transposase source or the transformants are transformed with a nucleic acid construct conferring expression of a transposase, transiently or stable. In some cases (approx. 10%), the transposon jumps out of the genome of the host cell once transformation has taken place successfully and is lost. In a further number of cases, the transposon jumps to a different location. In these cases the marker gene must be eliminated by performing crosses. In microbiology, techniques were developed which make possible, or facilitate, the detection of such events. A further advantageous method relies on what is known as recombination systems; whose advantage is that elimination by crossing can be dispensed with. The best-known system of this type is what is known as the Cre/lox system. Cre1 is a recombinase that removes the sequences located between the loxP sequences. If the marker gene is integrated between the loxP sequences, it is removed once transformation has taken place successfully, by expression of the recombinase. Further recombination systems are the HIN/HIX, FLP/FRT and REP/STB system (Tribble et al., J. Biol. Chem., 275, 2000: 22255-22267; Velmurugan et al., J. Cell Biol., 149, 2000: 553-566). A site-specific integration into the plant genome of the nucleic acid sequences according to the invention is possible. Naturally, these methods can also be applied to microorganisms such as yeast, fungi or bacteria.

In a preferred embodiment, there is provided a gene construct comprising:

- (i) A class I HDZip hox5 nucleic acid or variant thereof; or an NRT-encoding nucleic acid or variant thereof; or a Group I shaggy-like kinase-encoding nucleic acid or variant thereof;
- (ii) A constitutive promoter capable of driving expression of the nucleic acid sequence of (i); and optionally
- (iii) A transcription termination sequence.

The constitutive promoter is preferably a GOS2 promoter, more preferably the constitutive promoter is the rice GOS2 promoter, further preferably the constitutive promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 33 or SEQ ID NO: 178, most preferably the constitutive promoter is as represented by SEQ ID NO: 33 or SEQ ID NO: 178. The invention further provides use of a construct as defined hereinabove in the methods of the invention.

In another preferred embodiment, there is provided a gene construct comprising:

- (i) A YEP1 6-encoding nucleic acid or variant thereof;
- (ii) A seed-specific promoter capable of driving expression of the nucleic acid sequence of (i); and optionally
- (iii) A transcription termination sequence.

The present invention also encompasses plants obtainable by the methods according to the present invention. The present invention therefore provides plants, plant parts (including plant cells) obtainable by the methods according to the present invention, which plants or parts (including cells) comprise a transgene class I HDZip hox5 nucleic acid or variant thereof; a transgene NRT-encoding nucleic acid or variant thereof; a transgene YEP1 6-encoding nucleic acid or variant thereof; or a transgene Group I shaggy-like kinase-encoding nucleic acid or variant thereof.

The invention also provides a method for the production of transgenic plants having improved growth characteristics, particularly increased yield, relative to corresponding wild type or other control plants, comprising introduction and expression in a plant of any of the nucleic acids described herein as being useful in the methods of the invention.

For the purposes of the invention, "transgenic", "transgene" or "recombinant" means with regard to, for example, a nucleic acid sequence, an expression cassette, gene construct or a vector comprising the nucleic acid sequence or an organism transformed with the nucleic acid sequences, expression cassettes or vectors according to the invention, all those constructions brought about by recombinant methods in which either

- a) the nucleic acid sequences encoding proteins useful in the methods of the invention, or
- b) genetic control sequence(s) which is operably linked with the nucleic acid sequence according to the invention, for example a promoter, or
- c) a) and b)

are not located in their natural genetic environment or have been modified by recombinant methods, it being possible for the modification to take the form of, for example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. The natural genetic environment is understood as meaning the natural genomic or chromosomal locus in the original plant or the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the nucleic acid sequence is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least on one side and has a sequence

length of at least 50 bp, preferably at least 500 bp, especially preferably at least 1000 bp, most preferably at least 5000 bp. A naturally occurring expression cassette - for example the naturally occurring combination of the natural promoter of the nucleic acid sequences with the corresponding nucleic acid sequence encoding a polypeptide useful in the methods of the present invention, as defined above - becomes a transgenic expression cassette when this expression cassette is modified by non-natural, synthetic ("artificial") methods such as, for example, mutagenic treatment. Suitable methods are described, for example, in US 5,565,350 or WO 00/1 581 5.

More specifically, the present invention provides a method for the production of transgenic plants having improved growth characteristics (particularly increased yield) which method comprises:

- (i) introducing and expressing in a plant, plant part or plant cell a class I HDZip hox5 nucleic acid or variant thereof; an NRT-encoding nucleic acid or variant thereof; a YEP16-encoding nucleic acid or variant thereof; a Group I shaggy-like kinase-encoding nucleic acid or variant thereof; and
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

The nucleic acid may be introduced directly into a plant cell or into the plant itself (including introduction into a tissue, organ or any other part of a plant). According to a preferred feature of the present invention, the nucleic acid is preferably introduced into a plant by transformation.

The term "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant regenerated therefrom. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

Transformation of plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. *et al.* (1982) *Nature* 296, 72-74; Negrutiu I *et al.* (1987) *Plant Mol Biol* 8: 363-373); electroporation of protoplasts (Shillito R.D. *et al.* (1985) *Bio/Technol* 3, 1099-1102); microinjection into plant material (Crossway A *et al.* (1986) *Mol. Gen Genet* 202: 179-185); DNA or RNA-coated particle bombardment (Klein TM *et al.* (1987) *Nature* 327: 70) infection with (non-integrative) viruses and the like. Transgenic rice plants are preferably produced via *Agrobacterium*-mediated transformation using any of the well known methods for rice transformation, such as described in any of the following: published European patent application EP 1198985 A1, Aldemita and Hodges (*Planta* 199: 612-617, 1996); Chan *et al.* (*Plant Mol Biol* 22 (3): 491-506, 1993), Hiei *et al.* (*Plant J* 6 (2): 271-282, 1994), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida *et al.* (*Nat. Biotechnol* 14(6): 745-50, 1996) or Frame *et al.* (*Plant Physiol* 129(1): 13-22, 2002), which disclosures are incorporated by reference herein as if fully set forth.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant.

Following DNA transfer and regeneration, putatively transformed plants may be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, or quantitative PCR, all techniques being well known to persons having ordinary skill in the art.

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.

The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells

transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

The present invention clearly extends to any plant cell or plant produced by any of the methods described herein, and to all plant parts and propagules thereof. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced by the parent in the methods according to the invention.

The invention also includes host cells comprising an isolated class I HDZip hox5 nucleic acid or variant thereof; host cells comprising an isolated NRT-encoding nucleic acid or variant thereof; host cells comprising an isolated YEP16-encoding nucleic acid or variant thereof; host cells comprising a Group I shaggy-like kinase-encoding nucleic acid or variant thereof. Preferred host cells are plant cells.

The invention also extends to harvestable parts of a plant such as, but not limited to seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs. The invention furthermore relates to products derived from a harvestable part of such a plant, such as dry pellets or powders, oil, fat and fatty acids, starch or proteins.

The present invention also encompasses use of class I HDZip hox5 nucleic acids and variants thereof and use of class I HDZip hox5 polypeptides and homologues thereof; use of NRT-encoding nucleic acids and variants thereof and use of NRT polypeptides and homologues thereof; use of YEP16-encoding nucleic acids and variants thereof and use of YEP16 polypeptides and homologues thereof; use of Group I shaggy-like kinase-encoding nucleic acids and variants thereof and use of Group I shaggy-like kinase polypeptides and homologues thereof. Such uses relate to improving any of the plant growth characteristics as defined hereinabove.

Class I HDZip hox5 nucleic acids or variants thereof, or class I HDZip hox5 polypeptides or homologues thereof; NRT-encoding nucleic acids and variants thereof, or NRT polypeptides and homologues thereof; YEP16-encoding nucleic acids and variants thereof or YEP16 polypeptides and homologues thereof; Group I shaggy-like kinase-encoding nucleic acids and variants thereof, or Group I shaggy-like kinase polypeptides and homologues thereof may find use in breeding programmes in which a DNA marker is identified which may be genetically linked to one of the aforementioned nucleic acids or variants. The nucleic acids or variants, or

polypeptides or homologues thereof may be used to define a molecular marker. This DNA or protein marker may then be used in breeding programmes to select plants having improved growth characteristics (such as increased yield). The nucleic acids or variants are as defined hereinabove.

Allelic variants of a class I HDZip hox5 nucleic acid/gene; an NRT-encoding nucleic acid/gene; a YEP16-encoding nucleic acid/ gene; a Group I shaggy-like kinase-encoding nucleic acid/gene may also find use in marker-assisted breeding programmes. Such breeding programmes sometimes require introduction of allelic variation by mutagenic treatment of the plants, using for example EMS mutagenesis; alternatively, the programme may start with a collection of allelic variants of so called "natural" origin caused unintentionally. Identification of allelic variants then takes place, for example, by PCR. This is followed by a step for selection of superior allelic variants of the sequence in question and which give improved growth characteristics, such as increased yield. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question, for example, different allelic variants of any of the nucleic acids/genes described herein as being useful in the methods of the invention. Growth performance may be monitored in a greenhouse or in the field. Further optional steps include crossing plants in which the superior allelic variant was identified with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

The aforementioned nucleic acid and variants may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. Such use of the nucleic acids or variants requires only a nucleic acid sequence of at least 15 nucleotides in length. The nucleic acids or variants may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Sambrook J, Fritsch EF and Maniatis T (1989) Molecular Cloning, A Laboratory Manual) of restriction-digested plant genomic DNA may be probed with the nucleic acids or variants. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander *et al.* (1987) Genomics 1: 174-181) in order to construct a genetic map. In addition, the nucleic acids may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the nucleic acid or variant in the genetic map previously obtained using this population (Botstein *et al.* (1980) Am. J. Hum. Genet. 32:314-331).

The production and use of plant gene-derived probes for use in genetic mapping is described in Bematzky and Tanksley (1986) *Plant Mol. Biol. Reporter* 4: 37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

The nucleic acid probes may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel *et al. In: Non-mammalian Genomic Analysis: A Practical Guide*, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, the nucleic acid probes may be used in direct fluorescence *in situ* hybridisation (FISH) mapping (Trask (1991) *Trends Genet.* 7:149-154). Although current methods of FISH mapping favor use of large clones (several kb to several hundred kb; see Laan *et al.* (1995) *Genome Res.* 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

A variety of nucleic acid amplification-based methods for genetic and physical mapping may be carried out using the nucleic acids. Examples include allele-specific amplification (Kazazian (1989) *J. Lab. Clin. Med* 11:95-96), polymorphism of PCR-amplified fragments (CAPS; Sheffield *et al.* (1993) *Genomics* 16:325-332), allele-specific ligation (Landegren *et al.* (1988) *Science* 241:1077-1080), nucleotide extension reactions (Sokolov (1990) *Nucleic Acid Res.* 18:3671), Radiation Hybrid Mapping (Walter *et al.* (1997) *Nat. Genet.* 7:22-28) and Happy Mapping (Dear and Cook (1989) *Nucleic Acid Res.* 17:6795-6807). For these methods, the sequence of a nucleic acid is used to design and produce primer pairs for use in the amplification reaction or in primer extension reactions. The design of such primers is well known to those skilled in the art. In methods employing PCR-based genetic mapping, it may be necessary to identify DNA sequence differences between the parents of the mapping cross in the region corresponding to the instant nucleic acid sequence. This, however, is generally not necessary for mapping methods.

The methods according to the present invention result in plants having improved growth characteristics, as described hereinbefore. These improved growth characteristics may also be combined with other economically advantageous traits, such as further yield-enhancing traits, tolerance to other abiotic and biotic stresses, traits modifying various architectural features and/or biochemical and/or physiological features.

Description of figures

The present invention will now be described with reference to the following figures in which:

Fig. 1 shows a multiple alignment of class I HDZip homeodomains from different plant sources, using VNTI AlignX multiple alignment program, based on a modified ClustalW algorithm (InforMax, Bethesda, MD, <http://www.informaxinc.com>), with default settings for gap opening penalty of 10 and a gap extension of 0.05). The homeodomain invariant amino acids L₁₆, W₄₈, F₄₉, N₅₁ and R₅₃ are boxed vertically. HDZip Class I preferred amino acids A₄₆ and W₅₆ are equally boxed vertically. The three helixes necessary for DNA binding are marked as black boxes above the alignment. The six heptads are separated by a vertical line. The seven positions within each heptad are named a, b, c, d, e, f and g. The Leu occupies the d position within each heptad, and is boxed vertically.

Fig. 2 shows a multiple alignment of several plant class I HDZip hox5 polypeptides, using VNTI AlignX multiple alignment program, based on a modified ClustalW algorithm (InforMax, Bethesda, MD, <http://www.informaxinc.com>), with default settings for gap opening penalty of 10 and a gap extension of 0.05). The three main characterized domains, from N-terminal to C-terminal, are heavily boxed and identified as the acidic box, the class I homeodomain and the six heptad-leucine zipper. Additionally, the Trp tail and the RPFF amino acid motif are lightly boxed.

Fig. 3 shows a binary vector for expression in *Oryza sativa* of an *Oryza sativa* class I HDZip hox5 under the control of a GOS2 promoter.

Fig. 4 details examples of class I homeodomain leucine zipper (HDZip) hox5 sequences useful in performing the methods according to the present invention. Several sequences result from public EST assemblies (see Table A), with lesser quality sequencing. As a consequence, a few nucleic acid substitutions may be expected. The start (ATG) and stop codons delimit the nucleic acid sequences.

Fig. 5 shows the typical domain structure of an NRT protein useful in the methods of the present invention, here exemplified with SEQ ID NO: 53. The protein of SEQ ID NO: 53 comprises an MFS₁ domain starting at S69 and ending with F432, indicated in bold. C-terminally of this MFS₁ domain, a putative transmembrane domain (T441 to P463, underlined) is present.

Fig. 6 (a) shows a phylogenetic tree, in which SEQ ID NO: 126 represents the rice NRT1 protein sequence, comprising a PTR2 domain, and (b) a multiple alignment of the of the sequences listed in Table I of Example 14. The asterisks in the multiple alignment indicate amino acids that are identical among the aligned sequences, the semicolons indicate conservative substitutions and the dots represent less conserved substitutions.

Fig. 7 shows the binary vector for increased expression in *Oryza sativa* of an rice NRT protein-encoding nucleic acid under the control of a GOS2 promoter.

Fig. 8 details examples of NRT sequences useful (with the exception of SEQ ID NO: 125 and SEQ ID NO: 126) in performing the methods according to the present invention. The sequences SEQ ID NO: 123 and 124 are probably not full length sequences.

Fig. 9 shows a binary vector for expression in *Oryza sativa* of an *Arabidopsis thaliana* YEP16-encoding nucleic acid under the control of an oleosin promoter.

Fig. 10 shows YEP16 sequences useful in the methods of the invention.

Fig. 11 taken from Planta (2003) 218: 1-14 (Wang *et al.*), shows plant response to abiotic stress. Primary stresses, such as drought, salinity, cold, heat and chemical pollution are often interconnected, and cause cellular damage and secondary stresses, such as osmotic and oxidative stress. The initial stress signals (e.g. osmotic and ionic effects, or temperature, membrane fluidity changes) trigger the downstream signalling process and transcription controls which activate stress-responsive mechanism to re-establish homeostasis and protect and repair damaged proteins and membranes. Inadequate response at one or several steps in the signalling and gene activation may ultimately result in irreversible changes of cellular homeostasis and in destruction of functional and structural proteins and membranes, leading to cell death.

Fig. 12 taken from from TRENDS in plant Science Vol. 7, No. 10, Oct. 2002 (Claudia Jonak and Heribert Hirt) shows possible shaggy-like kinase pathways in plants. /A/GSK1 is a positive regulator of the high-salt response. WIG (wound-induced GSK) is implicated in wound signalling. /A/SK1 1 and AtSKI 2 are involved in correct flower patterning. Genetic and biochemical analyses indicate that BIN2 (brassinosteroid-insensitive 1)-mediated brassinosteroid (BR) signalling, which controls nuclear accumulation of BES1 (BR1 1-EMS-suppressor 1) and BRZ1 (brassinazole-resistant 1).

Fig. 13 taken from TRENDS in plant Science Vol. 7, No. 10, Oct. 2002 (Claudia Jonak and Heribert Hirt) shows: (a) Phylogenetic analysis of the ten *Arabidopsis* glycogen synthase kinase 3/SHAGGY-like protein kinases (GSKs). The *Arabidopsis* GSKs can be classified into four subgroups. (b) Phylogenetic tree of full-length GSK cDNAs of different plant species obtained from various BLAST searches. *Brassica napus*, BSK Θ (Y1 2674); *Medicago sativa*, MSK1 (X6841 1), MSK2 (X68410), MSK3 (X68409), MSK4 (AF432225), WIG (AJ295939); *Nicotiana tabacum*, NSK6 (Y08607), NSK59 (AJ00231 5), NSK91 (AJ224163), NSK1 11 (AJ002314), NTK-1 (X77763); *Oryza sativa*, OSK γ (AB59612), OSK η (Y1 3437); *Petunia hybrida*, PSK4 (X83619), PSK6 (AJ2241 64), PSK7 (AJ224165), SPK6 (X83620). Alignments were performed with Clustal X by the neighbor-joining method using *Arabidopsis* MPK1 (Q39021) as an out-group; trees were designed by the TreeView program.

Fig. 14 shows a CLUSTAL multiple alignment of plant Group I shaggy-like kinases. Motifs I and II are boxed.

Fig. 15 shows a binary vector for expression in *Oryza sativa* of a Group I shaggy-like kinase from *Oryza sativa* under the control of a GOS2 promoter

Fig. 16 details examples of Group I shaggy-like kinase sequences useful in performing the methods according to the present invention.

Examples

The present invention will now be described with reference to the following examples, which are by way of illustration alone and are not intended to completely define or to otherwise limit the scope of the invention.

Unless otherwise stated, recombinant DNA techniques were performed according to standard protocols described in (Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York) or in Volumes 1 and 2 of Ausubel *et al.* (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfase (1993) by R.D.D. Croy, published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

EXAMPLES Class I HDZip hox5 polypeptides and encoding sequences**Example 1: Identification of sequences related to SEQ ID NO: 1 and SEQ ID NO: 2**

Sequences (full length cDNA, ESTs or genomic) were identified amongst those maintained in the Entrez Nucleotides database at the National Center for Biotechnology Information (NCBI) using database sequence search tools, such as the Basic Local Alignment Tool (BLAST) (Altschul *et al.* (1990) J. Mol. Biol. 215:403-410; and Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402). The program was used to find regions of local similarity between sequences by comparing nucleic acid or polypeptide sequences to sequence databases and by calculating the statistical significance of matches. For example, the polypeptide encoded by the nucleic acid of SEQ ID NO: 1 was used for the TBLASTN algorithm, with default settings and the filter to ignore low complexity sequences set off. The output of the analysis was viewed by pairwise comparison, and ranked according to the probability score (E-value), where the score reflects the probability that a particular alignment occurs by chance (the lower the E-value, the more significant the hit). In addition to E-values, comparisons were also scored by percentage identity. Percentage identity refers to the number of identical nucleotides (or amino acids) between the two compared nucleic acid (or polypeptide) sequences over a particular length. In some instances, the default parameters may be adjusted to modify the stringency of the search. For example the E-value may be increased to show less stringent matches. This way, short nearly exact matches may be identified.

Table A below provides a list of nucleic acid sequences related to the nucleic acid sequence of SEQ ID NO: 1.

Table A: Examples of sequences related to the nucleic acid sequence of SEQ ID NO: 1

Name	NCBI nucleotide accession number	Nucleotide SEQ ID NO	Translated polypeptide SEQ ID NO	Source
Orysa_hox5	XM_482406	1	2	<i>Oryza sativa</i>
Orysa_hox16	XM_467603	3	4	<i>Oryza sativa</i>
Zeama_hox5*	CO458693 DV024016	5	6	<i>Zea mays</i>
Zeama_hox16	AY105265	7	8	<i>Zea mays</i>
Sacof_hox5*	CA088615 CA115362 CA142506	9	10	<i>Saccharum officinarum</i>

Sorbi_hox5*	BE363386 CD432381	11	12	<i>Sorghum bicolor</i>
Triae_hox16*	DR735359 DR741379 CD916488	13	14	<i>Triticum aestivum</i>
Arath_ATHB1	X58821	15	16	<i>Arabidopsis thaliana</i>
Dauca_CHB3**	D26575	17	18	<i>Daucus carota</i>
Glyma_HD157**	AF184278	19	20	<i>Glycine max</i>
Crapl_CPHB-5	AF443621	21	22	<i>Craterostigma plantagineum</i>
Goshi_hox5*	DT465649 CD486134	23	24	<i>Gossypium hirsutum</i>
Lyces_hox5	BT014213.1	25	26	<i>Lycopersicon esculentum</i>
Lyces_VaHOX1	X94947	27	28	<i>Lycopersicon esculentum</i>
Medsa_hox16*	CB892061 CA858059	29	30	<i>Medicago sativa</i>
Aqufo_hox5	DT758247	31	32	<i>Aquilegia formosa x Aquilegia pubescens</i>
Poptr_hox16_1	scaff_XV.439	40	41	<i>Populus tremuloides</i>
Poptr_hox16_2	scaff_XII.649	42	43	<i>Populus tremuloides</i>
Poptr_hox16_3	lcl scaff_VIII.1839	44	45	<i>Populus tremuloides</i>
Medtr_hox16_1	CR954197.2	46	47	<i>Medicago truncatula</i>
Phavu_hox16	AF402605	48	49	<i>Phaseolus vulgaris</i>
Lotco_hox16	AP006364	50	51	<i>Lotus corniculatus</i>

*Contig compiled from several EST accessions (main ones shown); EST sequencing quality being usually lower, a few nucleic acid substitutions may be expected.

**Sequences from *Daucus carota* and *Glycine max* have been corrected compared to their accession number.

Example 2: Alignment of class I HDZip hox5 polypeptide sequences

AlignX from the Vector NTI (Invitrogen) based on the popular Clustal algorithm of progressive alignment (Thompson *et al.* (1997) Nucleic Acids Res 25:4876-4882; Chenna *et al.* (2003). Nucleic Acids Res 31:3497-3500) was used. A phylogenetic tree can be constructed using a

neighbour-joining clustering algorithm. Default values are for the gap open penalty of 10, for the gap extension penalty of 0,1 and the selected weight matrix is Blosum 62 (if polypeptides are aligned).

The result of the multiple sequence alignment is shown in Figure 2. The three main characterized domains, from N-terminal to C-terminal, are heavily boxed and identified as the acidic box, the class I homeodomain and the six heptad- leucine zipper. The "Conserved Domain" comprises these three domains. Additionally, the Trp tail and the RPFF amino acid motif are lightly boxed.

Example 3: Calculation of global percentage Identity between class I HDZip hox5 polypeptides sequences

Global percentages of similarity and identity between full length class I HDZip hox5 polypeptide sequences were determined using the Matrix Global Alignment Tool (MatGAT) software (BMC Bioinformatics. 2003 4:29. MatGAT: an application that generates similarity/identity matrices using protein or DNA sequences. Campanella JJ, Bitincka L, Smalley J; software hosted by Ledion Bitincka). MatGAT software generates similarity/identity matrices for DNA or protein sequences without needing pre-alignment of the data. The program performs a series of pair-wise alignments using the Myers and Miller global alignment algorithm (with a gap opening penalty of 12, and a gap extension penalty of 2), calculates similarity and identity using for example Blosum 62 (for polypeptides), and then places the results in a distance matrix. Sequence similarity is shown in the bottom half of the dividing line and sequence identity is shown in the top half of the diagonal dividing line.

Parameters used in the comparison were:

Scoring matrix: Blosum62

First Gap: 12

Extending gap: 2

Results of the software analysis are shown in Table B 1 for the global similarity and identity over the full length of the polypeptide sequences (excluding the partial polypeptide sequences). Percentage identity is given above the diagonal and percentage similarity is given below the diagonal.

The percentage identity between the polypeptide sequences shown can be as low as 29% amino acid identity compared to SEQ ID NO: 2.

Table B 1: MatGAT results for global similarity and identity over the full length of the polypeptide sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1. Aqufo_Hox5		56	54	37	34	64	36	64	35	34	36	47	37	36	38	38	36	42	41	46	49	42
2. Arath_ATHB1	73		52	34	34	59	36	57	33	34	36	44	34	35	40	35	35	39	39	41	43	39
3. Crapl_CPHB-5	69	66		33	35	56	37	59	33	33	33	45	39	34	37	36	36	41	39	41	44	41
4. Dauca_CHB3	52	52	48		44	39	53	35	46	49	46	30	33	47	58	56	43	32	33	31	33	33
5. Glyma_HD157	50	47	48	58		33	44	32	43	43	72	33	31	84	48	48	47	32	31	31	31	32
6. Goshi_Hox5	79	74	71	53	49		38	64	36	36	37	46	38	35	39	36	35	40	39	46	49	40
7. Lotco_Hox16	51	53	51	66	62	53		35	45	66	50	29	31	49	62	59	49	30	31	30	32	31
8. Lyces_Hox5	75	70	72	51	45	75	50		34	34	36	46	38	34	37	36	33	41	41	45	47	41
9. Lyces_VaHOX1	49	48	47	63	58	48	62	47		45	44	31	32	47	53	49	44	33	33	32	33	33
10. Medtr_Hox16	48	48	50	65	64	49	78	48	63		46	30	30	45	59	55	42	31	30	31	31	30
11. Medtr_Hox16_1	52	49	50	61	81	49	67	49	61	64		33	28	77	51	48	50	32	31	29	29	32
12. Orysa_Hox16	62	59	58	50	50	60	47	58	45	50	51		49	34	32	31	30	46	45	73	76	45
13. Orysa_Hox5	53	47	52	48	48	52	48	50	44	45	46	59		32	32	32	30	66	66	49	50	65
14. Phavu_HOX16	51	51	48	64	89	49	65	47	63	65	88	49	48		56	55	51	34	32	31	32	33
15. Poptr_HOX16_1	54	54	52	71	66	52	75	50	66	73	69	48	49	71		92	48	35	35	32	34	34
16. Poptr_HOX16_2	51	49	51	70	66	50	73	49	65	70	66	47	46	71	96		47	34	33	32	32	34
17. Poptr_HOX16_3	52	51	47	59	59	52	63	45	59	59	62	44	44	65	63	63		34	33	30	31	33
18. Sacof_Hox5	62	58	57	47	44	60	48	57	44	45	46	56	69	46	48	47	47		95	46	46	94
19. Sorbi_Hox5	62	57	55	46	45	58	51	58	45	44	46	56	69	47	50	47	46	97		43	46	94
20. Triae_Hox16	62	54	56	48	48	59	47	58	47	49	47	82	61	48	52	51	46	56	55		72	45
21. Zeama_Hox16	63	58	59	51	49	62	51	60	49	50	47	81	62	51	49	48	46	56	57	81		45
22. Zeama_Hox5	62	58	56	46	44	59	49	57	45	45	45	55	68	46	50	46	48	96	96	57	56	

The "Conserved Domain" of class I HDZip hox5 polypeptide sequences comprises from N-terminal to C-terminal, an acidic box, a class I homeodomain and the six heptad-leucine zipper (see Figure 2), as defined hereinabove. When percentage identity analysis is performed on the conserved domains instead of on the full length polypeptide sequences, an increase in percentage identity is observed, as shown in Table B 2. Lowest values are now above 50% amino acid identity compared to SEQ ID NO: 2.

Table B 2: MatGAT results for global similarity and identity over the "Conserved Domain" of the polypeptide sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1. Aqufo_hox5_CD		81	74	66	82	62	82	62	61	75	66	61	67	63	60	68	67	73	76	67
2. Arath_ATHB1_CD	93		74	59	82	61	85	61	61	71	66	63	65	62	59	67	66	71	71	67
3. Crapl_CPHB-5_CD	85	85		61	78	62	77	57	60	69	63	62	62	58	65	65	64	66	68	65
4. Dauca_CHB3_CD	81	79	75		64	70	62	66	69	57	57	64	80	75	66	58	59	57	57	58
5. Goshi_hox5_CD	94	95	89	81		66	83	63	63	74	66	63	68	63	64	67	66	73	75	67
6. Lotco_hox16_CD	80	78	74	81	80		62	67	85	54	52	62	77	73	64	53	52	54	54	53
7. Lyces_hox5_CD	91	92	88	79	92	77		57	61	75	68	63	66	62	60	71	69	75	76	70
8. Lyces_VaHOX1_CD	77	75	71	79	76	84	74		71	56	57	62	73	68	60	58	58	57	57	58
9. Medtr_hox16_CD	77	75	74	81	77	93	75	84		59	57	61	75	71	62	57	57	58	59	57
10. Orysa_hox16_CD	93	92	85	77	92	79	92	74	75		84	58	60	58	58	82	82	94	96	82
11. Orysa_hox5_CD	90	87	83	78	88	77	88	71	74	91		59	58	57	57	92	93	81	84	94
12. Phavu_hox16_CD	79	79	75	80	79	81	76	75	80	76	75		71	71	65	60	60	57	58	60
13. Poptr_hox16_1_CD	81	80	75	88	82	90	79	84	87	79	80	86		93	65	59	60	58	61	59
14. Poptr_hox16_2_CD	79	77	74	85	79	87	76	82	84	75	75	85	98		62	57	57	56	58	57
15. Poptr_hox16_3_CD	74	75	73	80	75	76	71	76	77	73	71	78	77	77		57	57	56	58	58
16. Sacof_hox5_CD	89	86	80	77	87	77	86	71	73	88	96	74	79	75	72		98	79	82	98
17. Sorbi_hox5_CD	89	86	81	77	87	77	87	71	73	89	97	74	79	76	72	99		78	82	98
18. Triae_hox16_CD	93	92	85	79	92	80	92	74	75	98	91	77	80	77	73	88	89		95	79
19. Zeama_hox16_CD	93	92	86	78	92	81	92	75	77	98	92	79	80	76	74	90	91	98		82
20. Zeama_hox5_CD	89	86	81	77	87	77	87	71	73	89	97	74	79	75	72	99	100	89	91	

Example 4: Identification of domains comprised in class I HDZip hox5 polypeptide sequences

The Integrated Resource of Protein Families, Domains and Sites (InterPro) database is an integrated interface for the commonly used signature databases for text- and sequence-based searches. The InterPro database combines these databases, which use different methodologies and varying degrees of biological information about well-characterized proteins to derive protein signatures. Collaborating databases include SWISS-PROT, PROSITE, TrEMBL, PRINTS, ProDom and Pfam, Smart and TIGRFAMs. Interpro is hosted at the European Bioinformatics Institute in the United Kingdom.

The results of the InterPro scan of the polypeptide sequence as represented by SEQ ID NO: 2 are presented in Table C.

Table C: InterPro scan results of the polypeptide sequence as represented by SEQ ID NO: 2

InterPro	IPR000047	Helix-turn-helix motif, lambda-like repressor	
	PRINTS	PR00031	HTHREPRESSR

InterPro	IPR001356	Homeobox	
	PRODOM	PD000010	Homeobox
	PRINTS	PR00024	HOMEBOX
	PFAM	PF00046	Homeobox
	SMART	SM00389	HOX
	PROFILE	PS00027	HOMEBOX_1
	PROFILE	PS50071	HOMEBOX_2

InterPro	IPR003106	Leucine zipper, homeobox-associated	
	PFAM	PF02183	HALZ

InterPro	IPR009057	Homeodomain-like	
	SUPERFAMILY	SSF46689	Homeodomain_like

InterPro	IPR012287	Homeodomain-related	
	GENE3D	G3DSA:1.10.10.60	Homeodomain-rel

Primary amino acid composition (in %) to determine if a polypeptide domain is rich in specific amino acids (for example in an acidic box) may be calculated using software programs from the ExPASy server, in particular the ProtParam tool (Gasteiger E *et al.* (2003) ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Res 31:3784-3788). The composition of the polypeptide sequence of interest may then be compared to the average amino acid composition (in %) in the Swiss-Prot Protein Sequence data bank.

In the Table below (Table D), are compared the % Asp (D), % Glu (E) and their combined content in the acidic box of SEQ ID NO: 2 with the average in Swiss-Prot Protein Sequence databank.

Table D

	% Asp (D)	% Glu (E)	% Asp (D) + % Glu (E)
Average in Swiss-Prot Protein Sequence databank	5.3%	6.6%	11.9%
Acidic box of SEQ ID NO: 2	9.1%	54.5%	63.6%

An acidic box may be part of a transcription activation domain. Eukaryotic transcription activation domains have been classified according to their amino acid content, and major categories include acidic, glutamine-rich and proline-rich activation domains (Rutherford *et al.* (2005) Plant J. 43(5)769-88, and references therein).

The Gene Ontology (GO) Consortium is an international collaboration among scientists at various biological databases, with an Editorial Office based at the European Bioinformatics Institute. The objective of GO is to provide controlled vocabularies for the description of the molecular function, biological process and cellular component of gene products. When performing an InterPro scan as described above, the GO database is also searched. The class I HDZip hox5 polypeptide sequences have as molecular function transcription factor and sequence-specific DNA binding activity, and localised in the nucleus of the plant cell (see Table below (Table E)).

Table E

	Gene Ontology Entry
<i>Homeodomain</i>	Molecular Function: transcription factor activity (GO:0003700) Cellular Component: nucleus (GO:0005634) Molecular Function: sequence-specific DNA binding (GO:0043565)
<i>Leucine zipper, homeobox-associated</i>	Molecular Function: DNA binding (GO:0003677) Cellular Component: nucleus (GO:0005634)

Example 5: Topology prediction of class I HDZip hox5 polypeptide sequences

Leucine zipper prediction and heptad identification was carried out using specialised software such as 2ZIP, which combines a standard coiled coil prediction algorithm with an approximate search for the characteristic leucine repeat (Bornberg-Bauer *et al.* (1998) Nucleic Acids Res 26(11): 2740-2746; hosted at Max Planck Institut, Golm in Germany). A potential leucine zipper, a repeat of leucines or a coiled coil may be identified using this software.

The class I HDZip hox5 polypeptide sequences comprise a leucine zipper prediction, with at least 5, preferably 6 heptads. When the polypeptide of SEQ ID NO: 2 is submitted to this algorithm, a potential leucine zipper is between positions 143 and 178, as shown in the output below (numbers reflect amino acid position, C the coiled coil region, and L the leucine within the heptad):

Example 6: Assay for class I HDZlp hox5 polypeptide sequences

Class I HDZip hox5 polypeptides or homologues thereof have DNA binding activity, preferably to 5 bp half-sites that overlap at a central position, CAA(A/T)ATTG, as detected in yeast one-hybrid assays (Meijer *et al.* (2000) *Mol Gen Genet* 263:12-21). In transient assays on rice cell suspensions, co-bombardement of a class I HDZip hox5 polypeptide with the GUS reporter gene reportedly resulted in an increased number of stained spots, which were also more intense in color (Meijer *et al*, *supra*). This assay is useful to demonstrate the activator function of class I HDZip hox5 polypeptides or homologues.

Example 7: Cloning of *Oryza sativa* class I HDZip hox5 nucleic acid sequence

The *Oryza sativa* class I HDZip hox5 nucleic acid sequence was amplified by PCR using as template an *Oryza sativa* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.6 kb and the original number of clones was of the order of 1.67×10^7 cfu. Original titer was determined to be 3.34×10^6 cfu/ml after first amplification of 6×10^{10} cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 μ l PCR mix. Primers prm06000 (SEQ ID NO: 34; sense, start codon in bold, AttB1 site in italic: 5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGGATCCCGGCCG 3') and prm06001 (SEQ ID NO: 35; reverse, complementary, AttB2 site in italic: 5'-GGGG/ACC/AC TTTGTAC/MG/MGC7GGG7OATCAGCTCCAGAACCCAGG 3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Tag DNA polymerase in standard conditions. A PCR fragment of 1116 bp

(including attB sites; from start to stop 1050 bp) was amplified and purified also using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombines *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone". Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.

Example 8: Vector Construction

The entry clone comprising the nucleic acid sequences was subsequently used in an LR reaction with a "destination" vector used for *Oryza sativa* transformation. This vector contained as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already cloned in the entry clone. A rice GOS2 promoter (SEQ ID NO: 33 OR SEQ ID NO: 178) for constitutive expression was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector (Figure 3) was transformed into *Agrobacterium* strain LBA4044 according to methods well known in the art.

Example 9: Plant transformation

Rice transformation

The *Agrobacterium* containing the expression vector was used to transform *Oryza sativa* plants. Mature dry seeds of the rice japonica cultivar Nipponbare were dehusked. Sterilization was carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2%HgCl₂, followed by a 6 times 15 minutes wash with sterile distilled water. The sterile seeds were then germinated on a medium containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli were excised and propagated on the same medium. After two weeks, the calli were multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces were subcultured on fresh medium 3 days before co-cultivation (to boost cell division activity).

Agrobacterium strain LBA4404 containing the expression vector was used for cocultivation. *Agrobacterium* was inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28°C. The bacteria were then collected and suspended in liquid co-cultivation medium to a density (OD₆₀₀) of about 1. The suspension was then transferred to a Petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues were then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25°C. Co-cultivated calli were grown on 2,4-D-containing medium for 4

weeks in the dark at 28°C in the presence of a selection agent. During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential was released and shoots developed in the next four to five weeks. Shoots were excised from the calli and incubated for 2 to 3 weeks on an auxin-containing medium from which they were transferred to soil. Hardened shoots were grown under high humidity and short days in a greenhouse.

Approximately 35 independent T₀ rice transformants were generated for one construct. The primary transformants were transferred from a tissue culture chamber to a greenhouse. After a quantitative PCR analysis to verify copy number of the T-DNA insert, only single copy transgenic plants that exhibit tolerance to the selection agent were kept for harvest of T₁ seed. Seeds were then harvested three to five months after transplanting. The method yielded single locus transformants at a rate of over 50 % (Aldemita and Hodges1996, Chan et al. 1993, Hiei et al. 1994).

Example 10: Phenotypic evaluation procedure

10.1 Evaluation setup

Approximately 35 independent T₀ rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T₁ seed. Seven events, of which the T₁ progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T₁ seedlings containing the transgene (hetero- and homo-zygotes) and approximately 10 T₁ seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. The transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. Greenhouse conditions were of short days (12 hours light), 28°C in the light and 22°C in the dark, and a relative humidity of 70%.

All T₁ events were further evaluated in the T₂ generation following the same evaluation procedure as for the T₁ generation. From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point, digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

Salt stress screen

Plants from 4 events (T₂ seeds) were grown on a substrate made of coco fibers and argex (3 to 1 ratio). A normal nutrient solution was used during the first two weeks after transplanting

the plantlets in the greenhouse. After the first two weeks, 25 mM of salt (NaCl) was added to the nutrient solution, until the plants were harvested.

Drought screen

Plants from five events (T2 seeds) were grown in potting soil under normal conditions until they approached the heading stage. They were then transferred to a "dry" section where irrigation was withheld. Humidity probes were inserted in randomly chosen pots to monitor the soil water content (SWC). When SWC went below certain thresholds, the plants were automatically re-watered continuously until a normal level was reached again. The plants were then re-transferred again to normal conditions. The rest of the cultivation (plant maturation, seed harvest) was the same as for plants not grown under abiotic stress conditions. A confirmation round was performed consisting of repeating the screen with T2 seeds not harvested from plants of the first drought screen, but from plants grown under normal conditions.

Reduced nutrient (nitrogen) availability screen

The rice plants are grown in potting soil under normal conditions except for the nutrient solution. The pots are watered from transplantation to maturation with a specific nutrient solution containing reduced N nitrogen (N) content, usually between 7 to 8 times less. The rest of the cultivation (plant maturation, seed harvest) is the same as for plants not grown under abiotic stress. Seed-related parameters are then measured

10.2 Statistical analysis: F test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F test was carried out to check for an effect of the gene over all the transformation events and to verify for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F test. A significant F test value points to a gene effect, meaning that it is not only the mere presence or position of the gene that is causing the differences in phenotype.

10.3 Parameters measured

10.3.1 Biomass-related parameter measurement

From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

The plant aboveground area (or leafy biomass) was determined by counting the total number of pixels on the digital images from aboveground plant parts discriminated from the background. This value was averaged for the pictures taken on the same time point from the different angles and was converted to a physical surface value expressed in square mm by calibration. Experiments show that the aboveground plant area measured this way correlates with the biomass of plant parts above ground. The aboveground area is the time point at which the plant had reached its maximal leafy biomass. The early vigour is the plant (seedling) aboveground area three weeks post-germination.

An additional parameter was used to measure abiotic stress tolerance when necessary: the greenness index after drought, which gives an indication of the senescence of the plant. It is the proportion (expressed as %) of yellow pixels in the first imaging after drought.

To measure root-related parameters, plants were grown in specially designed pots with transparent bottoms to allow visualization of the roots. A digital camera recorded images through the bottom of the pot during plant growth. Root features such as total projected area (which can be correlated to total root volume), average diameter and length of roots above a certain thickness threshold (length of thick roots, or thick root length) were deduced from the picture using of appropriate software. Increase in root biomass is expressed as an increase in total root biomass (measured as maximum biomass of roots observed during the lifespan of a plant); or as an increase in the root/shoot index (measured as the ratio between root mass and shoot mass in the period of active growth of root and shoot).

10.3.2 Seed-related parameter measurements

The mature primary panicles were harvested, counted, bagged, barcode-labelled and then dried for three days in an oven at 37 °C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. The total seed yield was measured by weighing all filled husks harvested from a plant. Total seed number per plant was measured by counting the number of husks harvested from a plant. Thousand Kernel Weight (TKW) is extrapolated from the number of filled seeds counted and their total weight. The Harvest Index (HI) in the present invention is defined as the ratio between the total seed yield and the above ground area (mm²), multiplied by a factor 106. The total number of flowers per panicle as defined in the present invention is the ratio between the

total number of seeds and the number of mature primary panicles. The seed fill rate as defined in the present invention is the proportion (expressed as a %) of the number of filled seeds over the total number of seeds (or florets).

Example 11: Results of transgenic rice plants expressing a class I HDZip hox5 nucleic acid under normal growth conditions

The results of the evaluation of transgenic rice plants expressing the *class I HDZip hox5 nucleic acid* under normal growth conditions are presented in Table F. The percentage difference between the transgenics and the corresponding nullizygotes is shown, with a P value from the F test below 0.05.

Table F: Results of the evaluation of transgenic rice plants expressing a *class I HDZip hox5 nucleic acid* under normal growth conditions.

Trait	% Difference in T1	% Difference in T2
Average root diameter	2	1
Length of thick roots	9	17
Total seed yield	17	19
Number of filled seeds	15	17
Fill rate	7	9
Total number seeds	6	9
Number of flowers per panicle	8	9
TKW	2	2
Harvest index	16	16
Greenness index before flowering	2	4

Example 12: Results of transgenic rice plants expressing the nucleic acid sequence useful in performing the methods of the invention, under salt stress growth conditions

The results of the evaluation of transgenic rice plants expressing the nucleic acid encoding a class I HDZip hox5 polypeptide sequence under salt stress growth conditions are presented in Table G. The percentage difference between the transgenics and the corresponding nullizygotes is shown, with a P value from the F test below 0.05.

Table G : Results of the evaluation of transgenic rice plants expressing the *class I HDZip hoxδ* nucleic acid under salt stress growth conditions.

Trait	% Difference in T1
Total seed yield	41
Number of filled seeds	40
Fill rate	30
TKW	1
Harvest index	36
Greenness index before flowering	7

Example 13: Results of transgenic rice plants expressing the class I HDZip hoxδ nucleic acid under drought stress growth conditions

The results of the evaluation of transgenic rice plants expressing the nucleic acid sequence useful in performing the methods of the invention under drought stress growth conditions are presented in Table H. The percentage difference between the transgenics and the corresponding nullizygotes is shown, with a P value from the F test below 0.05.

Table H: Results of the evaluation of transgenic rice plants expressing the nucleic acid sequence useful in performing the methods of the invention, under drought stress growth conditions.

Trait	% Difference in T1	% Difference in T2
Average root diameter	2	1
Length of thick roots	9	14
Total seed yield	18	31
Number of filled seeds	21	33
Fill rate	15	33
Harvest index	18	34
Greenness index after drought	2	3

EXAMPLES NRT polypeptides and encoding nucleic acids

Example 14: Identification of sequences related to SEQ ID NO: 52 and SEQ ID NO: 53

Sequences (full length cDNA, ESTs or genomic) related to SEQ ID NO: 52 and/or protein sequences related to SEQ ID NO: 53 were identified amongst those maintained in the Entrez Nucleotides database at the National Center for Biotechnology Information (NCBI) using database sequence search tools, such as the Basic Local Alignment Tool (BLAST) (Altschul et

a/. (1990) J. Mol. Biol. 215:403-410; and Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402). The program is used to find regions of local similarity between sequences by comparing nucleic acid or polypeptide sequences to sequence databases and by calculating the statistical significance of matches. The polypeptide encoded by SEQ ID NO: 52 was used for the TBLASTN algorithm, with default settings and the filter to ignore low complexity sequences set off. The output of the analysis was viewed by pairwise comparison, and ranked according to the probability score (E-value), where the score reflects the probability that a particular alignment occurs by chance (the lower the E-value, the more significant the hit). In addition to E-values, comparisons were also scored by percentage identity. Percentage identity refers to the number of identical nucleotides (or amino acids) between the two compared nucleic acid (or polypeptide) sequences over a particular length. In some instances, the default parameters may be adjusted to modify the stringency of the search.

In addition to the publicly available nucleic acid sequences available at NCBI, proprietary sequence databases are also searched following the same procedure as described herein above.

Table I provides a list of nucleic acid and protein sequences related to the nucleic acid sequence as represented by SEQ ID NO: 1 and the protein sequence represented by SEQ ID NO: 2.

Table I: Nucleic acid sequences related to the nucleic acid sequence (SEQ ID NO: 1) useful in the methods of the present invention, and the corresponding deduced polypeptides.

Species	GenBank accession	Protein SEQ ID NO:	Nucleic acid SEQ ID NO:
<i>Oryza sativa</i>	BAA33382	53	1
<i>Phragmites australis</i>	BAC76606	66	65
<i>Zea mays</i>	AAT66252	68	67
<i>Zea mays</i>	AAN05088	70	69
<i>Hordeum vulgare</i>	AAC49531	72	71
<i>Triticum aestivum</i>	AAK19519	74	73
<i>Hordeum vulgare</i>	AAC49532	76	75
<i>Triticum aestivum</i>	AAG01172	78	77
<i>Triticum aestivum</i>	AAL11016	80	79
<i>Hordeum vulgare</i>	AAD28364	82	81
<i>Hordeum vulgare</i>	AAD28363	84	83

<i>Prunus persica</i>	BAD02939	86	85
<i>Prunus persica</i>	BAD04063	88	87
<i>Glycine max</i>	AAC09320	90	89
<i>Lotus japonicus</i>	Q9ARC5	92	91
<i>Nicotiana tabacum</i>	CAD89799	94	93
<i>Lycopersicon esculentum</i>	AAK72402	96	95
<i>Populus</i> sp.	CAG26716	98	97
<i>Nicotiana tabacum</i>	CAD89798	100	99
<i>Nicotiana plumbaginifolia</i>	CAA69387	102	101
<i>Lycopersicon esculentum</i>	AAF00053	104	103
<i>Arabidopsis thaliana</i>	AAC64170	106	105
<i>Lycopersicon esculentum</i>	AAF00054	108	107
<i>Brassica napus</i>	CAC05338	110	109
<i>Arabidopsis thaliana</i>	AAY78876	112	111
<i>Arabidopsis thaliana</i>	NP_172289	114	113
<i>Arabidopsis thaliana</i>	AAC35884	116	115
<i>Arabidopsis thaliana</i>	NP_200886	118	117
<i>Arabidopsis thaliana</i>	AAU05505	120	119
<i>Daucus carota</i>	AAL99362	122	121
<i>Zea mays</i>	CAC87729	124	123

Example 15: Alignment of relevant polypeptide sequences

AlignX from the Vector NTI (Invitrogen) is based on the popular Clustal algorithm of progressive alignment (Thompson *et al.* (1997) *Nucleic Acids Res* 25:4876-4882; Chenna *et al.* (2003). *Nucleic Acids Res* 31:3497-3500). A phylogenetic tree can be constructed using a neighbour-joining clustering algorithm. Default values are for the gap open penalty of 10, for the gap extension penalty of 0,1 and the selected weight matrix is Blosom 62 (if polypeptides are aligned).

The result of the multiple sequence alignment using polypeptides relevant in identifying the ones useful in performing the methods of the invention is shown in Figure 6 of the present application. The multiple alignment shows the high sequence conservation among NRT proteins of the various species. Proteins comprising a PTR2 domain (exemplified by SEQ ID NO: 126) clearly do not fall within the group of NRT proteins as defined herein.

Example 16: Calculation of global percentage identity between NRT polypeptide sequences

Global percentages of similarity and identity between full length polypeptide sequences useful in performing the methods of the invention were determined using MatGAT (Matrix Global Alignment Tool) software (BMC Bioinformatics. 2003 4:29. MatGAT: an application that generates similarity/identity matrices using protein or DNA sequences. Campanella JJ, Bitincka L, Smalley J; software hosted by Ledion Bitincka). MatGAT software generates similarity/identity matrices for DNA or protein sequences without needing pre-alignment of the data. The program performs a series of pair-wise alignments using the Myers and Miller global alignment algorithm (with a gap opening penalty of 12, and a gap extension penalty of 2), calculates similarity and identity using for example Blosom 62 (for polypeptides), and then places the results in a distance matrix. Sequence similarity is shown in the bottom half of the dividing line and sequence identity is shown in the top half of the diagonal dividing line.

Parameters used in the comparison were:

Scoring matrix: Blosom62

First Gap: 12

Extending gap: 2

Results of the software analysis are shown in Table I for the global similarity and identity over the full length of the polypeptide sequences (excluding the partial polypeptide sequences). Percentage identity is given above the diagonal and percentage similarity is given below the diagonal.

The percentage identity between the polypeptide sequences useful in performing the methods of the invention is usually above 60 % amino acid identity compared to SEQ ID NO: 53 (although exceptions may occur); whereas proteins comprising a PTR2 domain (such as rice nitrate transporter represented by SEQ ID NO: 126, line 31 in the table below) shows only very limited sequence identity with the NRT proteins (17% or lower).

Table J: MatGAT results for global similarity and identity over the full length of the polypeptide sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
1 SEQID53		87.4	87.2		79.9	79.9	80.7	80.1	79.7	79.9	79.4	75.4	75.0	75.7	73.7	73.7	73.9	73.5	72.6	72.4	72.6	71.5	72.4	71.8	71.5	66.9	66.7	66.1	66.1	66.3	14.9
2 SEQID66	91.9		88.7	87.4	82.7	83.1	83.1	83.1	82.4	82.7	82.2	75.5	75.1	76.0	75.1	73.4	72.9	73.8	71.9	71.3	72.3	71.4	72.1	70.6	71.1	67.3	67.1	66.0	65.5	65.2	15.2
3 SEQID68	91.7	92.7		98.5	80.9	81.1	80.7	81.3	81.1	80.5	80.7	75.1	74.8	75.9	73.6	70.8	71.2	73.9	70.9	70.8	71.5	70.8	71.1	71.1	71.1	67.3	67.1	64.4	64.6	64.1	13.7
4 SEQID70	90.2	91.4	98.5		79.4	79.5	79.2	79.7	79.5	79.0	79.2	73.8	73.4	74.4	72.1	69.2	69.7	72.6	69.4	69.2	70.0	69.6	69.6	70.0	69.9	66.2	66.0	63.5	63.7	62.6	13.7
5 SEQID72	85.7	88.5	87.4	85.9		98.2	91.9	98.4	97.4	98.0	98.6	73.2	72.8	73.5	71.3	68.3	68.7	71.7	68.3	67.5	67.9	68.9	67.7	68.1	68.1	64.9	64.9	64.8	63.9	61.3	14.5
6 SEQID74	85.7	88.9	87.8	86.3	99.2		91.9	98.4	97.8	97.6	97.8	73.5	73.2	73.4	71.1	68.1	68.3	71.5	68.3	67.5	67.4	68.7	67.2	68.1	67.2	64.7	64.7	64.8	63.5	60.9	13.8
7 SEQID76	86.5	88.5	87.2	85.7	96.3	96.1		92.3	91.6	91.6	91.4	72.8	72.4	72.8	71.1	68.7	68.5	70.9	67.2	67.0	67.7	68.0	67.5	68.5	67.5	64.9	64.9	63.3	62.2	61.6	16.6
8 SEQID78	85.6	88.5	87.2	85.7	99.0	98.8	96.3		98.2	97.4	98.2	73.7	73.4	74.1	71.9	68.5	68.9	72.2	68.1	67.4	68.1	69.0	67.9	68.3	67.9	65.1	65.0	64.1	61.5	61.5	14.3
9 SEQID80	85.6	88.3	87.2	85.7	98.6	98.8	95.9	98.8		97.0	97.2	73.7	73.4	73.9	71.3	67.9	68.3	72.2	68.1	67.4	68.1	69.0	67.9	68.3	67.9	65.1	65.1	64.4	63.5	61.1	13.8
10 SEQID82	85.4	88.3	86.8	85.3	98.6	98.8	95.9	98.8	98.2		97.6	73.0	72.6	73.0	70.7	67.9	68.3	70.7	67.7	67.0	67.4	68.5	67.2	67.7	67.5	64.3	64.3	64.4	63.7	60.9	12.9
11 SEQID84	85.0	88.0	87.0	85.5	99.0	98.8	95.7	98.8	98.4	98.0		72.8	72.4	73.2	70.9	68.1	68.5	71.5	68.1	67.4	67.9	68.9	67.7	67.9	67.4	67.4	64.9	64.1	63.2	61.1	14.5
12 SEQID86	85.6	84.5	84.7	83.2	83.0	83.0	83.4	83.2	83.0	82.6	82.5		99.1	90.4	87.4	81.7	80.8	88.3	82.6	82.8	82.6	81.7	82.3	81.1	80.8	75.3	75.1	73.7	74.0	71.9	14.9
13 SEQID88	85.4	84.3	84.5	83.0	82.8	82.8	83.2	83.0	82.8	82.5	82.3	99.6		90.0	87.0	81.1	80.2	87.4	81.9	82.1	81.9	81.1	81.5	80.6	80.6	74.7	74.5	73.8	73.8	71.4	14.7
14 SEQID90	86.1	85.3	85.3	83.8	83.8	83.0	84.2	84.0	83.6	83.0	83.2	95.8	95.7		91.3	82.6	81.4	87.9	81.5	81.1	81.9	79.8	81.5	79.6	80.8	74.5	74.3	73.7	72.9	72.9	15.7
15 SEQID92	85.2	85.8	84.9	83.4	82.8	82.3	83.4	83.0	83.0	82.3	82.3	94.3	94.2	96.2		80.6	78.5	85.5	80.4	80.4	80.0	78.3	79.8	78.1	79.4	73.8	73.6	72.0	72.0	70.3	15.8
16 SEQID94	84.8	84.0	82.1	80.6	81.3	80.6	81.5	81.5	81.1	80.6	81.1	91.9	91.3	91.7	90.9		93.4	81.3	90.4	90.4	89.8	77.4	89.6	76.6	77.7	72.6	72.5	67.5	66.6	82.9	15.2
17 SEQID96	85.0	83.6	81.9	80.4	80.8	80.0	81.0	81.0	80.6	80.0	80.8	91.0	90.4	90.4	89.6	96.2		81.2	89.1	88.9	89.1	76.1	88.9	75.3	76.3	71.4	71.2	66.8	66.6	88.5	15.8
18 SEQID98	85.0	84.1	84.5	83.0	82.6	81.9	83.4	82.8	82.6	81.7	82.4	94.5	94.2	94.0	93.2	91.3	90.2		82.8	82.6	83.4	80.2	83.0	79.6	80.0	74.9	74.7	71.4	70.1	72.7	14.8
19 SEQID100	82.6	82.3	80.9	79.4	80.0	80.0	79.2	79.8	79.6	79.2	79.8	91.3	90.9	90.6	89.4	89.5	94.4	91.7		97.5	95.3	78.3	95.1	77.9	78.3	73.8	73.6	66.8	66.8	79.0	14.9
20 SEQID102	82.9	82.1	80.9	79.4	80.2	80.2	79.4	80.0	79.8	79.4	80.0	91.7	91.3	90.9	89.6	95.7	94.4	92.1	99.2		95.1	77.9	94.7	77.4	77.9	73.2	73.0	66.4	66.6	79.2	14.6
21 SEQID104	82.7	82.3	80.6	79.1	79.4	78.7	79.4	79.6	79.4	78.7	79.2	90.4	90.0	90.4	89.2	95.3	93.8	90.6	97.5	97.7		77.9	99.6	77.0	77.7	72.6	72.5	67.3	66.6	79.6	17.2
22 SEQID106	83.7	82.8	82.1	80.8	80.4	80.0	81.5	80.6	80.4	79.8	79.8	90.6	90.4	88.5	88.5	87.5	86.6	87.9	87.2	87.2	86.6		77.7	94.7	82.8	87.0	86.8	68.5	68.1	68.4	14.9
23 SEQID108	82.6	82.1	80.2	78.7	79.2	78.5	79.2	79.4	79.2	78.5	79.1	90.0	89.6	90.0	89.1	95.1	93.6	90.2	97.4	97.4	99.6	86.4		76.8	77.4	72.5	72.3	67.3	66.2	79.4	17.2
24 SEQID110	83.7	83.2	82.1	80.8	80.8	80.8	81.7	80.9	80.8	80.2	80.2	90.6	90.4	89.1	89.1	88.1	87.2	88.9	87.7	87.7	86.6	97.7	86.4		82.1	85.5	85.3	67.9	67.5	67.5	15.5
25 SEQID112	83.7	82.7	82.5	81.2	80.6	80.6	80.6	81.0	80.8	80.3	80.3	90.4	90.2	89.2	88.3	87.9	86.8	89.0	87.5	88.1	86.8	90.6	86.4	90.4			78.4	70.3	69.9	68.8	15.4
26 SEQID114	81.8	81.8	82.1	80.7	79.5	79.3	80.8	79.7	79.5	78.7	79.1	86.6	86.4	85.7	85.5	84.2	83.1	85.3	83.6	83.6	82.5	90.9	82.3	90.8	87.9		99.8	64.4	63.7	63.8	13.8
27 SEQID116	81.6	81.6	81.9	80.5	79.5	79.5	80.8	79.7	79.5	78.7	79.1	86.4	86.2	85.5	85.3	84.0	82.9	85.1	83.4	83.4	82.3	90.8	82.1	90.6	87.7	99.8		64.2	63.1	63.6	13.6
28 SEQID118	79.0	77.6	76.3	75.0	75.7	75.7	76.1	75.9	75.5	75.3	75.1	83.3	83.5	84.6	82.9	82.4	81.6	82.9	81.3	81.4	81.8	82.4	81.6	82.2	82.9	79.0	78.8		89.3	59.2	16.0
29 SEQID120	78.6	77.5	76.9	75.6	75.1	74.7	74.9	75.1	74.7	74.7	74.4	83.0	83.2	83.4	81.2	81.5	81.2	81.7	80.4	80.6	80.8	81.2	80.6	80.8	82.1	78.4	77.7	93.9		59.4	16.4
30 SEQID122	79.1	77.0	75.1	73.6	73.5	73.1	73.8	74.0	73.6	73.1	73.5	82.8	82.2	82.4	82.1	87.3	90.3	82.6	86.0	86.4	85.6	78.9	85.4	79.3	79.4	75.7	75.3	75.3	74.9		15.6
31 SEQID126	28.8	29.5	26.4	26.2	30.3	28.6	33.4	29.5	28.6	28.8	29.1	28.8	28.6	28.1	30.5	29.8	29.6	29.6	28.8	28.6	32.4	27.9	32.4	28.8	30.7	31.8	31.8	32.0	31.8	31.0	

Example 17: Identification of domains comprised in polypeptide sequences useful in performing the methods of the invention

The Integrated Resource of Protein Families, Domains and Sites (InterPro) database is an integrated interface for the commonly used signature databases for text- and sequence-based searches. The InterPro database combines these databases, which use different methodologies and varying degrees of biological information about well-characterized proteins to derive protein signatures. Collaborating databases include SWISS-PROT, PROSITE, TrEMBL, PRINTS, ProDom and Pfam, Smart and TIGRFAMs. Interpro is hosted at the European Bioinformatics Institute in the United Kingdom.

The results of the InterPro scan of the polypeptide sequence as represented by SEQ ID NO: 53 are presented in Table K.

Table K: InterPro scan results of the polypeptide sequence as represented by SEQ ID NO: 53

Database	Accession number	Accession name
Pfam	PF07690	MFS_1

Example 18: Topology prediction of the NRT polypeptides (subcellular localization, transmembrane...)

TargetP 1.1 predicts the subcellular location of eukaryotic proteins. The location assignment is based on the predicted presence of any of the N-terminal pre-sequences: chloroplast transit peptide (cTP), mitochondrial targeting peptide (mTP) or secretory pathway signal peptide (SP). Scores on which the final prediction is based are not really probabilities, and they do not necessarily add to one. However, the location with the highest score is the most likely according to TargetP, and the relationship between the scores (the reliability class) may be an indication of how certain the prediction is. The reliability class (RC) ranges from 1 to 5, where 1 indicates the strongest prediction. TargetP is maintained at the server of the Center for Biological Sequence Analysis, Technical University of Denmark.

For the sequences predicted to contain an N-terminal presequence a potential cleavage site can also be predicted.

A number of parameters were selected, such as organism group (non-plant or plant), cutoff sets (none, predefined set of cutoffs, or user-specified set of cutoffs), and the calculation of prediction of cleavage sites (yes or no).

The results of TargetP 1.1 analysis of the polypeptide sequence as represented by SEQ ID NO: 53 are presented Table L. The "plant" organism group has been selected, no cutoffs defined, and the predicted length of the transit peptide requested. No subcellular localisation could be predicted.

Table L: TargetP 1.1 analysis of the polypeptide sequence as represented by SEQ ID NO: 53

Length (AA)	533
Chloroplastic transit peptide	0.116
Mitochondrial transit peptide	0.060
Secretory pathway signal peptide	0.008
Other subcellular targeting	0.874
Predicted Location	-
Reliability class	2
Predicted transit peptide length	-

Many other algorithms can be used to perform such analyses, including:

- ChloroP 1.1 hosted on the server of the Technical University of Denmark;
- Protein Prowler Subcellular Localisation Predictor version 1.2 hosted on the server of the Institute for Molecular Bioscience, University of Queensland, Brisbane, Australia;
- PENCE Proteome Analyst PA-GOSUB 2.5 hosted on the server of the University of Alberta, Edmonton, Alberta, Canada;

Using the TMHMM program (Center for Biological Sequence Analysis, Technical University of Denmark) the number of transmembrane helices was predicted to be 11, see Table M hereunder.

Table M:

Location	Region of amino acids involved
outside	1 67
TMhelix	68 90
inside	91 129
TMhelix	130 152
outside	153 155

TMhelix	156 178
inside	179 184
TMhelix	185 207
outside	208 221
TMhelix	222 244
inside	245 272
TMhelix	273 295
outside	296 314
TMhelix	315 332
inside	333 352
TMhelix	353 375
outside	376 379
TMhelix	380 402
inside	403 408
TMhelix	409 431
outside	432 440
TMhelix	441 463
inside	464 533

The expected number of amino acids in transmembrane helices was predicted to be at least 242 (if more than 18, the protein is very likely a transmembrane protein). Furthermore, the presence of a secretion signal is not very likely, since there is no predicted transmembrane helix within the first 60 amino acids, nor a N-terminal signal sequence (Exp number, first 60 AAs: 0.00085).

Example 19: Assay for NRT

To determine the transporter activity of NRT, the nitrate uptake assay as described by Tong et al. (Plant J. 41, 442-450, 2005). Briefly, mRNA is prepared from constructs in which the ORF encoding the NRT protein of interest is preceded by 5'-UTR of Xenopus β -globin gene and followed by the 3'-UTR of the same gene. This mRNA is injected in Xenopus stage V and VI oocytes whereafter the NRT protein of interest is expressed. The oocytes are incubated in a solution with $^{15}\text{NO}_3^-$ during 3 to 12 hrs at 18°C. Next, the oocytes are washed and dried at 60°C. The uptake of ^{15}N -enriched nitrate is measured by measuring the ratio $^{15}\text{N}/^{14}\text{N}$ with a mass spectrometer. Other suitable assays for measuring NO_3^- uptake are known to persons skilled in the art, see for example Filleur et al ($^{15}\text{NO}_3^-$ uptake in roots, FEBS Letters 489, 220-224, 2001), or Zhou et al (measurement of anion-elicited currents with the two-electrode

voltage-clamp method, J. Biol. Chem. 275, 39894-39899, 2000). If required, a *nar2* gene may be co-expressed to increase nitrate transport.

Alternatively, the activity of an NRT protein or homologue thereof may be assayed by expressing the NRT protein or homologue thereof under control of a GOS2 promoter in the *Oryza sativa* cultivar Nipponbare, which results in plants with increased aboveground biomass and/or increased seed yield compared to corresponding wild type plants. This increase in seed yield may be measured in several ways, for example as an increase of total seed weight, number of filled seeds or total number of seeds, as an increase of harvest index or as an increase of flowers per panicle.

Example 20: Cloning of nucleic acid sequence as represented by SEQ ID NO: 52

The *Oryza sativa* NRT gene was amplified by PCR using as template an *Oryza sativa* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.5 kb and the original number of clones was of the order of 1.59×10^7 cfu. Original titer was determined to be 9.6×10^5 cfu/ml after first amplification of 6×10^{11} cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 μ l PCR mix. Primers prm07061 (SEQ ID NO: 54; sense, start codon in bold, AttB1 site in italic: 5'-**ggggacaagttt**gtacaaaaaagcaggcttaaaca atggactcgtcgacggtg-3') and prm07062 (SEQ ID NO: 55 reverse, complementary, stop codon in bold, AttB2 site in italic: 5'-**ggggaccacttt**gtacaagaagctgggtc\cggl.cgcagaattgWlac-3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 1683 bp (including attB sites) was amplified and purified also using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombines *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone". Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.

Example 21: Expression vector construction using the nucleic acid sequence as represented by SEQ ID NO: 52

The entry clone was subsequently used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already cloned in the entry clone. A rice GOS2 promoter (nucleotides 1 to 2188 of SEQ ID NO: 56, the

promoter-gene combination) for constitutive expression was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector for *NRT* (Figure 7) was transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants.

Example 22: Plant transformation

Rice transformation

The *Agrobacterium* containing the expression vector was used to transform *Oryza sativa* plants. Mature dry seeds of the rice japonica cultivar Nipponbare were dehusked. Sterilization was carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2% HgCl_2 , followed by a 6 times 15 minutes wash with sterile distilled water. The sterile seeds were then germinated on a medium containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli were excised and propagated on the same medium. After two weeks, the calli were multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces were subcultured on fresh medium 3 days before co-cultivation (to boost cell division activity).

Agrobacterium strain LBA4404 containing the expression vector was used for cocultivation. *Agrobacterium* was inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28°C. The bacteria were then collected and suspended in liquid co-cultivation medium to a density (OD600) of about 1. The suspension was then transferred to a Petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues were then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25°C. Co-cultivated calli were grown on 2,4-D-containing medium for 4 weeks in the dark at 28°C in the presence of a selection agent. During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential was released and shoots developed in the next four to five weeks. Shoots were excised from the calli and incubated for 2 to 3 weeks on an auxin-containing medium from which they were transferred to soil. Hardened shoots were grown under high humidity and short days in a greenhouse.

Approximately 35 independent TO rice transformants were generated for one construct. The primary transformants were transferred from a tissue culture chamber to a greenhouse. After a quantitative PCR analysis to verify copy number of the T-DNA insert, only single copy transgenic plants that exhibit tolerance to the selection agent were kept for harvest of T1 seed. Seeds were then harvested three to five months after transplanting. The method yielded single

locus transformants at a rate of over 50 % (Aldemita and Hodges1996, Chan *et al.* 1993, Hiei *etal.* 1994).

Example 23: Phenotypic evaluation procedure

23.1 Evaluation setup

Approximately 35 independent TO rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T1 seed. Five events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homo-zygotes) and approximately 10 T1 seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. The transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions under the following environmental settings: photoperiod= 11.5 h, daylight intensity= 30,000 lux or more, daytime temperature= 28 °C or higher, night time temperature= 22 °C, relative humidity= 60-70%.

Four T1 events were further evaluated in the T2 generation following the same evaluation procedure as for the T1 generation but with more individuals per event. From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

23.2 Statistical analysis:

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and to verify for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the mere presence or position of the gene that is causing the differences in phenotype.

To check for an effect of the genes within an event, i.e., for a line-specific effect, a t-test was performed within each event using data sets from the transgenic plants and the corresponding null plants. "Null plants" or "null segregants" or "nullizygotes" are the plants treated in the same way as the transgenic plant, but from which the transgene has segregated. Null plants can also be described as the homozygous negative transformed plants. The threshold for

significance for the t-test is set at 10% probability level. The results for some events can be above or below this threshold. This is based on the hypothesis that a gene might only have an effect in certain positions in the genome, and that the occurrence of this position-dependent effect is not uncommon. This kind of gene effect is also named herein a "line effect of the gene". The p-value is obtained by comparing the t-value to the t-distribution or alternatively, by comparing the F-value to the F-distribution. The p-value then gives the probability that the null hypothesis (i.e., that there is no effect of the transgene) is correct.

Because two experiments with overlapping events had been carried out, a combined analysis was performed. This is useful to check consistency of the effects over the two experiments, and if this is the case, to accumulate evidence from both experiments in order to increase confidence in the conclusion. The method used was a mixed-model approach that takes into account the multilevel structure of the data (i.e. experiment - event - segregants). P-values are obtained by comparing likelihood ratio test to chi square distributions.

23.3 Parameters measured

Biomass-related parameter measurement

From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

The plant aboveground area (or leafy biomass) was determined by counting the total number of pixels on the digital images from aboveground plant parts discriminated from the background. This value was averaged for the pictures taken on the same time point from the different angles and was converted to a physical surface value expressed in square mm by calibration. Experiments show that the aboveground plant area measured this way correlates with the biomass of plant parts above ground. The aboveground area is the time point at which the plant had reached its maximal leafy biomass. The early vigour is the plant (seedling) aboveground area three weeks post-germination.

Seed-related parameter measurements

The mature primary panicles were harvested, counted, bagged, barcode-labelled and then dried for three days in an oven at 37°C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. The total seed yield was measured by weighing all filled husks harvested from a plant. Total

seed number per plant was measured by counting the number of husks harvested from a plant. Thousand Kernel Weight (TKW) is extrapolated from the number of filled seeds counted and their total weight. The Harvest Index (HI) in the present invention is defined as the ratio between the total seed yield and the above ground area (mm^2), multiplied by a factor 10^6 . The total number of flowers per panicle as defined in the present invention is the ratio between the total number of seeds and the number of mature primary panicles. The seed fill rate as defined in the present invention is the proportion (expressed as a %) of the number of filled seeds over the total number of seeds (or florets). The flowers-per-panicle is a parameter estimating the average number of florets per panicle on a plant, derived from the number of total seeds divided by the number of first panicles. The tallest panicle and all the panicles that overlapped with the tallest panicle when aligned vertically, were considered as first panicles and were counted manually.

Example 24: Results of the phenotypic evaluation of the transgenic plants

Upon analysis of the seeds as described above, the inventors found that plants transformed with the *NRT* gene construct had a higher seed yield, expressed as number of filled seeds (which may be at least in part the result of an increased fill rate), total weight of seeds and harvest index, compared to plants lacking the *NflT* transgene.

The results obtained for plants in the T1 generation are summarised in Table N:

Table N:

	% difference	p-value
Nr filled seeds	+48	0.0000
Total weight seeds	+54	0.0000
Harvest Index	+38	0.0000
Flowers/panicle	+14	0.0003
Total nr seeds	+13	0.0287

These positive results seed yield were again obtained in the T2 generation. In Table O, data show the overall % increases for the number of filled seeds, total weight of seeds and harvest index, calculated from the data of the individual lines of the T2 generation, and the respective p-values. These T2 data were re-evaluated in a combined analysis with the results for the T1 generation, and the obtained p-values show that the observed effects were highly significant.

Table O :

	T2 generation		Combined analysis
	% difference	p-value	p-value
Nr filled seeds	+100	0.0000	0.0000
Total weight seeds	+104	0.0000	0.0000
Harvest Index	+83	0.0000	0.0000
Flowers/panicle	+18	0.0000	0.0000
Total nr seeds	+20	0.0000	0.0000

In addition, the transgenic plants also showed an increase in biomass (areamax: +7% in the T1 generation and +4% in T2) which increase was significant (p-value of combined analysis: 0.0001).

Examples YEP16 polypeptides and encoding nucleic acids

Example 25: Gene Cloning of *Arabidopsis thaliana* YEP16-encoding nucleic acid

The *Arabidopsis thaliana* YEP16-encoding gene was amplified by PCR using as template an *Oryza sativa* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.6 kb and the original number of clones was of the order of 1.67×10^7 cfu. Original titer was determined to be 3.34×10^6 cfu/ml after first amplification of 6×10^{10} cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 μ l PCR mix. Primers prm00735 (SEQ ID NO: 144; sense, start codon in bold, AttB1 site in italic: 5'-*ggggacaagttgtacaaaaaagc* aggcffcacaatggatactctctcagcatcc-3') and prm00736 (SEQ ID NO: 145; reverse, complementary, AttB2 site in italic: 5'-*ggggaccactttgtacaagaaagctgggtt.gta*l.ca\caagaaaccaga-3'), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 12173 bp (including attB sites; from start to stop 1050 bp) was amplified and purified also using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombines *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone". Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.

Example 26: Vector Construction

The entry clone was subsequently used in an LR reaction with p00640, a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already

cloned in the entry clone. A rice oleosin promoter (SEQ ID NO: 143) for seed-specific expression was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector (Figure 9) was transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described in Example 27.

Example 27: Evaluation and Results of *Oryza sativa* YEP16-encoding nucleic acid under the control of the rice oleosin promoter in normal growth conditions

Approximately 15 to 20 independent T₀ rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T₁ seed. Seven events, of which the T₁ progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T₁ seedlings containing the transgene (hetero- and homo-zygotes) and approximately 10 T₁ seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. 4 T₁ events were further evaluated in the T₂ generation following the same evaluation procedure as for the T₁ generation but with more individuals per event.

27.1 Statistical analysis: F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the presence or position of the gene that is causing the differences in phenotype.

Seed-related parameter measurements

The mature primary panicles were harvested, counted, bagged, barcode-labelled and then dried for three days in an oven at 37 °C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. The total seed yield was measured by weighing all filled husks harvested from a plant. Total

seed number per plant was measured by counting the number of husks harvested from a plant. Thousand kernel weight (TKW) was extrapolated from the number of filled seeds counted and their total weight. The harvest index (HI) in the present invention is defined as the ratio between the total seed yield and the above ground area (mm²), multiplied by a factor 10⁶.

- 5 The total number of flowers per panicle as defined in the present invention is the ratio between the total number of seeds and the number of mature primary panicles.

The number of filled seeds, the total seed yield (total weight of seeds), fill rate of seeds (which is the number of filled seeds divided by the total number of seeds and multiplied by 100) and
10 the harvest index of transgenic plants transformed with a YEP16-encoding nucleic acid are shown in Table P. These parameters were significantly increased in the T1 generation compared to corresponding control plants. Average increases in the same parameters were also observed in the T2 generation.

- 15 **Table P:** Results of number of filled seeds, total seed weight, fill rate and harvest index in the T1 generation of transgenic plants transformed with a YEP16-encoding nucleic acid

Phenotype	T1 evaluation: Number of events showing an increase	P value of F test
Total weight of seeds	All 3 lines showed an average increase of 22%	Significant
Number of filled seeds	All 3 lines showed an average increase of 22%	Significant
Fill rate of seeds	All 3 lines showed an average increase of 15%	Significant
Harvest Index	All 3 lines showed an average increase of 18%	Significant

Examples: Group I sha $\alpha\alpha$ v-like kinase and encoding nucleic acids

Example 28: Gene Cloning

- 20 The *Oryza sativa* Group I shaggy-like kinase-encoding gene was amplified by PCR using as a template an *Arabidopsis thaliana* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.5 kb and the original number of clones was of the order of 1.59x10⁷ cfu. Original titer was determined to be 9.6x10⁵ cfu/ml after first
25 amplification of 6x10¹¹ cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 μ l PCR mix. Primers prm5797 (SEQ ID NO: 179; sense, start codon in bold, AttB1 site in italic: 5'-ggggacaagttgtacaaaaaagcaggcctaaacaa|ggg|Xcag|.agggg|Xg-3') and prm5798 (SEQ ID NO: 180; reverse, complementary, stop codon in bold, AttB2 site in italic: 5'-ggggaccactttgtacaaga
aagc/ggg.gaagctgtctcactactcctgc-3'), which include the AttB sites for Gateway recombination,
30 were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase in standard conditions. A PCR fragment of 1328 bp was amplified and purified also using

standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombines *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone". Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.

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Example 29: Vector Construction

The entry clone was subsequently used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already cloned in the entry clone. A GOS2 promoter from rice, for constitutive expression, was upstream of this Gateway cassette (De Pater *et al.*, Plant J. 1992 Nov; 2(6):837-44).

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After the LR recombination step, the resulting expression vector (Figure 15) was transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants as described in Example 30.

Example 30: Rice Transformation

Mature dry seeds of a rice japonica cultivar were dehusked. Sterilization was carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2%HgCl₂, followed by a 6X15 minute wash with sterile distilled water. The sterile seeds were then germinated on a medium containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli were excised and propagated on the same medium. After two weeks, the calli were multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces were sub-cultured on fresh medium 3 days before co-cultivation (to boost cell division activity). *Agrobacterium* strain LBA4404 harbouring binary T-DNA vectors were used for co-cultivation. *Agrobacterium* was inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28°C. The bacteria were then collected and suspended in liquid co-cultivation medium to a density (OD₆₀₀) of about 1. The suspension was then transferred to a petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues were then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25°C. Co-cultivated calli were grown on 2,4-D-containing medium for 4 weeks in the dark at 28°C in the presence of a suitable concentration of the selective agent. During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential was released and shoots developed in the next four to five weeks. Shoots were excised from the calli and incubated for

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2 to 3 weeks on an auxin-containing medium from which they were transferred to soil. Hardened shoots were grown under high humidity and short days in a greenhouse. Seeds were then harvested three to five months after transplanting. The method yielded single locus transformants at a rate of over 50 (Aldemita and Hodges, *Planta*, 199 612-617, 1996; Chan et al., *Plant Mol. Biol.* 22 (3) 491 -506, 1993, Hiei et al., *Plant J.*, 6 (2) 271 -282, 1994).

Example 31: Salt Stress Screen

Seeds were sown and seedlings selected by monitoring visual marker expression. Ten days after sowing, the seedlings were transplanted to plastic pots, 12cm in diameter, filled with a 1:1 mixture of moist sand and vermiculite. The pots were soaked in fresh water before transplantation. Seedlings were then transplanted from tissue culture chambers to a greenhouse for growing and harvest of T₁ seed. The pots were submitted to salt conditions one day after transplantation. Pots were watered 4 times a day at 8am, 12pm, 4pm, and 9pm with a salt-stress nutrient solution containing 25mM NaCl and the components listed below.

- NPK Nutrient mix, 20-20-20 Peters professional (Scotts, Marysville, OH, USA) at a concentration of 1 kg/m³.
- Magnesium chelate, Chelal Mg (BMS, Bornem, Belgium) at 333.33 ml / m³
- Iron chelate, Libfer (CIBA, Bradford, UK) at 21.67 g / m³
- NaCl 1.425 kg / m³

Salt concentration was monitored on a weekly basis and additions were made where necessary. Plants were grown under these conditions until the start of grain filling. They were then transferred to a different compartment of the greenhouse where they were irrigated daily with fresh water until seed harvest. Growth and yield parameters were recorded as detailed in Example 32.

Example 32: Evaluation and Results

Approximately 15 to 20 independent T₀ rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T₁ seed. At least 5 events for which the T₁ progeny segregated 3:1 for presence/absence of the transgene were retained. For each of these events, approximately 10 T₁ seedlings containing the transgene (hetero- and homo-zygotes) and approximately 10 T₁ seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. 4 of the best performing T₁ events were further evaluated in the T₂ generation following the same evaluation procedure as for the T₁ generation but with more individuals per event.

Statistical analysis: F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention.

The F-test was carried out to check for an effect of the gene over all the transformation events and for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level. A significant F-test value points to a gene effect, meaning that it is not only the presence or position of the gene that is causing the differences in phenotype.

32.1 Seed-related parameter measurements

Mature primary panicles were harvested, bagged, barcode-labelled and then dried for three days in the oven at 37 °C. The panicles were then threshed and all the seeds were collected and counted. Filled husks were separated from the empty ones using an air-blowing device.

The empty husks were discarded and the remaining fraction was counted again. Filled husks were weighed on an analytical balance. The total seed yield was measured by weighing all filled husks harvested from a plant. The harvest index in the present invention is defined as a ratio of total seed yield and the aboveground area (mm²) multiplied by a factor 106.

The Table of results below show the p values from the F test for T1 and T2 evaluations. The percentage difference between the transgenics and the corresponding nullizygotes (or plants without the transgene) is also shown. For example, for total seed weight in the T1 generation, 2 events were positive for total seed weight (i.e., showed an increase in total seed weight (of >54%, with a p-value from the F-test of <0.1938) compared to the seed weight of corresponding nullizygote plants in conditions of salt stress). In the T2 generation, 1 event was positive for total seed weight (i.e., showed an increase in total seed weight (of 65%, with a p-value from the F-test of 0.0252) compared to the seed weight of corresponding nullizygote plants in conditions of salt stress).

Table Q: T1 and T2 generation shaggy-like kinase transgenic plants and corresponding non-transgenic plants under salt-stress

Phenotype	T1	Diff	p-value	T2	Diff	p-value
Area max	1 event	47%	0.0254	1 event	19%	0.0951
Number filled seeds	1 event	58%	0.0376	1 event	61%	0.0313
Total number seeds	2 events	41%	<0.191	1 event	28%	0.0999
Flower per panicle	1 event	55%	0.0177	1 event	26%	0.0072
Total seed weight	2 events	>54%	<0.1938	1 event	65%	0.0252

TKW				1 event	6%	0.1008
Harvest Index	2 events	>57%	<0.0627	1 event	54%	0.0086

Transformation of corn, wheat, soybean, canola, alfalfa with sequences useful in the methods of the invention

Corn transformation

Transformation of maize (*Zea mays*) is performed with a modification of the method described by Ishida et al. (1996) Nature Biotech 14(6): 745-50. Transformation is genotype-dependent in corn and only specific genotypes are amenable to transformation and regeneration. The inbred line A188 (University of Minnesota) or hybrids with A188 as a parent are good sources of donor material for transformation, but other genotypes can be used successfully as well. Ears are harvested from corn plant approximately 11 days after pollination (DAP) when the length of the immature embryo is about 1 to 1.2 mm. Immature embryos are cocultivated with *Agrobacterium tumefaciens* containing the expression vector, and transgenic plants are recovered through organogenesis. Excised embryos are grown on callus induction medium, then maize regeneration medium, containing the selection agent (for example imidazolinone but various selection markers can be used). The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to maize rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Wheat transformation

Transformation of wheat is performed with the method described by Ishida et al. (1996) Nature Biotech 14(6): 745-50. The cultivar Bobwhite (available from CIMMYT, Mexico) is commonly used in transformation. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* containing the expression vector, and transgenic plants are recovered through organogenesis. After incubation with *Agrobacterium*, the embryos are grown in vitro on callus induction medium, then regeneration medium, containing the selection agent (for example imidazolinone but various selection markers can be used). The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Soybean transformation

Soybean is transformed according to a modification of the method described in the Texas A&M patent US 5,164,310. Several commercial soybean varieties are amenable to transformation by this method. The cultivar Jack (available from the Illinois Seed foundation) is commonly used for transformation. Soybean seeds are sterilised for in vitro sowing. The hypocotyl, the radicle and one cotyledon are excised from seven-day old young seedlings. The epicotyl and the remaining cotyledon are further grown to develop axillary nodes. These axillary nodes are excised and incubated with *Agrobacterium tumefaciens* containing the expression vector. After the cocultivation treatment, the explants are washed and transferred to selection media. Regenerated shoots are excised and placed on a shoot elongation medium. Shoots no longer than 1 cm are placed on rooting medium until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Rapeseed/canola transformation

Cotyledonary petioles and hypocotyls of 5-6 day old young seedling are used as explants for tissue culture and transformed according to Babic et al. (1998, Plant Cell Rep 17: 183-188). The commercial cultivar Westar (Agriculture Canada) is the standard variety used for transformation, but other varieties can also be used. Canola seeds are surface-sterilized for in vitro sowing. The cotyledon petiole explants with the cotyledon attached are excised from the in vitro seedlings, and inoculated with *Agrobacterium* (containing the expression vector) by dipping the cut end of the petiole explant into the bacterial suspension. The explants are then cultured for 2 days on MSBAP-3 medium containing 3 mg/l BAP, 3 % sucrose, 0.7 % Phytagar at 23 °C, 16 hr light. After two days of co-cultivation with *Agrobacterium*, the petiole explants are transferred to MSBAP-3 medium containing 3 mg/l BAP, cefotaxime, carbenicillin, or timentin (300 mg/l) for 7 days, and then cultured on MSBAP-3 medium with cefotaxime, carbenicillin, or timentin and selection agent until shoot regeneration. When the shoots are 5 - 10 mm in length, they are cut and transferred to shoot elongation medium (MSBAP-0.5, containing 0.5 mg/l BAP). Shoots of about 2 cm in length are transferred to the rooting medium (MSO) for root induction. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Alfalfa transformation

A regenerating clone of alfalfa (*Medicago sativa*) is transformed using the method of (McKersie et al., 1999 Plant Physiol 119: 839-847). Regeneration and transformation of alfalfa is genotype dependent and therefore a regenerating plant is required. Methods to obtain

regenerating plants have been described. For example, these can be selected from the cultivar Rangeland (Agriculture Canada) or any other commercial alfalfa variety as described by Brown DCW and A Atanassov (1985. Plant Cell Tissue Organ Culture 4: 111-112). Alternatively, the RA3 variety (University of Wisconsin) has been selected for use in tissue culture (Walker et al., 1978 Am J Bot 65:654-659). Petiole explants are cocultivated with an overnight culture of *Agrobacterium tumefaciens* C58C1 pMP90 (McKersie et al., 1999 Plant Physiol 119: 839-847) or LBA4404 containing the expression vector. The explants are cocultivated for 3 d in the dark on SH induction medium containing 288 mg/ L Pro, 53 mg/ L thioproline, 4.35 g/ L K₂SO₄, and 100 µm acetosyringone. The explants are washed in half-strength Murashige-Skoog medium (Murashige and Skoog, 1962) and plated on the same SH induction medium without acetosyringone but with a suitable selection agent and suitable antibiotic to inhibit *Agrobacterium* growth. After several weeks, somatic embryos are transferred to BOi2Y development medium containing no growth regulators, no antibiotics, and 50 g/ L sucrose. Somatic embryos are subsequently germinated on half-strength Murashige-Skoog medium. Rooted seedlings were transplanted into pots and grown in a greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Claims

1. Method for increasing plant yield relative to corresponding wild type plants comprising modulating expression in a plant of a nucleic acid encoding class I homeodomain leucine zipper (HDZip) hox5 polypeptide or homologue thereof, and optionally selecting for plants having increased yield, wherein said class I HDZip hox5 polypeptide or homologue comprises from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads.

2. Method according to claim 1, wherein said class I HDZip hox5 polypeptide or homologue thereof further comprises one or both of the following: (i) a Trp tail; and (ii) a RPFF amino acid motif, where R is Arg, P Pro and F Phe, and within this motif, allowing one or more conservative change(s) at any position, and/or one or two non-conservative change(s) at any position.

3. Method according to claim 1 or 2, wherein said modulated expression is effected by introducing a genetic modification preferably in the locus of a gene encoding a class I HDZip hox5 polypeptide or a homologue thereof.

4. Method according to claim 3, wherein said genetic modification is effected by one of: T-DNA activation, TILLING, site-directed mutagenesis or directed evolution.

5. Method for increasing plant yield relative to corresponding wild type plants comprising introducing and expressing in a plant a class I HDZip hox5 nucleic acid or a variant thereof.

6. Method according to claim 5, wherein said variant is a portion of a class I HDZip hox5 nucleic acid, which portion encodes a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads.

7. Method according to claim 5, wherein said variant is a sequence capable of hybridising to a class I HDZip hox5 nucleic acid, which hybridising sequence encodes a polypeptide comprising from N-terminal to C-terminal: (i) an acidic box; and (ii) a class I homeodomain; and (iii) a leucine zipper with more than 5 heptads.

8. Method according to claims 5 to 7, wherein said class I HDZip hox5 nucleic acid or variant thereof is overexpressed in a plant.

9. Method according to any one of claims 5 to 8, wherein said class I HDZip hox5 nucleic acid or variant thereof is of plant origin, preferably from a monocotyledon plant, further preferably from the family Poaceae, more preferably from the genus *Oryza*, most preferably from *Oryza sativa*.

10. Method according to any one of claims 5 to 9, wherein said variant encodes an orthologue or paralogue of the class I HDZip hox5 protein of SEQ ID NO: 2.

11. Method according to any one of claims 5 to 10, wherein said class I HDZip hox5 nucleic acid or variant thereof is operably linked to a constitutive promoter.

12. Method according to claim 11, wherein said constitutive promoter is a GOS2 promoter, more preferably the constitutive promoter is a rice GOS2 promoter, further preferably the constitutive promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 33 or SEQ ID NO: 178, most preferably the constitutive promoter is as represented by SEQ ID NO: 33 or SEQ ID NO: 178.

13. Method according to any one of claims 1 to 12, wherein said increased yield is selected from one or more of: increased number of filled seeds, increased total seed yield, increased number of flowers per panicle, increased seed fill rate, increased harvest index (HI), increased thousand kernel weight (TKW), increased root length or increased root diameter, each relative to corresponding wild type plants.

14. Method according to any one of claims 1 to 13, wherein said increased yield occurs under abiotic stress.

15. Method according to claim 14, wherein said abiotic stress is an osmotic stress, selected from one or more of: water stress, salt stress, oxidative stress and ionic stress, preferably wherein said water stress is drought stress.

16. Method according to claim 14 or 15, wherein said abiotic stress tolerance is manifested as increased yield selected from one or more of: increased number of filled seeds, increased total seed yield, increased number of flowers per panicle, increased seed fill rate, increased HI, increased TKW, increased root length or increased root diameter, each relative to corresponding wild type plants.

17. Method according to claims 13 to 16, wherein said increased yield comprises increased greenness index.

18. Plant, plant part or plant cell obtainable by a method according to any one of claims 1 to 17.

19. Use of a construct comprising:

- (i) a class I HDZip hox5 nucleic acid or variant thereof
- (ii) one or more control sequences capable of driving expression of the nucleic acid sequence of (i), and optionally
- (iii) a transcription termination sequence

in a method according to any one of claims 5 to 17.

20. Construct according to claim 19, wherein said control sequence is a constitutive promoter.

21. Construct according to claim 20, wherein said constitutive promoter is a GOS2 promoter, preferably the rice GOS2 promoter, further preferably the constitutive promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 33 or SEQ ID NO: 178, most preferably the constitutive promoter is as represented by SEQ ID NO: 33 or SEQ ID NO: 178.

22. Plant, plant part or plant cell transformed with a construct comprising a class I HDZip hox5 nucleic acid or variant thereof under the control of a GOS2 promoter.

23. Method for the production of a transgenic plant having increased yield relative corresponding wild type plant, which method comprises:

- (i) introducing and expressing in a plant or plant cell a class I HDZip hox5 nucleic acid or variant thereof ;
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

24. Method according to claim 23 wherein said increased yield occurs under increased abiotic stress.

25. Transgenic plant having increased yield relative to corresponding wild type plant, said increased yield resulting from a class I HDZip hox5 nucleic acid or a variant thereof introduced into said plant.

26. Transgenic plant according to claim 18, 22 or 25, wherein said plant is a monocotyledonous plant, such as sugar cane or wherein the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, oats or sorghum.

27. Harvestable parts of a plant according to any one of claims 18, 22, 25 or 26.

28. Harvestable parts of a plant according to claim 27, wherein said harvestable parts are seeds.

29. Products derived from a plant according to claim 26 and/or from harvestable parts of a plant according to claims 27 or 28.

30. Use of a class I HDZip hox5 nucleic acid/gene or variant thereof, or use of a class I HDZip hox5 polypeptide or homologue thereof, in increasing plant yield relative to corresponding wild type plants.

31. Use according to claim 30, wherein said increased yield is selected from one or more of: increased number of filled seeds, increased total seed yield, increased number of flowers per panicle, increased seed fill rate, increased HI, increased TKW, increased root length or increased root diameter, each relative to corresponding wild type plants.

32. Use according to claims 30 or 31, wherein said increased yield occurs under increased abiotic stress.

33. Use according to claim 32, wherein said increased yield comprises increased greenness index.

34. Use of a class I HDZip hox5 nucleic acid/gene or variant thereof, or use of a class I HDZip hox5 polypeptide or homologue thereof, as a molecular marker.

35. Method for improving growth characteristics of plants relative to corresponding wild type plants, comprising modulating expression in a plant of a nucleic acid encoding an NRT

polypeptide or a homologue thereof, and optionally selecting for plants having improved growth characteristics.

36. Method according to claim 35, wherein said modulated expression is effected by introducing a genetic modification preferably in the locus of a gene encoding an NRT polypeptide or a homologue thereof.

37. Method according to claim 36, wherein said genetic modification is effected by one of: T-DNA activation, TILLING, site-directed mutagenesis, homologous recombination or directed evolution.

38. Method for improving growth characteristics relative to corresponding wild type plants, comprising introducing and expressing in a plant an *NRT* nucleic acid or a variant thereof.

39. Method according to claim 38, wherein said nucleic acid encodes a homologue of the NRT protein of SEQ ID NO: 53, preferably said nucleic acid encodes an orthologue or paralogue of the NRT protein of SEQ ID NO: 53.

40. Method according to claim 38, wherein said variant is a portion of an *NRT* nucleic acid or a sequence capable of hybridising to an *NRT* nucleic acid, which portion or hybridising sequence encodes a polypeptide comprising (i) an MFS_1 domain, (ii) a transmembrane domain located C-terminally of the MFS_1 domain and preferably also having NRT activity.

41. Method according to any of claims 38 to 40, wherein said *NRT* nucleic acid or variant thereof is overexpressed in a plant.

42. Method according to any one of claims 38 to 41, wherein said *NRT* nucleic acid or variant thereof is of plant origin, preferably from a monocotyledonous plant, more preferably from the family Poaceae, most preferably the nucleic acid is from *Oryza sativa*.

43. Method according to any one of claims 38 to 42, wherein said *NRT* nucleic acid or variant thereof is operably linked to a constitutive promoter.

44. Method according to claim 43, wherein said constitutive promoter is a GOS2 promoter.

45. Method according to any one of claims 35 to 44, wherein said improved growth characteristic is increased yield.

46. Method according to claim 45, wherein said increased yield is increased seed yield.

47. Method according to claim 46, wherein said increased seed yield is selected from:
increased total weight of seeds, increased total number of seeds, increased number of filled
seeds, increased number of flowers per panicle or increased harvest index.

48. Plant or plant cell obtainable by a method according to any one of claims 35 to 47.

49. Construct comprising:

- (i) an *NRT* nucleic acid or a variant thereof;
- (ii) one or more control sequences capable of driving expression of the nucleic acid sequence of (i); and optionally
- (iii) a transcription termination sequence.

50. Construct according to claim 49, wherein said control sequence is a constitutive promoter.

51. Construct according to claim 50, wherein said constitutive promoter is a GOS2 promoter.

52. Construct according to claim 51, wherein said GOS2 promoter is as represented by nucleotides 1 to 2193 in SEQ ID NO: 56.

53. Plant or plant cell transformed with a construct according to any one of claims 49 to 52.

54. Method for the production of a transgenic plant having increased yield compared to corresponding wild type plants, which method comprises:

- (i) introducing and expressing in a plant or plant cell an *NRT* nucleic acid or variant thereof;
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

55. Transgenic plant or plant cell having improved growth characteristics resulting from an *NRT* nucleic acid or a variant thereof introduced into said plant.

56. Transgenic plant or plant cell according to claim 48, 53 or 55, wherein said plant is a monocotyledonous plant, such as sugar cane or wherein the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, oats or sorghum, or wherein said transgenic plant cell is derived from a monocotyledonous plant, such as sugar cane or wherein the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, oats or sorghum.

57. Harvestable parts of a plant according to any one of claims 48, 53, 55 or 56.

58. Harvestable parts of a plant according to claim 57 wherein said harvestable parts are seeds.

59. Products directly derived from a plant according to claim 56 and/or from harvestable parts of a plant according to claims 57 or 58.

60. Use of an *NRT* nucleic acid/gene or variant thereof, or use of an *NRT* polypeptide or a homologue thereof, in improving growth characteristics of plants, preferably in improving yield, especially seed yield, relative to corresponding wild type plants.

61. Use according to claim 60, wherein said seed yield is one or more of: increased total weight of seeds, increased total number of seeds, increased number of filled seeds, increased number of flowers per panicle or increased harvest index.

62. Use of an *NRT* nucleic acid/gene or variant thereof, or use of an *NRT* polypeptide or a homologue thereof, as a molecular marker.

63. Method for improving plant yield relative to corresponding wild type plants, comprising modulating expression in a plant of a nucleic acid encoding a YEP16 polypeptide or a homologue thereof, wherein said YEP16 polypeptide or a homologue thereof comprises, in increasing order of preference, at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128.

64. Method according to claim 63, wherein said modulated expression is increased expression.

65. Method according to claim 63 or 64, wherein said modulated expression is effected by introducing a genetic modification preferably in the locus of a gene encoding a YEP16 polypeptide or a homologue thereof.

66. Method according to claim 65, wherein said genetic modification is effected by one of: T-DNA activation, TILLING, site-directed mutagenesis or directed evolution.

67. Method for improving plant yield relative to corresponding wild type plants comprising introducing and expressing in a plant a nucleic acid encoding a YEP16 polypeptide or a homologue thereof, wherein said YEP16 polypeptide or a homologue thereof comprises in increasing order of preference at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128.

68. Method according to any one of claims 63 to 67, wherein said YEP16 polypeptide or homologue thereof is targeted to a plastid.

69. Method according to claim 68, wherein said plastid is a chloroplast.

70. Method according to any one of claims 67 to 69, wherein said nucleic acid encoding a YEP16 polypeptide or a homologue thereof is a nucleic acid sequence capable of hybridising under reduced stringency conditions to a nucleic acid as represented by SEQ ID NO: 127 or SEQ ID NO: 129.

71. Method according to any one of claims 67 to 70, wherein said nucleic acid encoding a YEP16 polypeptide or a homologue thereof is a nucleic acid sequence having in increasing order of preference, at least 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575 consecutive nucleotides of a nucleic acid as represented by SEQ ID NO: 127 or SEQ ID NO: 129.

72. Method according to any one of claims 67 to 71, wherein said nucleic acid encoding a YEP16 polypeptide or a homologue thereof encodes an orthologue or paralogue of the YEP16 polypeptide of SEQ ID NO: 128 or SEQ ID NO: 130.

73. Method according to claims 67 to 72, wherein said nucleic acid encoding a YEP16 polypeptide or a homologue thereof is overexpressed in a plant.

74. Method according to any one of claims 67 to 73, wherein said nucleic acid encoding a YEP16 polypeptide or a homologue thereof is of plant origin, preferably from a dicotyledonous species, further preferably from the family Brassicaceae, more preferably from *Arabidopsis thaliana*.

75. Method according to any one of claims 67 to 74, wherein said nucleic acid encoding a YEP1 6 polypeptide or a homologue thereof is operably linked to a seed-specific promoter.

76. Method according to claim 75, wherein said seed-specific promoter is an oleosin promoter, preferably the oleosin promoter from rice, further preferably as represented by SEQ ID NO: 143.

77. Method according to any one of claims 63 to 76, wherein said improved yield is improved seed yield relative to corresponding wild type plants.

78. Method according to claim 77, wherein said improved seed yield is selected from any one or more of increased seed weight, increased number of filled seeds, increased seed fill rate and increased harvest index.

79. Plant or plant cell obtainable by a method according to any one of claims 63 to 78.

80. Construct comprising:

- (i) a nucleic acid encoding a YEP1 6 polypeptide or a homologue thereof, wherein said YEP1 6 polypeptide or a homologue thereof comprises in increasing order of preference at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128;
- (ii) one or more control sequences capable of driving expression of the nucleic acid sequence of (i); and optionally
- (iii) a transcription termination sequence.

81. Construct according to claim 80, wherein said control sequence is a seed-specific promoter.

82. Construct according to claim 81, wherein said seed-specific promoter is an oleosin promoter, preferably the oleosin promoter from rice.

83. Plant, plant part or plant cell transformed with a construct according to any one of claims 80 to 82.

84. Method for the production of a transgenic plant having improved yield relative to a corresponding wild type plant, which method comprises:

(i) introducing and expressing in a plant or plant cell a nucleic acid encoding a YEP1 6 polypeptide or a homologue thereof, wherein said YEP16 polypeptide or a homologue thereof comprises in increasing order of preference at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128;

(ii) cultivating the plant cell under conditions promoting plant growth and development.

85. Transgenic plant having improved yield relative to corresponding wild type plant resulting from a nucleic acid encoding a YEP1 6 polypeptide or a homologue thereof, wherein said YEP1 6 polypeptide or a homologue thereof comprises in increasing order of preference at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128.

86. Transgenic plant according to claim 79, 83 or 85, wherein said plant is a monocotyledonous plant, such as sugar cane or wherein the plant is a cereal, such as rice, maize, wheat, barley, millet, rye, oats or sorghum.

87. Harvestable parts of a plant according to any one of claims 79, 83, 85 or 86.

88. Harvestable parts of a plant according to claim 87 wherein said harvestable parts are seeds.

89. Products directly derived from a plant according to claim 86 and/or from harvestable parts of a plant according to claims 87 or 88.

90. Use of a nucleic acid encoding a YEP1 6 polypeptide or a homologue thereof, wherein said YEP1 6 polypeptide or a homologue thereof comprises in increasing order of preference at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128 in improving plant yield relative to corresponding wild type plants.

91. Use according to claim 90, wherein said improved yield is selected from one or more or all of: increased seed weight, increased number of filled seeds, increased fill rate and increased harvest index.

92. Use of a nucleic acid encoding a YEP16 polypeptide or a homologue thereof as a molecular marker, wherein said YEP16 polypeptide or a homologue thereof comprises in increasing order of preference at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to the amino acid sequence of SEQ ID NO: 128.

93. Method for improving abiotic stress tolerance in plants, comprising increasing activity in a plant of a Group I shaggy-like kinase or a homologue thereof, which Group I shaggy-like kinase is one having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid.

94. Method according to claim 93, wherein said increased activity is effected by introducing a genetic modification, preferably in the locus of a Group I shaggy-like kinase-encoding gene, said locus being a genomic region which includes the gene of interest and 10KB up- or downstream of the coding region.

95. Method according to claim 94, wherein said genetic modification is effected by any one of: site-directed mutagenesis, homologous recombination, tilling, T-DNA activation and by introducing and expressing in a plant a nucleic acid encoding a Group I shaggy-like kinase or homologue thereof.

96. Method for improving abiotic stress tolerance in plants, comprising introducing and expressing in a plant a Group I shaggy-like kinase-encoding nucleic acid/gene or variant thereof.

97. Method according to claim 96, wherein said variant is a portion of a Group I shaggy-like kinase-encoding nucleic acid/gene and/or is a nucleic acid capable of hybridising with a Group I shaggy-like kinase-encoding nucleic acid/gene, which portion or hybridising sequence is at least 1,200 nucleotides in length, and which portion or hybridising sequence encodes a polypeptide having: (i) at least 77% sequence identity to the amino acid sequence represented by SEQ ID NO: 147; and (ii) having motif I: R/H/V/N/Q E/G LK G/N and motif II: K Q/N CXXX G/A/S, where X may be any amino acid.

98. Method according to claim 96 or 97, wherein said Group I shaggy-like kinase-encoding nucleic acid/gene or variant thereof is overexpressed in a plant.

99. Method according to any one of claims 96 to 98, wherein said Group I shaggy-like kinase-encoding nucleic acid/gene or variant thereof is of plant origin, preferably from a monocotyledonous plant, further preferably from the family Poaceae, more preferably from the genus *Oryza*, most preferably from *Oryza sativa*.

100. Method according to any one of claims 96 to 99, wherein said Group I shaggy-like kinase-encoding nucleic acid/gene or variant thereof is operably linked to a constitutive promoter, preferably to a GOS 2 promoter, such as the GOS2 promoter from rice.

101. Method according to any one of claims 93 to 100, wherein said abiotic stress is any one or more of: water stress, anaerobic stress, salt stress, temperature stress, chemical toxicity stress and oxidative stress.

102. Method according to any one of claims 93 to 101, wherein said abiotic stress is an osmotic stress, selected from salt stress, water stress, oxidative stress, ionic stress.

103. Plant or plant cell obtainable by a method according to any one of claims 93 to 102, which plant or plant cell has increased activity of a Group I shaggy-like kinase and/or increased expression of a Group I shaggy-like kinase-encoding nucleic acid.

104. Construct comprising:

- (i) A Group I shaggy-like kinase-encoding nucleic acid or variant thereof;
- (ii) one or more control sequences capable of driving expression of the nucleic acid sequence of (i); and optionally
- (iii) a transcription termination sequence.

105. Construct according to claim 104, wherein said control sequence comprises a constitutive promoter, preferably the GOS2 promoter, such as the GOS2 promoter from rice.

106. Plant or plant cell transformed with a construct according to claim 104 or 105.

107. Method for the production of transgenic plants having improved tolerance to abiotic stress, which method comprises:

- (i) introducing into a plant or plant cell a Group I shaggy-like kinase-encoding nucleic acid or variant thereof; and
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

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108. Method according to claim 107, wherein said abiotic stress is an osmotic stress, selected from salt stress, water stress, oxidative stress, ionic stress.

109. Transgenic plant having improved tolerance to abiotic stress relative to corresponding wild-type plants, which transgenic plant has increased activity of a Group I shaggy-like kinase and/or increased expression of a Group I shaggy-like kinase-encoding nucleic acid.

110. Transgenic plant according to any one of claims 103, 106 and 109, which transgenic plant is a crop plant such as soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco, further preferably a monocotyledonous plant, such as sugar cane, more preferably a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum or oats.

111. Harvestable parts, including seeds, of transgenic plant according to any one of claims 103, 106, 109 to 110.

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112. Use of a Group I shaggy-like kinase-encoding nucleic acid or variant thereof or use of a Group I shaggy-like kinase or homologue thereof in increasing plant tolerance to abiotic stress.

113. Use according to claim 112, wherein said abiotic stress is an osmotic stress, selected from salt stress, water stress, oxidative stress, ionic stress.

25

114. Use of a Group I shaggy-like kinase-encoding nucleic acid or variant thereof or use of a Group I shaggy-like kinase or homologue thereof as a molecular marker.

30

Class I homeodomain of HDZip

	Helix 1	Helix 2	Helix 3
1			60
Zeama_hox5 (SEQ ID NO 06)	APEKKRRLLTAEQVQVILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Glyma_HD157 (SEQ ID NO 20)	QPGKKRRLLTSEQVQVILERNFEVENKLEPERKVKQLAKELGLQPRQVAIWFCNRRARFVKTKQ		
Lyces_VaHOX1 (SEQ ID NO 28)	QAEKKRRLLTDNQVQVILLEKSFGEENKLEPERKVKQLAKELGLQPRQVAIWFCNRRARWTKTKQ		
Dauca_CHB3 (SEQ ID NO 18)	QPEKKRRLLKADQIQHLEKSFETDNKLEPERKVKQLAKELGLQPRQVAIWFCNRRARWTKTKT		
Medtr_hox16 (SEQ ID NO 30)	QSEKKRRLLSVDQVQVILLEKSFEEEDNKLEPERKTKLAKDLGLQPRQVAIWFCNRRARWTKTKQ		
Triae_hox16 (SEQ ID NO 14)	LPEKKRRLLTPEQVQHILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKT		
Goshi_hox5 (SEQ ID NO 24)	LPEKKRRLLTSEQVYILLEKSFEEENKLEPERKVKQLAKELGLQPRQVAVWFQNRARWTKTKQ		
Sorbi_hox5 (SEQ ID NO 12)	APEKKRRLLTAEQVQVILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Sacof_hox5 (SEQ ID NO 10)	APEKKRRLLTAEQVQVILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Aqufo_hox5 (SEQ ID NO 32)	LPEKKRRLLTSEQVHILLEKSFETENKLEPDRKTQLAKKLGLQPRQVAVWFQNRARWTKTKQ		
Orysa_hox5 (SEQ ID NO 02)	APEKKRRLLTAEQVQVILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Zeama_hox16 (SEQ ID NO 08)	LPEKKRRLLTPEQVQLILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Orysa_hox16 (SEQ ID NO 04)	LPEKKRRLLTPEQVHILERSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Lyces_hox5 (SEQ ID NO 26)	SPEKKRRLLTPEQVHILLEKSFETENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Arath_ATHB1 (SEQ ID NO 16)	LPEKKRRLLTPEQVHILLEKSFETENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Crapl_CPHB-5 (SEQ ID NO 22)	LPEKKRRLLTAEQVHILLEKSFEEENKLEPERKTELRRLGMAPRQVAVWFQNRARWTKTKQ		
Orysa_hox6 (SEQ ID NO 39)	AADKKRFRFSEEQIKSLESMFATQTKLEPRQKLQARELGLQPRQVAIWFCNRRARWTKSKQ		
Orysa_hox4 (SEQ ID NO 37)	GGEKKRRLLSVEQVRALLERSFEVENKLEPERKARLARDLGLQPRQVAVWFQNRARWTKTKQ		
Consensus	PEKKRRLLTAEQV ILERSFEEENKLEPERKT LARKLGLQPRQVAVWFQNRARWTKTKQ		

Homeodomain invariant amino acids	L ₁₆	W ₄₈ F ₄₉ N ₅₁ R ₅₃	
HDZip Class I preferred amino acids		A ₄₆	W ₅₆

FIGURE 1

Class I leucine zipper of HDzip									
Zeama_hox5	(SEQ ID NO 06)	TKQLETDYDRLLKAAAYDALAADHQQGLADNDNLRAQVISL	TEK						
Glyma_HD157	(SEQ ID NO 20)	TKQLEKDYGVLLKASYDRLLKSDYESLVQENDKLKAEVNSLES	K						
Lyces_VaHOX1	(SEQ ID NO 28)	TKQLEKDYDELRNRYDITLKSNNVNLKEDLLRTEVFRLLTGK							
Dauca_CHB3	(SEQ ID NO 18)	TKTLEKDYDVLLQNSYNLSKADYDNLAEKEKLKAEVLDLTDK							
Medtr_hox16	(SEQ ID NO 30)	TKQLEKDYDSLNDGYESLKTEDNLLKEKDRLLQSEVASL	TEK						
Triae_hox16	(SEQ ID NO 14)	TKTILERDFDRLKASFDALRADHDALLQDNHRLRSQVVTL	TEK						
Goshi_hox5	(SEQ ID NO 24)	TKQLERDYYDILLKSSFDSLQSNYDTILLKENEKLKSEVASL	TEK						
Sorbi_hox5	(SEQ ID NO 12)	TKQLETDYDRLLKAAAYDALAADHQQGLADNDSLRAQVISL	TDK						
Sacof_hox5	(SEQ ID NO 10)	TKQLETDYDHLKAAAYDALAADHQQGLADNDSLRAQVVS	LTEK						
Agufo_hox5	(SEQ ID NO 32)	TKQLERDYYDILLKASYDSLRSNDYDDIVKENEKLKSEVVS	LTKG						
Orysa_hox5	(SEQ ID NO 02)	TKQLEHDFDRLKAAAYDALAADHALLSDNDRLRAQVISL	TEK						
Zeama_hox16	(SEQ ID NO 08)	TKQLERDFDRLKASFDALRADHDALLQDNHRLRSQVVS	LTEK						
Orysa_hox16	(SEQ ID NO 04)	TKQLERDFDRLKASFDALRADHDALLQDNHRLHSQWMS	LTEK*						
Lyces_hox5	(SEQ ID NO 26)	TKQLERDYYDQLKSSYDSLSDFSVRKDNNDKLKSEVVS	LMEK						
Arath_ATHB1	(SEQ ID NO 16)	TKQLERDYYDILLKSTYDQLLSNYDSIVMDNDKLRS	SEVTSLTEK						
Crapl_CPHB-5	(SEQ ID NO 22)	TKQLERDYYDKLLKSSYDSLSTYDSIRQENDKLKAE	LKSLNEK						
Orysa_hox6	(SEQ ID NO 39)	SKQLEREYSALRDDYDALLCSSYESLKKEKLALI	KQLEKLAEM						
Orysa_hox4	(SEQ ID NO 37)	TKQLERDYAALRHYSYDSLRLDHDALRRDKDAL	LAEIKELKAK						
Consensus		TKQLERDYYD LKASYDALRADYDALL DNDKLRAE	VVS	LTEK					
		abcdefgabcde	fgabcde	fgabcde	fgabcde	fgabcde	fgabcde	fgabcde	fg

heptad1heptad2heptad3heptad4heptad5heptad6

FIGURE 1 (continued)

3/104

	1	50
Zeama_hox5	(1) ---MDPSAVSFDSGGARRGGG-----AQMLLFGGGGGSAN	
Aqufo_hox5	(1) ---MDSTTSRLFFDGSCHGN-----MLLLGSGDPV	
Arath_ATHB1	(1) ---MESNSFFFDPASHGNS-----MFFLCNLNPV	
Orysa_hox5	(1) ---MDPCRNVFDSGVARRACPGG-----AQMLLFGGGGGSAN	
Crapl_CPHB-5	(1) ---MNSARIFDPPSHGNMLQ-----FLGNAGGDSSV	
Dauca_CHB3	(1) ---MAGRRVFG---EGANTTSAS-----LLFHSQRPEPFLLSAPSPS	
Glyma_HD157	(1) ---MAGCKLYAGSNMSLLLQNER-----LPCSSEVLESLSWAQTSNPAS	
Goshi_Hox5	(1) ---MESGRLFFNPSTTHRN-----MLLLGNTPEI	
Lyces_hox5	(1) ---MGSCHIFFDPPSCHGN-----MLFLGSGDPV	
Lyces_VaHOX1	(1) ---MAPGILYGGSSNFDGVFTQKQRDVFSSTAPKGLGSLFAPASSSSN	
Medtr_HOX16_1	(1) ---MAGCKLFGGSNMSLLLQNER-----LPCTSEVLESLSWVHT--PAS	
Orysa_hox16	(1) ---MESGRLIFSTAGS---GAGQ-----MLFLDCGAGGGGVG	
Sacof_hox5	(1) ---MDPSAVSFNSGGARRGGGG-----TQMLLFGGGGGSAN	
Sorbi_hox5	(1) ---MDPSAVSFDSGGARRGGGG-----GAQMLLFGGGGGSAN	
Triae_hox16	(1) ---MEPCRLIENTSGS---GNGQ-----MLFMDCGAGGIA-G	
Zeama_hox16	(1) ---MESGRLIFNAPGS---GAGQ-----MLFLDCGAGGG--P	
Poptr_HOX16_1	(1) ---MAGGTGGSNNSLVLLQSQRG-----PCAASQPLESFFLSCS-SPS	
Poptr_HOX16_2	(1) MAACGGGGGGSNPNLSVLVQSQRG-----PCAASQPLEAFFLSCS-SPS	
Poptr_HOX16_3	(1) ---MAGDKDCGSSKMTIFLRNGR-----LPPCESLCILTS-FST	
Phavu_hox16	(1) ---MAGCKLHPGNSNMSLLLQNDR-----LPCSSEVLESLSWAHTSNAAS	
Lotco_HOX16	(1) ---MAGGRVFGSGSAAPANVSDTS-----LLLQNPDPDSSLFLSTSAS	
Medtr_HOX unknown	(1) MHEMAFFQANFMLQTPHHHDDHHQ-----PSSLNSILPQD	
Piclg_hox unknown	(1) ---MACDRSALYTSSVIMNTEDN-----SSAHAIAAMIASCTPPAT	
Orysa_hox4	(1) -----MKRPGGAGG	
Medtr_HOX unknown2	(1) -----MKRLNNTSDS	
Orysa_hox6	(1) -----	
Consensus	(1) M G F	G

	51	100
Zeama_hox5	(32) SNCFFRGVPMVAVLGMDDATRVG-----KRPFFTTHRE--ELLEEEYDE	
Aqufo_hox5	(28) LRCSR-----SFINMEDSL-----KRPFFYSST--DELEEEFYDE	
Arath_ATHB1	(28) VQGGGAR---SMMNMEETS-----KRPFFSSP--EDLYDDDFYDD	
Orysa_hox5	(34) SGCFFRGVPAAVLGMDESRRSSSAAGAGAKRPFFTTHRE--ELLEEEYDE	
Crapl_CPHB-5	(30) FRCTRSS---SVLNMEESS-----LHQIFSGGGDEFYDEEYDE	
Dauca_CHB3	(38) LIGS-----KSMVSFQDAKRKNP-----YDGFMRSYDEEEIGDEEYDE	
Glyma_HD157	(41) FOCS-----KPVVDFENVSGSR-----MTIRPFFQAIKEBENC-DEDEYEG	
Goshi_Hox5	(27) FREAR-----TMVSMEENP-----KRLFFSSP--EDLYDEEYDE	
Lyces_hox5	(27) FRCPRS---TMMKMEEDSS-----KRPFFSSP--EDLYDEEYDE	
Lyces_VaHOX1	(48) FLCS-----SSMVSFRGVNGG-----KRSFFDSFD-QDDNEADELGE	
Medtr_HOX16_1	(39) FOCS-----NSVVFENGSGSNRV--VTIRPFFQAIKEBENCDEDEYEA	
Orysa_hox16	(32) GGAMFHRGARFVLGMEEGG-----RGVIRPFFTTHD--ELLEEEYDE	
Sacof_hox5	(33) SNCFFRGVPMVAVLGMDDATRVG-----KRPFFTTHRE--ELLEEEYDE	
Sorbi_hox5	(35) SNCFFRGVPMVAVLGMDDATRVG-----KRPFFTTHRE--ELLEEEYDE	
Triae_hox16	(31) AACMFHRGVRPVLGGMEEG-----RGVIRPFFTTHD--DMLEEEYDE	
Zeama_hox16	(30) GGELFHRGGRPMLGLEEG-----RGVIRPFFTTHD--ELLEEEYDE	
Poptr_HOX16_1	(41) FLCS-----RSMMSFEDVHQANG-----STRPFFRSDDHEDNG-DDDLDE	
Poptr_HOX16_2	(44) FLCS-----RSMMSFADVHQANG-----STRPFFRPYDHEDNG-DDDLDE	
Poptr_HOX16_3	(36) LHCA-----KSMVNFNRNDGGDT-----VIMSFFQPHVKEESS-DEDEYDA	
Phavu_hox16	(41) FOCS-----KSMVDFENVSGGR-----VTIRPFFQAIKEKEDNC-DDDYEG	
Lotco_HOX16	(41) FLCS-----RSMVSFADNKLQ-----TRSFFSADLDENG-DEVMDE	
Medtr_HOX unknown	(36) YHCG-----PSFLGKRCMS-----KSSGIELGEEANIPEDLSDD	
Piclg_hox unknown	(40) FOCTR-----SISVFETGNERKRP-----AGNSYSALELSDDIGDEGSD	
Orysa_hox4	(10) GGCS-----PSLVTMANSS-----IDGYGGVGMEAGDVEEEMMA	
Medtr_HOX unknown2	(11) FSTP-----LITISPSTEEHSPRNKHVYGMFQSMMLDGFEEEGCVEE	
Orysa_hox6	(1) -----MDGSEDS-----EWMMDVG--GKGG--KGGG	
Consensus	(51) G S E	RPFF E EE YDE

conserved domain

FIGURE 2

4/104

		Class I homeodomain	
		101	150
Zeama_hox5	(73)	CAP--	EKKRRLTAEQVQLERSFEEENKLEPERKTELARRLGMAPROVAV
Aqufo_hox5	(62)	CLP--	EKKRRLTSEOVHLLKSFETENKLEEDRKTLQAKKLGLOPROVAV
Arath_ATHB1	(64)	CLP--	EKKRRLTSEOVHLLKSFETENKLEPERKTLQAKKLGLOPROVAV
Orysa_hox5	(82)	CAP--	EKKRRLTAEQVQLERSFEEENKLEPERKTELARRLGMAPROVAV
Crapl_CPHB-5	(68)	CLLP-	EKKRRLTAEQVHLLKSFEEAENKLEPERKAEAKKLGLOPROVAI
Dauca_CHB3	(77)	YFQPF	EKKRRLKADQIQFLEKSFETDNKLEPERKVQLAKELGLQPROVAI
Glyma_HD157	(80)	CFHQPG	EKKRRLTSEOVQFLERNFEVENKLEPERKVQLAKELGLQPROVAI
Goshi_Hox5	(61)	CLP--	EKKRRLTSEOVYLLKSFEEAENKLEPERKSLAKKLGLOPROVAV
Lyces_hox5	(62)	CSP--	EKKRRLTSEOVHLLKSFETENKLEPERKTLQAKKLGLOPROVAV
Lyces_VaHOX1	(84)	YLHQA	EKKRRLTDNQVQFLEKSFGEENKLEPERKVQLAKELGLQPROVAI
Medtr_HOX16_1	(81)	CYHQGG	EKKRRLTSEOVQFLEKSFEEVENKLEEDRKVQLAKELGLQPROVAI
Orysa_hox16	(73)	CLP--	EKKRRLTSEOVHLLERSFEEENKLEPERKTELARKLGLOPROVAV
Sacof_hox5	(74)	CAP--	EKKRRLTAEQVQLERSFEEENKLEPERKTELARRLGMAPROVAV
Sorbi_hox5	(76)	CAP--	EKKRRLTAEQVQLERSFEEENKLEPERKTELARRLGMAPROVAV
Triae_hox16	(72)	CLP--	EKKRRLTSEOVHLLERSFEEENKLEPERKTELARKLGLOPROVAV
Zeama_hox16	(70)	CLP--	EKKRRLTSEOVLLERSFEEENKLEPERKTELARKLGLOPROVAV
Poptr_HOX16_1	(80)	YFHQP	EKKRRLTVDQVQFLEKSFLENKLEPERKIQLAKDLGLQPROVAI
Poptr_HOX16_2	(83)	YFHQP	EKKRRLTVDQVQFLERSFEVENKLEPERKIQLAKDLGLQPROVAI
Poptr_HOX16_3	(74)	HLKPS	EKKRRLTAAQVQFLEKSFEEAENKLEPERKMQLAKELGLQPROVAI
Phavu_hox16	(80)	CFHQPG	EKKRRLTSEOVQFLERNFEVENKLEPERKVQLAKELGLQPROVAI
Lotco_HOX16	(78)	YFHQS	EKKRRLSVDQVQFLEKSFVDNKLEEDRKTKIAKDLGLQPROVAI
Medtr_HOX unknown	(71)	GSQAG	EKKRRLTNMQVKTLEKSFELGNKLEPERKMQLARALNLOPROVAI
Piclg_hox unknown	(81)	CIHLG	EKKRRLTLEQVRALEKNFEEMANKLEPEKKMQLAKALGLQPROTAV
Orysa_hox4	(45)	CGGGG	EKKRRLSVEQVRALEKSFEEVENKLEPERKARLARDLGLOPROVAV
Medtr_HOX unknown2	(54)	TGHHSE	EKKRRLRVDQVKALEKNFEVENKLEPERKEKLALBELGLQPROVAV
Orysa_hox6	(24)	GGGAADR	KKRFSEEQIKSLESMTATQTKLEFRQKLQLARELGLOPROVAI
Consensus	(101)		EKKRRLT EQVQ LEKSFE ENKLEPERK QLAK LGLQPROVAV
		conserved domain	
		Class I	
		Homeodomain Leucine zipper	
		151	200
Zeama_hox5	(121)	WFQNRRA	WTKQLETDYDRLKAAYDALAADHQGLTADNDNLRQVLSLT
Aqufo_hox5	(110)	WFQNRRA	WTKQLERDYDLLKASYDSLRSYDDIVKENEKIKSEVVSILT
Arath_ATHB1	(112)	WFQNRRA	WTKQLERDYDLLKSTYDQLLSNYDSIVMDNDKLRSEVTSILT
Orysa_hox5	(130)	WFQNRRA	WTKQLEHDFDRLKAAYDALAADHHAITSNDRLRQVLSILT
Crapl_CPHB-5	(117)	WFQNRRA	WTKQLERDYDKLKSSYDSLSTYDSIROENDKIKAEILLSN
Dauca_CHB3	(127)	WFQNRRA	WTKLEKDYDVLONSYNSLKADYDNLTAEEKLKAEVNLSLT
Glyma_HD157	(130)	WFQNRRA	WTKQLEKDYGVLKASYDRILKSDYESLVQENDKIKAEVNSLT
Goshi_Hox5	(109)	WFQNRRA	WTKQLERDYDLLKSSFDLSQSNYDTILKENEKIKSEVASILT
Lyces_hox5	(110)	WFQNRRA	WTKQLERDYDQLKSSYDSLSTDFDVRKDNKIKSEVVSIM
Lyces_VaHOX1	(134)	WFQNRRA	WTKQLEKDYDELRNRYDTILKSNYNLLKKEEDLRTEVFRILT
Medtr_HOX16_1	(131)	WFQNRRA	WTKQLEKDYGTILKASFDSLKDDYDNLLOENDKIKEEVNSIK
Orysa_hox16	(121)	WFQNRRA	WTKQLERDFDRLKASFDAIRADHDALIQDNHRLHSQVMSILT
Sacof_hox5	(122)	WFQNRRA	WTKQLETDYDHLKAAYDALAADHQGLTADNDNLRQVVSILT
Sorbi_hox5	(124)	WFQNRRA	WTKQLETDYDRLKAAYDALAADHQGLTADNDNLRQVVSILT
Triae_hox16	(120)	WFQNRRA	WTKLERDFDRLKASFDAIRADHDALIQDNHRLRSQVVTILT
Zeama_hox16	(118)	WFQNRRA	WTKQLERDFDRLKASFDAIRADHDALIQDNHRLRSQVVSILT
Poptr_HOX16_1	(130)	WFQNRRA	WTKQLEKDYDVLOSSYNSLKADYDNLKEKEKIKAEVNLILT
Poptr_HOX16_2	(133)	WFQNRRA	WTKQLEKDYEVLOSSYNGLKADYDNLKKEKIKAEVNLILT
Poptr_HOX16_3	(124)	WFQNRRA	WTKQLERDYDSLRIISFDKIKADYDKLLLEKQNLKNELLSIK
Phavu_hox16	(130)	WFQNRRA	WTKQLEKDYGTILKASYDRILKGDYESLVQENDKIKAEVNSLT
Lotco_HOX16	(128)	WFQNRRA	WTKQLEKDYDSLHSSFESLSKNYDNLKEKQMLKAEVASILT
Medtr_HOX unknown	(121)	WFQNRRA	WTKQLEKDYDVLRQYDAIKLNDALQAQNKQLQAEILAIK
Piclg_hox unknown	(131)	WFQNRRA	WTKQLEKDFNVLLKQDYDAIKQDYDNLMEENNLQAMIERMS
Orysa_hox4	(95)	WFQNRRA	WTKQLERDYAALRHSYDSLRLDHDALRRDKDALLAEIKELIK
Medtr_HOX unknown2	(104)	WFQNRRA	WTKQLERDYGVLYANYDAIKLKFDALIAQDNKAFHKEIKELIK
Orysa_hox6	(74)	WFQNRRA	WTKQLEREYSAIRDDYDALCSYESLKKELALIKQLEKTA
Consensus	(151)	WFQNRRA	WTKQLE DYD LK SYD L DYD LL EN L AEV SLT
		conserved domain	

FIGURE 2 (continued)

SUBSTITUTE SHEET (RULE 26)

5/104

		201		250
Zeama_hox5	(171)	ERLQCKETSPS-----	ATTAAQEVDPDEHTAVSGTEELL	
Aqufo_hox5	(160)	GRLOVKEGAGM-----	ELNQISDPPLS--TEENVDTVTT	
Arath_ATHB1	(162)	ERLQCKQOETAN-----	EPPGQVPEP-----NQLDPVYI	
Orysa_hox5	(180)	ERLQDKETSPS-----	SATITTAAQEVDPDEHTAASTTGFA	
Crapl_CPHB-5	(167)	ERLQPKDDDDP-----	SAEIGRNLSSSSPVDAAEPPC	
Dauca_CHB3	(177)	DRLLLEKEDKGS-----	KTVVFDKQKVSAAFQQERVSNDIS	
Glyma_HD157	(180)	SKLLLRDKEKEE-----	NSDDKSSPDADVNSSSPHNNKEPMDLLI	
Goshi_Hox5	(159)	ERLQAKDVATE-----	AIAGEKDEG-----LAAEMASA	
Lyces_hox5	(160)	ERLQCKVVGGA-----	GGNEKSD-----ILEVDAMTI	
Lyces_VaHOX1	(184)	GRLFIEKEKNG-----	QLDLRDEHKHSNALAKETVVDPMIS	
Medtr_HOX16_1	(181)	NKLIIPRDKEKV-----	NSEDKSS-PEAINSP--HNNIDPMDIIS	
Orysa_hox16	(171)	ERLQCKETTTEGSAGAAVDVPG-PAADVKVAVPDAEPALEEEAAAFE		
Sacof_hox5	(172)	ERLQCKETSPS-----	ATTAAQEVDPDEHTAASGTEKLL	
Sorbi_hox5	(174)	DKLQCKETSPS-----	ATTAAQEVDPDEHTAASGTEKLL	
Triae_hox16	(170)	ERLQCKEAPESFGAAADASEPE-QAAAEAKASLADAEQAAAAAEFEV		
Zeama_hox16	(168)	ERLQCKEDATEGGATADTAAP---AVDVEASLADDVEEPAEPAATFEV		
Poptr_HOX16_1	(180)	DKLLLEKEKEG-----	ISELSDKDALSQEPPKRAIADSAS	
Poptr_HOX16_2	(183)	NELLLEKEKEG-----	SSELSDKDALSQEPPKRAIADSAS	
Poptr_HOX16_3	(174)	ERLQSRRESME-----	SSEPFVDVIHS-PDAELEPIPDIVS	
Phavu_hox16	(180)	SKLLLRDKEKE-----	NSDDKSS-PDAVNSP---HKEPMDLIS	
Lotco_HOX16	(178)	ERVLARENLKQ-----	VESETKGLVEPPQRPRLDSVS	
Medtr_HOX unknown	(171)	NREPTESINLN-----	KETEGSSSNRSENSEIKLMS	
Piclg_hox unknown	(181)	SKSCSCNDQKFQAN-----	SSKLQKDDQDLQLLMMSATKVDCA	
Orysa_hox4	(145)	ARLGDEEAAAS-----	FTSVKEEPAASDGPAAAGFGSSDS	
Medtr_HOX unknown2	(154)	SKLGEEEEKSTIN-----	VLVKEELTMLESCDEDKHNPSS	
Orysa_hox6	(124)	ERLQEPGRKYG-----	DNAGDDARSGGVAGMKKEEFVG	
Consensus	(201)	ERLQ KE		
		conserved domain		
		251		300
Zeama_hox5	(206)	AQQ-----	LKDNLHSSG-----	
Aqufo_hox5	(191)	MQFN-----	VKVEDRLSSGSGVSAVVDDEEC	
Arath_ATHB1	(190)	NAAA-----	IKTEDRLSSGSGVSAVLDODA	
Orysa_hox5	(218)	TVDGALA-----	APPPGHQPPHKDLVSSSGTNDGDDGGAA	
Crapl_CPHB-5	(200)	LKLT-----	VKVEDRLSTGSGVSAVMDGCG	
Dauca_CHB3	(212)	VGE-----	VLSNSVMDCKOEDHNSVK--SDAVDSDS	
Glyma_HD157	(220)	ISKNATTTTTTSENGTKVLSPLPLPIMVTCCOEDANSK--SDVLDSDS		
Goshi_Hox5	(187)	LQFS-----	MKVEDRLSSGSGVSAVVDDEDA	
Lyces_hox5	(187)	LQVK-----	VKACDRLSSGSGVSAVVDHES	
Lyces_VaHOX1	(219)	NVP-----	ALVVKHQOEDLSSAK--SDVFDSES	
Medtr_HOX16_1	(217)	ITN-----	SENGSKMS---LPNMVLKCOEDANSK--SDVLDSDS	
Orysa_hox16	(220)	EQQE-----	QQVKAEDRLSTGSGVSAVVDODA	
Sacof_hox5	(207)	AQQ-----	LKDDLHSSG-----	
Sorbi_hox5	(209)	VQQ-----	LKDDLHSSG-----	
Triae_hox16	(219)	QQQ-----	LHVKEERLSPGSGVSAVLDARD	
Zeama_hox16	(213)	LQ-----	EVKSEDRLSTGSGVSAVVDADA	
Poptr_HOX16_1	(215)	EGE-----	VSKISTVACQOEDISSAK--SDIFDSDS	
Poptr_HOX16_2	(218)	EGE-----	VSKTSTVACQOEDISSAK--SDMFDSDS	
Poptr_HOX16_3	(208)	EN-----	VSAIVPMVTPKQESSAK--NDVFNSDS	
Phavu_hox16	(214)	N-----	STSENGTKVS---LPIMVT-COEDANSK--SDVLDSDS	
Lotco_HOX16	(210)	EGEE-----	SKVSVGACQOEDISSAR--SESLSDS	
Medtr_HOX unknown	(204)	RTP-----	ASDSPLSTHQHTTSRTFFPPS	
Piclg_hox unknown	(219)	DKEN-----	NNEGPSSICSEGSSVLDMD	
Orysa_hox4	(180)	DSS-----	AVLNDVDAAGAAPAATDALAPEA	
Medtr_HOX unknown2	(189)	TSNP-----	SSESKDHLDYDCIINNNDVGIG	
Orysa_hox6	(157)	AGG-----	AATLYSSAEGGTTTTTAKL	
Consensus	(251)		K ED S G S V D D	

FIGURE 2 (continued)

6/104

		301		350
Zeama_hox5	(218)	-----DCTGHGTLSE		
Aqufo_hox5	(216)	RQ-----LVDSVDSYFPGD---DYGCIG-----PVDGVQS		
Arath_ATHB1	(215)	EQ-----LLDSCDSYFP-----SIVPI		
Orysa_hox5	(255)	VVVF-----DVTEGANDRLSCESAYFADAAEAYERDCAGHYALS--SE		
Crapl_CPHB-5	(225)	EQQL-----LDDSGDSYFEND---EEYDCAA-----ASLAAA		
Dauca_CHB3	(241)	PHYSD---EVYSSFMEPVDRSYVFEPAQSE-----DISQD		
Glyma_HD157	(267)	PHCTS-----FVEPADSSHAFEPEDHSE-----DFSQD		
Goshi_Hox5	(212)	EQ-----LVDSGNSYFPSD---EYSRGIG-----PFDGVQS		
Lyces_hox5	(212)	SQ-----LVDSGDSYFHTD---HEEYPGPGGCNVPPPMDGLQS		
Lyces_VaHOX1	(245)	PRYTSR--MHSSVVDQDD SARAFETDQS-----DSSQD		
Medtr_HOX16_1	(253)	PHCNDG--NNLSSFIEPTDSDFS-----QD		
Orysa_hox16	(247)	QLVVGCGRQHLLAAVDSSVESYFPGG---DEYHDC-VMGPMDDHAAGGIQS		
Sacof_hox5	(219)	-----DCTGHGALS--SE		
Sorbi_hox5	(221)	-----DFTGHGALS--SE		
Triae_hox16	(245)	ALLG-SGCGLAGVVDSSVDSYCFPGGAGGDEYHEC---VVGPPVAGG-IQS		
Zeama_hox16	(237)	LLYG---RFAAAVDSSVESYFPGGE---DHYHDCGTMGPNVNHGAGGGIQ		
Poptr_HOX16_1	(244)	PHYAD---GVHSSLLEAGDSYVFEPDQSE-----DLSQD		
Poptr_HOX16_2	(247)	PHFAD---GVHSSLLEAGDSHVFEPDQSE-----DLSQD		
Poptr_HOX16_3	(236)	PRSFL-----EPRDCYRVFESDQP-----DFSQV		
Phavu_hox16	(249)	PHCTDG--NHPSFVEPADSSHAFEPDHS-----DFSQD		
Lotco_HOX16	(239)	PRYRDG-YGVNSAVLETCDSYVVEPDQSE-----DMSQD		
Medtr_HOX unknown	(228)	ARPS-----SGIAQLFQTSRPE-----IQC		
Piclg_hox unknown	(243)	EGTIDS-----QQNIDSIGFSN-----VKA		
Orysa_hox4	(206)	CTFLGAPPAAGAGAGAAAAASHVEVFFHG-----NFLKV		
Medtr_HOX unknown2	(215)	ETSSLFPVDLKDGSDDSDSSAIISSSGVLQSQ-----QHLLL		
Orysa_hox6	(181)	MPHFG-----SDDVDAGLFLRPS-----SQHHP		
Consensus	(301)	P DS Q		
		351		400
Zeama_hox5	(229)	EEDGGVVSDEGCS-----FALPDAMFAAGFTHHG-----AEEVQ		
Aqufo_hox5	(244)	EEDDISDDS---R-----SYFSDVFPAAPEQNHQ-----ES-E		
Arath_ATHB1	(232)	QDNSNASDHDNDR-----SCFADVFVPTTSPSHD-----HHGE		
Orysa_hox5	(296)	EEDGGAVSDEGCS-----FDLPDAAAAAAMFGAAGVVHDAADDEEAQ		
Crapl_CPHB-5	(254)	KEDDGSDEGG-----CYFTEALAAEEEE-----A		
Dauca_CHB3	(272)	EEDDMGNNLFLPS--YHVFSKTEGYSYDQPSNSSF-----GFPVE		
Glyma_HD157	(295)	EEDNLSENLLMTFPSSCCLPKVEEHCHYDGPENSCNF-----GFQVE		
Goshi_Hox5	(240)	EEDDGSNDG-----SYFSDVFATTEQG-----		
Lyces_hox5	(247)	EEDDGSDDHGSC-----GYFSNVFVAEEQHHEQ-----GE-E		
Lyces_VaHOX1	(276)	DDENFSKNMLSTAN---LLGKDAADDYPATSSNLSYFG-----FPVE		
Medtr_HOX16_1	(276)	EEDNDNLSHNLLTLP--CLPKVEDVCYDDPHENSCNF-----GFPVE		
Orysa_hox16	(292)	EEDDGAGSDEGCS-----YYADDAGVLFADHGHHHHQHADDDEEDGQQ		
Sacof_hox5	(230)	EEDGGVVSDEG-S-----FDLPDAMFAAGVTHHGA-----DAEEAQ		
Sorbi_hox5	(232)	EEDGGVVSDEGCS-----FDLPDAMFAAGVTHHG-----AEEAQ		
Triae_hox16	(290)	EEDDGAGSDEGCS-----YYPDLAAVFFAAAQGHGHHRTDDDDQQDDGQ		
Zeama_hox16	(280)	SDDDGAGSDEGCS-----YYADEAAAAAFAFHATHHHHADEDEDAGQ		
Poptr_HOX16_1	(275)	EEDNFSKSLPP---YVFPKLEDYSDPPAS-----FE		
Poptr_HOX16_2	(278)	EEDNLSKSLPP---YVFPKLEDYSDPPAS-----FE		
Poptr_HOX16_3	(260)	EEDNLTRSFLPP-----PYFPKLYREPPASSRNF-----EFSAE		
Phavu_hox16	(281)	EEDNLSESLLTLP---CLPKVEEACVDDPPENPCNF-----GFHVE		
Lotco_HOX16	(272)	EEDNLTKTLLPPY---MFSKLGDMYSDPPESSCNF-----GFPBE		
Medtr_HOX unknown	(249)	QKIDQMVKEES-----LSNMFCGMDDQAG-----		
Piclg_hox unknown	(263)	RDLRLECNRFP-----KVEENVSQADEPCNYLFYN-----NLETGP		
Orysa_hox4	(240)	EEDETGFLDDDEP-----CGGFFADDQPPP-----LSSWW		
Medtr_HOX unknown2	(251)	SPSSSMNCFQYQKSYHVKMEHNFLSADEACN-----FFSDE		
Orysa_hox6	(204)	PPHAGAGFTSSE-----PAADHQSFNFHSSWPSS-----TEQTCS		
Consensus	(351)	EED D E		

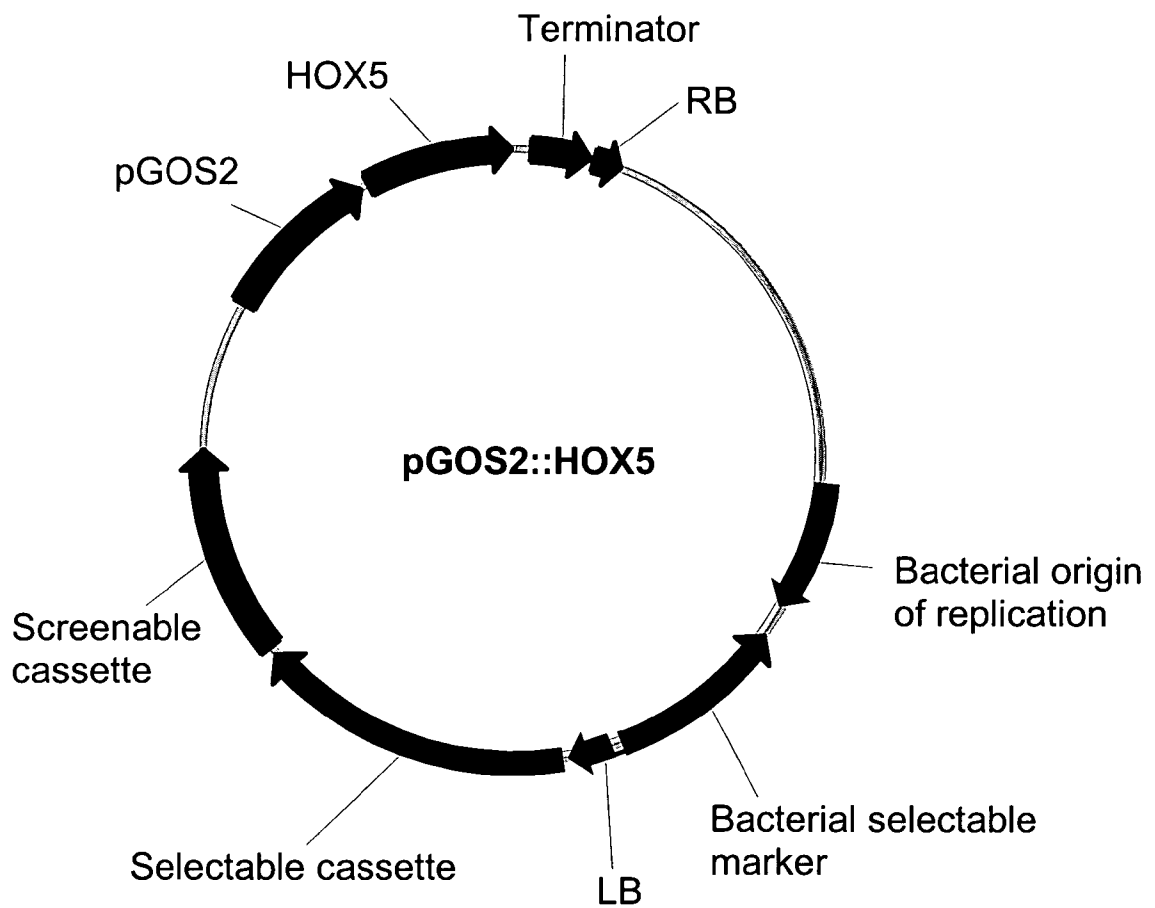
FIGURE 2 (continued)

7/104

Trp tail		
	401	414
Zeama_hox5 (263)	LANWTSMFWN----	
Aqufo_hox5 (273)	TLGWWDWA-----	
Arath_ATHB1 (265)	SLAFWCWP-----	
Orysa_hox5 (340)	IGSWTAFWFS----	
Crapl_CPHB-5 (278)	HFAWCIMS-----	
Dauca_CHB3 (312)	LHTFGFWGTEL---	
Glyma_HD157 (337)	DQTFCFWPY-----	
Goshi_Hox5 (263)	ALGLWAWX-----	
Lyces_hox5 (279)	HIGWFWS-----	
Lyces_VaHOX1 (315)	DQGFGFWTY-----	
Medtr_HOX16_1 (316)	DQTFCFWPY-----	
Orysa_hox16 (336)	ISCWWMNN-----	
Sacof_hox5 (265)	LANWTSMFWN----	
Sorbi_hox5 (266)	LANWTSWFWN----	
Triae_hox16 (334)	IS-YWMNN-----	
Zeama_hox16 (324)	IS-WWMNN-----	
Poptr_HOX16_1 (306)	DHAFWSWSY-----	
Poptr_HOX16_2 (309)	DHAFWCWSY-----	
Poptr_HOX16_3 (294)	DQPFWSWIY-----	
Phavu_hox16 (319)	DQTFCFWPY-----	
Lotco_HOX16 (310)	DHALWSWSY-----	
Medtr_HOX unknown (273)	---FWPWLQQHFN	
Piclg_hox unknown (299)	LLWDYNWSSGL---	
Orysa_hox4 (270)	AEPTEHNN-----	
Medtr_HOX unknown2 (289)	CAPTLOWYCPDQWS	
Orysa_hox6 (240)	STPWWEFESE----	
Consensus (401)	W	

FIGURE 2 (continued)

8/104

**FIGURE 3**

9/104

SEQ ID NO: 1 *Oryza sativa* *Oryza_hox5* cDNA sequence XM_482406.1
ATGGATCCCGGCCGCGTCTGTTCGACTCCGGCGTGGCGCGGCGGGCGTCCCCGGCGGGCGC
GCAGATGCTTCTCTTCGGCGGCGGCGGCAGCGCCAACAGCGGCGGCTTCTTCCGAGGCGTG
CGGCGGCGGTGCTGGGGATGGATGAATCGCGGTCGTCGTCGTCGCGCGGCGGGGGCGGGGGCG
AAGCGGCCGTTCTTCACGACGCACGAGGAGCTCCTGGAGGAGGAGTACTACGACGAGCAGGC
GCCGGAAGAAGCGGCGGCTGACGGCGGAGCAGGTGCAGATGCTGGAGCGGAGCTTCGAGG
AGGAGAACAAGCTGGAGCCGGAGCGGAAGACGGAGCTCGCCCGCCGCTCGGCATGGCCCCC
CGGCAGGTCGCCGTCTGGTTCCAGAACC GCCCGCGCCCGCTGGAAGACCAAGCAGCTCGAGCA
CGACTTCGACCGCCTCAAGGCCGCTACGACGCCCTCGCCGCCGACCACCATGCCCTCCTCT
CCGACAACGACCGCCTCCGCGCGCAGGTAATCTCATTAACCGAGAAGCTGCAAGACAAGGAG
ACGTCGCCGTCGTCGGCGACCATCACCACCGCGCGCAGGAGGTCGACCAGCCGGACGAACA
CACGGAGGCCGCGTCAACCACCGGCTTCGCCACCGTCGACGGCGCATTTGGCGGCGCCACCGC
CCGGCCACCAGCAGCCGCCGCATAAAGATGATCTTGTGAGCAGCGGCGGCACCAACGACGAC
GGCGATGGCGGCGCGGCCGCTGGTGGTCTTCGACGTCACCGAGGGCGCCAACGACCGCCTCAG
CTGCGAGTCGGCGTACTTCGCCGACGCCGCGGAGGCGTACGAGCGCGACTGCGCCGGGCACT
ACGCCCTCTCGTCGGAGGAGGAGGACGGCGGCGCGGTGAGCGACGAGGGCTGCAGCTTCGAC
CTCCCCGACGCCGCCGCCGCCGCCGCCATGTTGGCGCGCCGGAGTTGTGCACCACGA
CGCCGCGGACGACGAGGAGGCGCAGCTCGGCAGCTGGACCGCCTGGTTCTGGAGCTGA

SEQ ID NO: 2 *Oryza sativa* *Oryza_hox5* translated amino acid sequence

MDPGRVVFDSGVARRACPGGAQMLLFGGGGSANSGGFFRGVPAAVLGMDESRSSSSAAGAGA
KRPFFTTHEELLLEEEYYDEQAPEKKRRLTAEQVQMLERSFEEENKLEPERKTELARRLGMAP
RQVAVWFQNRRLRWKTKQLEHDFDRLKAAFDALAADHALLSDNDRRLRAQVISLTEKLQDKE
TSPSSATITTAQEVDPDEHTEAASTTGATVDGALAAPPPGHQPPHKDDLVSSTGGTND
GDGGAADVVFVTEGANDRLSCESAYFADAAEAYERDCAGHYALSSEEDGGAVSDEGCSFD
LPDAAAAAAMFGAAGVVHDAADDEEAQLGSWTAWFWS

SEQ ID NO : 3 *Oryza sativa* *Oryza_hox16* cDNA sequence XM_467603.1

ATGGAGTCCGGCCGGCTCATCTTCAGCACGGCGGGCTCCGGCGCCGGGCAGATGCTCTTCTT
GGACTGCGGCGCTGGCGGCGGCGGCGTCCGGCGCGGGGCCATGTTCCATCGAGGGGCGAGAC
CGGTGCTCGGCATGGAGGAAGGAGGGCGCGGCGTCAAGCGGCCCTTCTTACCACCCCCGAC
GAGCTCCTCGAAGAGGAGTACTACGACGAGCAGCTCCCGGAGAAGAAGCGGCGCCTCACGCC
GGAGCAGGTGCATCTGCTGGAGAGGAGCTTCGAGGAGGAGAACAAGCTGGAGCCGGAGCGGA
AGACGGAGCTGGCGCGGAAGCTAGGGCTGCAGCCGCGGCAGGTCGCCGTGTGGTTCCAGAAC
CGCCGCGCGCGCTGGAAGACCAAGCAGCTCGAGCGGCACTTCGACCGCCTCAAGGCGTCGTT
CGACGCCCTCCGCGCCGACCACGACGCCCTCCTCCAGGACAACCACCGCCTCCACTCTCAGG
TCATGTCGTTGACCGAGAAGCTGCAAGAGAAGGAGACGACGACCGAGGGCAGCGCCGGCGCG
GCCGTTGACGTCCCGGGCTTGCCCTGCGGCGGCGGACGTGAAGGTCGCCGTCCCGGACGCGGA
GGAACCGGCGCTGGAGGAGGCGGCGGCGGCGTTCGAGGAGCAGCAGGAGCAGCAGGTGAAGG
CCGAGGACAGGCTGAGCACGGGCAGCGGCGGGAGCGCGGTGGTGGACACGGACGCGCAACTG
GTGGTTCGGGTGCGGCCGGCAAGCATCTCGCCGCCGTGGACAGCAGCGTGGAGTCGTACTTCC
CGGGCGGCGACGAGTACCACGACTGCGTGATGGGCCCCATGGACCACGCCGCGGGGGGCATC
CAGTCGGAGGAGGACGACGGCGCCGGCAGCGACGAGGGCTGCAGTACTACGCCGACGACGC
CGGCGTCCTCTTCGCCGACCACGGCCACCACCACCACCAACACGCGGACGACGACGAGG
AGGACGGCCAGCAGATCAGCTGCTGGTGGATGTGGAAGTAGATTTCTCGCGCGCGCGCGTCC
TCGTGCATTCAATTCTCGTGTTAAAAAATCGTTCTCTTTTTCATTTTCCGCTTCTTTGTC
TGTAATGTTGAGTTTCGATCGGCTATGAGAAGGAAGGAGGTGTATGCATGTGCATGGTATGG
TAGGGTAACACATCGGTGA

FIGURE 4 (continued)

10/104

SEQ ID NO: 4 *Oryza sativa* *Oryza_hox16* translated amino acid sequence

MESGRLLIFSTAGSGAGQMLFLDCGAGGGGVGGGAMFHRGARPVLGMEEGGRGVKRPFFTTTPD
ELLEEEYYDEQLPEKKRRLTPEQVHLLERSFEEENKLEPERKTELARKLGLQPRQVAVWFQN
RRARWKTQQLERDFDRLKASFDALRADHDALLQDNHRLHSQVMSLTEKLQEKETTTEGSAGA
AVDVPGLPAAADVQVAVPDAAEPALEEAAAAFEEQQEQVKAEDRLSTGSGGSAAVVDTDALQ
VVGCGRQHLLAAVDSSVESYFPGGDEYHDCVMGPMDDHAAGGIQSEEDDGAGSDEGCSYYADDA
GVLFADHGHHHHHQHADDDEEDGQQISCWWMWN

SEQ ID NO: 5 *Zea mays* *Zeama_hox5* cDNA sequence contig from essentially CO458693 & DV024016

ATGGATCCGAGCGCGGTCTAGTTTCGACTCTGGCGGCGCGCGCGGGGCGGCGCGCGCAGAT
GCTGCTCTTCGGCGGCGGAGGCAGCGCCAACAGCAACGGCTTCTTCCGAGGTGTTCCGATGG
CGGTCTTGGGCATGGACGACGCGACGCGCGTGGGCAAGCGGCCCTTCTTCACGACACACGAG
GAGCTCCTAGAGGAGGAGTACTACGACGAGCAGGCGCCGAGAAGAAGCGCCGACTGACGGC
GGAGCAGGTGCAGCTGCTGGAGCGGAGCTTCGAAGAAGAGAACAAGCTGGAGCCGGAGCGCA
AGACCGAGCTGGCTCGCCGCCTGGGGATGGCGCCCCGCCAGGTAGCTGTTTGGTTCCAGAAC
CGCCGCGCGCGCTGGAAGACCAAGCAACTCGAGACCGACTATGACCGCCTCAAGGCTGCTTA
CGACGCACTCGCCGCCGACCACCAGGGCCTCCTGGCCGACAACGATAACCTCCGGGCACAGG
TGATCTCCCTGACGGAGAAGCTGCAAGGCAAGGAGACATCCCCGTGCGCAACCACTGCTGCC
CAAGAGGTCGACCAGCCAGACGAACACACCGCTGTGTGTCAGGCACGGAAGAACTGCTGGCGCA
GCAGCTCAAGGACAACCTCCACAGCAGCGGCGACTGCACTGGCCATGGCACCTCTCTTCGG
AAGAAGACGACGGTGGCGTGGTCACTGACGAGGGCTGCAGCTTCGCTCTCCCGGATGCCATG
TTCGCTGCCGGGTTACCCACCATGGCGCCGAGGAGGTGCAGCTGGCCAACTGGACATCCAT
GTTCTGGAAGTGA

SEQ ID NO : 6 *Zea mays* *Zeama_hox5* translated amino acid sequence

MDPSAVSFDSSGGARRGGGAQMLLFGGGGSANSNGFFRGVPMVAVLGMDDATRVGKRPFFTTHE
ELLEEEYYDEQAPEKKRRLTAEQVQLLERSFEEENKLEPERKTELARRLGMAPRQVAVWFQN
RRARWKTQQLTDYDRLKAAYDALADHQGLLADNDNLRAQVISLTEKLQKETSPPSATTAA
QEVDQPDHTAVSGTEELLAQQLKDNHLHSSGDCTGHGTLSSSEEDDGGVVSDEGCSFALPDAM
FAAGFTHHGAEEVQLANWTSMFWN

SEQ ID NO: 7 *Zea mays* *Zeama_hox16* cDNA sequence AY105265

ATGGAGTCTGGACGGCTCATCTTCAACGCGCCGGGCTCTGGCGCCGGGCAGATGCTCTTCCT
CGACTGCGGCGCAGGCGGCGGTCCCGGCGGCGGCTTGTTCCATCGAGGCGGGAGACCGATGC
TTGGCCTTGAAGAAGGGCGCGGCGTAAACGGCCCTTCTTCACCTCGCCCGACGAGCTCCTC
GAGGAAGAGTACTACGACGAGCAGCTGCCGAGAAGAAGCGCCGCTCACCCAGAGCAGGT
GCTTCTGCTGGAGAGGAGCTTCGAGGAGGAGAACAAGCTGGAGCCGGAGCGCAAGACGGAGC
TGGCGCGCAAGCTGGGCCTGCAGCCTCGCCAGGTGGCCGTCTGGTTCCAGAACCGCCGCGCC
CGGTGGAAGACCAAGCAGCTCGAGCGCGACTTCGACCGCCTCAAGGCCTCCTTCGACGCTCT
CCGAGCGGACCACGACGCCCTCCTCCAGGACAACAACCGCCTCCGCTCACAGGTTGTGTCTG
TGACCGAGAAGCTGCAAGAGAAGGAGGATGCGACGGAGGGCGGCGCCACCGCTGACACCGCC
GCGCCGGCGGTGGACGTCGAGGCTTCCCTGGCCGACGACGTCGAGGAGCCAGCAGAGCCTGC
GGCGACGTTTCGAGGTGCTGCAGGAGGTGAAGTCCGAGGACAGGCTGAGCACCGGCAGCGGCG
GGAGCGCGGTGGTGGACGCGGACGCGCTGCTGTACGGCAGGTTCCCGCGGCAGTTGATAGC
AGCGTGGAGTCGTACTTCCCCGGCGGCGAGGACCACTACCACGACTGCGGGACGATGGGCCC

FIGURE 4 (continued)

11/104

CGTGAATCATGGCGCCGGAGGAGGCATCCAGTCGGACGACGACGGCGCCGGCAGCGACGAGG
GGTGCAGCTACTACGCCGACGAAGCCGCCGCCGCCGCCGCGTTCTTCGCCGGACACGCC
ACCCACCACCACGCGGACGAGGACGAGGACGCCGCCGATCAGCTGGTGGATGTGGAAC
TA
G

SEQ ID NO: 8 Zea mays Zeama_hox16 translated amino acid sequence

MESGRLI FNAPGSGAGQMLFLDCGAGGGPGGGLFHRGGRPMLGLEEGRGVKRPFFTS PDELL
EEEEYYDEQLPEKKRRLTPEQVLLLLERSFEEENKLEPERKTELARKLGLQPRQVAVWFQNRRA
RWKTKQLERDFDLRKASFDALRADHDALLQDNNRLRSQVVS LTEKLQEKEDATEGGATADTA
APAVDVEASLADDVEEPAEPAATFEVLQEVKSEDLSTGSGGSAVVDADALLYGRFAAAVDS
SVESYFPGGEDHYHDCGTMGPVNHGAGGGI QSDDDGAGSDEGCSYYADEAAAAAAAFFAGHA
THHHADEDEDAGQISWWMWN

**SEQ ID NO: 9 Saccharum officinarum Sacof_hox5 cDNA sequence
contig from essentially CA088615, CA115362 & CA142506**

ATGGATCCGAGCGCGGT CAGTTTCAACTCCGGCGGCGCGCGCGGGGCGGCGGGCAGCGCA
GATGCTGCTCTTCGGCGGCGGAGGCAGCGCCAACAGCAACGGCTTCTTCCGAGGTGTTCCGA
TGGCGGTCTTGGGCATGGACGACGCGACGCGCGTGGGCAAGCGGCCCTTCTTACCACACAC
GAGGAGCTCCTGGAGGAGGAGTACTACGACGAGCAGGCGCCCGAGAAGAAGCGCCGTCTGAC
GGCGGAGCAGGTGCAGCTGCTGGAGCGGAGCTTCGAGGAAGAGAACAAGCTGGAGCCCGAGC
GCAAGACCGAGCTGGCTCGCCGCCTCGGGATGGCGCCCCGCCAGGTGGCCGTCTGGTTCCAG
AACCGCCGCGCGCGCTGGAAGACCAAGCAGCTCGAGACCGACTATGACCACCTCAAGGCTGC
CTACGACGCGCTCGCCGCCGACCACCAGGGCCTCTTGCCGACAACGATAGCCTCCGGGCAC
AGGTGGTCTCCCTAACAGAGAAGCTGCAAGGCAAGGAGACATCCCCGTCGGCCACCACTGCT
GCCCAAGAGGTGCGACCAGCCAGACGAACACACCGCGGCGTCAGGCACTGAGAACTGCTGGC
GCAGCAGCTCAAGGACGACCTCCACAGCAGCGGCGACTGCACTGGCCATGGTGCCCTCTCCT
CAGAGGAAGAAGATGGTGGTGTGGT CAGTGACGAGGGCAGCTTTGATCTCCCGGATGCCATG
TTTGCTGCCGGGGTCACCCACCATGGCGCCGACGCCGAGGAGGCACAGCTGGCCAACTGGAC
ATCCTGGTTCTGGAAC TGA

**SEQ ID NO: 10 Saccharum officinarum Sacof_hox5 translated
amino acid sequence**

MDPSAVSFNSGGARRGGGGTQMLLFGGGGGSANSNGFFRGVPMAVLGMDDATRVGKRPFFTTH
EELLEEEYYDEQAPEKKRRLTAEQVQLLERSFEEENKLEPERKTELARRLGMAPRQVAVWFQ
NRRARWTKQLETDYDHLKAA YDALADHQGLLADNDSLRAQVVS LTEKLQKETS PPSATTA
AQEVDQPDHETAASGTEKLLAQQLKDDLHSSGDCTGHGALSSEEEDGGVVSDEGSFDLPDAM
FAAGVTHHGADAEEAQLANWTSWFWN

SEQ ID NO: 11 Sorghum bicolor Sorbi_hox5 BE363386, CD432381

ATGGATCCGAGCGCGGT CAGTTTCGACTCCGGCGGCGCGCGGGGCGGCGGGCAGCGCGG
CGCGCAGATGCTGCTCTTCGGCGGCGGAGGCAGCGCCAACAGCAACGGCTTCTTCCGAGGTG
TTCCGATGGCGGTCTTGGGCATGGACGACGCGACGCGCGTGGGCAAGCGGCCTTTCTTACC
ACGCACGAGGAGCTCCTGGAGGAGGAGTACTACGACGAGCAGGCGCCCGAGAAGAAGCGCCG
TCTGACGGCGGAGCAGGTGCAGCTGCTGGAGCGGAGCTTCGAGGAAGAGAACAAGCTGGAGC
CGGAGCGCAAGACCGAGCTGGCTCGCCGCCTCGGGATGGCGCCTCGCCAGGTGGCCGTCTGG
TTCCAGAACCGCCGCGCGCTGGAAGACTAAGCAGCTCGAGACCGACTATGACCGCCTCAA
GGCTGCCTACGACGCGCTCGCCGCCGACCACCAGGGCCTCCTGGCCGACAACGATAGCCTCC

FIGURE 4 (continued)

12/104

GGGCACAGGTGATCTCCCTAACGGATAAGCTGCAACGCAAGGAGACATCCCCGTGGGCGACC
 ACTGCTGCCCCAAGAGGTGCGACCAGCCAGACGAACACACCGCTGCGTCAGGCACTGAGAACT
 GCTGGTGACAGCAGCTCAAGGACGACCTCCACAGCAGCGGCGACTTCACTGGCCATGGTGCCC
 TCTCTTCAGAGGAAGAGGATGGTGGTGTGGTCAGCGACGAGGGCTGCAGCTTTGATCTCCCC
 GATGCCATGTTTCGCTGCCGGGGTCACCCACCATGGCGCCGAGGAGGCGCAGCTGGCCAACTG
 GACATCCTGGTTCTGGAAC**TGA**

SEQ ID NO: 12 Sorghum bicolor Sorbi_hox5 translated amino acid sequence

MDPSAVSFDSGGARRGGGGGAQMLLFGGGGSANSNGFFRGVPMAVLGMDDATRVGKRPFFT
 THEELLEEEYYDEQAPEKKRRLTAEQVQLLERSFEEENKLEPERKTELARRLGMAPRQVAVW
 FQNRRLRWKTKQLETDYDRLKAAYDALADHQLLADNDSLRAQVISLTDKLQRKETSPSAT
 TAAQEVDQPDHTAASGTEKLLVQQLKDDLHSSGDFTHGALSSEEDGGVVSDEGCSFDLP
 DAMFAAGVTHHGAEAAQLANWTSWFWN

SEQ ID NO: 13 Triticum aestivum Triae_hox16 DR735359,DR741379, CD916488

ATGGAGCCCGCCGGCTCATCTTCAACACGTCGGGCTCCGGCAACGGACAGATGCTCTTCAT
 GGACTGCGGCGCGGGCGGCATCGCCGGCGCGGCGGCATGTTCCATCGAGGGGTGAGACCGG
 TCCTCGGCGGCATGGAAGAAGGGCGCGCGGTGAAGCGGCCCTTCTTCACCTCGCCGGATGAC
 ATGCTCGAGGAGGAGTACTACGACGAGCAGCTCCCGGAGAAGAAGCGGCGCCTCACCCCGGA
 GCAGGTCCACCTGCTGGAGAGGAGCTTCGAGGAGGAGAACAAAGCTGGAGCCGGAGAGGAAGA
 CGGAGCTGGCCCGCAAGCTCGGGCTGCAGCCACGCCAGGTGGCCGTCTGGTTCCAGAACCGC
 CGCGCCCGGTGGAAGACAAAGACGCTGGAGCGCGACTTCGACCGCCTCAAGGCGTCCTTCGA
 CGCCCTCCGGGCCGACCACGACGCCCTCCTCCAGGACAACCACCGGCTCCGGTCACAGGTGG
 TAACGTTGACCGAGAAGATGCAAGATAAGGAGGCGCCGGAAGGCAGCTTCGGTGCAGCCGCC
 GACGCCTCGGAGCCGGAGCAGGCGGCGGCGGAGGCGAAGGCTTCCTTGGCCGACGCCGAGGA
 GCAGGCCGCGGCAGCGGAGGCGTTTCGAGGTGGTGCAGCAGCAGCTGCACGTGAAGGACGAGG
 AGAGGCTGAGCCCGGGGAGCGGCGGGAGCGCGGTGCTGGACGCGAGGGACGCGCTGCTCGGG
 AGCGGATGCGGCCTCGCCGGCGTGGTGGACAGCAGCGTGGACTCGTACTGCTTCCCGGGGGG
 CGCCGGCGGCGACGAGTACCACGAGTGCGTGGTGGGCCCCGTGGCGGGCGGCATCCAGTCGG
 AGGAGGACGACGCGCGGGCAGCGACGAGGGCTGCAGCTACTACCCGACGACGCCGCCGCTC
 TTCTTCGCCGCCGCGCAAGGGCACGGCCACCATCGCACGGACGACGACGATCAGCAGGACGA
 CGGCCAGATCAGCTACTGGATGTGGAAC**TAG**

SEQ ID NO: 14 Triticum aestivum Triae_hox16 translated amino acid sequence

MEPGRLIFNTSGSGNGQMLFMDCGAGGIAGAAGMFHRGVRPVLGGMEEGRGVKRPFFFTSPDD
 MLEEEYYDEQLPEKKRRLTPEQVHLLERSFEEENKLEPERKTELARKLGLQPRQVAVWFQNR
 RARWKTTLERDFDRLKASFDALRADHDALLQDNHRLRSQVVTLTEKMQDKEAPEGSFGAAA
 DASEPEQAAAEAKASLADAEQAAAAEAFEVVQQQLHVKDEERLSPSGSSAVLDARDALLG
 SGCGLAGVVDSSVDSYCFPGGAGGDEYHECVVGPVAGGIQSEEDDGAGSDEGCSYYPDDAAV
 FFAAQGHGHRDDEDDQDDGQISYWMWN

FIGURE 4 (continued)

13/104

SEQ ID NO: 15 *Arabidopsis thaliana* Arath_ATHB1 cDNA sequence X58821

ATGGAATCCAATTCGTTTTTCTTCGATCCATCTGCTTCACACGGCAACAGCATGTTCTTCCT
TGGGAATCTCAATCCCGTCGTCCAAGGAGGAGGAGCAAGATCGATGATGAACATGGAGGAAA
CTTCGAAGCGAAGGCCCTTCTTTAGCTCCCCTGAGGATCTCTACGACGATGACTTTTACGAC
GACCAGTTGCCTGAAAAGAAGCGTCGCCTCACTACCGAACAAGTGCATCTGCTGGAGAAAAG
CTTCGAGACAGAGAACAAGCTAGAGCCTGAACGCAAGACTCAGCTTGCCAAGAAGCTTGCTC
TACAGCCAAGGCAAGTGGCTGTCTGGTTTCAGAATCGCCGAGCTCGTTGGAAAACAAAACAG
CTTGAGAGAGACTACGATCTTCTCAAGTCCACTTACGACCAACTTCTTTCTAACTACGACTC
CATCGTCATGGACAACGATAAGCTCAGATCCGAGGTTACTTCCCTGACCGAAAAGCTTCAGG
GCAAACAAGAGACAGCTAATGAACCACCTGGTCAAGTGCCCGAACCACCAACTTGATCCG
GTTTACATTAATGCGGCAGCAATCAAAACCGAGGACCGGTTAAGTTTCAGGGAGCGTTGGGAG
CGCGGTACTAGACGACGACGCACCTCACTACTAGACAGCTGTGACTCTTACTTCCCAAGCA
TCGTACCCATCCAAGACAACAGCAACGCCAGTGATCATGACAATGACCGGAGCTGTTTCGCC
GACGTCTTTGTGCCACCACTTCACCGTCGCACGATCATCACGGTGAATCATTGGCTTTCTG
GGGATGGCCTTAG

SEQ ID NO: 16 *Arabidopsis thaliana* Arath_ATHB1 translated amino acid sequence

MESNSFFFDPSASHGNSMFFLGNLNPVVQGGGARSMMNMEETSKRRPFFSSPEDLYDDDFYD
DQLPEKKRRLTTEQVHLLLEKSFETENKLEPERKTQLAKKLGLQPRQVAVWFQNRARWKTQ
LERDYDLLKSTYDQLLSNYDSIVMDNDKLRSEVTSLTEKLQKQETANEPGQVPEPNQLDP
VYINAAAIAKTEDRLSSGSVGSVAVLDDDDAPQLLDSCDSYFPSIVPIQDNSNASDHDNDRSCFA
DV FVPTTSPSHDHHGESLAFWGP

SEQ ID NO: 17 *Daucus carota* Dauca_CHB3 cDNA sequence D26575

ATGGCGGGTCGGAGGGTGTTCATGGGGAGGGAGCCAATACGACGTCCGCTAGCCTGTTGTT
TCATAGTCAAAGACCTGAGCCTTTCTTTCTTTCTGCACCTTCTCCTTCTCTAATTGGTTCAA
AATCCATGGTTAGCTTTCAAGATGCTAAGCGAAAAAATCCCTACGATGGGTTCTTTATGCGG
TCATATGATGAAGAAGAAATTGGGGATGAAGAATATGATGAATACTTTTCAGCAGCCTGAGAA
GAAGAGGAGGCTCAAGGCTGATCAAATCCAGTTTCTTGAGAAAAGTTTTGAGACTGATAACA
AGCTTGAGCCTGAAAGAAAAGTTTCACTTGCAAAAGAACTCGGCTTGACGCAAGACAGGTT
GCGATATGGTTTCAGAACCGTCGAGCACGGTGGAAGACCAAAACACTAGAAAAAGATTATGA
TGTATTGCAAAATAGCTACAACAGCCTCAAGGCTGACTATGACAATCTACTTGCCGAGAAAG
AAAAACTTAAAGCCGAGGTTCTCGACCTGACAGACAAGCTACTTCTCAAAGAAGATAAGGGG
AGCAAGACAGTAGTTTTTGTATAAGCAAAAGGTGTCTGCAGCATTCCAACAAGAACGTGTTAG
TAATGACATATCTGTGGGTGAAGTACTCAGTAACTCAGTTATGGACTGCAAGCAAGAAGATC
ATAACTCTGTGAAAAGTGATGCAGTTGATTCTGACAGTCCACACTACAGTGATGAAGTCTAC
TCCAGTTTTATGGAGCCAGTGATCGCTCTTATGTTTTTGAACCTGCTCAGTCGGATATATC
TCAAGATGAAGAAGATGACATGGGGAACAACCTTATTTCTCCCATCATATCATGTTTTCTCAA
AGACTGAAGACGGTAGTTACTCCGACCAGCCTTCGAACCTTTCGTACTTTGGCTTCCAGTT
GAAGATCATACGTTTGGCTTTTGGGGTACTGAATTATAA

FIGURE 4 (continued)

14/104

SEQ ID NO: 18 *Daucus carota* Dauca_CHB3 translated amino acid sequence

MAGRRVFYGEANTTSASLLFHSQRPEPFFLSAPSPSLIGSKSMVSFQDAKRKNPYDGFMR
SYDEEEIGDEEYDEYFQQPEKKRRLKADQIQFLEKSFETDNKLEPERKVQLAKELGLQPRQV
AIWFQNRRLRWKTKTLEKDYDVLQNSYNLKYADYNLLAEKEKLKAEVLDLTDKLLLLKEDKG
SKTVVFDKQKVSAAFQQERVSNDISVGEVLSNSVMDCKQEDHNSVKSDAVDSDSPHYSDEVY
SSFMEPVDRSYVFEPAQSDISQDEEDDMGNNLFLPSYHVFVSKTEDGSYSQPSNSSYFGFPV
EDHTFGFWGTEL

SEQ ID NO: 19 *Glycine max* Glyma_HD157 cDNA sequence AF184278

ATGGCGAGTGGCAAGCTTTATGCGGGTTCAAACATGTCACTTCTCCTCCAAAACGAAAGGCT
CCCTTGCTCCTCTGAAGTCCTTGAGTCTCTTTGGGCTCAGACCTCTAACCTTGCTTCCCTTCC
AAGGTTCAAACCCGTGGTTGATTTTGAAGAATGTAAGTGGGAGCAGGATGACGGATAGGCCT
TTCTTTCAAGCGTTGGAGAAGGAAGAGAACTGTGATGAGGATTACGAGGGGTGTTTCCACCA
ACCGGGGAAGAAAAGGAGGCTCACAAGCGAACAAGTTCAAGTTTCTTGAAAGGAAGTTTGAGG
TAGAGAACAAAGCTTGAACCCGAAAGGAAAGTCCAAGTTGCAAAAGAGCTTGGCTTGCAGCCA
AGGCAAGTTGCTATATGGTTCCAAAACCGAAGGGCAAGGTTCAAGACCAAGCAGCTAGAAAA
AGACTATGGCGTGTGAAAGCTAGTTATGACAGACTCAAAAGTGACTATGAAAGTCTTGTTTC
AAGAGAATGACAAGTTAAAAGCAGAGGTGAATTCTCTGGAGAGCAAATTGATTCTTAGAGAT
AAAGAGAAGGAGGAGAATTTCGGATGACAAGTCATCTCCTGATGATGCTGTCAATTCTTCTTC
ACCCCAACAACAAGGAGCCTATGGATTTATTAATTATTTCAAAAAATGCAACAACAACAA
CAACATCTGAAAATGGGACCAAAGTGTGTCACCACTCCCACTCCCTATTATGGTAACATGC
TGCAAGCAAGAAGATGCCAACTCAGCCAAAAGTGATGTCTTGATTTCGGATAGCCACATTG
CACTTCATTTCGTGGAGCCTGCTGATTCCTCTCATGCCTTTGAACCAGAAGACCACTCAGAAG
ACTTCTCCCAAGATGAAGAGGATAACCTTAGTGAAAACCTTTTGATGACCTTCCCTTCTTCT
TGTTGCTTACCTAAGGTTGAAGAACACTGCTATGACGGCCCTCCTGAAAACCTCTTGTAATTT
TGGCTTCCAGGTTGAGGATCAAACCTTCTGTTTCTGGCCCTATTGA

SEQ ID NO: 20 *Glycine max* Glyma_HD157 translated amino acid sequence

MASGKLYAGSNMSLLLQNERLPCSSSEVLESLSWAQTSNPASFQGSKPVVDFENVSGSRMTDRP
FFQALEKEENCDEDYEGCFHQPGKKRRLTSEQVQFLERNFEVENKLEPERKVQLAKELGLQP
RQVAIWQNRRLRFKTKQLEKDYGVLKASYDRLKSDYESLVQENDKLKAEVNSLESKLIIRD
KEKEENSDDKSSPDDAVNSSSPHNNKEPMDLLIIISKNAATTTTTSENGTKVLSPLPLPIMVTC
CKQEDANSAKSDVLDSDSPHCTSFVEPADSSSHAFEPEDHSEDFSQDEEDNLSENLLMTFPSS
CCLPKVEEHCYDGPPEPNSCNFGFQVEDQTFCFWPY

SEQ ID NO: 21 *Craterostigma plantagineum* CPHB-5 AF443621

ATGAACTCTGCTCGGATTTTCTTCGACCCATCTTCCACGGCAACATGCTGCAGTTTCTTGG
GAACGCCGCGCGGCGATTTCATCCGTTTTCCGAGGAACAAGATCGTCGTCGGTGCTGAACATGG
AGGAGAGCTCGTTAAAACGACAGATTTTCAGCGCGCGCGCGCGGCGATGAATTCTACGACGAG
GAATACTACGACGAGCAGTTGTTGCCTGAGAAGAAGCGCCGACTCACCGCCGAGCAGGTTCA
CTTGCTTGAGAAGAGCTTCGAGGCTGAGAACAAGCTTGAGCCTGAGCGAAAGGCTGAGCTGG
CGAAGAAGCTCGGATTGCAGCCGAGGCAAGTCGCCATTTGGTTCCAAAACCGCCGAGCACGG
TGGAAGACTAAGCAGTTAGAGAGGGACTACGACAAGCTTAAGTCTTCTATGATTCTTCTTCT
CTCAACCTACGACTCTATTTCGCCAGGAAAACGACAAGCTCAAAGCCGAGCTCCTTTCCCTGA
ACGAGAAATTGCAACCCAAAGACGACGACGACCCATCGGCCGAAATAGGTGCAAATCTCAGT

FIGURE 4 (continued)

15/104

TCATCGTCGCCGCCTGTCGACGCGGCTGAGCCGCCGTGCCTGAAGCTGACGGTGAAGGTGGA
 GGACCGCCTGAGCACGGGGAGCAACGGCAGCGCAGTAATGGACGGCGACGGACCTCAGCAGC
 TCCTCGACGACAGCGGCGACTCGTACTTCGAGAACGACGAGGAATACGACTGCGCCGCCGCA
 AGTTTGGCTGCTGCGAAGGAGGACGACGGCAGCGATGAGGGCGGGTGTACTTCACCGAGGC
 TCTCGCGGCGGAGGAGGAGGAGGCGCCGTTTGTCTGGTGTATTTGGTCTTAA

SEQ ID NO: 22 Craterostigma plantagineum CPHB-5 translated amino acid sequence

MNSARIFFDPSSHGNMLQFLGNAGGDSSVFRGTRSSSVLNMEESSLKRQIFSGGGGDEFYDE
 EYYDEQLLPEKKRRLTAEQVHLLKSF EAENKLEPERKAELAKKLGLQPRQVAIWFQNRARR
 WKTKQLERD YDKLKSSYDSLSTYDSIRQENDKLKAELLSLNEKLQPKDDDDPSAEIGRNL
 SSSPPVDAAEPPCLKLTVKVEDRLSTGSNGSAVMDGDGPQQLLDDSGDSYFENDEEYDCAA
 SLAAAKEDDGSDEGGCYFTEALAAEEEEAPFAWCIWS

SEQ ID NO: 23 Gossypium hirsutum Goshi_hox5 cDNA sequence DT465649, CD486134

ATGGAGTCTGGCCGTCTTTTTTTCAATCCCTCCACTACCCACCGCAACATGTTGCTTCTCGG
 GAACACTGAACCCATCTTTCGAGGGGCAAGAACAATGGTTAGCATGGAGGAAAACCCAAAGA
 AGCGACTGTTCTTCAGCTCGCCGGAGGATTTGTACGACGAAGAGTACTACGACGAGCAGTTG
 CCCGAGAAAAAGCGTCGCCTTACGTCGGAGCAGGTGTATCTGCTAGAGAAGAGCTTTGAGGC
 AGAGAACAAAGCTGGAGCCGGAGAGGAAGAGCCAGTTGGCCAAGAAGTTAGGACTGCAACCAA
 GGCAGGTGGCGGTATGGTTCCAGAACCGCCGTGCAAGGTGGAAGACAAAGCAGCTTGAAAGG
 GACTATGACCTCCTCAAATCTTCCTTTGATTCCCTTCAGTCCAATTATGACACTATTCTCAA
 AGAAAATGAGAAGCTCAAATCTGAGGTAGCTTCCTTGAAGTGAAGGACTACAAGCCAAAGATG
 TGGCAACAGAAGCAATAGCAGGTGAAAAGGATGAAGGGTTAGCAGCTGAGATGGCCTCCGCC
 CTCCAATTCAGTATGAAGGTGGAGGACCGTCTTAGTAGCGGCAGTGTGGAAGCGCGGTGGT
 GGATGAGGATGCCCCACAGCTGGTGGACAGCGGCAATTCTACTTTCCAAGCGATGAATACT
 CCAGAGGCATTGGCCCTTTTCGATGGGGTTTCAGTCGGAAGATGAGGATGGCAGTGATAATTGC
 GGGAGTTACTTCTCCGATGTGTTTCGCAACCACAGAGCAGGGAGCATTAGGATTGTGGGCCTG
 GNTCTAA

SEQ ID NO: 24 Gossypium hirsutum Goshi_hox5 translated amino acid sequence

MESGRLFFNPSTTHRNMLLLGNTEPIFRGARTMVSMEENPKKRLFFSSPEDLYDEEYYDEQL
 PEKKRRLTSEQVYLLEKSF EAENKLEPERKSQ LAKKLGLQPRQVAVWFQNRARRWKTKQLER
 DYDLLKSSFDSLQSNYDTILKENELKSEVASLTEKLQAKDVATEA IAGEKDEGLAAEMASA
 LQFSMKVEDRLSSGSVGS AVVDEDA PQLVDSGNSYFPSDEYSRGIGPFDGVQSEDEDGSDNC
 GSYFSDVFATTEQ GALGLWAWX

SEQ ID NO: 25 Lycopersicon esculentum Lyces_hox5 cDNA sequence BT014213.1

ATGGGATCTGGGCATATATTTTTTCGACCCGTCGTCGTGTCACGGCAACATGCTGTTCTTGG
 GAGCGGAGATCCTGTTTTCCGAGGACCAAGATCGACGATGATGAAGATGGAGGACTCCTCGA
 AGAGGCGACCTTCTTTAGCTCGCCGGAGGATCTATATGACGAGGAATACTACGACGAGCAG
 TCACCGGAGAAGAAGCGCCGTCTCACTCCTGAGCAGGTGCACTTGTTGGAGAAGAGCTTTGA
 GACAGAAAACAAGCTGGAGCCCGAGCGCAAAACCCAGCTGGCCTANAAGCTGGGGCTGCAGC

FIGURE 4 (continued)

16/104

CCAGACAGGTGGCTGTATGGTTCCAAAACCGCCGTGCCCGGTGGAAGACCAAGCAGCTCGAG
 AGGGATTATGATCAGCTCAAATCCTCTTATGACTCCCTTCTCTCTGATTTTACTCCGTTTCG
 CAAAGATAACGATAAGCTCAAATCTGAGGTTGTTTCATTGATGAAAAGTTACAGGGGAAAG
 TGGTTGGAGGAGCAGGGGGAAATGAAAAATCTGACATCTTGGAGGTGGATGCTATGACGATC
 CTTCAAGTGAAGGTGAAGGCTGGGGACCGGTTGAGCAGTGGCAGTGGTGGGAGCGCGGTGGT
 AGATGAGCATAGTTCACAGCTGGTGGACAGTGGGGACTCATATTTTCACACTGATCATGAGG
 AGTATCCAGGGCCTGGAGGATGCAATGTTCCCTCCACCCATGGATGGTTTACAATCGGAGGAA
 GATGATGGTAGTGATGATCATGGCAGTTGCCATGGCTACTTCTCTAACGTCTTTGTGGCAGA
 AGAGCAGCACCATGAACAAGGAGAAGAGCCTATTGGATGGTTCTGGTCTTAA

SEQ ID NO: 26 *Lycopersicon esculentum* Lyces_hox5 translated amino acid sequence

MMSGHIFFDPSCHGNMFLGSGDPVFRGPRSTMMKMEDSSKRRPFFSSPEDLYDEEYYDEQ
 SPEKKRRLTPEQVHLLKESFETENKLEPERKTQLAXKLGLQPRQVAVWFQNRARWKTQLE
 RDYDQLKSSYDSLLSDFDSVRKDNDKLKSEVVSLEKLGKVVGGAGGNEKSDILEVDAMTI
 LQVKVKAGDRLSSGSGSAVVDEHSSQLVDSGDSYFHTDHEEYPGPGGCNVPVPPMDGLQSEE
 DDGSDDHGSCHGYFSNVFVAEEQHHEQGEEPIGWFW

SEQ ID NO: 27 *Lycopersicon esculentum* VaHOX1 cDNA sequence X94947

ATGGCTCCAGGGATTCTCTATGGTGGTTCTTCTAATTTTCGATGGCGTTTTTACTCAAAAACA
 GAGAGACGTGTTTTCTTCATCTACTGCACCGAAAGGGCATCTTGGTTCCCTTTTTGCCCTG
 CCTCTTCTTCTTCTAATTTCTTGGGATCCAGTTCTATGGTGAGTTTTTCGCGGTGTTAATGGA
 GGGAAGAGATCATTCTTTGATTCGTTCGATCAGGATGACAATGAAGCTGATGAATTGGGGGA
 ATATCTTCATCAAGCGGAGAAGAAGAGGCGACTTACTGACAACCAAGTTCAGTTTCTTGAGA
 AGAGTTTTGGGGAAGAGAACAACTTGAACCAGAAAGAAAAGTTCAGCTTGCTAAAGAACTT
 GGTCTGCAGCCTCGCCAAATTGCAATTTGGTTTCAGAATCGTCGTGCGCGATGGAAGACTAA
 GCAGCTCGAGAAAGATTATGATGAATTGAGGAATAGATACGATACTCTGAAATCAAATTACA
 ATAATCTTCTCAAGGAAAAAGAAGATCTTCAAGTGAAGTTTTCCGTCTCACCGGTAAGCTG
 TTTATCAAAGAGAAAGGAAATGGGCAATTGGATTGCGCGATGAACACAAACACTCCAATGC
 ATTGGCAAAGAAACCGTGGTTGATCCAATGTCCAATGTACCAGCTCTGGTTGTTAAGCACC
 AGCAGGAAGATTTAAGCTCTGCTAAGAGTGATGTTTTCGACTCAGAAAGCCACGTTACACC
 AGTAGAATGCATTCCTCAGTCGTAGATCAGGATGATTCTGCTCGCGCATTGAAACTGATCA
 GTCGGATTCTCTCAGGATGATGATGAAACTTCAGCAAGAATATGCTTTCTACTGCCAACC
 TACTTGGCAAAGACGCGGATGATGATTATCCCGCGACATCATCAAATTTGAGTTACTTTGGA
 TTTCCAGTTGAAGACCAAGGTTTTGGTTTCTGGACTTATTAA

SEQ ID NO: 28 *Lycopersicon esculentum* VaHOX1 translated amino acid sequence

MAPGILYGGSSNFDGVFTQKQRDVFSSSTAPKGLHLSLFPASSSSNFGSSSMVSFRGVNG
 GKRSFFDSFDQDDNEADELGEYLHQAEKKRRLTDNQVQFLEKSFGEENKLEPERKVQLAKEL
 GLQPRQIAIWQNRARWKTQLEKDYDELNRNYDTLKSNNLLKEKEDLRTEVFRLTGKL
 FIKEKNGQLDLRDEHKHSNALAKETVVDPMSPALVVKHQEDLSSAKSDVFDSESPRYT
 SRMHSSVVDQDDSARAFETDQSDSSQDDDENFSKNMLSTANLLGKDADDDYPATSSNLSYFG
 FPVEDQGFGWFTY

FIGURE 4 (continued)

17/104

SEQ ID NO: 29 *Medicago sativa* Medsa_hox16 cDNA sequence CB892061, CA858059

ATGGCGGGTGGGAGAGTTTTTTCAAATGGTCCTGCAAATATTTCAAATATAAATATGAATAT
 TTTGCTTCAGAATCAACAACAACTCCTCGTGGAACCTCTTCTCAACAACCTCTTGATTCTC
 TTTTCCTTTCTTCTTCTGCTTCTTTCTTTGGTTCAAGATCTATGGTGAGTTTTGAAGATGTT
 CAAGGAAGGAAAAGGCGCAACAGGTCTTTCTTTGGAGGATTTGATCTTGACGAAAACGGAGA
 GGATGAGATGGATGAGTACTTTTCATCAATCCGAGAAGAAACGGCGTCTCTCAGTGGATCAAG
 TTCAGTTTCTTGAGAAAAGCTTTGAGGAGGACAACAACTTGAACCAGAGAGGAAAACCAAG
 CTAGCTAAAGACCTTGGTTTGCAGCCACGGCAAGTTGCTATTTGGTTTCAAACCGTCGTGC
 AAGGTGGAAGACTAAACAGCTTGAGAAGGATTATGATTCTCTTAATGATGGTTATGAGTCTC
 TTAAGACAGAGTATGACAACCTTCTCAAAGAGAAAGATAGGTTACAATCTGAGGTGGCAAGC
 CTAAGTGAAGGTTACTTGAAAGAGAGAAACAAGAGGGGAAAATTCAAACAAGGTGAAAGTGA
 AACAAAGGAATTCTTGAAGGAACCAACAATTAATAAGCCTTTGGTTGATTGAGTTTCTGAGG
 GTGAAGGATCCAAATTGTCAATTGTTGAGGCTTCTAATAATAATAATAATAACAACTT
 GAAGATATTAGTTTCAAGGAGTGACATATTGGATTGTGAAAGTCCACGCTACACTGATGG
 AGTGTTAGAGACATGTGATTCTTCTATGTATTTGAACCTGAATATCAATCGGACCTATCAC
 AAGATGAAGAAGATCACAATTTATTGCCTCCTTACATCTTTACAAAACCTTGAAGATGTGAAT
 TACTCCGACCCGCCACATAATTCAACAAGTTATGGATTTCAAGAGGAAGATCATCATCAAGC
 TCTTTGGCCTTGGTCTTATTAG

SEQ ID NO: 30 *Medicago sativa* Medsa_hox16 translated amino acid sequence

MAGGRVFSNGPANISNINMNILLQNQQQTTPRGNSSQQPLDSLFLSSSASFSGSRSMVSFEDV
 QGRKRRNRSFFGGFDLDENGEDEMDEYFHQSEKKRRLSVDQVQFLEKSFEEDNKLPERKTK
 LAKDLGLQPRQVAIWQNRARRWKTKQLEKDYDSLNDGYESLKTEYDNLLEKEDRLQSEVAS
 LTEKVLEREKQEGKFKQGESETKEFLKEPTINKPLVDSVSEGEKSKLSIVEASNNNNNNNKL
 EDISSARSDILDCESPRYTDGVLETCDSSYVFEPEYQSDLSQDEEDHNLPPYIFTKLEDVN
 YSDPPHNSTSYGFQEEDHHQALWPWSY

SEQ ID NO: 31 *Aquilegia formosa* x *Aquilegia pubescens* Aqufo_hox5 cDNA sequence DT758247

ATGGATTCAACAACAAGCCGTCTTTTCTTTGATGGTTCCTGCCATGGGAACATGTTGCTTTT
 AGGGAGTGGAGATCCCGTTCTTCGAGGTTCAAGATCATTCAATTAATATGGAAGATTCTTTGA
 AAAGACGTCCTTTTTATAGTTCAACAGATGAACTAATTGAAGAGGAGTTTTATGATGAACAG
 CTACCTGAAAAGAAACGTCGTCTTACTTCTGAGCAGGTTTCTATTGGAGAAGAGCTTTGA
 GACAGAGAACAAGCTGGAACAGATCGTAAGACCCAGCTTGCTAAGAAGCTTGGGTTGCAAC
 CGAGACAAGTTGCAGTTTGGTTTCAGAATAGACGAGCTCGTTGGAAGACTAAGCAACTAGAG
 AGAGATTATGATCTTCTTAAAGCTTCTTATGATTCCCTTCGTTCTGATTACGATGACATTGT
 TAAAGAGAATGAGAAGCTCAAATCTGAGGTGGTTTCTTAACTGGGAAGTTGCAGGTCAAGG
 AGGGAGCTGGGATGGAGTTAAATCAGATATCTGACCCACCACTCTCCACTGAAGAAAATGTT
 GATGTAACACTACGATGCAATTTAATGTTAAGGTTGAGGATCGCTTGAGCTCTGGCAGTGGGGT
 AAGTGCTGTGGTTGATGAGGAATGTCGACAGCTTGTTGACAGTGTTGATTCTTATTTCCCTG
 GCGATGACTATGGTCAATGCATAGGCCAGTAGATGGAGTCCAGTCAGAAGAAGATGACATT
 AGTGACGACAGCCGGAGCTATTTCTCAGATGTCTTTCCAGCTGCACCAGAGCAGAACCACCA
 GGAGAGTGAGACATTGGGTTGGTGGGACTGGGCTTAA

FIGURE 4 (continued)

18/104

**SEQ ID NO: 32 *Aquilegia formosa* x *Aquilegia pubescens*
Aqufo_hox5 translated amino acid sequence**

MDSTTSRLFFDGSCHGNMLLLGSGDPVLRGSRSFINMEDSLKRRPFYSSTDELIEEEFYDEQ
LPEKKRRLTSEQVHLLLEKSFETENKLEPDRKTQLAKKLGLQPRQVAVWVFQNRRLRWKTKQLE
RDYDLLKASYDSLRSYDDIVKENEKLKSEVVS LTGKLQVKEGAGMELNQISDPPLSTEENV
DVTMMQFNVKVEDRLSSSGSGVSAVVDEECRQLVDSVDSYFPGDDYGQCIGPVDGVQSEEDDI
SDDRSYFSDVFPAAPEQNHQSESETLGWWDWA

SEQ ID NO: 33 *Oryza sativa* GOS2 promoter

AATCCGAAAAGTTTCTGCACCGTTTTTCACCCCCTAACTAACAATATAGGGAACGTGTGCTAA
ATATAAAATGAGACCTTATATATGTAGCGCTGATAACTAGAACTATGCAAGAAAACTCATC
CACCTACTTTAGTGGCAATCGGGCTAAATAAAAAAGAGTCGCTACACTAGTTTCGTTTTCTT
TAGTAATTAAGTGGGAAAATGAAATCATTATTGCTTAGAATATACGTTACATCTCTGTGCAT
GAAGTTAAATTATTTCGAGGTAGCCATAATTGTTCATCAAACTCTTCTTGAATAAAAAAATCTT
TCTAGCTGAACTCAATGGGTAAAGAGAGAGATTTTTTTTTAAAAAATAGAATGAAGATATTC
TGAACGTATTGGCAAAGATTTAAACATATAATTATATAATTTTATAGTTTGTGCATTTCGTCA
TATCGCACATCATTAAGGACATGTCTTACTCCATCCCAATTTTTATTAGTAATTAAAGACA
ATTGACTTATTTTTATTATTTATCTTTTTTCGATTAGATGCAAGGTACTTACGCACACACTT
TGTGCTCATGTGCATGTGTGAGTGCACCTCCTCAATACACGTTCAACTAGCAACACATCTCT
AATATCACTCGCCTATTTAATACATTTAGGTAGCAATATCTGAATTCAGCACTCCACCATC
ACCAGACCACTTTTAATAATATCTAAAATACAAAAATAATTTTACAGAATAGCATGAAAAG
TATGAAACGAACTATTTAGGTTTTTCACATACAAAAAAGAAATTTTGCTCGTGCGCGA
GCGCCAACTCTCCCATATTGGGCACACAGGCAACAACAGAGTGGCTGCCACAGAACACCCA
CAAAAAACGATGATCTAACGGAGGACAGCAAGTCCGCAACAACCTTTTAACAGCAGGCTTTG
CGGCCAGGAGAGAGGAGGAGAGGCAAGAAAACCAAGCATCCTCCTCCTCCCATCTATAAAT
TCCTCCCCCTTTTCCCCTCTCTATATAGGAGGCATCCAAGCCAAGAAGAGGGAGAGCACCA
AGGACACGCGACTAGCAGAAGCCGAGCGACCGCCTTCTTCGATCCATATCTTCCGGTTCGAGT
TCTTGGTCGATCTCTTCCCTCCTCCACCTCCTCCTCACAGGGTATGTGCCCTTCGGTTGTTT
TTGGATTTATTGTTCTAGGTTGTGTAGTACGGGCGTTGATGTTAGGAAAGGGGATCTGTATC
TGTGATGATTCTGTTCTTGGATTTGGGATAGAGGGGTTCTTGATGTTGCATGTTATCGGTT
CGGTTTGTATTAGTAGTATGGTTTTCAATCGTCTGGAGAGCTCTATGGAAATGAAATGGTTTA
GGGTACGGAATCTTGCGATTTTGTGAGTACCTTTTGTGTTGAGGTAAAATCAGAGCACCGGTG
ATTTTGCTTGGTGTAATAAAAGTACGGTTGTTTGGTCCTCGATTCTGGTAGTGATGCTTCTC
GATTTGACGAAGCTATCCTTTGTTTATTCCCTATTGAACAAAATAATCCAACCTTTGAAGAC
GGTCCCGTTGATGAGATTGAATGATTGATTCTTAAGCCTGTCCAAATTTTCGAGCTGGCTT
GTTTAGATACAGTAGTCCCATCACGAAATTCATGGAAACAGTTATAATCCTCAGGAACAGG
GGATTCCCTGTTCTTCCGATTTGCTTTAGTCCCAGAATTTTTTTTTCCCAAATATCTTAAAAA
GTCACCTTCTGGTTTCAGTTCAATGAATTGATTGCTACAAATAATGCTTTTATAGCGTTATCC
TAGCTGTAGTTCAGTTAATAGGTAATAACCCCTATAGTTTAGTCAGGAGAAGAACTTATCCGA
TTTCTGATCTCCATTTTAAATTATATGAAATGAACTGTAGCATAAGCAGTATTCATTTGGAT
TATTTTTTTTTATTAGCTCTCACCCCTTCATTATTCTGAGCTGAAAGTCTGGCATGAACTGTC
CTCAATTTTGTGTTTCAAATTCACATCGATTATCTATGCATTATCCTCTTGTATCTACCTGTA
GAAGTTTCTTTTGGTTATTCCTTGACTGCTTGATTACAGAAAGAAATTTATGAAGCTGTAA
TCGGGATAGTTATACTGCTTGTTCTTATGATTCAATTCCTTTGTGCAGTTCTTGGTGTAGCT
TGCCACTTTCACCAGCAAAGTTC

FIGURE 4 (continued)

19/104

SEQ ID NO: 34 primer prm6000

GGGGACAAGTTTGTACAAAAAGCAGGCTTAAACAATGGATCCCGGCCG

SEQ ID NO: 35 primer prm6001

GGGGACCACTTTGTACAAGAAAGCTGGGTGATCAGCTCCAGAACCAGG

SEQ ID NO : 36 *Oryza sativa* *Oryza hox4* cDNA sequence AF145728

ATGAAGCGACCCGGCGGTGCCGGCGGCGGCGGAGGCCACCCATCGCTCGTCACGATGGCTAA
TTCTAGTGATGATGGATATGGAGGGGTTGGGATGGAGCGGAGGGGGACGTGGAGGAGGAGA
TGATGGCGTGCGGCGGCGGCGGGGAGAAGAAGCGGCGGCTGAGCGTGGAGCAGGTTTCGCGCG
CTGGAGCGGAGCTTCGAGGTGGAGAACAAAGCTTGAGCCTGAGCGGAAGGCGCGGCTGGCGCG
CGACCTCGGCCTGCAGCCGCGCCAGGTCGCCGTCTGGTTCCAGAACCGCCGCGCGCGGTGGA
AGACCAAGCAGCTCGAGCGCGACTACGCCGCGCTCCGCCATTCTACGACTCCCTGCGCCTC
GATCACGACGCGCTCCGCCGCGACAAGGACGCCCTCCTCGCCGAGATCAAGGAGCTGAAGGC
GAAGCTCGGGGACGAGGAGGCGGCGGCGAGCTTCACGTCGGTGAAGGAGGAGCCGGCGGCCT
CCGACGGGCCACCGGCGGCGGGATTTGGGTCGTCCGACAGCGACTCAAGCGCGGTGCTGAAC
GACGTGGACGCGGCCGGCGCGCCGCGGCGGCGACGGACGCGCTGGCTCCGGAGGCGTGCAC
GTTTCTCGGTGCGCCGCCCGCCGCGGGCGCGGGCGCGGGCGCAGCGGCGGCGGCGAGCCACG
AGGAGGTGTTCTTCCACGGCAATTTCTCAAGGTGGAGGAGGACGAGACGGGGTTCTTCGAC
GACGACGAGCCGTGCGGCGGGTTCTTCGCCGACGATCAGCCCCGCGCTCTCGTCGTGGTG
GGCCGAACCCACGGAGCACTGGAAC**TGA**

SEQ ID NO : 37 *Oryza sativa* Orysa_hox4 translated amino acid sequence

MKRPGGAGGGGSPSLVTMANSSDDGYGGVGMEEAGDVEEEMMACGGGGGEKKRRLSVEQVRA
 LERSFEVENKLEPERKARLARDLGLQPRQVAVWFQNRRLRWKTKQLERDYAALRHSYDSLRL
 DHDALRRDKDALLAEIKELKAKLGDDEEAAASFTSVKEEPAASDGPAAAGFGSSDSDSSAVLN
 DVDAAGAAPAATDALAPEACTFLGAPPAAGAGAGAAAAASHEEVFFHGNFLKVEEDETGFLD
 DDEPCGGFFADDOPPLSSWWAEPTEHWN

SEQ ID NO : 38 *Oryza sativa* *Oryza hox6* cDNA sequence AK103160

ATGGATGGGGAGGAGGACAGCGAGTGGATGATGATGGACGTTGGAGGGAAGGGCGGGAAGGG
 CGGCGGCGGCGGCGGCGCGGCGGACAGGAAGAAGCGGTTTCAGCGAGGAGCAGATCAAGTCGC
 TGGAGTCCATGTTCGCGACGCAGACCAAGCTGGAGCCGAGGCAGAAGCTGCAGCTCGCCAGG
 GAGCTCGGCCTGCAGCCTCGCCAGGTCGCCATCTGGTTCCAGAACAAGCGCGCGCGGTGGAA
 GTCCAAGCAGCTCGAGCGCGAGTACTCCGCCCTCCGCGACGACTACGACGCCCTCCTCTGCA
 GCTACGAGTCCCTCAAGAAGGAGAAGCTCGCCCTCATCAAGCAGCTGGAGAAGCTGGCGGAG
 ATGCTGCAGGAGCCACGGGGGAAGTACGGCGATAATGCCGGGGACGACGCGCGGTTCGGGCGG
 CGTCGCCCGGCATGAAGAAGGAGGAGTTCGTCGGCGCGGGCGGCGCCGCCACGCTCTACTCGT
 CGGCCGAGGGTGGCGGGACGACGACGACGACGACGGCCAAGTTGATGCCCCACTTTCGGCAGC
 GACGACGTCGACGCGGGGCTCTTCCTCCGGCCGTCGTCGCAGCATCATCCGCCGCCGCCGCA
 CGCCGGTGCCGGCTTCACGTCCTCCGAGCCGGCCGCCGACCACAGTCCTTCAACTTCCACT
 CGAGCTGGCCGTCGTCCACGGAGCAGACCTGCAGCAGCACGCCATGGTGGGAATTTCGAGAGC
GAGTGA

FIGURE 4 (continued)

20/104**SEQ ID NO : 39 *Oryza sativa* Orysa_hox6 translated amino acid sequence**

MDGEEDSEWMMMDVGGKGGKGGGGGAADRKKRFSEEQIKSLESFMFATQTKLEPRQKLQLAR
ELGLQPRQVAIWQNKRRRWKSKQLEREYSALRDDYDALLCSYESLKKEKLALIKQLEKLAE
MLQEPRGKYGDNAGDDARSGGVAGMKKEEFVGAGGAATLYSSAEGGGTTTTTTAKLMPHFGS
DDVDAGLFLRPSSQHHPPPHAGAGFTSSEPAADHQSFNFHSSWPSSTEQTCSSTPWWEFES
E

SEQ ID NO: 40 *Populus tremuloides* Poptr_HOX16_1 cDNA sequence

ATGGCGGGTGGTACCGGTGGTTCTAATTCCAATTTGTCTGTTTTGCTTCAAAGCCAAAGAGG
CCCTTGTGCTGCTTCACAACCTCTTGAATCTTTTTCTCTTCTGGCTCTTCTCCTTCTTTTC
TTGGTTCAAGATCCATGATGAGTTTTGAAGATGTTTCATCAAGCAAACGGATCAACCAGGCCT
TTTTTCCGCTCGTTTTGATCACGAAGACAATGGAGACGATGATCTGGATGAATATTTTCATCA
ACCTGAAAAGAAGAGGAGACTTACTGTTGATCAAGTTCAGTTTCTTGAAAAGAGTTTTGAGC
TTGAGAACAAAGCTTGAACCTGAAAGGAAAATCCAGCTTGCAAAGGATCTTGGCCTTCAGCCG
CGTCAGGTTGCTATATGGTTTCAAACCGCCGAGCAAGATGGAAGACTAAACAGCTGGAAAA
GGATTATGACGTTTTTGCAATCTAGCTACAATAGCCTTAAGGCTGACTATGACAACCTCCTCA
AGGAGAAGGAGAACTAAAAGCTGAGGTTAATCTTCTCACCGACAAGTTGCTCCTCAAAGAG
AAAGAGAAGGGAATCTCAGAATTGTCTGATAAAGATGCATTATCGCAAGAGCCACCTAAAAG
GGCTATAGCTGATTACAGCTTCCGAGGGTGAAGTGTGCAAAAATCTCAACAGTGGCCTGTAAGC
AGGAAGATATCAGCTCAGCCAAAAGCGACATATTTGATTACAGACAGCCACATTACGCTGAT
GGGGTGCATTCTCTCACTCTTAGAGGCAGGAGATTCTTCATATGTTTTCGAACCCGATCAATC
AGATTTGTCAACAAGATGAAGAAGATACTTTAGCAAGAGCTTATTGCCTCCATACGTCTTTC
CGAAGCTTGAAGATGACGATTACTCTGACCCGCCTGCAAGTTTTGAAGATCATGCCTTTTGG
TCCTGGTCATACTAA

SEQ ID NO: 41 *Populus tremuloides* Poptr_HOX16_1 translated amino acid sequence

MAGGTGGSNSNLSVLLQSQRGPAAASQPLESFFLSGSSPSFLGSRSMMSFEDVHQANGSTRP
FFRSFDHEDNGDDDLDEYFHQPEKKRRLTVDQVQFLEKSFLENKLEPERKIQIAKDLGLQP
RQVAIWQNRNRARWTKQLEKDYDVLQSSYNLSKADYDNLKEKEKLKAEVNLLTDKLLLKE
KEKGISELSDKDALSQEPKRAIADSASEGEVSKIISTVACKQEDISSAKSDIFDSDSPHYAD
GVHSSLLEAGDSSYVFEPDQSDLSQDEEDNFSKSLPPYVFPKLEDDDYSDPPASFEDHAFW
WSY

SEQ ID NO: 42 *Populus tremuloides* Poptr_HOX16_2 cDNA sequence

ATGGCGGCTTGTGGTGGTGGTGGTGGTCTAATCCCAATTTGTCTGTTTTAGTTCAAAG
CCAAAGAGGCCCTTGTGCTGCTTCTCAACCTCTTGAAGCTTTTTCTCTTCTGGCTCTTCTC
CTTCTTTTCTTGGTTCAAGATCCATGATGAGTTTTGCAGATGTTACCAAGCAAATGGATCA
ACTAGACCGTTTTTCCGCCCATATGATCACGAAGACAACGGCGACGATGATTTGGATGAATA
TTTTCATCAACCTGAAAAGAAGAGGAGACTTACTGTTGATCAAGTTCAGTTTCTTGAAAGAA
GTTTTGAGGTTGAGAACAAAGCTTGAACCCGAAAGGAAAATCCAGCTGGCGAAGGATCTTGGC
TTGCAGCCTCGGCAGGTTGCCATATGGTTTCAAACCGCCGGGCAAGATGGAAGACGAAACA
GCTTGAAAAAGATTATGAGGTTCTGCAATCTAGCTACAATGGCCTTAAGGCTGACTACGACA
ACCTCTTCAAGGAGAAGGAGAACTAAAAGCTGAGGTTAATCTTCTCACCAACGAGTTGCTC
CTTAAAGAGAAAGAGAAAGGAAGCTCAGAATTGTCTGATAAAGATGCATTATCTCAAGAGCC
ACCCAAAAGGCAATAGCCGATTCAGCTTCAGAGGGTGAAGTGTGCAAACTTCAACCGTGG

FIGURE 4 (continued)

21/104

CCTGCCAGCAGGAAGATATTAGCTCAGCCAAAAGTGATATGTTTGATTTCAGACAGCCCACAT
 TTTGCGGATGGGGTACATTCTCTACTCTTAGAGGCAGGTGATTCTTCACATGTCTTCGAGCC
 CGACCAATCGGATTTATCACAAGATGAAGAAGATAACTTGAGCAAGAGTCTTTTGCCTCCGT
 ACGTCTTTCCAAAGCTTGAAGATGGTGATTACTCTGACCCGCCAGCAAGTTTTGAAGATCAT
 GCCTTTTGGTGCTGGTCATACTAA

SEQ ID NO: 43 Populus tremuloides Poptr_HOX16_2 translated amino acid sequence

MAACGGGGGGSNPNLSVLVQSQRGPCAASQPLEAFFLSGSSPSFLGSRSMMSFADVHQANGS
 TRPFFRPYDHEDNGDDDLDEYFHQPEKKRRLTVQVQFLERSFEVENKLEPERKIQQLAKDLG
 LQPRQVAIWFQNRRLRWKTKQLEKDYEVLQSSYNGLKADYDNLFEKEKEKLKAEVNLLTNELL
 LKEKEKGSSELSKDALSQEPPKKAADSASEGEVSKTSTVACQQEDISSAKSDMFDSDSPH
 FADGVHSSLLEAGDSSHVFEPDQSDLSQDEEDNLSKSLPPYVFPKLEDGDYSDPPASFEDH
 AFWCWSY

SEQ ID NO: 44 Populus tremuloides Poptr_HOX16_3 cDNA sequence

ATGGCGGGTGATAAAGACTGTGGCAGTTCTAAAATGACCATTTTTCTTCGAAACGGCAGGCT
 CCCTCCTTGTGAATCTCTCTGTATTCTCACCTCTTTTAGCACTCTTCATGGTGCAAAATCTA
 TGGTTAATTTTAGGAATGATGGAGGAGACACTGTAGACATGTCTTTTTTCCAACCACATGTC
 AAAGAAGAAAGTAGCGATGAGGATTATGATGCGCACCTTAAGCCATCTGAAAAGAAAAGGCG
 GCTTACAGCTGCTCAAGTCCAGTTTCTTGAGAAGAGCTTTGAGGCGGAGAATAAGCTTGAAC
 CAGAGAGGAAGATGCAGCTTGCTAAAGAACTCGGCTTGACGCCTCGCCAGGTTGCAATATGG
 TTTCAAACCGTAGAGCTCGGTTCAAGAACAAGCAGCTGGAAAGGGACTACGACTCCTTGAG
 AATCAGCTTTGACAACTCAAGGCTGATTATGACAACTCCTCCTCGAGAAGCAGAATTTGA
 AAAACGAGCTTCTTTCACTGAAAGAAAAATTGCTTAGCAGAGAGGAAAGTATGGAAAGTTCA
 GAACCATTTGATGTCATCCATTCACCGGATGCAGAACTTGAGCCTATTCCTGATACAGTGTC
 TGAAAATGTTTCCGCCATTGTGCCAATGGTGACACCCAAACAAGAAGAAAGTTCAGCTAAAA
 ATGATGTTTTCAACTCAGACAGCCACGTTCAATTTTGGAGCCCCGTGATTGTTATCGTGTT
 TTCGAGTCAGACCAACCAGATTTTTCCCAAGTTGAAGAAGATAATCTCACCAGGAGCTTTCT
 ACCCCCTCCGTACTTTCCAAAACCTCTACCGAGAGCCACCTGCAAGTTCACGTAATTTTGAAT
 TCTCAGCGGAAGATCAGCCCTTTTGGTCCTGGATTACTGA

SEQ ID NO 45 Populus tremuloides Poptr_HOX16_3 translated amino acid sequence

MAGDKDCGSSKMTIFLRNGRLPPCESLCILTSFSTLHGAKSMVNFNRNDGGDTVDMSFFQPHV
 KEESDEDYDAHLKPSEKKRRLTAAQVQFLEKSFEAENKLEPERKMQQLAKELGLQPRQVAIW
 FQNRRLRFKNQQLERDYDSLRI SFDKLKADYDKLLLEKQNLKNELLSLKEKLLSREESMESS
 EPFDVIHSPDAELEPI PDTVSENVSAI VPMVTPKQEESSAKNDVFNSDSPRSFLEPRDCYRV
 FESDQPDFSQVEEDNLTRSFLPPPYFPKLYREPPASSRNFEFSAEDQPFWSWIY

SEQ ID NO 46 Medicago truncatula Medr_HOX16_1 cDNA sequence

ATGGCAGGTGGCAAGCTTTTTGGTGTTCTAATATGTCACTTTTGCTTCAAATGAAAGACT
 CCCTTGTAATTCTGAAGTCCTTGAATCTCTTTGGGTTACACCCCTGCTTCTTTTCAAGGTT
 CAAATTCAAGTGGTTAATTTTGAGAATGGTGGTGGTAGCAACAGAGTGGTAACAGATAGACCC
 TTCTTTCAACAACCTTGAGAAAGAAGAGAATTGTGGTGATGAAGATTATGAAGCATGCTACCA
 TCAACAAGGAAAGAAAAGGAGGCTTTCAAGTGAACAAGTTCAATTTCTTGAAAAGAGTTTTG
 AGGTAGAAAACAAGCTTGAACCTGATAGGAAAGTTCAACTTGCAAAGAGCTTGTTTGCAA

FIGURE 4 (continued)

22/104

CCAAGACAAGTTGCTATATGGTTTCAAAACAGAAGGGCAAGGTTCAAAACTAAACAGCTTGA
 AAAAGATTATGGCACATTGAAAGCTAGCTTTGATAGTCTCAAAGATGATTATGATAATCTTC
 TTCAAGAGAATGACAAGTTAAAAGAAGAGGTGAATTCTCTCAAGAACAAATTGATCCCAAGA
 GATAAAGAAAAAGTGAATTGAGAAGACAAATCATCACCAGAAGCAATCAATTCACCTCATAA
 CAACATAGATCCAATGGATATAATTTCAATTACAAATTCAGAAAATGGGTCCAAAATGTCAC
 TCCCTAATATGGTACTAAATGTAAGCAAGAAGATGCCAATTCAGCTAAAAGTGATGTGCTT
 GATTCTGATAGCCACATTGCAATGATGGGAACAATCTTTCTTCTTTTCATAGAGCCTACAGA
 TTCAGATTTCTCACAAGATGAAGAGGATAATGATACTTGAGTCATAATCTTTTGACTCTTC
 CTTGCTTACCAAAAGTTGAAGATGTTTGCTATGATGACCCACATGAAAATTCTTGTAATTTT
 GGGTTCCTGTTGAAGATCAAACCTTTTGTCTTCTGGCCTTATTGA

SEQ ID NO 47 *Medicago truncatula* Medtr_HOX16_1 translated amino acid sequence

MAGGKLFGGSNMSLLLLQNERLPCTSEVLES LWVHTPASFQGSNSVNFENGGSNRVVTDRP
 FFQQLKEKENCDEDEYACYHQQKKRRLSSEQVQFLEKSFEVENKLEPDRKVQLAKELGLQ
 PRQVAIWFQNRARRFKTKQLEKDYGLKASFDSLKDDYDNLQENDKLKEEVNSLKNKLI PR
 DKEKVNSDKSSPEAINSPHNNIDPMDIISITNSENGSKMSLPNMVLKCKQEDANSKSDVL
 DSDSPHCNDGNNLSSFIEPTDSDFSQDEEDNDNLSHNLLTLPCLPKVEDVCYDDPHENSCNF
 GFPVEDQTFCFWPY

SEQ ID NO 48 *Phaseolus vulgaris* Phavu_HOX16 cDNA sequence

ATGGCGGGTGGCAAGCTTCATCCTGGTTCAAACATGTCACTTCTCCTCCAAAACGACAGGCT
 CCCTTGCTCCTCTGAAGTCCTTGAGTCTCTTTGGGCTCACACCTCTAACGCTGCTTCCTTCC
 AAGGTTCAAAATCTATGGTTGATTTTGAGAATGTTAGTGGGGGCAGGGTGACGGATAGGCCC
 TTTTTTCAAGCGTTGGAGAAGGAAGATAACTGTGATGATGATTATGAGGGTTGCTTCCATCA
 ACCGGGTAAGAAAAGGAGGCTCACAAGCGAACAAGTTCAGTTCCTTGAAAGGAACCTTGAGG
 TCGAGAACAAGCTTGAACCTGAAAGGAAGGTCCAACCTTGCAAAGGAGCTTGGCTTGCAGCCA
 AGGCAAGTGGCTATATGGTTCCAAAACCGAAGGGCAAGGTTCAAGACCAAGCAGCTAGAAAA
 AGATTATGGCACATTGAAAGCTAGCTATGACAGACTCAAAGGTGACTATGAAAGTCTTCTTC
 AAGAGAATGACAAGTTAAAAGCAGAGGTGAATTCTCTGGAGAGCAAATTGATTCTTAGAGAT
 AAAGAGAAGGAGAATTTCGGACGACAAGTCATCTCTGATGCTGTCAATTCACCCACAAAGA
 GCCTATGGATTTAATTTCAAATTCACATCTGAAAATGGGACCAAAGTGTCACTCCCTATTA
 TGGTAACATGCAAGCAAGAAGATGCCAATTCAGCCAAAAGTGATGTGCTTGATTTCGGACAGC
 CCACATTGCACTGATGGGAACCATCCCTCTTCATTCTGAGGCTGCTGATTCTCCTCCCATGC
 TTTTGAACCAGACCACTCCGACTTCTCCAAGATGAAGAGGATAATCTTAGTGAAAGCCTTT
 TGACCCTCCCTTGCTTACCAAAGGTTGAAGAAGCCTGCTATGATGACCTCCTGAAAACCTT
 TGTAATTTTGGCTTCCATGTGCGAGGATCAAACCTTCTGTTTCTGGCCCTATTGA

SEQ ID NO 49 *Phaseolus vulgaris* Phavu_HOX16 translated amino acid sequence

MAGGKLHPGSNMSLLLLQNDRLPCSSEVLES LWHTSNAASFQGSKSMVDFENVSGGRVTD RP
 FFQALEKEDNCDDEYEGCFHQPGKKRRLTSEQVQFLERNFEVENKLEPERKVQLAKELGLQP
 RQVAIWFQNRARRFKTKQLEKDYGLKASYDRLKGDYESLLQENDKLKAEVNSLESKLI LRD
 KEKENSDDKSSPDVNSPHKEPMDLISNSTSENGTKVSLPIMVTCKQEDANSKSDVLDSDS
 PHCTDGNHPSSFVEPADSSSHAFEPDHSDFSQDEEDNLSESLTLPCLPKVEEACYDDPPENP
 CNFGFHVVEDQTFCFWPY

FIGURE 4 (continued)

23/104**SEQ ID NO 50 Lotus corniculatus Lotco_Hox16 cDNA sequence**

ATGGCGGGAGGGAGGGTCTTTAGCGGCGGTTCTGCTGCTCCTGCAAATGTTTCCGATACCAG
TCTTTTGCTTCAGAATCAACCTCCTGATTCTTCTCTCTCCTCTCTACCTCTGCTTCTTTTC
TCGGTTCAAGATCCATGGTGAGCTTCGCAGATAATAAATTAGGGCAAACGCGGTCTGTTCTTC
TCCGCGTTTGACCTCGATGAGAACGGCGATGAGGTCATGGACGAGTACTTTACCAATCGGA
GAAGAAGCGCCGTCTCTCTGTTGACCAAGTTCAGTTTCTGGAGAAGAGCTTCGAGGTGGATA
ACAAGCTCGAACCTGACAGGAAAACCAAGATTGCCAAGGACCTTGGTTTGCAGCCACGCCAA
GTCGCAATCTGGTTCCAGAACCGCCGTGCACGGTGGAAGACGAAACAGCTTGAGAAGGATTA
TGATTCTCTGCATAGTAGCTTTGAGAGTCTCAAATCCAATATGATAATCTTCTCAAGGAGA
AAGACATGTTAAAAGCTGAGGTGGCAAGTCTCACTGAGAAGGTGCTTGCAAGAGAGAATTTG
AAACAAGTTGAAAGTGAAACAAAGGGATTGGTTGAACCACCCCAAAGGCCTTTACTTGATTCT
AGTTTCAGAGGGTGAAGAATCTAAAGTCTCTGTTGGGGCTTGTAACATGAGGATATCAGTT
CAGCCAGGAGTGAGAGTTTGGATTCTGATAGCCACGTTACAGGGATGGATATGGAGTTAAC
TCAGCAGTGCTAGAGACATGTGATTCTTCTTATGTGGTTGAACCTGATCAATCGGATATGTC
ACAGGATGAGGAAGACAACCTGACCAAGACCCTGTTGCCTCCATACATGTTTTCCAACTTG
GAGATATGGATTACTCCGACCCGCCTGAAAGTTCATGTAATTTCCGATTTCCGGAGGAAGAT
CATGCCCTTTGGTCATGGTCTTACTGA

SEQ ID NO 51 Lotus corniculatus Lotco_Hox16 translated amino acid sequence

MAGGRVFSGGSAA PANVSDTSLLLQNQPPDSSLFLSTSASFLGSRSMVSFADNKLQTRSF
SAFDLDENGDEVMDEYFHQSEKKRRLSVDQVQFLEKSFEVDNKLEPDRKTKIAKDLGLQPRQ
VAIWFQNRRLRWKTKQLEKDYDSLHSSFESLKSNYDNLLKEKDMLKAEVASLTEKVLARENL
KQVESETKGLVEPPQRPLLDVSEGEESKVS VGACKHEDISSARSES LDDSPRYRDGYGVN
SAVLETCDSSYVVEPDQSDMSQDEEDNLTKTLLPPYMF SKLGDM DYSDPPESSCNFGFPEED
HALWSWSY

FIGURE 4 (continued)

SUBSTITUTE SHEET (RULE 26)

24/104

MDSSTVGAPGSSSLHGVTGREPAFAFSTEVGGEDAAAASKFDLPVDSEHKAKTI
RLLSFANPHMRTFHL**SWISFFSCFVSTFAAAPLVPIIRDNLNLTKADIGNAGV**
ASVSGSIFSRLAMGAICDMLGPRYGCAFLIMLAAPTVFCMSLIDSAAGYIAVR
FLIGFSLATFVSCQYWMSTMFNSKIIGLVNGLAAGWGNMGGGATQLIMPLVYD
VIRKCGATPFTAWRLAYFVPGTLHVVMGVLVLTLGQDLPDGNLRS**LQKKGDVN**
RDSFSRVLWYAVTNYRTWIFVLLYGYSMGVELTTDNVIAEYFYDRFDL**DLRVA**
GIIAASFGMANIVARPTGGLLSDLGARYFGMRARLWNIWILQTAGGAFCLLLG
RASTLPTSVVCMVLFSFCAQAACGAIFGVIPFVSRRSLGIISGMTGAGGNFGA
GLTQLLFFTSSRYSTGTGLEYMGIMIMACTLPVVLVHFPQWGS**MFLPPNAGAE**
EEHYYGSEWSEQESKGLHGASLKFAENSRSERGRNVINAAAAAATPPNNSP
EHA

FIGURE 5

SUBSTITUTE SHEET (RULE 26)

25/104

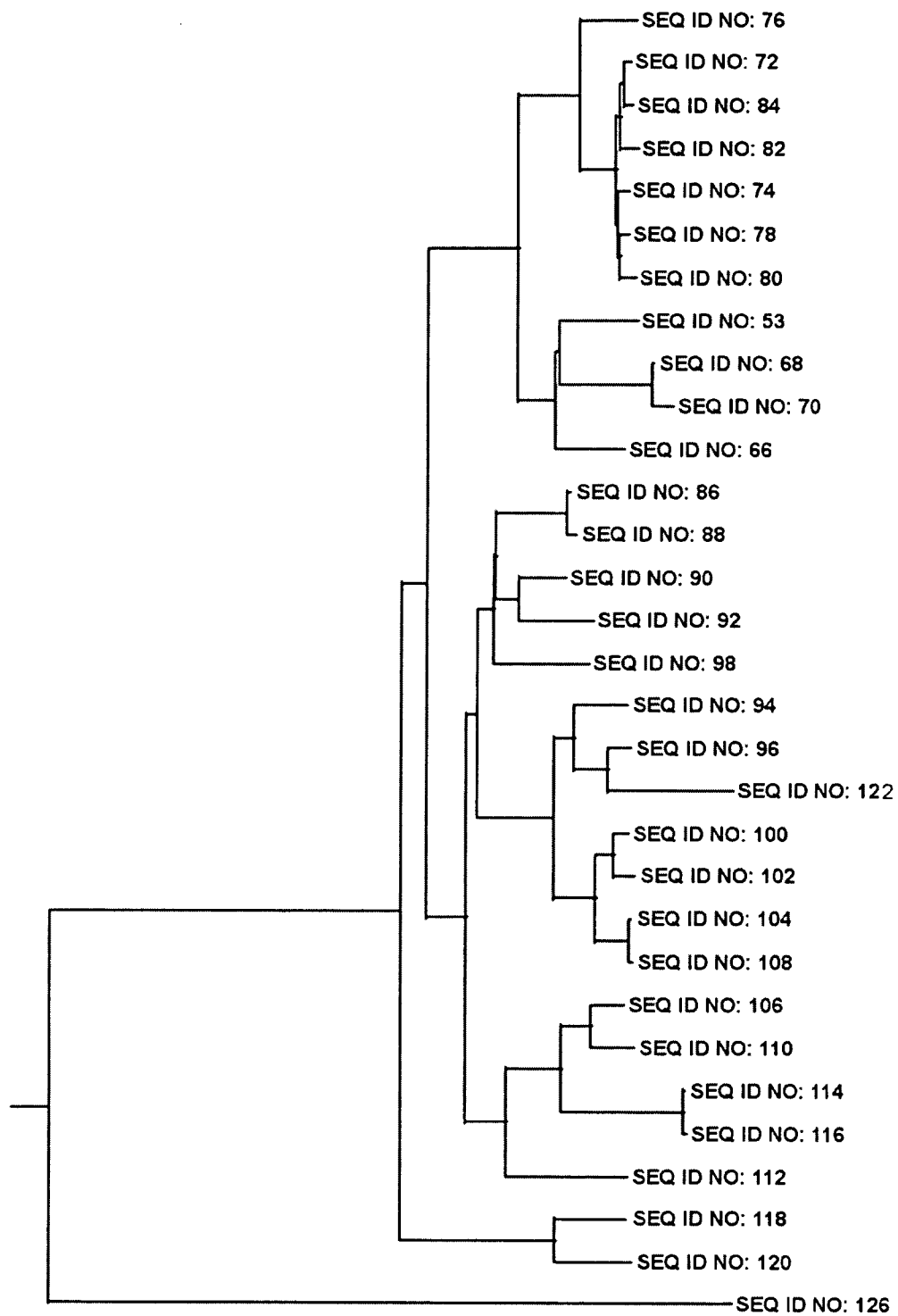


FIGURE 6 A

CLUSTAL W (1.83) multiple sequence alignment

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-----MAAVGAPGSSSLHGVGTGREPAFAFSTEHEE--AASNG-----GKFDLPVDSEHKAK
-----MAAVGAPGSSSLHGVGTGREPAFAFSTEHEE--AASNG-----GKFDLPVDSEHKAK
-----MEVGAPGSSSLHGVGTGREPAFAFSTSAPV-DDDAA-----SKFDLPVDSEHKAK
---MDSSTVGAPGSSSLHGVGTGREPAFAFSTEVGGEDAAAA-----SKFDLPVDSEHKAK
-----MEVEASAHGDTAA-----SKFTLPVDSEHKAK
-----MEVESSAHGDAAA-----SKFTLPVDSEHKAK
-----MEVQAGSHADAAA-----SKFTLPVDSEHKAK
-----MEVEAGAHGDTAA-----SKFTLPVDSEHKAK
-----MEVEAGAHGDTAA-----SKFTLPVDSEHKAK
-----MEVESSSHGAGDEAA-----SKFSLPVDSEHKAK
-----MAEVEGEPGSSMHGVTGREQTFAFSVASPIVP-----TDPTAKFDLPVDSEHKAK
-----MAEVEGEPGSSMHGVTGREQTFAFSVASPIVP-----TDPTAKFDLPVDSEHKAK
-----MAEIEGSPGSSMHGVTGREQTFVAVASPIVP-----TDTTAKFDLPVDSEHKAK
-----MVEIEGSPGTSMHGVTGREQTFISSVSSPMVP-----TDTTAKFDLPVDSQHKAK
-----MADVEGSPGSSMHGVTGREQSFASFASPTVP-----TDTTAKFALPVDSEHKAK
-----MGDIEGSPGSSMHGVTGREPVLAFFVASLI VP-----TDTSANFKVPVDSEHKAK
-----MGDMEGSPGSSMHGVTGREPSSLAFSVASRID-----TSAEFHVPVDSEHKAK
-----MVDIEGSPGSSMHGVTGREPVLAFFSVASPMVQ-----TDTTAHFKVPVDSEHKAK
-----MGDIEGEPGSSMHGVTGREPVLAFFSVASPMVP-----TDTTAKFSVPVDTEHKAK
-----MADIEGEPGSSMHGVTGREPVLAFFSVASPMVP-----TDTTAKFSVPVDTEHKAK
-----MADVEGSPGSSMHGVTGREPVLAFFSVASPMVP-----TDTSAKFSVPVDTEHKAK
-----MTDVEGSPGSSMHGVTGREPVLAFFSVASPMVP-----TDTSAKFSVPVDTEHKAK
-----MGDSTGEPGSSMHGVTGREQSFASFVQSPIVH-----TDKTAKFDLPVDTEHKAT
-----MGDSTGEPGSSMHGVTGREQTFAFSVASPIVP-----TDKTAKFDLPVDSEHKAT
-----MGSTDPEGSSMHGVTGREQSYAFSVDG-SEP-----TNTKKKYNLPVDAEDKAT
-----MGSTDPEPRSSMHGVTGREQSYAFSVDG-SEP-----TNTKKKYNLPVDAEDKAT
-----MADGFGEPGSSMHGVTGREQSYAFSVESPAVP-----SDSSAKFSLPVDTEHKAK
MTHNHSNEEGSIGTSLHGVGTAREQVFSFSDASS---QTVQSDDDPTAKFALPVDSEHRAK
MAHNHSDGGSIGTSLHGVGTAREQVFSFVSQEDVPSSQAVRTNDPTAKFALPVDSEHRAK
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SEQID68
SEQID70
SEQID66
SEQID53
SEQID78
SEQID80
SEQID74
SEQID72
SEQID84
SEQID82
SEQID76
SEQID86
SEQID88
SEQID90
SEQID92
SEQID98
SEQID96
SEQID122
SEQID94
SEQID100
SEQID102
SEQID104
SEQID108
SEQID106
SEQID110
SEQID114
SEQID116
SEQID112
SEQID118
SEQID120

FIGURE 6 B

27/104

SEQID68	SVRLFSVANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSG
SEQID70	SVRLFSVANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSG
SEQID66	SIRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSG
SEQID53	TIRLLSFANPHMRTFHLWSISFFSCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSG
SEQID78	SFRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID80	SFRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID74	SFRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID72	SFRLFSFANPHMRTFHLWSISFFTCFISTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID84	SFRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID82	SFRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID76	SIRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLAKADIGNAGVASVSG
SEQID86	VFKIFSLANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKQDIGNAGVASVSG
SEQID88	VFKIFSLANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKQDIGNAGVASVSG
SEQID90	VFKLFSLANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKSDIGNAGVASVSG
SEQID92	VFKLFSLANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKSDIGNAGVASVSG
SEQID98	VFKIFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKSDIGNAGVASVSG
SEQID96	VFKFYFSKPHGLTFQLWSISFCTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSG
SEQID122	VFKFKSFPHPGLTFQLTWISFPTCFVSTFAAAPLVPIIRDNLNPTKMDVGNAGVASVSG
SEQID94	VFKFYFSKPHGLTFQLWSISFPTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSG
SEQID100	IFKFYFSKPHGLTFQLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSG
SEQID102	VFKFYFSKPHGLTFQLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSG
SEQID104	QFKFYFSKPHGLTFQLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSG
SEQID108	QFKFYFSKPHGLTFQLWSISFFTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSG
SEQID106	VFKLFSFAKPHMRTFHLWSISFSTCFVSTFAAAPLVPIIRENINLTKMDVGNAGVASVSG
SEQID110	VFKLFSFAKPHMRTFHLWSISFSTCFVSTFAAAPLVPIIRENINLTKQDIGNAGVASVSG
SEQID114	VFKLFSFAKPHMRTFHLWSISFSTCFVSTFAAAPLVPIIRENINLTKHDIGNAGVASVSG
SEQID116	VFKLFSFAKPHMRTFHLWSISFSTCFVSTFAAAPLVPIIRENINLTKHDIGNAGVASVSG
SEQID112	VFKLLSFEAPHMRTFHLAWSIFFTCFISTFAAAPLVPIIRDNLNLTRQDIGNAGVASVSG
SEQID118	VFNPLSFAKPHMRAFHGLWSIFFTCFISTFAAAPLVPIIRDNLDLTKTDIGNAGVASVSG
SEQID120	VFKPLSFAKPHMRAFHGLWSIFFTCFISTFAAAPLVPIIRDNLDLTKTDIGNAGVASVSG

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FIGURE 6 B (continued)

28/104

SEQID68	SIFSRLTMGAVCDLLGPRYGC AFLIMLSAPT VFCMSLIDD AAGYITVRFLIGFSLATFVS
SEQID70	SIFSRLTMGAVCDLLGPRYGC AFLIMLSAPT VFCMSLIDD AAGYITVRFLIGFSLATFVS
SEQID66	SIFSRLAMGAI CDLLGPRYGC AFLIMLTAPT VFCMSLIDD AAGYIVVRFLIGFSLATFVS
SEQID53	SIFSRLAMGAI CDM LGPRYGC AFLIMLAAPT VFCMSLIDS AAGYIAVRF LIGFSLATFVS
SEQID78	SIFSRLAMGAI CDLLGPRYGC AFLVMLSAPT VFCMAA ID DASYIAVRF LIGFSLATFVS
SEQID80	SIFSRLAMGAVCDLLGPRYGC AFLVMLSAPT VFCMAVIDD ASGYIAVRF LIGFSLAAFVS
SEQID74	SIFSRLAMGAI CDLLGPRYGC AFLVMLSAPT VFCMAVIDD ASGYIAVRF LIGFSLATFVS
SEQID72	SIFSRLAMGAI CDLLGPRYGC AFLVMLSAPT VFCMAVIDD ASGYIAVRF LIGFSLATFVS
SEQID84	SIFSRLAMGAI CDLLGPRYGC AFLVMLSAPT VFCMAVIDD ASGYIAVRF LIGFSLATFVS
SEQID82	SIFSRLAMGAI CDLLGPRYGC AFLVMLSAPT VFCMAVIDD ASGYIAVRF LIGFSLATFVS
SEQID76	SIFSRLAMGAI CDLLGPRYGC AFLVMLAAPT VFCMSLIDD AAGYITVRFLIGFSLATFVS
SEQID86	SIFSRLVMGAVCDLLGPRYGC AFLIMLSAPT VFCMSFVS D AGGYLA VRFMIGFSLATFVS
SEQID88	SIFSRLVMGAVCDLLGPRYGC AFLIMLSAPT VFCMSFVS D AGGYLA VRFMIGFSLATFVS
SEQID90	SIFSRLAMGAVCDML GPRYGC AFLIMLSAPT VFCMSFVKDAAGYIAVRF LIGFSLATFVS
SEQID92	SIFSRLTMGVI CDLLGPRYGC AFLIMLSAPT VFCMSFVNDAAGYI VVRFMIGFSLATFVS
SEQID98	SIFSRLVMGAVCDLLGPRYGC AFLIMLSAPT VFCMSFVS D AGGYLA VRFMIGFSLATFVS
SEQID96	SILSRLAMGAI CDM LGPRYGC AFLIMLSAPT VCLCMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID122	SILSRGAMGAI CDM LGPRYGC AFLIMLSAP KVL CMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID94	SILSRLAMGAI CDM LGPRYGC AFLIMLSAPT VFCMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID100	SILSRLVMGAVCDML GPRYGC AFLIMLSAPT VFCMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID102	SILSRLVMGAVCDML GPRYGC AFLIMLSAPT VFCMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID104	SILSRLTMGAVCDLLGPRYGC AFLIMLSAPT VFCMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID108	SILSRLTMGAVCDLLGPRYGC AFLIMLSAPT VFCMSFVS SAGGYVA VRFMIGFSLATFVS
SEQID106	SIFSRLVMGAVCDLLGPRYGC AFLVMLSAPT VFSMSFVS DAAGFI TVR FMIGFCLATFVS
SEQID110	SIFSRLVMGAVCDLLGPRYGC AFLVMLSAPT VFSMSFVS GAAGFI TVR FMIGFCLATFVS
SEQID114	SIFSRLVMGAVCDLLGPRYGC AFLVMLSAPT VFSMSFVS DAAGFI TVR FMIGFCLATFVS
SEQID116	SIFSRLVMGAVCDLLGPRYGC AFLVMLSAPT VFSMSFVS DAAGFI TVR FMIGFCLATFVS
SEQID112	SIFSRLVMGAVCDLLGPRYGC AFLVMLSAPT VFSMSFVG GAGGYI TVR FMIGFCLATFVS
SEQID118	AIFSRLAMGAVCDLLGARYGTAFSLMLTAPT VFSMSFVG GPSGYLGVR FMIGFCLATFVS
SEQID120	AIFSRLAMGAVCDLLGARYGTAFSLMLTAPA VFSMSFVADAGSYLA VRFMIGFCLATFVS
	:*: *. * *: *. * *: *. * *: *. * *: *. * *: *. * *: *. * *: *

FIGURE 6 B (contiuned)

29/104

SEQID68 CQYWMSTMFSSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID70 CQYWMSTMFSSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID66 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID53 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID78 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID80 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID74 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID72 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID84 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID82 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID76 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID86 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID88 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID90 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID92 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID98 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID96 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID122 CRYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID94 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID100 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID102 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID104 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID108 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID106 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID110 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID114 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID116 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID112 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID118 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV
 SEQID120 CQYWMSTMFNSKIIIGTVNGLAAGWGNMGGGATQQLIMPLVYDVIRKCGATPFTAWRLAYFV

FIGURE 6 B (continued)

30/104

SEQID68	PGLMHVVMGVLVLTGQDLPDG--NLRSLQKKGNVKNKDSFSKVMWYAVINYRTWIFVLL
SEQID70	PGLMHVVMGVLVLTGQDLPDG--NLRSLQKKGNVKNKDSFSKVMWYAVINYRTWIFVLL
SEQID66	PGLMHVVMGILVLTGQDLPDG--NLRSLQKKGDANKDFSKVLWYAVTNYRTWIFVLL
SEQID53	PGTLHVVMGVLVLTGQDLPDG--NLRSLQKKGDVNRDVSFSRVLWYAVTNYRTWIFVLL
SEQID78	PGMHMIVMGLLVLTMGQDLPDG--NLASLQKKGDMAKDFSKVLWGAVTNYRTWIFVLL
SEQID80	PGMHMIVMGLLVLTMGQDLPDG--NLASLQKKGDMAKDFSKVLWGAVTNYRTWIFVLL
SEQID74	PGMHMIVMGLLVLTMGQDLPDG--NLASLQKKGDMAKDFSKVLWGAVTNYRTWIFVLL
SEQID72	PGMHMIVMGLLVLTMGQDLPDG--NLASLQKKGDMAKDFSKVLWGAVTNYRTWIFVLL
SEQID84	PGMHMIVMGLLVLTMGQDLPDG--NLASLQKRGDMAKDFSKVLWGAVTNYRTWIFVLL
SEQID82	PGMHMIVMGLLVLTMGQDLPDG--NLASLQKKGDMAKDFSKVLWGAVTNYRTWIFVLL
SEQID76	PGMHVVVMGLLVLTMGQDLPDG--NLASLQKKGEMAKDFSKVVMGAVTNYRTWIFVLL
SEQID86	PGLHVIIMGIMVLVLTGQDLPDG--NLAALQKKGDVAKDQFSKVLWHAVTNRTWIFVLL
SEQID88	PGLHVIIMGIMVLVLTGQDLPDG--NLAALQKKGDVAKDQFSKVLWHAITNRTWIFVLL
SEQID90	PGFMHVIMGILVLTGQDLPDG--NLGALRKKGDVAKDFSKVLWYAITNRTWIFALL
SEQID92	PGFMHVFMGILVLTGQDLPDG--NLSALQKKGDVAKDFSKVLWYAITNRTWIFALL
SEQID98	PGLHVIIMGILVLTGQDLPDG--NLGALKKKGDVAKDFSKVLWYAVTNYRTWIFVLL
SEQID96	PGLHVIIMGILVLTGQDLPDG--NLASLQKKGDVSKDKFSKILWYAAATNRTWILVLL
SESEQID122	PGLHVIISGILVLTGQDLPDGENAQNEASLRKKGRVHKDKFSKILRYAATNRTWILVLL
SESEQID94	PGLHVIIMGILVLTGQDLPDG--NLASLQKKGDVSKDKFSKILWYAAATNRTWIFVLL
SESEQID100	PGLHVIIMGILVLTGQDLPDG--NRGDLQKKGDVSKDKFSNILWYAAATNRTWIFVLL
SESEQID102	PGLHVVVMGILVLTGQDLPDG--NRGDLQKKGGVSKDKFTNILWYAAATNRTWIFVLL
SESEQID104	PGLHVVVMGILVLTGQDLPDG--NRGTLQKTGTVAKDKFGNILWYAAATNRTWIFVLL
SESEQID108	PGLHVVVMGILVLTGQDLPDG--NRGTLQKTGTVAKDKFGNILWYAAATNRTWIFVLL
SESEQID106	PGLLHIIMGILVLTGQDLPDG--NLRATLEKAGEVAKDFGKILWYAVTNYRTWIFVLL
SESEQID110	PGLLHIIMGVVLVLTGQDLPDG--NRSALKKGEVAKDFGKIMWYAVTNYRTWIFVLL
SESEQID114	PGLLHIIMGILVLTGQDLPDG--NRAAMEKAGEVAKDFGKILWYAVTNYRTWIFVLL
SESEQID116	PGLLHIIMGILVLTGQDLPDG--NRAAMEKAGEVAKDFGKILWYAVTNYRTWIFVLL
SESEQID112	PGLHVIIMGILVLTGQDLPDG--NRSTLEKKGAVTKDKFSKVLWYAITNRTWIFVLL
SESEQID118	PGLQVVMGILVLTGQDLPDG--NLSTLQKSGQVSKDKFSKVFWFVAVKNYRTWILFVL
SESEQID120	PGLQVVMGILVLTGQDLPDG--NLSTLQKSGQVSKDKFSKVFWFVAVKNYRTWILFVL
	** : : : . * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *

FIGURE 6 B (contiuned)

SEQID68	YGYCMGVELTTDNVIAEYMYDRFDLRLRVAGTIAACFGMANIVARPMGGIMSDMGARYWYG
SEQID70	YGYCMGVELTTDNVIAEYMYDRFDLRLRVAGTIAACFGMANIVARPMGGIMSDMGARYWYG
SEQID66	YGYCMGVELTTDNVIAEYYYYDHFDLRLVAGI IAAACFGMANIVARPLGGILSLDIGARYWG
SEQID53	YGYSMGVELTTDNVIAEYFYDRFDLRLVAGIIAASFGMANIVARPTGGLLSDLGARIFYG
SEQID78	YGYCMGVELTTDNVIAEYYYYDHFDLRLAAAGTIAACFGMANIVARPMGGYLSDLGARIFYG
SEQID80	YGYCMGVELTTDNVIAEYYYYDHFDHLHRAAGTIAACFGMANIVARPMGGYLSDLGARIFYG
SEQID74	YGYCMGVELTTDNVIAEYYYYDHFDLRLAAAGTIAACFGMANIVARPMGGYLSDLGARIFYG
SEQID72	YGYCMGVELTTDNVIAEYFFDHFHLDLRLAAAGTIAACFGMANIVARPTGGYLSDLGARIFYG
SEQID84	YGYCMGVELTTDNVIAEYFFDHFHLDLRLAAAGTIAACFGMANIVARPMGGYLSDLGARIFYG
SEQID82	YGYCMGVELTTGNVIAEYFFDHFHLNLRAAAGTIAACFGMANIVARPMGGYLSDLGARIFYG
SEQID76	YGYCMGVELTTDNVIAEYFFDHFHLLDLRTSGTIAACFGMANIVARPAGGYLSDLGARIFYG
SEQID86	YGYSMGVELSTDNVIAEYFYDRFNLKLHTAGI IAAATFGMANLVARPFGGFASDRAARYFG
SEQID88	YGYSMGVELS IDNVIAEYFYDRFNLKLHTAGI IAAAFGMANIVARPFGGFASDRAARYFG
SEQID90	YGYSMGVELTTDNVIAEYFYDRFNLKLHTAGI IAAASFGMANLVARPFGGYASDVAAARLFG
SEQID92	YGYSMGVELTTDNVIAEYFYDRFNLKLHTVGI IAAASFGMANLVARPFGGYVSDVAARLFG
SEQID98	YGYSMGVELSTDNVIAEYFYNRFDLKLHTAGVIAATFGMANLVARPFGGYFSDVAARYFG
SEQID96	YGYSMGVELTTDNVIAEYFFDRFDLKLHTAGI IAAATFGMANLLARPFGGWSSDVAAKHFG
SEQID122	YGYSMGVELTTDNVIAEYFFDRFDLKLHTPGI IAAATFGMANLLARPFGGWSSDVAAKHFG
SEQID94	YGYSMGVELTTDNVIAEYFFDRFDLKLHTAGI IAAATFGMANLLARPFGGWSSDIAAKHFG
SEQID100	YGYSMGVELSTDNVIAEYFFDRFDLKLHTAGI IAAATFGMANLLARPFGGFSSDYAAKRFG
SEQID102	YGYSMGVELSTDNVIAEYFFDRFDLKLHTAGI IAAATFGMANLLARPFGGFSSDFAAKRFG
SEQID104	YGYSMGVELSTDNVIAEYFFDRFDLKLSTAGI IAAATFGMANLLARPFGGFSSDYAAKKFG
SEQID108	YGYSMGVELSTDNVIAEYFFDRFDLKLSTAGI IAAATFGMANLLARPFGGFSSDYAAKKFG
SEQID106	YGYSMGVELSTDNVIAEYFFDRFHCLKHTAGLIAACFGMANFFARPAGGYASDFAAKIFYG
SEQID110	YGYSMGVELSTDNVIAEYFFDRFHCLKHTAGI IAAACFGMANFFARPAGGYASDLAAKIFYG
SEQID114	YGYSMGVELSTDNVIAEYFFDRFHCLKHTAGI IAAACFGMANFFARPAGGWASDIAAKRFG
SEQID116	YGYSMGVELSTDNVIAEYFFDRFHCLKHTAGI IAAACFGMANFFARPAGGWASDIAAKRFG
SEQID112	YGYSMGVELTTDNVIAEYFFDRFHCLKHTAGI IAAASFGMANFFARPIGGWASDIAARRFG
SEQID118	YGSSMGIELTINNVISGYFYDRFNCLKQTAGIVAASFGMANFIARPFGGYASDVAAARVFG
SEQID120	YGFMSGVELTINNVISGYFYDRFNLTHTAGIIAASFGMANFFARPFGGYASDVAAARLFG
	** . ** : ** : . *** : * : : : * * * . * : * * * * : * * * * : *

SUBSTITUTE SHEET (RULE 26)

[illegible]

SUBSTITUTE SHEET (RULE 26)

33/104

SEQID68	RRSLGIIISGMTGAGGNFGAGLTQLLFFTSSTYSTGRGLEYMGINIMACTLPVVVFVHFFPQW
SEQID70	RRSLGIIISGMTGAGGNFGAGLTQLLFFTSSTYSTGRGLEYMGINIMACTLPVVVFVHFFPQW
SEQID66	RRSLGIMSGMTGAGGNFGAGLTQLLFFTSSTKYSTGMGLEYMGINIMACTLPVVVFVHFFPQW
SEQID53	RRSLGIIISGMTGAGGNFGAGLTQLLFFTSSTRYSTGTGLEYMGINIMACTLPVVVLVHFFPQW
SEQID78	RRSLGIIISGLTGAGGNVGAGLTQLLFFTSSTQYSTGRGLEYMGINIMACTLPVALVHFFPQW
SEQID80	RRSLGIIISGLTGAGGNVGAGLTQLLFFTSSTQYSTGRGLEYMGINIMACTLPITLVHFFPQW
SEQID74	RRSLGIIISGLTGAGGNVGAGLTQLLFFTSSTQYSTGRGLEYMGINIMACTLPVALVHFFPQW
SEQID72	RRSLGIIISGLTGAGGNVGAGLTQLLFFTSSTQYSTGRGLEYMGINIMACTLPVALVHFFPQW
SEQID84	RRSLGIIISGLTGAGGNVGAGLTQLLFFTSSTQYSTGRGLEYMGINIMACTLPVALVHFFPQW
SEQID82	RRSLGIIISGLTGAGGNVGAGLTQLLFFTSSTQYSTGRGLEYMGINIMACTLPVALVHFFPQW
SEQID76	RRSLGIIISGLSAGGNFGAGLTQLLFFTSSTKYSTGRGLEYMGINIMACTLPVALVHFFPQW
SEQID86	RRSLGIIISGLTGAGGNFGSGLTQLVFFSSSAFSTATGLSLMGVMI VCCTLPVTLVHFFPQW
SEQID88	RRSLGIIISGLTGAGGNFGSGLTQLVFFSSAAFSATATGLSLMGVMI VCCTLPVTLVHFFPQW
SEQID90	RRSLGIIISGLTGAGGNFGSGLTQLVFFSTSKFSTATGLSLMGVMI VACTLPVSVVHFFPQW
SEQID92	KRSLGIIISGLTGAGGNFGSGLTQLVFFSTSRFSTGAGLSWMGVMI VGCTLPVTLVHFFPQW
SEQID98	RRSLGIIISGLTGAGGNFGSGLTQLVFFSSSSLSAAGLSWMGVMI CGCTLPVTLVYFFPQW
SEQID96	RRSLGIIISGMTGAGGNFGSGLTQLLFFTSSTKYSTGTGLTYMGMMI IACTLPVMLVRFPPQW
SEQID122	RRYLGIIISQMTGANGNFGSGQTQPLEFSDSTKYNTGLGLTYMGMMI IACTLPMLVWFQD
SEQID94	RRSLGIIISGMTGAGGNFGSGLTQLLFFTTTKWSTETGLSYMGIMI IACTLPVSLVHFFPQW
SEQID100	RRSLGIIISGMTGAGGNFGSGLTQLLFFTSSTKYSTATGLTYMGLMI IGCTLPVTFFCHFPPQW
SEQID102	RRSLGIIISGMTGAGGNFGSGLTQLLFFTSSTKYSTATGLTYMGMMI IGCTLPVTLCCHFPPQW
SEQID104	RRSLGIIISGMTGAGGNFGSGLTQLLFFTSSTKYSTATGLTYMGFMI IGCTLPVTFCCHFPPQW
SEQID108	RRSLGIIISGMTGAGGNFGSGLTQLLFFTSSTKYSTATGLTYMGFMI IGCTLPVTFFCHFPPQW
SEQID106	RRALGIIISGLTGAGGNFGSGLTQLLFFTSSTHFTTEQGLTWMGVMI VACTLPVTLVHFFPQW
SEQID110	RRALGIIISGLTGAGGNFGSGLTQLIFFSTSRFTTEQGLTWMGVMI VACTLPVTLIHFFPQW
SEQID114	RRALGIIISGLTGAGGNFGSGLTQLVFFSTSRFTTEEGLTWMGVMI VACTLPVTLIHFFPQW
SEQID116	RRALGIIISGLTGAGGNFGSGLTQLVFFSTSRFTTEEGLTWMGVMI VACTLPVTLIHFFPQW
SEQID112	RRSLGIIISGLTGAGGNFGSGLTQLVFFSTSTFSTEQGLTWMGVMI ACTLPVTLVHFFPQW
SEQID118	RRSLGLISGLTGAGGNFGSGLTQLLFFSSARFSTAEGLSLMGVMAVLCTLPVAFIHFFPQW
SESEQID120	RRSLGLISGLTGAGGNFGSGVTQLLFFSSSRFSTAEGLSLMGVMAVVCSLPVAFIHFFPQW
	: * * * : : * * * : * : : * * * * * : * * * * * : * * *

FIGURE 6 B (contiuned)

34/104

SEQID68	GSMFFPPSATADDEE---GYAYASEWNDDEKSKGLHSASLKF AENSR SERGRNVIQADAA
SEQID70	GSMFFPPSATADDEE---GYAYASEWNDDEKSKGLHSASLKF AENSR SERGRNVIQADAA
SEQID66	GSMFLPPSAGAVEE---HYYSSEWSEEEKSKGLHSSSLKFSENCR SERGRNVI LAAPN
SEQID53	GSMFLPPNAGAE E---HYYGSEWSEEEKSKGLHGASLKF AENSR SERGRNVI NA AAA
SEQID78	GSMFFPASADATEE---EYAYSEWSEEEKGKLHI TGQKFAENSR SERGRNVI LATS A
SEQID80	GSMFFPASADATEE---EYAYSEWSEEEKGKLHI AGQKFAENSR SERGRNVI LATS A
SEQID74	GSMFFPASADATEE---EYAYSEWSEEEKKGLHI AGQKFAENSR SERGRNVI LATS A
SEQID72	GSMFFPASADATEE---EYAYSEWSEEEKAKGLHI AGQKFAENSR SERGRNVI LATS A
SEQID84	GSMFFPASADATEE---EYAYSEWSEEEKGKLHI AGQKFAENSR SERGRNVI FATS A
SEQID82	GSMFLAASADATEE---EYAYSEWSEEEKSKGLHI AGQKFAENSR SERGRNVI LATS A
SEQID76	GSMFLPPNANATEE---EFYAAEWSEEEKKKGLHI PGQKFAENSR SERGRNVI LATA A
SEQID86	GSMFLPPSKDVVKS---TEEFYGAENWNEEEKQGLHQQSLRFAENSR SERGR -RVASAP TP
SEQID88	GSMFLPPSKDVVKS---TEEFYGAENWNEEEKQGLHQQSLRFAENSR SERGR -RVASAP TP
SEQID90	GSMFLPPSKDVKS---TEEFYTTSEWNEEEKQGLHQQSLKFAENSR SERGK -RVASAP TP
SEQID92	GSMFLPPSKDINKS---SEEHYTTAEWDEEEKKGLHQSLKFAENSR SERGK -RVSSAP TP
SEQID98	GGMFFPPSKDVVKS---TEESYYASEWDEDEKQGMHQSKSLKFAENSR SERGK -RIASAP TP
SEQID96	GSMFLPPSKDPIKG---TEEHYFGSEYTEDEKQGMHQNSIKFAENSR TERGKKRVGSA TP
SEQID122	GSMFLPPSKDPIKGTEPEHYFGSEYTEDEKVKGMHQNSIKFAENSR TEFGKKRVGSA TP
SEQID94	GSMFLPPTKDPVKS---TEEHYFTSEYTEAEKQGMHQNSIKFAENCR SERGK -RVGSAL TP
SEQID100	GSMFFPPTKDPVKG---SEEHYAAEYTEAEKQGMHQNSLKF AENCR SERGK -RVGSAP TP
SEQID102	GSMFFPPTKDPVKG---SEEHYAAEYTEAEKQGMHQNSLKF AENCR SERGK -RVGSAP TP
SEQID104	GSMFLPPTKDPVKG---TEEHYTTSEYTEAEKQGMHQNSLKF AENCR SERGK -RVGSAP TP
SEQID108	GSMFLPPTKDPVKG---TEEHYTTSEYTEAEKQGMHQNSLKF AENCR SERGK -RVGSAP TP
SEQID106	GSMFLPPSTD---PVKGTEAHYVGSEWNEEQKQKNMHQSLRFAENAKSEGGR -RVRSAAT P
SEQID110	GSMFLPPSTD---PVKGPKEHYAYASEWNEQKQKNMHQSLRFAENAKSEGGR -RVRSAAT P
SEQID114	GSMFFPPSND---SVDAT-EHYVVG EYSKEEQQIGMHLKSLFADGAKTEGGS -SVHKG NAT
SEQID116	GSMFFPPSND---SVDAT-EHYVVG EYSKEEQQIGMHLKSLFADGAKTEGGS -SVHKG NAT
SEQID112	GSMFLPSTED-EVKSTEYYMKWETETEKRGKMHGSLKF AVNSR SERGR -RVASAP SP
SEQID118	GSMFLRPSDTERS---QEEYYGSEWTENEKQGLHEGSIKF AENSR SERGRKVALANI PT
SEQID120	GSMFLRPSQDGEKS---KEEHYGAEWTEEEKSLGLHEGSIKF AENSR SERGRKAMLADI PT

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FIGURE 6 B (continued)

35/104

SEQID68	ATPEHV-----
SEQID70	ATPEHV-----
SEQID66	STPEHV-----
SEQID53	AATPPNNSPEHA
SEQID78	TPPNNTPQHVV--
SEQID80	TPPNNTPQHVV--
SEQID74	TPPNNTPQHVV--
SEQID72	TPPNNTPQHVV--
SEQID84	TPPNNTPQQVV--
SEQID82	TPPNNTPPLHV--
SEQID76	TPPNNTPQHA--
SEQID86	PNTTPSHV-----
SEQID88	PNTTPSHV-----
SEQID90	PNATPTHV-----
SEQID92	PNTTPTHV-----
SEQID98	PSTTPNR-----
SEQID96	PNVTPNRV-----
SEQID122	PNVYPNRV-----
SEQID94	PNVTPNRV-----
SEQID100	PNLTPNRV-----
SEQID102	PNLTPNRV-----
SEQID104	PNLTPNRV-----
SEQID108	PNLTPNRV-----
SEQID106	PENTPNNV-----
SEQID110	PENTPNNV-----
SEQID114	NNA-----
SEQID116	NNA-----
SEQID112	PPEHV-----
SEQID118	PENGTPSHV----
SEQID120	PETGSPAHV----

FIGURE 6 B (contiuned)

36/104

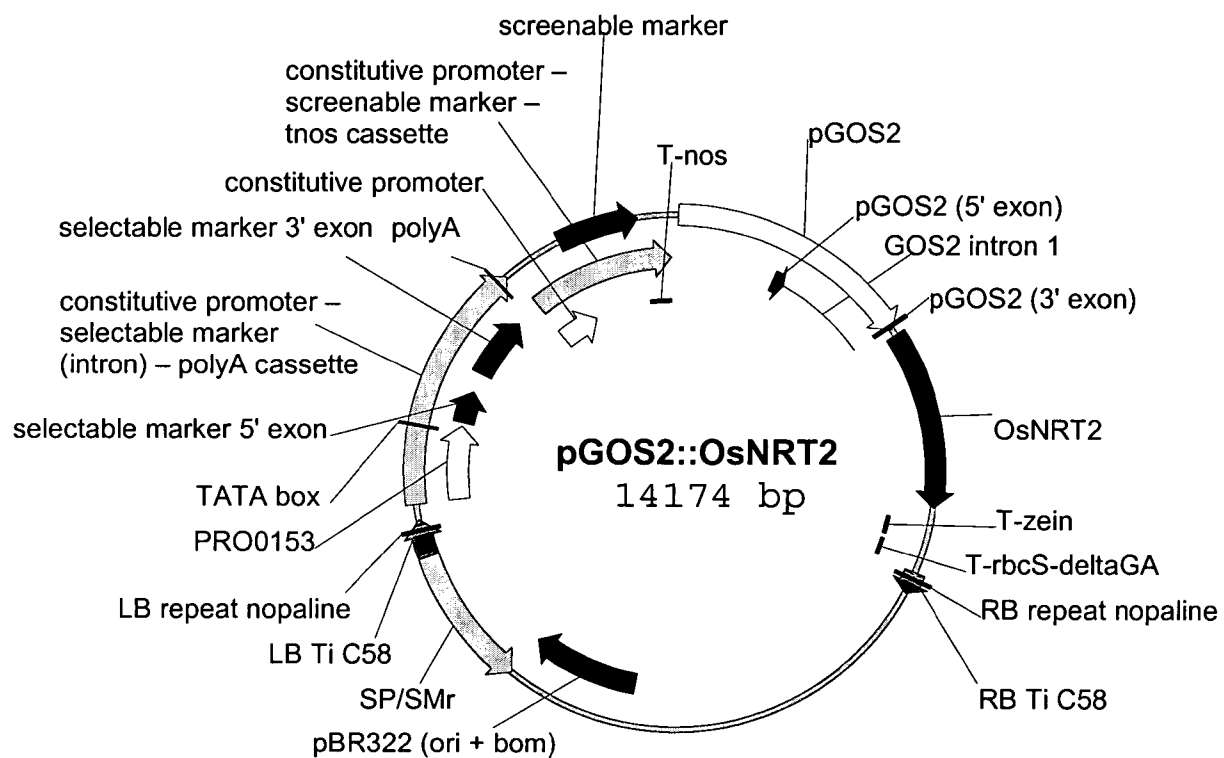


FIGURE 7

37/104

SEQ ID NO: 52, OsNRT coding sequence

ATGGACTCGTCGACGGTGGGCGCTCCGGGGAGCTCGCTGCACGGCGTGACGGGGCGCGAGCCGGCG
 TTCGCGTTCTCGACGGAGGTGGGCGGCGAGGACGCGGCGGCGGCGAGCAAGTTGCACTTGCCGGTG
 GACTCGGAGCACAAGGCGAAGACGATCAGGTTGCTGTCGTTTCGCGAACCCGCATATGAGGACGTTT
 CACCTATCATGGATCTCCTTCTTCTCCTGCTTCGTCTCCACCTTCGCCGCCGCCCTCTCGTCCCC
 ATCATCCGCGACAACCTCAACCTCACCAAGGCCGACATCGGCAACGCCGGCGTCGCCTCCGTCTCC
 GGCTCCATCTTCTCCAGGCTCGCCATGGGCGCCATCTGCGACATGCTCGGCCCGCGCTACGGCTGC
 GCCTTCCTCATCATGCTCGCCGCGCCCAACGCTTCTGTCATGTCGCTCATCGACTCCGCCGCGGGG
 TACATCGCCGTGCGCTTCCTCATCGGCTTCTCCCTCGCCACCTTCGTGTTCATGCCAGTACTGGATG
 AGCACCATGTTCAACAGCAAGATCATCGGCCTCGTCAACGGCCTTCGCCGCCGGGTGGGGAAACATG
 GGCGGCGGCGCGACGCGAGCTCATCATGCCGCTCGTCTACGACGTGATCCGCAAGTGCGGCGCGACG
 CCGTTACGGCGTGGAGGCTGGCCTACTTCGTGCCGGGGACGCTGCACGTGGTGATGGGCGTGCTG
 GTGCTGACGCTGGGGCAGGACCTCCCCGACGGCAACCTGCGCAGCCTGCAGAAGAAGGGTGACGTC
 AACAGGGACAGCTTCTCCAGGGTGCTCTGGTACGCCGTACCAACTACCGCACCTGGATCTTCGTC
 CTCCTCTACGGCTACTCCATGGGCGTCGAGCTCACCACCGACAACGTCATCGCCGAGTACTTCTAC
 GATCGCTTCGACCTCGACCTCCGCGTCGCCGGCATCATCGCCGCATCCTTCGGCATGGCCAACATC
 GTCGCGCGCCCCACCGGCGGCCCTCCTCTCGGACCTCGGCGCGCGCTACTTCGGCATGCGCGCCCGC
 CTCTGGAACATTTGGATCCTCCAGACCGCCGGCGGCGCGTTCTGCCTCCTGCTCGGCCGCGCATCC
 ACCCTCCCCACCTCCGTCTGTCATGGTCCTTCTCCTTCTGCGCGCAGGCCGCCTGCGGCGCC
 ATCTTCGGCGTCATCCCCTTCGTCTCCCGCCGCTCGCTCGGCATCATCTCCGGCATGACCGGCGCC
 GGCGGCAACTTCGGCGCCGGGCTCACGCAGCTGCTCTTCTTCACGTGCTCGAGGTACTCCACGGGC
 ACGGGGCTGGAGTACATGGGCATCATGATCATGGCGTGACGCTGCCGGTGGTGCTCGTCCATTTT
 CCGCAGTGGGGTCCATGTTCTCCTCCCGCCCAACGCCGGCGCCGAGGAGGAGCACTACTACGGCTCC
 GAGTGGAGCGAACAGGAGAAGAGCAAGGGCCTCCACGGTGCAAGTCTCAAGTTCGCCGAGAACTCC
 CGCTCCGAGCGTGGCCGCGCAACGTCATCAACGCCGCCGCCGCCGCCGCCACGCCGCCCAACAAC
 TCGCCGGAGCACGCCTAA

SEQ ID NO: 53, OsNRT deduced protein sequence

MDSSTVGAPGSSLHGVTGREPAFAFSTEVGGEDAAAASKFDLPVDSEHKAKTIRLLSFANPHMRTF
 HLSWISFFSCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSGSIFSRLAMGAICDMLGPRYGC
 AFLIMLAAPTVMFCMSLIDSAAGYIAVRFLIGFSLATFVSCQYWMSTMFNSKIIGLVNGLAAGWGNM
 GGGATQLIMPLVYDVIRKCGATPFTAWRLAYFVPGTLHVVMGVVLVLTGLQDLDPGNLRSLOKKGDV
 NRDSFSRVLWYAVTNYRTWIFVLLYGYSMGVELTDDNVIAEYFYDRFDLRLVAGIIAASFMANI
 VARPTGGLLSDLGARYFGMRARLWNIWILQTAGGAFCLLLGRASLTPTSVVCMVLFSFCAQAACGA
 IFGVIPFVSRRSLGIIISGMTGAGGNFGAGLTQLLFFTSRYSTGTGLEYMIMIMACTLPVVLVHF
 PQWGSMLPFPNAGAEHEHYGSEWSEQEKSGLHGASLKFAENSRSERGRNVINAAAAAATPPNN
 SPEHA

SEQ ID NO: 54, prm07061, start codon in bold, AttB1 site in italics

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACA**AT**GGACTCGTCGACGGTG

FIGURE 8

38/104

SEQ ID NO: 55, prm07062, reverse, complementary, stop codon in bold, AttB2 site in italic

GGGGACCACTTTGTACAAGAAAGCTGGGTCTCGGTTCGAGAATTGTTTAC

SEQ ID NO: 56, *NRT* expression cassette with the promoter-gene combination, promoter sequence in italics, start and stop codon of the *NRT* ORF in bold and underlined

AATCCGAAAAGTTTCTGCACCGTTTTTCACCCCCTAACTAACAATATAGGGAACGTGTGCTAAATAT
AAAATGAGACCTTATATATGTAGCGCTGATAACTAGAACTATGCAAGAAAACTCATCCACCTACT
TTAGTGGCAATCGGGCTAAATAAAAAAAGAGTCGCTACACTAGTTTTCGTTTTCTTAGTAATTAAGT
GGGAAAATGAAATCATTATTGCTTAGAATATACGTTACATCTCTGTCATGAAGTTAAATTATTTCG
AGGTAGCCATAATTGTCATCAAACCTCTTCTTGAATAAAAAAATCTTTCTAGCTGAACTCAATGGGT
AAAGAGAGAGATTTTTTTTTTAAAAAATAGAATGAAGATATTCTGAACGTATTGGCAAAGATTTAAA
CATATAATTATATAATTTTTATAGTTTGTGCATTTCGTCATATCGCACATCATTAAAGACATGTCTTA
CTCCATCCCAATTTTTATTAGTAATTAAAGACAATTGACTTATTTTTATTATTTATCTTTTTTCG
ATTAGATGCAAGGTAATTACGCACACACTTTGTGCTCATGTGCATGTGTGAGTGCACCTCCTCAAT
ACACGTTCAACTAGCAACACATCTCTAATATCACTCGCCTATTTAATACATTTAGGTAGCAATATC
TGAATTCAAGCACTCCACCATCACCAGACCACTTTTAATAATATCTAAAAATACAAAAATAATTTT
ACAGAATAGCATGAAAAGTATGAAACGAACATTTAGGTTTTTCACATACAAAAAAGAAATT
TTGCTCGTGCGCGAGCGCAATCTCCCATATTGGGCACACAGGCAACAACAGAGTGGCTGCCCACA
GAACAACCCACAAAAACGATGATCTAACGGAGGACAGCAAGTCCGCAACAACCTTTTAACAGCAG
GCTTTGCGGCCAGGAGAGAGGAGGAGGCAAGAAAACCAAGCATCCTCCTCCTCCCATCTATAA
ATTCTCCCCCTTTTCCCCCTCTCTATATAGGAGGCATCCAAGCCAAGAAGAGGGAGAGCACCAG
GACACGCGACTAGCAGAAGCCGAGCGACCGCCTTCTTCGATCCATATCTTCCGGTTCGAGTTCTTGG
TCGATCTCTTCCCTCCTCCACCTCCTCCTCACAGGGTATGTGCCCTTCGGTTGTTCTTGGATTAT
TGTTCTAGGTTGTGTAGTACGGGCGTTGATGTTAGGAAAGGGGATCTGTATCTGTGATGATTCCTG
TTCTTGGATTGTTGGGATAGAGGGGTTCTTGATGTTGCATGTTATCGGTTCCGTTTGATTAGTAGTAT
GGTTTTCAATCGTCTGGAGAGCTCTATGGAAATGAAATGGTTTAGGGTACGGAATCTTGCGATTTT
GTGAGTACCTTTTGTGTTGAGGTAAAATCAGAGCACCGGTGATTTTGCTTGGTGTAATAAAAGTACG
GTTGTTTGGTCCTCGATTCTGGTAGTGATGCTTCTCGATTTGACGAAGCTATCCTTTGTTTATTCC
CTATTGAACAAAAATAATCCAACCTTTGAAGACGGTCCCGTTGATGAGATTGAATGATTGATTCTTA
AGCCTGTCCAAAATTTTCGAGCTGGCTTGTTTAGATACAGTAGTCCCATCACGAAATTCATGGAA
ACAGTTATAATCCTCAGGAACAGGGGATTCCCTGTTCTTCCGATTTGCTTTAGTCCAGAAATTTTT
TTTCCCAAATATCTTAAAAAGTCACTTTCTGGTTCAGTTCAATGAATTGATTGCTACAAATAATGC
TTTTATAGCGTTATCCTAGCTGTAGTTTCAAGTTAATAGGTAATACCCCTATAGTTTAGTCAGGAGAA
GAACTTATCCGATTTCTGATCTCCATTTTTTAATTATATGAAATGAACTGTAGCATAAGCAGTATTC
ATTTGGATTATTTTTTTTTTATTAGCTCTCACCCCTTCATTATTCTGAGCTGAAAGTCTGGCATGAAC
TGTCTCAATTTTGTGTTTCAAATTCACATCGATTATCTATGCATTATCCTCTTGATCTACCTGTA
GAAGTTTCTTTTGGTTATTCCTTGACTGCTTGATTACAGAAAGAAATTTATGAAGCTGTAATCGG
GATAGTTATACTGCTTGTTCTTATGATTCAATTCCTTTGTGCGAGTTCTTGGTGTAGCTTGCCACTT
TCACCAGCAAAGTTCAATTTAAATCAACTAGGGATATCACAAGTTTGTACAAAAAAGCAGGCTTAAA
CAATGGACTCGTCGACGGTGGGCGCTCCGGGGAGCTCGCTGCACGGCGTG

FIGURE 8 (continued)

39/104

ACGGGGCGCGAGCCGGCGTTTCGCGTTCTCGACGGAGGTGGGCGGCGAGGACGCGGCGGCGGCGAGC
 AAGTTCGACTTGCCGGTGGACTCGGAGCACAAGGCGAAGACGATCAGGTTGCTGTCGTTTCGCGAAC
 CCGCATATGAGGACGTTCCACCTATCATGGATCTCCTTCTTCTCCTGCTTCGTCTCCACCTTCGCC
 GCCGCCCTCTCGTCCCCATCATCCGCGACAACCTCAACCTCACCAGGCCGACATCGGCAACGCC
 GGCGTCGCCTCCGTCTCCGGCTCCATCTTCTCCAGGCTCGCCATGGGCGCCATCTGCGACATGCTC
 GGCCCGCGCTACGGCTGCGCCTTCCTCATCATGCTCGCCGCGCCACCGTCTTCTGCATGTCGCTC
 ATCGACTCCGCCGCGGGGTACATCGCCGTGCGCTTCCTCATCGGCTTCTCCCTCGCCACCTTCGTG
 TCATGCCAGTACTGGATGAGCACCATGTTCAACAGCAAGATCATCGGCCTCGTCAACGGCCTCGCC
 GCCGGGTGGGGAACATGGGCGGCGGCGCGACGCGAGCTCATCATGCCGCTCGTCTACGACGTGATC
 CGCAAGTGCGGCGCGACGCCGTTACGGCGTGAGGCTGGCCTACTTCGTGCCGGGGACGCTGCAC
 GTGGTGATGGGCGTGCTGGTGCTGACGCTGGGGCAGGACCTCCCCGACGGCAACCTGCGCAGCCTG
 CAGAAGAAGGGTGACGTCAACAGGGACAGCTTCTCCAGGGTGCTCTGGTACGCCGTACCAACTAC
 CGCACCTGGATCTTCGTCTCTCTACGGCTACTCCATGGGCGTCGAGCTCACCACCGACAACGTC
 ATCGCCGAGTACTTCTACGATCGCTTCGACCTCGACCTCCGCGTCGCCGGCATCATCGCCGCATCC
 TTCGGCATGGCCAACATCGTCGCGCGCCCCACCGCGGCCTCCTCTCGGACCTCGGCGCGCGCTAC
 TTCGGCATGCGCGCCCGCCTCTGGAACATTTGGATCCTCCAGACCGCCGGCGGCGCGTTCGCTC
 CTGCTCGGCCGCGCATCCACCCTCCCCACCTCCGTCTGTCATGGTCCTCTTCTCCTTCTGCGCG
 CAGGCCGCTGCGGCGCCATCTTCGGCGTCATCCCCTTCGTCTCCCGCCGCTCGCTCGGCATCATC
 TCCGGCATGACCGGCGCCGGCGGCAACTTCGGCGCCGGGCTCACGCAGCTGCTCTTCTTCACGTG
 TCGAGGTACTCCACGGGCACGGGGCTGGAGTACATGGGCATCATGATCATGGCGTGACGCTGCCG
 GTGGTGCTCGTCCATTTCCCGCAGTGGGGCTCCATGTTCTCCCGCCCAACGCCGGCGCCGAGGAG
 GAGCACTACTACGGCTCCGAGTGGAGCGAACAGGAGAAGAGCAAGGGCCTCCACGGTGCAAGTCTC
 AAGTTCGCCGAGAACTCCCGCTCCGAGCGTGGCCGCGCAACGTCATCAACGCCGCGCCGCCGCC
 GCCACGCCGCCCAACAACCTCGCCGGAGCACGCCTAA

SEQ ID NO: 57, signature sequence 1

(N/S) (Y/P) (T/G/S/A) W(I/V/L) (F/L/T) (V/A/F/L) (L/V/M/I) (L/T/I/A/N) YG(
 Y/F) (S/C/T) (M/F/Y) G(V/I) EL(T/S) (T/I/V) (D/G/N) N(V/I/N) (I/V) (A/S/H/V
) (E/Q/G) Y

SEQ ID NO: 58, signature sequence 2

LG(P/A) RYG(C/T) AF(L/S)

SEQ ID NO: 59, signature sequence 3

STFAA(A/R) PL(V/I) (P/V) (I/L/V) IR(D/E) NL(N/D) (L/P)

SEQ ID NO: 60, signature sequence 4

VRF(L/M) IGF(S/C) LA

FIGURE 8 (continued)

40/104

SEQ ID NO: 61, signature sequence 5

FVSC (Q/R) YW (M/T) S (T/V) (M/S) (F/M)

SEQ ID NO: 62, signature sequence 6

K (A/Q/S/M/H/T) D (I/V) GNAGVASV (S/T) G (S/A) I (F/L) SR (L/G)

SEQ ID NO: 63, signature sequence 7

NG (L/T/C) A (A/G) GWG

SEQ ID NO: 64, signature sequence 8

G (A/S) G (L/V/Q) TQ (L/P) (L/V/I) (F/E) F (T/S/D) (S/T) (S/A/T) .

SEQ ID NO: 65, *Phragmites australis* NRT2 mRNA for putative high affinity nitrate transporter, complete cds (AB096061)

ACAACAGCTCAGATCAAGCACCTGCATTTGCATAAGAGCTAGCAAGCAAGCAAGTCCAAGAAAGAA
GCTAGCTAGCTTGTATCAGATCAAGACTCGAGAGGCCAGCTATGGAGGTTGGCGCGCCGGGGAGCT
CGCTGCACGGCGTACAGGGGCGCGAGCCGGCGTTTCGCCTTCTCGACGTCTGCGGTGCCCGACGACG
ATGCAGCGAGCAAGTTCGACCTGCCGGTGGACTCGGAGCACAAGGCCAAGAGCATCCGGCTCTTCT
CCTTCGCCAACCCGCACATGCGCACCTTCCATCTCTCGTGGATCTCCTTCTTCACCTGCTTCGTCT
CCACCTTCGCCGCCGCGCCGCTCGTCCCCATCATCCGCGACAACCTCAACCTCACCAAGGCCGACA
TCGGCAACGCCGGCGTGGCCTCCGTCTCGGGATCCATCTTCTCCCGTCTCGCCATGGGCGCCATCT
GCGACCTCCTCGGCCCGCGCTACGGCTGCGCCTTCTCATCATGCTCACGGCGCCCACCGTCTTCT
GCATGTCCCTCATCGACGACGCAGCCGGCTACATCGTTCGTTCAGGTTCTTGATCGGCTTCTCTCTGG
CCACGTTTCGTGTCGTGCCAGTACTGGATGAGCACCATGTTCAATAGCAAGATCATCGGGACGGTGA
ACGGGCTGGCGGCTGGGTGGGGGAACATGGGCGGGCGGCCACGCAGCTCCCCATGCCGCTCGTCT
ACGACGTCATCCGCAAGTGCGGCGCGACGCCCTTACGGCGTGGCGCATCGCCTACTTCGTGCCGG
GGCTAATGCACGTGGTGATGGGCATCCTGGTGCTCACGCTGGGGCAGGACCTCCCCGACGGCAACC
TGAGGAGCCTCCAGAAGAAGGGCGACGCCAACAAGGACAAGTTCTCCAAGGTGCTCTGGTACGCCG
TCACCAACTATCGCACCTGGATCTTCGTGCTGCTCTACGGCTACTGCATGGGCGTGGAGCTGACCA
CCGACAACGTTCATCGCCGAGTACTACTACGACCACTTCGACCTAGACCTCCGCGTCCGCCGCATCA
TCGCCGCTTGCTTCGGAATGGCCAACATCGTGGCACGGCCCTTGGGCGGCATCCTCTCCGACATCG
GCGCGCGCTACTGGGGCATGCGCGCGCGCCTCTGGAACATCTGGATCCTCCAGACTGCTGGCGGCG
CCTTCTGCCTCTGGCTCGGCCGCGCCAGCACGCTTCTGCCTCCATTACCGCCATGGTGCTCTTCT
CCTTCTGCGCCCAGGCCGCTGCGGCGCCATTTTCGGCGTCACCCCTTTCGTACCCGCGCGCTCCC
TCGGCATCATGTCCGGGATGACGGGGGCTGGCGGCAACTTCGGCGCGGGGCTCACGCAGCTGCTCT
TCTTCACCTCGTCCAAGTACTCCACGGGCATGGGGCTGGAGTACATGGGCATCATGATCATGGCGT
GCACGCTGCCCCGTGGTGTTTCGTGCACTTCCCGCAATGGGGATCCATGCTCCTCCCGCCAGCGCCG
GCGCCGTCGAGGAGCACTACTACAGCTCGGAG

FIGURE 8 (continued)

SUBSTITUTE SHEET (RULE 26)

41/104

TGGAGTGAGGAGGAGAAGAGCAAGGGGCTCCACAGCTCCAGCCTCAAGTTTTTCAGAGAACTGCCGT
TCAGAGCGCGGCAACCGCAACGTCATCCTCGCGGCACCAAACAGCACGCCCCGAGCACGTATAAGAC
GCACGTATATGTCCGCATTTCGTACCCCTGTGCGCGTATACGCATACGCCAGCGGTTTGTTTAATAA
GGTGCGCATATATATATATGTAACTAGCTATAATGCGTATCACCGTTATGCGCACGCACACGAAAT
ATATATAATTCGATGTTGACGCATATACAAAAAAAAAAAAAAAAA

SEQ ID NO: 66, *Phragmites australis* putative high affinity nitrate transporter (BAC76606)

MEVGAPGSSSLHGVTGREPAFAFSTSAVPDDDAASKFDLPVDSEHKAKSIRLFSFANPHMRTFHL
ISFFTCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSGSIFSRILAMGAICDLLGPRYGCAFLI
MLTAPTVCMSLIDDAAGYIVVRFLIGFSLATFVSCQYWMSTMFNSKIIGTVNGLAAGWGNMGGGA
TQLPMPPLVYDVIRKCGATPFTAWRIAYFVPGLMHVVMGILVLTGLQDLPDGNLRSLLQKKGDANKDK
FSKVLWYAVTNYRTWIFVLLYGYCMGVELTDDNVIAEYYYDHFDDLRLVAGIIAACFGMANIVARP
LGGILSDIGARYWGMRLRLWNIWILQTAGGAFCLWLGRASTLPASITAMVLFSCAQAACGAI FGV
TPFVTRRSLGIMSGMTGAGGNFAGLTQLLFFTSSKYSTGMGLEYMIMIMACTLPVVFVHFPQWG
SMLLPPSAGAVEEHYYSSEWSEEEKSKGLHSSSLKFSENCRSEGRNRNVILAAPNSTPEHV

SEQ ID NO: 67, *Zea mays* putative high affinity nitrate transporter (nrt2.2) mRNA, complete cds (AY559405)

CCAAGGGAAAGGGATACATCACCTGCTGCTCTAGCTCTGCTATAGCGCTAGCAGCAATATAATGGC
GGCCGTCGCGCTCCGGGAGCTCTCTGCACGGAGTCACGGGGCGCGAGCCGGCGTTCGCATTCTC
CACGGAGCACGAGGAGGCGGCGAGCAATGGCGGCAAGTTCGACCTGCCGGTGGACTCGGAGCACA
GGCGAAGAGCGTCCGGCTCTTCTCCGTGGCGAACCCGCACATGCGCACCTTCCACCTCTCCTGGAT
CTCCTTCTTCACCTGCTTCGTGTCCACCTTCGCCGCCGCGCGCTGGTCCCCATCATCCGCGACAA
CCTCAACCTCACCAAGGCCGACATCGGCAACGCGGGCGTGGCCTCCGTGTGCGGGCTCCATCTTCTC
CCGCCTCACCATGGGCGCCGTCTGCGACCTGCTGGGCCCGCGCTACGGCTGCGCCTTCTCATCAT
GCTGTCCGCGCCACCGTGTTCTGCATGTGCTCATCGACGACGCCGCGGGCTACATCACCGTCAG
GTTCTCATCGGCTTCTCCCTCGCCACCTTCGTCTCCTGCCAGTACTGGATGAGCACCATGTTTCA
CAGCAAGATCATCGGCACCGTCAACGGGCTCGCCGCCGGATGGGGCAACATGGGAGGCGGCGCCAC
GCAGCTCATCATGCCGCTCGTCTACGACGTCATCCGCAAGTGCGGCGCCACGCCCTTCACGGCGTG
GCGCCTCGCCTACTTCTGTGCCGGGCCTCATGCACGTCGTTCATGGGCGTCTTGGTGCTCACGCTGGG
GCAGGACCTCCCCGACGGCAACCTCAGGTGCTGCAGAAGAAGGGCAACGTCAACAAGGACAGCTT
CTCCAAGGTCATGTGGTACGCCGTCATCAACTACCGCACCTGGATCTTCGTCTCCTCTACGGCTA
CTGCATGGGCGTCGAGCTCACCACCGACAACGTCATCGCCGAGTACATGTACGACCGCTTCGACCT
CGACCTCCGCGTCGCCGGGACCATCGCCGCCTGCTTCGGCATGGCCAACATCGTCGCGCGCCCCAT
GGGCGGCATCATGTCCGACATGGGCGCGCGCTACTGGGGCATGCGCGCTCGCCTCTGGAACATCTG
GATCCTCCAGACCGCCGGCGGCGCCTTCTGCCTCTGGCTGGGACGCGCCAGCACCTCCCCGTCTC
CGTCGTGCGCATGGTGCTCTTCTCCTTCTGCGCGCAGGCGGCCTGCGGCGCCATCTTCGGGGTCAT
CCCCCTTCGTCTCCCGCCGCTCCCTCGGCATCATCTCCGGCATGACGGGCGCCGGCGGCAACTTCGG
CGCGGGGCTCACGCAGCTGCTCTTCTTACCTCCTCAACCTACTCCACGGGCAGGGGGCTAGAGTA
CATGGGCATCATGATCATGGCGTGCACGCTACCTGTGGTG

FIGURE 8 (continued)

42/104

TTCGTGCACTTCCCGCAGTGGGGGTCCATGTTCTTCCCGCCCAGCGCCACCGCCGACGAGGAGGGC
TACTACGCCTCCGAGTGGAAACGACGACGAGAAGAGCAAGGGACTCCATAGCGCCAGCCTCAAGTTT
GCCGAGAACAGCCGCTCAGAGCGCGGCAAGCGAAACGTCATCCAGGCCGATGCCGCCGCCACGCCG
GAGCATGTCTAAGTCTACTACTAATAAGATGGATCGATCCATCATCCATGTTACCTGCTACCTAC
C

**SEQ ID NO: 68, Zea mays putative high affinity nitrate transporter
(AAT66252)**

MAAVGAPGSSSLHGVTGREPAFAFSTEHEEAASNGGKFDLPVDSEHKAKSVRLFSVANPHMRTFHLS
WISFFTCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSGSIFSRLTMGAVCDLLGPRYGCAFL
IMLSAPTVCMSLIDDAAGYITVRFLIGFSLATFVSCQYWMSTMFSSKIIGTVNGLAAGWGNMGGG
ATQLIMPLVYDVIRKCGATPFTAWRLAYFVPGLMHVVMGVLVLTGQDLPDGNLRSLOKKGNVNKD
SFSKVMWYAVINYRTWIFVLLYGYCMGVELTTDNVIAEYMYDRFDLRLRVAGTIAACFGMANIVAR
PMGGIMSDMGARYWGMRLWNIWILQTAGGAFLWLGRASTLPVSVVAMVLFSSCAQAACGAIFG
VIPFVSRRSLGIISGMTGAGGNFGAGLTQLLFSTSSTYSTGRGLEYMIMIMACTLPVVFVHFPQW
GSMFFPPSATADEEGYYASEWNDDEKSKGLHSASLKFAENSRSERGKRNVIQADAAATPEHV

**SEQ ID NO: 69, Zea mays putative high affinity nitrate transporter
(nrt2.1) mRNA, complete cds (AY129953)**

ACGCGGGGAAGCACAAGCAACCAGCCAGCTAGTTTCCAAGGGATCACCTGCTCTCTAGCACTAGCA
GCAATGGCGGCCGTCGCGCTCCGGGCAGCTCTCTGCACGGAGTCACGGGGCGCGAGCCGGCGTTC
GCCTTCTCCACGGAGCACGAGGAGGCGGCGAGCAATGGTGGCAAGTTCGACCTGCCGGTGGACTCA
GAGCACAAGGCGAAGAGCGTCCGTCTCTTCTCCGTGGCGAACCACACATGCGCACCTTCCACCTC
TCCTGGATCTCCTTCTTACCTGCTTCGTGTCCACCTTCGCCGCCGCGCCGCTGGTCCCCATCATC
CGCGACAACCTCAACCTACCAAGGCCGACATCGGCAACGCGGGCGTGGCCTCGGTGTGGGCTCC
ATCTTCTCCCGCCTCACCATGGGCGCCGTCTGCGACCTGCTGGGCCCCGCGCTACGGCTGCGCCTTC
CTCATCATGCTGTCCGCGCCACCGTGTTCTGCATGTGCTCATCGACGACGCCGCGGGCTACATC
ACCGTCAGGTTCTCATCGGCTTCTCCCTCGCCACCTTCGTCTCCTGCCAGTACTGGATGAGCACC
ATGTTTCAGCAGCAAGATCATCGGCACCGTCAACGGGCTCGCCGCCGGATGGGGCACAATGGGAAGG
CGGCGCCACGCAGCTCATATGCCGCTCGTCTACGACGTATCCGCAAGTGCGGCGCCACGCCATTC
ACGGCCTGGCGCCTCGCCTACTTCGTGCCGGGCCTCATGCACGTCGTCATGGGCGTCTGGTGCTC
ACGCTGGGGCAGGACCTCCCCGACGGCAACCTCAGGTGCTGCAGAAGAAGGGCAACGTCAACAAG
GACAGCTTCTCCAAGGTCATGTGGTACGCCGTATCAACTACCGTACCTGGATCTTTGTCTCTCTC
TACGGCTACTGCATGGGCGTCGAGCTCACCACCGACAACGTATCGCCGAGTACATGTACGACCGC
TTCGACCTCGACCTCCGCGTCGCTGGGACCATCGCCGCCTGCTTCGGCATGGCCAACATCGTCGCA
CGCCCCATGGGCGGCATCATGTCCGACATGGGCGCGCGCTACTGGGGCATGCGCGCTCGCCTCTGG
AACATCTGGATCCTCCAGACCGCCGGCGGCGCCTTCTGCCTCTGGCTGGGGCGCGCCAGCACCCTC
CCCGTCTCCGTGCTCGCCATGGTGCTCTTCTCTCTTCTGCGCGCAGGCGGCATGCGGCGCCATCTTC
GGGGTTATCCCTTTGTCTCCCGCCGCTCCCTCGGCATCATCTCCGGCATGACGGGCGCCGGCGGC
AACTTCGGGCGCCGGGCTCACGCAGCTGCTCTTTACCTCCTCGACCTACTCCACGGGCAGGGGG
CTGGAGTACATGGGCATCATGATCATGGCGTGCACGCTGC

FIGURE 8 (continued)

43/104

CCGTGGTGTTCGTGCACTTCCCTCAGTGGGGGTCCATGTTCTTTCCGCCCAGCGCCACCGCCGACG
AGGAGGGCTACTACGCCTCCGAGTGGAACGACGACGAGAAGAGCAAGGGACTCCATAGCGCCAGCC
TCAAGTTCGCCGAGAACAGCCGCTCAGAGCGCGGCAAGCGAAACGTCATCCAGGCCGACGCCGCCG
CCACGCCGAGCATGTCTAAGTCTACTACTAAGATGGATCGATCGACGATCACCTATACCTCTTTG
TATGTACGAATATGCCTTGTTATTACTGCGCGCGCGCATATACAATACACGTGTGCTCCGTTGACA
TGAGTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 70, *Zea mays* putative high affinity nitrate transporter (AAN05088)

MAAVGAPGSSLHGVTGREPAFAFSTEHEEAASNGGKFDLPVDSEHKAKSVRLFSVANPHMRTFHLS
WISFFTCFVSTFAAAPLVPIIRDNLNLTKADIGNAGVASVSGSIFSRLTMGAVCDLLGPRYGCAFL
IMLSAPTVCMSLIDDAAGYITVRFLIGFSLATFVSCQYWMSTMFSSKIIGTVNGLAAGWGTMGRR
RHAAHMLPLVYDVIRKCGATPFTAWRLAYFVPGLMHVVMGVLVLTGQDLPDGNLRS LQKKGNVNKD
SFSKVMWYAVINYRTWIFVLLYGYCMGVELTTDNVIAEYMYDRFDLDRVAGTIAACFGMANIVAR
PMGGIMSDMGARYWGMRLWNIWILQTAGGAFLWLGRASTLPVSVVAMVLF SFCQAACGAIFG
VIPFVSRRSLGIISGMTGAGGNFGAGLTQLLFFTSSTYSTGRGLEYMIMIMACTLPVVFVHFPQW
GSMFFPPSATADEEGYYASEWNDDEKSKGLHSASLKFAENSRSERGKRNV IQADAAATPEHV

SEQ ID NO: 71, *Hordeum vulgare* high affinity nitrate transporter homolog BCH1 mRNA, complete cds (HVU34198)

GAATTCGCGGCCGCTCCCTTACTACATTGCAAGCCAAGCTCAAGAGCAGCAGCAACAGCCACCATT
AGCTGCTTCTAGTTGTTGGCAAAGATGGAGGTGCGAGGCGGGCGCCCATGGCGACACTGCCGCGAGC
AAGTTCACGCTGCCGGTAGACTCCGAGCACAAGGCCAAGTCCTTCAGGCTCTTCTCCTTCGCCAAC
CCGCACATGCGCACCTTCCATCTCTCGTGGATCTCCTTCTTCACTTGCTTCATCTCCACCTTCGCC
GCAGCGCCCCTTGTCCCCATCATTCTGTGATAACCTCAACCTTGCCAAGGCCGACATCGGCAATGCC
GGTGTGGCATCCGTTTCTGGGTCCATCTTCTCCAGGCTTGCCATGGGTGCCATCTGCGATCTCCTC
GGGCCGCGGTATGGATGTGCATTCTCTCGTCATGCTCTCGGCACCGACCGT TTTCTGCATGGCCGTT
ATCGATGATGCCTCAGGGTACATCGCCGTCCGCTTCTCATTGGCTTCTCGCTTGCTACGTTTCGTG
TCATGCCAATATTGGATGAGCACCATGTTTAATAGCAAGATCATCGGCACAGTCAACGGCCTCGCT
GCTGGATGGGGCAACATGGGTGGTGGCGCCACGCAGCTCATCATGCCGCTCGTCTTCCATGCAATC
CAGAAGTGTGGTGCCACGCCCTTCTAGCGTGGCGTATTGCCTACTTCTGTGCCCGGAATGATGCAC
ATCGTGATGGGCTTGTTGGTACTCACCATGGGGCAAGATCTCCCTGATGGGAACCTCGCAAGTCTC
CAGAAGAAGGGAGACATGGCCAAGGACAAGTTCTCCAAGGTCCTTTGGGGCGCCGTTACCAACTAC
CGAACATGGATCTTTGTCTCTCTATGGCTACTGCATGGGTGTCGAGCTCACCACCGACAATGTC
ATTGCCGAGTACTACTTTCGACCACTTCCACCTAGACCTCCGTGCCGCCGGTACCATCGCTGCCTGC
TTCGGCATGGCCAACATCGTCGCACGTCTACGGGTGGCTACCTCTCTGACCTTGGCGCCCGCTAT
TTCGGCATGCGTGCTCGCCTCTGGAATATCTGGATCCTCAAACCGCTGGTGGCGCTTCTTCTGCATC
TGGCTCGGTGCTGCATCGGCCCTCCCTGCCTCGGTGACCGCCATGGTCTCTTCTCCATCTGCGCC
CAGGCTGCGTGTGGTGCTATCTTTGGTGTGCGACCCTTCGTCTCCAGGCGTTCCCTTGGCATCATT
TCCGGGTTGACCGGTGCTGGTGGAACGTGGGCGCAGGGCTCACACAGCTTCTCTTCTTCACGTCA
TCGCAATACTCCACTGGTAGGGGTCTCGAGTACATGGGCATCATGATCATGGCATGCACGCTGCC
GTCGCTCTTGTCACCTTCCCACAATGGGGATCCATGTTCT

FIGURE 8 (continued)

44/104

TCCCTGCCAGCGCCGACGCCACGGAGGAGGAGTACTACGCCTCGGAGTGGTCCGAAGAGGAGAAAG
 CCAAGGGTCTCCATATCGCCGGCCAAAATTTGCTGAGAATTCCTCGCTCGGAGCGCGGTAGGCGCA
 ACGTCATCCTTGCCACGTCCGCCACACCACCAACAATACGCCCCAGCACGTATGAGACTGGATTG
 TTTTTCATACCTATGTACAAGTACTGAACTACAGTGCACGTTTCGTATATATATACGCCTGCAACAT
 CGGCTGTAATAAGGCGTATGAATTTACATTTGTAGTGTAGGCCTGTGTAATGCGTTTCTTACGCAC
 GAAATGTTTGGTCTGTGCATGCACGCATGCGAGGGTACCTGTGCTCTGAATTTACAACAGCTTTGA
 GCGGCCCGCAATTC

**SEQ ID NO: 72, *Hordeum vulgare* high affinity nitrate transporter
 homolog BCH1 (AAC49531)**

MEVEAGAHGDTAASKFTLPVDSEHKAKSFRLFSFANPHMRTFHLWSISFFTCTFISTFAAAPLVPII
 RDNLNLAKADIGNAGVASVSGSIFSRLAMGAICDLLGPRYGCAFLVMSAPT VFCMAVIDDASGYI
 AVRFLIGFSLATFVSCQYWMSTMFNSKI IGTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGATPF
 VAWRIAYFVPGMMHIVMGLLVLTMGQDLPDGNLASLQKKGDMAKDKFSKVLWGAVTNYRTWIFVLL
 YGYCMGVELTTDNVIAEYYFDHFHLDLRAAGTIAACFGMANIVARPTGGYLSDLGARYFGMRARLW
 NIWILQTAGGAFCIWLGRASALPASVTAMVLFSICAQAACGAIFGVAPFVSRRSLGIISGLTGAGG
 NVGAGLTQLLFFTSSQYSTGRGLEYMIMIMACTLPVALVHFPQWGSMMFFPASADATEEEYYASEW
 SEEEKAKGLHIAGQKFAENSRSERGRNVILATSATPPNNTPOHV

**SEQ ID NO: 73, *Triticum aestivum* high affinity nitrate transporter
 mRNA, complete cds (AF332214)**

TAGTTTTGAGTGCAACTAGGCTAGCTCAAGAAAGATGGAGGTGCAGGCCGGCTCTCATGCCGACGC
 CGCGGCGAGCAAGTTCACGCTGCCGGTGGACTCCGAGCACAAGGCCAAGTCCTTCAGGCTCTTCTC
 CTTCGCCAACCCCCACATGCGCACCTTTACCTCTCGTGGATCTCCTTCTTCACCTGCTTCGTCTC
 CACCTTTGCTGCGGCGCCCCCTCGTGCCCATCATCCGCGACAACCTCAACCTTGCCAAGGCTGACAT
 CGGCAATGCCGGTGTGCGGTCCGTGTCTGGGTCCATCTTCTCCAGGCTGGCCATGGGCGCTATCTG
 TGACTTGCTTGCCCCACGGTATGGTTGTGCCTTCCTCGTCATGCTCTCGGCACCGACCGTCTTCTG
 CATGGCCGTCATCGATGATGCCTCAGGGTACATCGCCGTCCGGTTCCTCATTGGCTTCTCCCTCGC
 CACCTTCGTGTCATGCCAATACTGGATGAGCACCATGTTCAATAGCAAGATCATTGGCACGGTCAA
 TGGCTTGGCTGCAGGCTGGGGCAACATGGGTGGCGGCCACGCAGCTCATCATGCCGCTTGTCTT
 CCACGCAATCCAGAAGTGTGGCGCCACGCCCTTCGTGGCATGGCGTATTGCCTACTTCGTGCCGGG
 AATGATGCACATCGTGATGGGCTTGCTGGTCCTCACCATGGGGCAAGATCTCCCTGACGGGAACCT
 TGCGAGCCTCCARAAGAAGGGAGACATGGCCAAGGACAAGTTCTCCAAGGTCTTTGGGGCGCYGT
 CACCAACTACCGGACATGGATCTTCGTCTCTCTACGGCTACTGCATGGGYGTGAGCTCACCAC
 SGACAATGTCATCGCCGAGTACTACTACGACCACTTCCACCTAGACCTCCGCGCYGCWGGCACCAT
 TGCYGCTTGYYTYGGCATGGCAAACATYGTGCGCGTCCTATGGGKGGCTACCTCTCYGACCTTGG
 TGCCCGCTACTTTGGCATGCGTGCTCGCCTTTGGAACATCTGGATCCTMCAAACYGCCGGTGGCGC
 TTTCTGCATCTGGCTCGGTGCTGCGTCAGCCCTCCCTGCCTCAGTGACTGCCATGGTTCTCTTCTC
 CATCTGCGCCCAAGCCGCGTGTGGTGCTGTATTTGGCGTCGCACCCTTCGTTTCTAGACGTTCCCT
 TGGCATCATCTCNGGGCTGACCGGTGCTGGTGGAACGTGGGTGCRGGGCTCACGCAGCTTCTCTT
 CTTTACTTCATCACAATACTCCACYGGAAGGGGTCTCGAGTACATGGG

FIGURE 8 (continued)

45/104

CATCATGATCATGGCATGCACGCTGCCTGTCGCTCTTGTGCACTTCCCACAGTGGGGCTCGATGTT
CTTCCCGGCCAGCGCCGACGCCACAGAGGAGGAATACTATGCCTCTGAGTGGTTCGGAGGAGGAGAA
GAACAAGGGTCTCCATATTGCTGGCCAAAAGTTTGCCGAGAACTCACGATCGGAGCGTGGAAGGCG
CAACGTCATCCTTGCCACGTCCGCCACGCCACCCAACAATACGCCCCAGCACGTATAAGACCGGAT
TGTTTTTTCATATACTATGTACAAGTACTGAACATCGGCTGTAATAAGGTGTACGCATTTATATTTC
CAGTGTAGACTTGTGTAATGCGTTTCTTACGCACGAAATGTTTTGGTGTGTGCATGCACGCATGCG
AGGTACCTGTGGTCTGAATTTACAGCAACTTTGAGACTAAAAAAAAAAAAA

SEQ ID NO: 74, *Triticum aestivum* high affinity nitrate transporter (AAK19519)

MEVQAGSHADAAASKFTLPVDSEHKAKSFRLFSFANPHMRTFHLWSISFFTFCFVSTFAAAPLVPII
RDNLNLAKADIGNAGVASVSGSIFSRLAMGAICDLLGPRYGCAFLVMLSAPTVCMAVIDDASGYI
AVRFLIGFSLATFVSCQYWMSTMFNSKIIGTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGATPF
VAWRIAYFVPGMMHIVMGLLVLTMGQDLPDGNLASLQKKGDMAKDKFSKVLWGAVTNYRTWIFVLL
YGYCMGVELTTDNVIAEYYYYDHFHLDLRAAGTIAACFGMANIVARPMGGYLSDLGARYFGMRARLW
NIWILQTAGGAFCIWLGRASALPASVTAMVLFISICAQAACGAVFGVAPFVSRRSLGIISGLTGAGG
NVGAGLTQLLFFTSSQYSTGRGLEYMIMIMACTLPVALVHFPQWGSMMFFPASADATEEEYYASEW
SEEEKNKGLHIAGQKFAENSRSERGRNVILATSATPPNNTPPQHV

SEQ ID NO: 75, *Hordeum vulgare* high affinity nitrate transporter homolog BCH2 mRNA, complete cds (U34290)

TTACAAGCTCCATCTGAGAGCAGCAGCAACCACCATTAGAGACACACTTAGTTGCCAGTGCGACTA
AGCTAGCTAGCTCGAGGAAGATGGAGGTGGAGTCGAGCTCGCATGGCGCCGGCGACGAGGCTGCGA
GCAAGTTCTCGCTGCCCCTGGACTCGGAGCACAAGGCCAAGTCCATCAGGCTCTTCTCCTTCGCCA
ACCCCCACATGCGCACCTTCCACCTCTCCTGGATCTCCTTCTTACCTGCTTCGTCTCCACCTTCG
CTGCCGCGCCCCCTCGTCCCTATCATCCGCGACAACCTAAACCTCGCCAAGGCCGACATCGGCAACG
CCGGTGTGGCGTCCGTGTCCGGGTCTATCTTCTCGAGGCTCGCCATGGGGGCCATCTGCGATCTCC
TTGGCCCTCGATATGGATGCGCCTTCCTCGTCATGCTCGCAGCACCACCGTCTTCTGCATGTCCC
TCATCGATGATGCGGCGGGCTACATCACGGTCCGCTTCCTCATCGGCTTCTCCCTCGCGACGTTTG
TGTCGTGCCAGTATTGGATGAGCACCATGTTCAACAGCAAGATCATCGGCACCGTCAACGGCCTGG
CGGCCGGCTGGGGCAACATGGGTGGTGGTGCCACCCAGCTCATTATGCCACTCGTCTTCCACGCCA
TCCAGAAGTGTGGTGCCACGCCCTTCGTGCGATGGCGCATCGCCTACTTCGTGCCAGGAATGATGC
ACGTGGTGTATGGGCTTGCTCGTGCTCACCATGGGACAGGATCTCCCCGATGGTAACCTTGCAAGCC
TCCAGAAGAAGGGGGAGATGGCCAAGGACAAGTTCTCCAAGGTTGTGTGGGGTGCTGTTACAAACT
ACCGTACATGGATCTTCGTTCTTCTTTACGGATACTGCATGGGTGTTGAGCTCACCACCGACAACG
TCATCGCCGAGTACTACTTCGACCACTTTCACCTTGACCTTCGAACATCCGGCACCATTGCCGCCT
GTTTTGGCATGGCCAACATCGTTGCTCGGCCTGCGGGTGGCTACCTCTCCGACCTCGGTGCCCGCT
ACTTCGGCATGCGTGCCCGCCTCTGGAACATCTGGATCCTCCAGACCGCTGGTGGCGCATTTCTGCC
TCTGGCTCGGCCGTGCAAAAGCCCTCCCCGAATCCATCACTGCCATGGTCTCTTCTCCATCTGCG
CTCAGGCAGCATGTGGTGCAGTCTTTGGTGTGATCCCCTTCGTCTCCCGCCGCTCCCTCGGCATCA
TTTCGGGCTTGAGTGGAGCCGGTGGGAACCTTTGGCGCCGGGCTGACAC

FIGURE 8 (continued)

46/104

AATTGCTCTTCTTCACTTCGTCTGAAGTATGGCACCGGCAGGGGGCTTGAGTACATGGGTATCATGA
TCATGGCCTGCACGCTCCCTGTGGCGCTTGTGCACTTCCACAGTGGGGTTCCATGCTCTTGCCGC
CAAACGCCAACGCCACCGAGGAGGAGTTCTATGCCGCCGAATGGAGCGAGGAGGAGAAGAAGAAGG
GTCTCCATATCCCTGGCCAAAAGTTTGCCGAGAATTCGCCGCTCGGAGCGTGGCAGGCGCAACGTCA
TCCTTGCCACAGCCGCCACACCCCCCAACAACACTCCCCAACACGCATAAGACTCGAGCTTTTCTT
TACCTGTGTACACGTACAGTGC GCGTATTATACACACATCGATCGTGTATATACGCCTGGAATCCG
CAAGCAGTATGTTTTTTGAAAAAAAAAAGCGGCCGCGAATTC

**SEQ ID NO: 76, *Hordeum vulgare* high affinity nitrate transporter
homolog BCH2 (AAC49532)**

MEVESSSHGAGDEAASKFSLPVDSEHKAKSIRLFSFANPHMRTFHLISWISFFTCTFVSTFAAAPLVP
IIRDNLNLAKADIGNAGVASVSGSIFSRLLAMGAICDLLGPRYGCAFLVMLAAPTVFCMSLIDDAAG
YITVRFLIGFSLATFVSCQYWMSTMFNSKIIGTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGAT
PFVAWRIAYFVPGMMHVVMGLLVLTMGQDLPDGNLASLQKKGEMAKDKFSKVVGAVTNYRTWIFV
LLYGYCMGVELTDDNVIAEYFFDHFLDLRTSGTIAACFGMANIVARPAGGYLSDLGARYFGMRAR
LWNIWILQTAGGAFCLWLGRAKALPESITAMVLFSICAQAACGAVFGVIPPVSRRLGIISGLSGA
GGNFGAGLTQLLFFTSSKYGTGRGLEYMIMIMACTLPVALVHFPOWGSMLLPNANATEEEFYAA
EWSEEEKKKGLHIPGQKFAENSRSERGRRNVILATAATPPNNTPQHA

**SEQ ID NO: 77, *Triticum aestivum* high affinity nitrate transporter
TaNRT2 mRNA, complete cds (AF288688)**

AAGCTAGCACCAAGCCTCCAAGGAGCAAGAAGAGAAGAAGCCTTGCTCGATCAAGCAAGGTCGAAA
TGGAGGTGGAGGCCAGCGCCCATGGCGACACGGCGGCGAGCAAGTTCACGCTGCCCGTGGACTCCG
AGCACAAGGCCAAGTCCTTCAGACTCTTCTCCTTCGCCAACCCCCACATGCGTACCTTCCACCTCT
CCTGGATATCCTTCTTCACCTGCTTCGTCTCCACCTTCGCGGCGGCACCGTTGGTGCCCATCATCC
GTGACAACCTCAACCTCGCTAAGGCCGACATAGGGAATGCCGGTGTGGCATCTGTGTCTGGGTCCA
TCTTCTCCAGGCTTGCCATGGGTGCCATCTGCGACCTTTTAGGGCCGCGGTATGGCTGCGCCTTCC
TCGTATGCTCTCAGCACCCACTGTGTTTTGCATGGCTGCTATCGACGATGCGTCAGGCTACATCG
CCGTACGCTTCTTCATTGGCTTCTCCCTCGCCACCTTCGTGTATGCCAATATTGGATGAGCACC
TGTTCAACAGTAAGATCATTGGCACGGTGAATGGCCTCGCGGCCGGCTGGGGCAACATGGGCGGTG
GTGCCACACAACCTCATCATGCCGCTTGTTTTCCATGCCATCCAAAAGTGTGGTGCCACACCCTTCG
TGGCATGGCGTATTGCCTATTTTCGTGCCGGAATGATGCACATCGTCATGGGGTTGCTTGTGCTCA
CTATGGGCCAAGATCTCCCCGACGGCAACCTTGCGAGTCTCCAGAAGAAGGGGGACATGGCCAAGG
ACAAATTCTCGAAGGTCCTTTGGGGTGCGGTCAACCACTACCGGACATGGATATTTCGTCCTCCTCT
ACGGCTACTGCATGGGTGTGAGCTCACCACCGACAACGTCATCGCCGAGTACTACTACGACCACT
TCCACCTTGACCTTCGCGCCGCTGGCACCATTGCCGCTTGCTTCGGCATGGCCAACATCGTCGCGC
GTCCTATGGGTGGCTATCTCTTGACCTTGGTGCCCGCTACTTCGGCATGCGTGCTCGGCTCTGGA
ACATCTGGATCTCCAGACCGCTGGTGGCGCTTCTGCATCTGGCTCGGTGCTGCATCGGCCCTTC
CTGCCTCAGTCACGGCCATGGTCCTCTTTTCCATTTGTGCACAAGCTGCTTGTGGTGCTGTATTTG
GCGTCGCACCCTTCGTTTCCAGGCGTTCCCTTGGCATCATCTCCGGGCTGAC

FIGURE 8 (continued)

47/104

CGGCGCTGGTGGCAATGTTGGCGCAGGGCTAACGCAACTTCTTTTCTTCACATCGTCGCAATACTC
CACCGGGAGGGGTCTCGAGTACATGGGCATCATGATCATGGCATGCACATTACCCGTCGCTCTGGT
GCACTTCCCCCAATGGGGCTCCATGTTCTTCCCGGCTAGCGCTGATGCCACGGAAGAGGAATACTA
TGCTTCTGAGTGGTTCGGAGGAGGAGAAGGGCAAGGGTCTCCATATTACAGGCCAAAAGTTTCGAGA
GAACTCCCGCTCAGAGCGCGGCAGGCGCAACGTCATCCTTGCCACATCCGCCACGCCACCCAACAA
CACACCCCAGCACGTATAAGGCCCTTATTTTTATGTACCTAAGAATTTTACTGTTTCATCACGTAT
ATATACAAACCGTATATCTACGTCTGCAGCCCCAGCGTAATAAGTTGTATGGGGATTTATGTTTCT
ACTAGTAACTTAAGGAAACGCTGCTTTTGCCTCCTGCTCTGTACGCATGAAATGTAATATCAAT
TTGAGTCCGAAATTACTACAAAAAAA

**SEQ ID NO: 78, *Triticum aestivum* high affinity nitrate transporter
(AAG01172)**

MEVEASAHGDTAASKFTLPVDSEHKAKSFRLFSFANPHMRTFHLWSISFFTFCFVSTFAAAPLVPII
RDNLNLAKADIGNAGVASVSGSIFSRAMGAI CDLLGPRYGCAFLVMSLAPTVCMAAIDDASGYI
AVRFLIGFSLATFVSCQYWMSTMFNSKIIGTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGATPF
VAWRIAYFVPGMMHIVMGLLVLTMGQDLPDGNLASLQKKGDMAKDKFSKVLWGAVTNYRTWI FVLL
YGYCMGVELTTDNVIAEYYYDHFHLDLRAAGTIAACFGMANIVARPMGGYLSDLGARYFGMRARLW
NIWILQTAGGAFCIWLGRASALPASVTAMVLFSICAQAACGAVFGVAPFVSRRSLGIISGLTGAGG
NVGAGLTQLLFFTSSQYSTGRGLEYMIMIMACTLPVALVHFPQWGSMMFFPASADATEEEYYASEW
SEEEKGKGLHITGQKFAENSRSERGRRNVILATSATPPNNTPPQHV

**SEQ ID NO: 79, *Triticum aestivum* high-affinity nitrate transporter
(NRT2.3) mRNA, complete cds (AY053452)**

GCAGTATAATCAAGCAAGCTAGCTGCAAGCCGAGGAGCCTAGCTCGATCAAGCAAGGTGCGAAATGG
AGGTGGAGTCTAGCGCCCATGGCGACGCCGCGGCGAGCAAGTTCACGCTGCCTGTGGACTCCGAGC
ACAAGGCCAAGTCCTTCAGGCTCTTCTCCTTCGCCAACCCCCACATGCGCACCTTCCACCTCTCCT
GGATATCCTTCTTCACCTGCTTTGTCTCCACCTTCGCCGCCGCGCGCTTGGTGCCCATCATCCGTG
ACAACCTCAACCTCGCCAAGGCCGACATAGGGAATGCCGGTGTGGCATCTGTGTGTCAGGGTCCATCT
TCTCCAGGCTTGCCATGGGCGCCGTCTGCGACCTTTTGGGGCCGCGGTATGGCTGTGCCTTCCTCG
TCATGCTCTCAGCGCCAACGGTCTTCTGCATGGCCGTCATCGATGACGCCTCGGGGTACATCGCTG
TACGCTTCCTCATTGGCTTCTCCCTCGCCGCCTTTGTGTCTGCTGCAATACTGGATGAGCACCATGT
TCAACAGTAAGATCATTGGCACGGTGAATGGCCTCGCGCCGGCTGGGGCAACATGGGGGGCGGTG
CCACACAACCTCATTATGCCACTTGTTTTCCATGCCATCCAAAAGTGCGGTGCCACACCCTTCGTGG
CATGGCGTATCGCCTACTTCGTGCCGGGAATGATGCACATCGTCATGGGGTTGCTTGCTCCTCACA
TGGGCCAAGATCTCCCCGACGGCAACCTTGCGAGCCTCCAGAAGAAGGGAGACATGGCCAAGGACA
AGTTCTCCAAGGTCCTTTGGGGCGCCGTACCAACTACCGGACATGGATCTTCGTCTCTCTCTACG
GCTACTGCATGGGTGTGAGCTCACCCTGACAACGTCATCGCCGAGTACTACTACGACCATTTCC
ACCTACACCTTCGCGCTGCAGGCACCATCGCCGCTGCTTTGGCATGGCCAATATCGTTCGCACGTC
CTATGGGAGGTTACCTCTCTGACCTTGGCGCTCGCTACTTTGGTATGCGTGCTCGCCTATGGAACA
TCTGGATCCTCCAGACCGCCGGCGGCGCTTTCTGCATCTGGCTCGGTGCTGCATCGGCCCTCCCCG
CCTCAGTGAAGTCCATGTTTCTTCTCCATCTGCGCCCAAGCTGCATGTGGCGCTGTCTTTGGTG
TTGCACCATTCGTTTCCAGGCGTTCCCTTGGCATCATCTCTGGGTAAACCG

FIGURE 8 (continued)

48/104

CGCTGGTGGCAATGTGGGCGCGGGGCTCACACAACCTTCTCTTCTTCACTTCGTCGCAATACTCCAC
CGGGAGGGGTCTCGAGTACATGGGCATCATGATCATGGCATGCACATTACCTATCACTCTGGTGCA
CTTCCCACAATGGGGCTCCATGTTCTTCCCGGCCAGTGCTGATGCTACGGAGGAGGAGTACTACGC
TTCCGAGTGGTCAGAGGAGGAGAAGGGCAAGGGTCTCCATATCGCAGGCCAGAAGTTTGAGAGAA
CTCCCGCTCGGAGCGTGGTAGGCGCAATGTTATCCTCGCCACATCCGCCACGCCGCCCAACAATAC
ACCCAGCATGTATAAGGCCCTTGTCTTCTGTACCTATGAATTGTACGGTTCGTCACGTACATAT
ACAAACCGTATATCTACGTCGGCAGCCCCAGCGTAATAAGTTGTATGGGGATTTATCTTTCTACTA
GTAAACTTAAGGAAACGCTGGTTTTGCGTTCCTGCTCTGTAC

SEQ ID NO: 80, *Triticum aestivum* high-affinity nitrate transporter (AAL11016)

MEVESSAHGDAAASKFTLPVDSEHKAKSFRLFSFANPHMRTFHLWSISFFTCFVSTFAAAPLVPII
RDNLNLAKADIGNAGVASVSGSIFSRAMGAVCDLLGPRYGCAFLVMSAPTVFCMAVIDDASGYI
AVRFLIGFSLAAFVSCQYWMSTMFNSKIIGTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGATPF
VAWRIAYFVPGMMHIVMGLLVLTMGQDLPDGNLASLQKKGDMAKDKFSKVLWGAVTNYRTWIFVLL
YGYCMGVELTTDNVIAEYYYDHFHLHLRAAGTIAACFGMANIVARPMGGYLSDLGARYFGMRARLW
NIWILQTAGGAFCIWLGRASALPASVTAMVLFSICAQAACGAVFGVAPFVSRRSLGIISGLTGAGG
NVGAGLTQLLFFTSSQYSTGRGLEMYGIMIMACTLPITLVHFPQWGSMMFFPASADATEEEYYASEW
SEEEKGKGLHIAGQKFAENSRSERGRRNVILATSATPPNNTPHV

SEQ ID NO: 81, *Hordeum vulgare* putative high affinity nitrate transporter (BCH4) mRNA, complete cds (AF091116)

CACCACTGCAAGCATATTTAGGCTTAGTTAGCTCCAAGGAGCAAAGCTAAAAAGAACCTAGCTAGG
CTAGCTCGATCCAGCTAGCTCAGTAGATATGGAGGTGGAGGCCGAGCTCATGGCGATGCGGCGGC
GAGCAAGTTCACGCTGCCCCGTGGACTCCGAGCACAAGGCCAAGTCCTTCAGGCTCTTCTCCTTCGC
CAACCCGCACATGCGCACCTTCCACCTCTCGTGATCTCCTTCTTACCTGCTTCGTCTCCACCTT
TGCCGCTGCTCCGTTGGTGCCCATCATCCGCGACAACCTCAACCTCGCCAAGGCCGACATCGGCAA
TGCCGGTGTGGCGTCCGTGTCCGGCTCCATCTTCTCGAGGCTCGCCATGGGCGCCATTTGTGACCT
GCTTGGCCCGCGGTACGGTTGTGCCTTTCTCGTCATGCTATCGGCGCCAACCGTCTTCTGCATGGC
CGTCATCGACGACGCGTCGGGATACATCGCAGTCCGCTTCTCATCGGCTTCTCCCTCGCAACCTT
CGTGTCATGCCAGTACTGGATGAGCACAATGTTCAACAGTAAAATCATCGGCACGGTTAATGGCCT
CGCAGCCGGGTGGGGCAACATGGGTGGCGGGGCCACACAGCTCATCATGCCCCCTCGTCTTCCATGC
CATCCAAAAGTGTTGGTGCCACACCTTTGTGGCATGGCGTATCGCCTACTTCGTGCCGGGGATGAT
GCACATCGTGATGGGCCACTCGTGCTCACCATGGGACAAGACCTCCCTGATGGGAACCTCGCAAG
CCTGCAGAAGAAGGGAGACATGGCCAAGGACAAGTTCTCCAAGGTCCTTTGGGGCGCCGTTACCAA
CTACCGGACATGGATCTTTGTCTCTCTATGGCTACTGCATGGGTGTGAGCTCACCAGTGGCAA
TGTCATTGCCGAGTACTACTTCGATCACTTCCACCTAAACCTCCGTGCCGCCGGTACCATCGCCGC
TTGCTTCGGCATGGCCAACATCGTCGCACGTCTATGGGCGGCTACCTCTCCGACCTTGGTGCTCG
CTACTTCGGTATGCGTGCTCGCCTTTGGAACATCTGGATCCTTCAGACAGCTGGCGGCGCCTTTTG
CATCTGGCTTGGGCGCGCCTCGGCCCTCCCCGCCTCAGTGACTGCCATGGTCCTCTTCTCCATCTG
CGCCAGGCTGCGTGTGGTGCTATCTTTGGTGTCGAACCTTTCGTCTCCAGG

FIGURE 8 (continued)

49/104

CGTTCCCTTGGCATCATTTCCGGGTGACCGGTGCTGGTGGAAACGTGGGCGCAGGGCTCACACAG
CTTCTCTTCTTCACTTCGTCGCAATACTCCACTGGCAGGGGTCTTGAGTACATGGGCATCATGATC
ATGGCATGCACCTTACCCGTCGCTCTCGTTCACTTCCCTCAGTGGGGCTCTATGTTCTTGGCTGCC
AGTGCCGACGCCACGGAGGAGGAGTACTACGCCTCAGAGTGGTCAGAGGAGGAGAAGAGCAAGGGT
CTCCATATCGCAGGACAAAAGTTTGCTGAGAACTCCCGCTCGGAACGCGGCAGGCGCAACGTCATC
CTTGCCACATCCGCCACACCACCCAACAACACGCCCTACACGTATAAGTTTCAAATTTTGTGTTA
CACAAGAAATGTACATCTTGCTGAGTATATATACACATCGTATATTTTAGTAAAAAAAAAAAAAAAA
AA

SEQ ID NO: 82, *Hordeum vulgare* putative high affinity nitrate transporter (AAD28364)

MEVEAGAHGDAAASKFTLPVDSEHKAKSFRLFSFANPHMRTFHLWSISFFTFCFVSTFAAAPLVPII
RDNLNLAKADIGNAGVASVSGSIFSRLAMGAICDLLGPRYGCAFLVMSAPTVCMAVIDDASGYI
AVRFLIGFSLATFVSCQYWMSTMFNSKII GTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGATPF
VAWRIAYFVPGMMHIVMGLLVLTMGQDLPDGNLASLQKKGDMAKDKFSKVLWGAVTNYRTWIFVLL
YGYCMGVELTTGNVIAEYYFDHFHLNLRAGTIAACFGMANIVARPMGGYLSDLGARYFGMRARLW
NIWILQTAGGAFCIWLGRASALPASVTAMVLFSICAQAACGAIFGVEPFVSRRSLGIISGLTGAGG
NVGAGLTQLLFFTSSQYSTGRGLEYMGIMIMACTLPVALVHFPPQWGSMLAASADATEEEYYASEW
SEEEKSKGLHIAGQKFAENSRSERGRNVILATSATPPNNTPLHV

SEQ ID NO: 83, *Hordeum vulgare* putative high affinity nitrate transporter (BCH3) mRNA, complete cds (AF091115)

TCTCAGTTGCCACTGCAGCTGATCAAGCAAGCTAGCTCCAAACCTCCAAGGAGGAAGCAGAGAAGG
AGACTAGCTCGATCAAGCAAGGTCCAAATGGAGGTGGAGGCTGGTGCCCATGGCGACACGGCGGCG
AGCAAGTTCACGTTGCCCGTGGACTCCGAGCACAAGGCCAAGTCCTTCAGGCTCTTCTCCTTCGCC
AACCCACACATGCGCACCTTTCACCTATCGTGGATATCCTTCTTCACATGCTTCGTCTCCACCTTT
GCCGCGGCGCCCCCTGGTGCCCATCATCCGCGACAACCTGAACCTCGCCAAGGCCGACATAGGGAAT
GCCGGTGTGGCATCTGTGTCTGGGTCTATCTTCTCGAGGCTTGCCATGGGCGCCATCTGCGACCTT
TTGGGGCCGCGGTATGGGTGTGCCTTCCTCGTCATGCTCTCAGCGCCAACCGTCTTCTGCATGGCC
GTCATCGATGACGCCTCAGGGTACATCGCCGTACGCTTCCTCATCGGCTTCTCCCTTGCCACCTTT
GTGTCGTGCCAATACTGGATGAGCACCATGTTCAACAGTAAATCATCGGCACGGTCAATGGCCTC
GCGGCCGGCTGGGGCAACATGGGCGGTGGTGCCACACAACCTCATCATGCCGCTTGTTTTCCACGCC
ATCCAAAAATGTGGTGCCACACCATTTGTGGCATGGCGTATTGCCTACTTCGTGCCCGGAATGATG
CACATCGTGATGGGCTTGCTGGTACTCACCATGGGGCAAGATCTCCCTGATGGGAACCTCGCGAGC
CTCCAGAAGAGAGGAGACATGGCCAAGGACAAGTTCTCCAAGGTCCTTTGGGGCGCCGTACCAAC
TACCGGACATGGATCTTTGTCTCCTATATGGCTACTGCATGGGTGTGGAACCTCACCCTGACAAT
GTCATTGCCGAGTACTACTTCGACCACTTCCACCTAGACCTTCGCGCCGCTGGTACCATCGCCGCC
TGCTTCGGTATGGCCAACATAGTCGCACGTCCTATGGGCGGCTACCTCTCTGACCTTGCGGCCCGC
TATTTCCGCATGCGTGCCCTTTGGAACATCTGGATCCTCCAACCGCTGGTGGCGCTTTCTGCATC
TGGCTCGGTGCTGCATCGGCCCTCCCTGCCTCGGTGACCGCCATGGTCCTCTTCTCCATCTGTGCC
CAGGCTGCCTGTGGTGCTATCTTTGGTGTGCGACCCTTCGTCTCCAGGCGTTCCCTTGGCATCATT
TCCGGGTGACCGGTGCCGGTGGAACGTGGGCGCAGGACTCACACAA

FIGURE 8 (continued)

50/104

CTTCTATTCTTCACCTCATCGCAATACTCCACTGGTAGGGGTCTCGAGTACATGGGCATCATGATC
ATGGCATGCACGCTGCCCCGTCGCTCTTGTGCACTTTCCGCAATGGGGATCCATGTTCTTCCCGGCC
AGCGCTGATGCCACTGAGGAGGAGTACTATGCTTCCGAGTGGTCGGAGGAGGAGAAGGGCAAGGGT
CTCCATATCGCAGGCCAAAAGTTCGCCGAGAACTCCCGCTCGGAGCGCGGCAGGCGCAACGTCATC
TTTGCCACATCCGCCACGCCGCCCAACAACACACCCACAGCAGGTATAAGGCATTTTTTTTTTGTAC
CTATGAATTTTACAGCTCATGGCGTATATATACAAACAGTATATTTACGTTTGCAGCCCCAGCGTA
ATAAGTTGTATGGGGGTTTATCTTTTTACTATGGTAAACCTAAGGACATGTATTGTCAAATTGAGT
CCGAAATTAATACATGAACAGTGTTGATGTTTGTGTATGCTTGAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 84, *Hordeum vulgare* putative high affinity nitrate transporter (AAD28363)

MEVEAGAHGDTAASKFTLPVDSEHKAKSFRLFSFANPHMRTFHLWSISFFTCTFVSTFAAAPLVPII
RDNLNLAKADIGNAGVASVSGSIFSRAMGAI CDLLGPRYGCAFLVMSAPT VFCMAVIDDASGYI
AVRFLIGFSLATFVSCQYWMSTMFNSKI IGTVNGLAAGWGNMGGGATQLIMPLVFHAIQKCGATPF
VAWRIAYFVPGMMHIVMGLLVLTMGQDLPDGNLASLQKRGDMAKDKFSKVLWGAVTNYRTWIFVLL
YGYCMGVELTTDNVIAEYYFDHFHLDLRAAGTIAACFGMANIVARPMGGYLSDLGARYFGMRALWN
IWILQTAGGAFCIWLGRASALPASVTAMVLF SICAQAACGAI FGVAPFVSRRSLGI ISGLTGAGGN
VGAGLTQLLFFTSSQYSTGRGLEYM GIMIMACTLPVALVHF PQWGSMMFFPASADATEEEYYASEWS
EEKKGKGLHIAGQKFAENSRSERGRNVIFATSATPPNNTPQQV

SEQ ID NO: 85, *Prunus persica* PpNRT2;1 mRNA for high-affinity nitrate transporter, complete cds (AB097402)

CATTTAGTCTAAGTAGTTTCTAAATTCGAAACTTGAGTGCTGAAACTCGAGATTCAAAATCCAAAC
TCCAAACCCCAAATTCAAACCCCAAAAACATGGCCGAAGTCGAAGGTGAACCCGGAAGCTCCATG
CATGGAGTGACAGGCAGAGAGCAAACCTTTCGCTTCTCGGTAGCTTCCCCCATCGTCCCAACAGAC
CCAACAGCCAAATTTGACCTACCAGTTGATTCAGAGCACAAGGCCAAAGTTTTCAAATCTTCTCT
TTGGCCAACCTCACATGAGAACTTTCCACTTGTCTTGGATCTCTTTCTTCACTTGCTTTGTCTCA
ACTTTTGCAGCGGCCCCACTTGTCCCTATAATCCGAGACAACCTCAACCTCACAAGCAAGACATT
GGAAATGCTGGGGTTGCCTCTGTCTCAGGCAGCATATTCTCAAGACTTGTAATGGGTGCAGTGTGT
GATTTGCTAGGGCCACGATATGGGTGTGCCTTTCTCATAATGCTCAGCGCACCCACTGTGTTTTGC
ATGTCATTTGTATCTGATGCTGGGGGCTACTTGGCAGTGAGATTCATGATTGGTTTTTCGCTTGCT
ACATTCGTGTCATGCCAGTATTGGATGAGTACCATGTTTAACAGTAAGATTATTGGGCTGGTTAAT
GGGACAGCTGCTGGGTGGGGAAACATGGGTGGTGGGGCCACCCAGCTCTTGATGCCATTGGTGTTT
GATATAATTGGAAGAGTTGGTGCAACTCCTTTCACTGCTTGGAGAATTGCCTTTTTTCATTCCCTGGC
TGGCTTCATGTCATTATGGGAATAATGGTCTTGACCCTTGGCCAAGACTTGCTGATGGGAATCTT
GCTGCCCTGCAAAAGAAGGGTGATGTTGCCAAAGATCAATTCTCCAAGGTATTGTGGCATGCTGTA
ACAAATTACAGGACATGGATCTTTGTCCTTCTCTATGGCTACTCCATGGGTGTTGAATTGTCCACT
GATAATGTCATTGCTGAATACTTCTATGACAGGTTCAATCTCAAGCTTCACACAGCTGGAATCATT
GCTGCAACATTTGGCATGGCCAACCTAGTAGCCCGTCCCTTTGGAGGATTTGCGTCTGATCGAGCA
GCCAGGTACTTTGGCATGAGGGGCAGGCTATGGACTCTTGGATCCTCCAAACACTAGGAGGAGTC
TTCTGCATCTGGCTCGGCCGAGCAAACCTCACTCCCCATTGCGGTCTTTGCCA

FIGURE 8 (continued)

51/104

TGATCCTCTTCTCTGTAGGAGCCCAAGCTGCATGCGGAGCCACCTTTGGCGTCATCCCCTTCATCT
CCCGGCGATCCCTCGGCATCATATCGGGCCTCACTGGAGCGGGTGGGAACCTTCGGGTCCGGGCTGA
CCCAACTAGTGTCTTCTCAAGCTCAGCATTCTCAACTGCGACAGGGTGTCTCTGATGGGGGTAA
TGATCGTGTGCTGCACACTTCCAGTGACTTTGGTGCATTTCCCTCAGTGGGGGAGCATGTTCTTC
CGCCTTCAAAGATGTCGTGAAATCGACGGAAGAGTTTTACTATGGAGCTGAGTGGAATGAGGAGG
AGAAGCAGAAGGGGCTACACCAGCAGAGTTTGAGGTTTGAGAGAGAATAGTAGGTCTGAGCGTGGTA
GGCGTGTGCTCAGCTCCAACCCACCCAACACCACACCTTCCCATGTTTAGGTTATGTTATGAT
CTCATGAGAATTGTTTCTTTGAAATGCTTTGCAAACCTCATGCGCCCAATTATTCTCCTTAAGT
TGACCGAGAAGCTTACTTCTCTCTTGGGGAAATTTTTCTTTATTATTATCAGTTTTTTTCCCAAGC
ATATAAGTGAAGTATGATTATTTTTATTTTTCAGAAAAAAAAAAAAAAAAAAAAA

**SEQ ID NO: 86, *Prunus persica* high-affinity nitrate transporter
(BAD02939)**

MAEVEGEPGSSMHGVTGREQTFAFSVASPIVPTDPTAKFDLPVDSEHKAKVFKIFSLANPHMRTFH
LSWISFFTCFVSTFAAAPLVPIIRDNLNLTKQDIGNAGVASVSGSIFSRMLVMGAVCDLLGPRYGCA
FLIMLSAPTVCMSFVSDAGGYLAVRFMIGFSLATFVSCQYWMSTMFNSKIIGLVNGTAAGWGNMG
GGATQLLMPLVFDIIGRVGATPPTAWRIAFFIPGWLHVIMGIMVLTGQDLPDGNLAALQKKGDA
KDQFSKVLWHAVTNYRTWIFVLLYGYSMVELSTDNVIAEYFYDRFNLKLHTAGIIAATFGMANLV
ARPFGGFASDRAARYFGMRGRLWTLWILQTLGGVFCIWLGRANSLPIAVFAMILFSVGAQAACGAT
FGVIPFISRRSLGIIISGLTGAGGNFGSGLTQLVFFSSSAFSTATGLSLMGVMIVCCTLPVTLVHFP
QWGSMLPSPKDVVKSTEEFYGAEWNEEEKQKGLHQQLRFAENSRSERGRRVASAPTPPNTTPS
HV

**SEQ ID NO: 87, *Prunus persica* PpNRT2;2 mRNA for high-affinity
nitrate transporter, complete cds (AB097676)**

GCTTCATTTAGTCTAAGTAGTTTCTAAATTCGAAACTCGAGTTTTGAAACTCGAGATTCAAAATCC
AAACTCCAAACCCCAAATAATGGCCGAAGTCGAAGGTGAACCCGGAAGCTCCATGCATGGAGTGAC
AGGCAGAGAGCAAACCTTTGCGTTCTCAGTAGCTTCCCCCATCGTCCCAACAGACCCAACAGCTAA
ATTTGACCTACCTGTTGATTTCAGAGCACAAGGCCAAAGTTTTCAAATCTTCTCTTTGGCCAACCC
GCACATGAGAACCTTCCACTTGTCTTGGATCTCCTTCTTCACTTGCTTTGTCTCAACTTTTGCAGC
GGCCCCACTTGTCCCTATAATCCGAGACAACCTCAACCTCACAAGCAAGACATTGGAAATGCTGG
GGTTGCCTCTGTCTCAGGCAGCATATTCTCAAGACTTGTAATGGGTGCAGTGTGTGATTTGCTAGG
GCCACGATATGGGTGTGCCTTTCTCATAATGCTCAGCGCACCCACTGTGTTTTGCATGTCATTTGT
ATCTGATGCTGGGGGCTACTTGGCAGTGAGATTTCATGATTGGTTTTTTCGCTTGCTACATTCGTGTC
ATGCCAGTATTGGATGAGTACCATGTTTAACAGTAAGATTATTGGGCTGGTTAATGGGACAGCTGC
TGGGTGGGGAAACATGGGTGGTGGGGCCACCCAGCTCTTGATGCCATTGGTGTGTTGATATAATTGG
AAGAGTTGGTGCAACTCCTTTCACTGCTTGGAGAATTGCCTTTTTTCATCCCTGGCTGGCTTCATGT
CATTATGGGAATAATGGTCTTGACCCTTGGCCAAGACTTGCCTGATGGAAATCTTGCTGCCCTGCA
AAAGAAGGGTGATGTTGCCAAAGATCAATTCTCCAAGGTATTGTGGCATGCTATAACAACTACAG
GACATGGATCTTTGTCCTTCTCTATGGCTACTCCATGGGTGTTGAATTGTCCATTGATAATGTCAT
TGCTGAATACTTCTATGACAGGTTCAATCTCAAGCTTCACACAGCTGGAATCATTGCTGCAGCA

FIGURE 8 (continued)

52/104

TTTGGCATGGCCAACATAGTGGCCCGTCCCTTTGGAGGATTTGCGTCTGATCGAGCAGCCAGGTAC
TTTGGCATGAGGGGAGGCTATGGACTCTTTGGATCCTCCAAACACTAGGAGGAGTCTTTTGCATC
TGGCTCGGCCGAGCAAACACTCACTCCCCATTGCGGTCTTTGCCATGATCCTCTTCTGTAGGAGCC
CAAGCTGCATGCGGAGCCACCTTTGGCGTCATCCCCTTCATCTCCCGGCGATCCCTCGGCATCATA
TCGGGCCCTCACTGGAGCGGGTGGGAACCTTCGGATCCGGGCTGACCCAACTAGTGTTCTTCTCAAGC
GCAGCATTCTCAACTGCGACAGGGTTGTCTCTGATGGGGGTAATGATCGTGTGCTGCACACTTCCA
GTGACTTTGGTGCACTTCCCTCAGTGGGGGAGCATGTTCTTCCGCCTTCAAAGATGTCGTGAAA
TCAACGGAAGAGTTTTACTATGGAGCTGAGTGGAATGAGGAGGAGAAGCAGAAGGGGCTACACCAG
CAGAGTTTGAGGTTTGCAGAGAATAGTAGGTCTGAGCGTGGTAGGCGTGTTGCCTCAGCTCCAACC
CCACCCAACACCACACCTTCCCATGTTTGTAGTCAAACAAGGGAAAAAGGTCAACATGCACCAAGGTG
CATATGTGGTGTGGAACAAACCAATAATCAGAGAAGTGCTATTTTGTATCATCTCAATCAATCATA
TGTGTACTGTATTTCTATTAGAAATACAAGAGATGATCAGTTGAGTTGATACAAGTAGTTTTATT
GTAATGAAAATAGAGTTGCCATATAGCGTGTGCCTCTATATATGTATCTTGTACACAAATGTTTTT
ACTTTCAAGGTTTAACTTATGATAATTTTCAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 88, *Prunus persica* high-affinity nitrate transporter (BAD04063)

MAEVEGEPGSSMHGVTGREQTFAFSVASPIVPTDPTAKFDLPVDSEHKAKVFKIFSLANPHMRTFH
LSWISFFTCFVSTFAAAPLVPIIRDNLNLTKQDIGNAGVASVSGSIFSRVLMGAVCDLLGPRYGCA
FLIMLSAPTVCMSFVSDAGGYLAVRFMIGFSLATFVSCQYWMSTMFSKII GLVNGTAAGWGNMG
GGATQLLMPLVFDI IGRVGATPFTAWRIAFFIPGWLHVIMGIMVLTLGQDLPDGNLAALQKKGDVA
KDQFSKVLWHAITNYRTWIFVLLYGYSMGGVELSIDNVIAEYFYDRFNLKLHTAGIIAAAFGMANIV
ARPFGGFASDRAARYFGMRGRLWTLWILQTLGGVFCIWLGRANSLPIAVFAMILFSVGAQAACGAT
FGVIPFISRRSLGIIISGLTGAGGNFGSGLTQLVFFSSAAFSTATGLSLMGVMIVCCTLPVTLVHFP
QWGSMLPSPKDVVKSTEEFYGAEWNEEEKQKGLHQQLRFAENSRSERGRRVASAPTPPNTTPS
HV

SEQ ID NO: 89, *Glycine max* putative high affinity nitrate transporter (NRT2) mRNA, complete cds (AF047718)

TCACACTTTCTTCCTTAATTTTCTAGCTCTTGCTACGTACTTGAATTCAATTAGTTATTAATGGCT
GAGATTGAGGGTTCTCCCGGAAGCTCCATGCATGGAGTAACAGGAAGAGAACAAACATTTGTAGCC
TCAGTTGCTTCTCCAATTGTCCCTACAGACACCACAGCCAAATTTGCTCTCCAGTGATTTCAGAA
CACAAGGCCAAGGTTTTCAAACCTCTCTCCCTGGCCAATCCCCACATGAGAACCTTCCACCTTTCT
TGGATCTCCTTCTTACCTGCTTCGTCTCGACATTTCGACGAGCACCTCTTGTGCCCATCATCCGC
GACAACCTTAACCTCACCAAAGCGACATTGGAACGCCGGGGTGTCTTCTGTCTCCGGAAGCATC
TTCTCAAGGCTCGCAATGGGTGCAGTCTGTGACATGTTGGGTCCACGCTATGGCTGCGCCTTCCTC
ATCATGCTTTTCGGCCCCCTACGGTGTCTGCATGTCCTTTGTGAAAGATGCTGCGGGGTACATAGCG
GTTTCGGTTCTTGATTGGGTCTCGTTGGCGACGTTTGTGTCGTGCCAGTACTGGATGAGCACGATG
TTCAACAGTAAGATTATAGGGCTTGCGAATGGGACTGCTGCGGGGTGGGGGAACATGGGTGGTGGA
GCCACTCAGCTCATAATGCCTTTGGTGTATGAGCTTATCAGAAGAGCTGGGGCTACTCCCTTCACT
GCTTGAGGATTGCCTTCTTTGTTCCGGGTTTCATGCATGTCATCATGGGGATTCTTGTCTCACT
CTAGGCCAGGACTT

FIGURE 8 (continued)

53/104

GCCTGATGGAAACCTCGGGGCCTTGCGGAAGAAGGGTGATGTAGCTAAAGACAAGTTTTCCAAGGT
GCTATGGTATGCCATAACAAATTACAGGACATGGATTTTTGCTCTCCTCTATGGGTACTCCATGGG
AGTTGAATTAACAACTGACAATGTCATTGCTGAGTATTTCTATGACAGATTTAATCTCAAGCTACA
CACTGCTGGAATCATTGCTGCTTCATTTGGAATGGCAAACCTTAGTTGCTCGACCTTTTGGTGGATA
TGCTTCAGATGTTGCAGCCAGGCTGTTTGGCATGAGGGGAAGACTCTGGACCCTTTGGATCCTCCA
AACCTTAGGAGGGGTTTTCTGTATTTGGCTTGGCCGTGCCAATTCTCTTCCTATTGCTGTATTGGC
CATGATCCTGTTCTCTATAGGAGCTCAAGCTGCATGTGGTGCAACTTTTGGCATCATTCCTTTTCAT
CTCAAGAAGGTCTTTGGGGATCATATCAGGTCTAACTGGTGCAGGTGGAACTTTGGGTCTGGCCT
CACCCAATTGGTCTTCTTTTCAACCTCCAAATTCTCTACTGCCACAGGTCTCTCCTTGATGGGTGT
AATGATAGTGGCTTGCACCTCTACCAGTGAGTGTTGTTCACTTCCCACAGTGGGGTAGCATGTTTCT
ACCACCCTCAAAAGATGTCAGCAAATCCACTGAAGAATTCTATTACACCTCTGAATGGAATGAGGA
AGAGAAGCAGAAGGGTTTGCACCAGCAAAGTCTCAAATTTGCTGAGAATAGCCGATCTGAGAGAGG
AAAGCGAGTGGCTTCAGCACCAACACCTCCAAATGCAACTCCCACTCATGTCTAGCCATAGCACTT
CAATCAAAGAAGATCATGAAACATAATTACTGAGCAGTATTGGGAATGAAGAACCATGAGTTGAAG
AATTTTCTAATAAGAAATCTTGTAACATGTAGACATAGAATGTTCTGGTTCTGGTTTGGCTGTGGT
GTAAGAGTTGTCTACTTGTGGTAAGTCATAAGTATCATAATCAGTATGTCAATGCAGATCTTGATG
CTGAGTATCAATAGTATCAAAAAAAAAA

SEQ ID NO: 90, Glycine max putative high affinity nitrate transporter; GmNRT2 (AAC09320)

MAEIEGSPGSSMHGVTGREQTFVASVASPIVPTDITAKFALPVDSEHKAKVFKLFLSLANPHMRTFH
LSWISFFTCTFVSTFAAAPLVPIIRDNLNLTKSDIGNAGVASVSGSIFSRAMGAVCDMLGPRYGCA
FLIMLSAPTVCMSFVKDAAGYIAVRFLIGFSLATFVSCQYWMSTMFNSKIIGLANGTAAGWGNMG
GGATQLIMPLVYELIRRAGATPFTAWRIAFFVPGFMHVIMGILVLTLLGQDLPDGNLGLRKKGDVA
KDKFSKVLWYAITNYRTWIFALLYGYSMGVELTTDNVIAEYFYDRFNLKLHTAGIIAASFGMANLV
ARPFGGYASDVAARLFGMRGRLWTLWILQTLGGVFCIWLGRANSLPIAVLAMILFSIGAQAACGAT
FGIIPFISRRSLGIIISGLTGAGGNFGSGLTQLVFFSTSKFSTATGLSLMGVMIVACTLPVSVVHFP
QWGSMLPSPKDVSKSTEEFYTSEWNEEEKQKGLHQQLKFAENSRSERGKRVASAPTPPNATPT
HV

SEQ ID NO: 91, Lotus japonicus mRNA for membrane transporter (nrt2 gene) (AJ292342)

GCACAAGTTTTTCTCTGTTGCATGTTCTGTTTCTGAATTACTTTAATTACTTCACACAACAACATT
CAACAATGGTTGAAATTGAAGGATCTCCAGGAACCTCCATGCATGGAGTAACAGGGAGGGAAACAAA
CCTTCATATCCTCAGTTTCTTCCCCAATGGTCCCAACAGACACCACAGCCAAATTTCGATTTACCAG
TTGATTCACAGCACAAAGCCAAAGTTTTCAAACCTGTTCTCATTAGCTAATCCTCACATGACAACCT
TCCACTTATCATGGATTTCTTCTTACCTGCTTTGTCTCTACCTTTGCAGCAGCTCCTCTTGTCC
CCATCATCCGAGACAACCTCAATCTCACAAAAGCGACATTGGCAACGCCGGTGTGCGCTCTGTCT
CCGGCAGCATTTTCTCCAGGCTCACCATGGGTGTAATTTGTGACCTCTTAGGCCCACGTTACGGGT
GTGCCTTCCTGATCATGCTGTCTGCACCAACTGTGTTCTGCATGTCGTTTGTGAATGATGCTGCAG
GCTACATTGTGGTTTCGTTTCATGATCGGGTTCTCATTGGCCACGTTTGTTCGTGCCAGTACTGGA
TGAGTACCATGTTTAAACAGTAAGATTATTGGGCTTGTTAATGGAAGTGCAGCTGGTTGGGGTAACA
TGGGTGGTGGAGCCACTCAGCT

FIGURE 8 (continued)

54/104

CATCATGCCTATTGTCTATGAATTGATCAGGAGAGCGGGGTCCACTGGGTTCCTGCTTGGAGGAT
TGCCTTCTTCATCCCTGGTTTCATGCATGTTTTTCATGGGGATCCTTGTCTTAACCTTGGCCAAGA
CTTGCCTGATGGCAACCTCAGTGCCCTCCAGAAGAAGGGTGATGTTGCTAAAGACAAATTCTCCAA
GGTGTTATGGTATGCCATAACAAATTACAGGACATGGATCTTTGCACTTCTCTATGGATACTCTAT
GGGAGTCGAATTAACCACTGACAATGTCATTGCTGAGTATTTTTATGACAGATTTAATCTGAAGTT
GCACACAGTTGGAATCATTGCTGCTTCTTTTGAATGGCAAATCTTGTGCTCGCCCCCTTTGGCGG
ATATGTATCTGATGTTGCAGCCCGTTGTTTGGTATGAGAGGAAGACTGTGGACTCTGTGGATCCT
CCAAACACTTGGAGGAGTGTCTGTATATGGCTTGGGCGTGCGAATTCACTTCCAATTGCGGTGTT
GGCGATGATCCTTTTCTCAGTTGGAGCTCAAGCTGCTTGTGGTGCAACATTTGGAATCATTCCTTT
CATCTCAAAAAGGTCTTTGGGGATCATTTTCAGGTCTAACTGGTGCAGGTGGCAACTTTGGTCTGG
ATTGACACAGTTGGTATTCTTTTCTACTTCAAGATTCTCCACAGGTGCAGGATTGTCTATGGATGGG
TGTGATGATTGTTGGTGCACCTCTCCGGTGACTCTTGTTCCTTCCCACAGTGGGGTAGCATGTT
CCTTCCTCCTTCAAAAAGACATCAACAAGTCCAGTGAGGAACACTATTACACTGCTGAATGGGATGA
GGAAGAGAGGAAGAAGGGGTTGCACTCTCAAAGTCTTAAGTTTGCAGAGAATAGTCGCTCTGAGAG
AGGAAAACGTGTTTCTCTGCTCCAACCTCTCCAAACACAACCCCTACCCATGTCTAAGATGGATG
GATGATCACCACAGTGGAAAGCTAATGAGGAAAAGAGTATATGGATCCCTTGATTGAATAATTTAT
CCTTAAGCCTTTAAAGATACTTTGGCATCCAGAAATTTGGTGTGTTGCCCTTCAAATTCTACTTGTT
ATAGAAATTTGGTGTGATTTTCTATAAGGGACTTTGGTGTCTGTGGGAGTGTGGGTCTATCAGTTA
ATTATACAAACAGGTGGTGTACAAAAATAATATATTGAGTTTTTTAATTTTGGTGTGATATATATT
AATGAATGTTACTCAAAAAAAAAAAAAAAAAAAAACTCGAGGGGGGGCCCGGTA

SEQ ID NO: 92, Membrane transporter - Lotus japonicus (Q9ARC5)

MVEIEGSPGTSMHGVTGREQTFISSVSSPMVPTDTTAKFDLPVDSQHKAKVFKLFSLANPHMTTFH
LSWISFFTCFVSTFAAAPLVPIIRDNLNLTKSDIGNAGVASVSGSIFSRMTMGVICDLLGPRYGCA
FLIMLSAPTVCMSFVNDAAGYIVVRFMIGFSLATFVSCQYWMSTMFNSKIIGLVNGTAAGWGNMG
GGATQLIMPVYELIRRAGSTGFTAWRIAFFIPGFMHVFMGILVLTGLQDLDPGNLSALQKKGDVA
KDKFSKVLWYAITNYRTWIFALLYGYSMGVELTTDNVIAEYFYDRFNLKLHTVGI IAASFGMANLV
ARPFGGYVSDVAARLFGMRGRLWTLWILQTLGGVFCIWLGRANSLPIAVLAMILFSVGAQAACGAT
FGIIPFISKRLGIIISGLTGAGGNFGSGLTQLVFFSTSRFSTGAGLSWMGVMIVGCTLPVTLVHFP
QWGSMLPSPKDKINKSSEEHYYTAEWDEEERKKGLHSQSLKFAENSRSERGKRVSSAPTPPNTTPT
HV

SEQ ID NO: 93, Nicotiana tabacum mRNA for high affinity nitrate transporter protein (nrt2.2 gene) (AJ557584)

TTAAAGAAGAAATTA AAAATGGTTGATATTGAAGGATCACCAGGTAGTTCTATGCATGGAGTTACA
GGTAGAGAACCAGTTCTTGCTTTCTCTGTTGCATCTCCAATGGTACAAACTGATACCACTGCACAT
TTTAAAGTTCCGGTCGATTCTGAACACAAGGCCAAGGTTTTCAAATTCTACTCATTTTCAAAACCT
CACGGTCTAACTTTTCAACTTTCTTGGAATTTCTTTCTTACTTGTTTTGTTTTCTACTTTTGCTGCT
GCCCCTTTAGTTCCTATTATTAGAGACAACCTTAACTTGACCAAAATGGACGTTGGTAATGCTGGG
GTTGCCTCTGTTTCCGGAAGTATTCTATCTAGGCTTGCAATGGGTGCGATTTGTGACATGTTGGGA
CCAAGATATGGATGCGCGTTTCTTATCATGTTATCAGCTCCGACTGTTTTTTGCATGTCTTTCGTG
TCTTCGGCTGGTGGCTACGTTGCTGTGAGATTCA

FIGURE 8 (continued)

SUBSTITUTE SHEET (RULE 26)

55/104

TGATTGGATTCTCACTCGCGACGTTTGTGTGTCGTGTCAATATTGGATGAGTACGATGTTTAATAGTC
 AGATTATTGGACTTGTTAATGGAACAGCAGCAGGATGGGGAAATATGGGGGGTGGAGCTACTCAGC
 TTATTATGCCTATTCTCTATGATATTATTAGAAGAGCAGGAGCCACCCCTTTTACTGCTTGGAGAA
 TTGCTTTCTTTATTCTGCTGGTGGCTTCATGTTATTATGGGAATTTTAGTGTTAACTCTTGGCCAAG
 ATTTGCCTGATGGTAACCTTGCTTCCCTACAGAAGAAAGGCGATGTTTCTAAAGATAAGTTCTCTA
 AGATATTGTGGTATGCTGCAACAAATTACAGGACATGGATCTTTGTCTGCTCTATGGTTACTCCA
 TGGGAGTTGAATTGACTACAGATAATGTGATTGCTGAGTACTTCTTTGATAGATTTGATCTAAAGC
 TTCACACGGCTGGAATCATTGCTGCCACATTTGGTATGGCTAATCTCTTAGCTCGACCTTTTGGAG
 GATGGTCATCAGATATTGCAGCCAAACATTTTGGAAATGAGAGGCAGATTATGGAACCTTATGGATTT
 TACAAACACTTGGTGGTGTCTTTCTGTTTCTTACTTGGAAAAGCAAACACACTTCCTATGGCTATAG
 CTTGGATGATCATATTCTCCTTAGGTGCTCAAGCAGCATGTGGAGCTACATTTGGTATTATTCCTT
 TCATTTTCGCGTCGATCGTTAGGTATAATCTCAGGTATGACAGGAGCTGGAGGAAATTTTGGTTCTG
 GATTGACACAACCTTGTCTTTTCACTACAAAATGGTCAACAGAAACAGGATTGAGTTATATGG
 GGATTATGATTATAGCTTGTACACTTCCTGTATCTTTGGTTTCAATTTCCACAATGGGGAAGTATGT
 TTTTGCCTCCAATAAAGATCCTGTAAAGAGTACTGAAGAGCATTACTTCACGTCTGAGTACACTG
 AGGCTGAGAAGCAAAGGGTATGCACCAAACAGCATCAAGTTTGTGAAAACGTGTCGGTCGGAGC
 GTGGTAAGCGTGTGGGTTCAGCTCTTACTCCGCCTAATGTAACGCCAAACCGTGTCTGAG
 CTTGAGTCTCACGGATCAGTACGGAGAAATAGTGATTTTGAAGGCTTACTTGCTTAATTGGTGT
 TGTATCAACACAATAAACGTGTGATATGTGTCTTTTAATGAGCTTTATATTACCAAGTGTGAGTA
 GTTAATTTGTATTATCACTTTGTGTGTGAGACTGATCTTAATATTAACAGTTGATTTGGTGTA
 AACTTTCATTAAAAA

SEQ ID NO: 94, *Nicotiana tabacum* high affinity nitrate transporter protein (CAD89799)

MVDIEGSPGSSMHGVTGREPVLAFSVASPMVQTDTTAHFKVPVDSEHKAKVFKFYSFSKPHGLTFQ
 LSWISFFTFCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSGSILSRLAMGAICDMLGPRYGCA
 FLIMLSAPTVCMSFVSSAGGYVAVRFMIGFSLATFVSCQYWMSTMFNSQIIIGLVNGTAAGWGNMG
 GGATQLIMPILYDIIRRAGATPFTAWRIAFFIPGWLHVIMGILVLTGQDLDPGNLASLQKKGDVS
 KDKFSKILWYAATNYRTWIFVLLYGYSMGVELTTDNVIAEYFFDRFDLKLHTAGIIAATFGMANLL
 ARPFGGWSSDIAAKHFGMRGRLWNLWILQTLGGVFCFLGKANTLPMAIAWMIIFSLGAQAACGAT
 FGIIPFISRRSLGIIISGMTGAGGNFGSLTQLLFFTTTKWSTETGLSYMGIIMIIACTLPVSLVHFP
 QWGSMLPPTKDPVKSTEEHYFTSEYTEAEKQKGMHQNSIKFAENCRSERGKRVGSALTTPPNVTPN
 RV

SEQ ID NO: 95, *Lycopersicon esculentum* putative high-affinity nitrate transporter (NRT2;3) mRNA, complete cds (AY038800)

GCCTAAAATGGGTGATATTGAAGGATCACCAGGAAGTTCAATGCATGGTGTTACTGGTAGAGAGCC
 AGTTCTTGCAATTTTTCAGTTGCTTCACTAATTGTACCAACTGATACATCAGCCAATTTCAAAGTCCC
 TGTTGATTCTGAACATAAAGCTAAAGTTTAAATTTTATTCGTTTTCGAAACCTCATGGACTAAC
 GTTTCAACTCTCATGGATTTCAATTTGTACTTGTTCGTATCGACTTTTGTGTCAGCCCTTTAGT
 CCCTATTATTAGGGACAATCTTAATCTAACTAAAATGGATGTTGGTAATGCTGGAGTTGCCTCTGT
 TTCGGGTAGTATCTTGTCTAGGCTAGCTATGGGCGCGATTTGTGACATGTTAGGTCCTAGATATGG
 TTGCGCGTTTCTTATAATGTTATCAGCCCCAACTGTTT

FIGURE 8 (continued)

56/104

TATGTATGTCTTTTGTGTCATCGGCTGGAGGGTACGTTGCTGTGAGGTTTATGATTGGGTTTTTCAC
TAGCAACGTTTGTGTCATGTGAGTATTGGATGAGTACGATGTTTAATAGTCAAATCATTGGACTTG
TGAATGGTACAGCTGCTGGATGGGGTAATATGGGTGGTGGTGTCTACTCAACTTATTATGCCTTTGC
TCTACGATATAATACGTAGAGCAGGGGCAACCCCGTTCACTGCTTGGAGAATCGCATTTTTTTATTC
CTGGATGGCTTCATGTTATTATGGGAATTTTAGTTTTAACTCTTGGACAAGATTTACCTGATGGTA
ACCTCGCTTCTTTACAGAAGAAAGGCGATGTTTCTAAAGATAAATTCTCAAAGATATTATGGTATG
CTGCAACAAATTACAGAACATGGATCCTTGTCTGCTCTATGGATACTCAATGGGAGTTGAATTAA
CTACAGATAACGTGATTGCTGAGTATTTCTTCGATAGATTTGATTTGAAGCTTCATACGGCTGGAA
TCATCGCTGCAACATTTGGCATGGCTAACTTATTAGCGCGACCATTGGAGGATGGTCATCAGATG
TTGCAGCTAAACATTTCTGGGATGAGAGGCAGATTATGGAATTCATGGATTTTACAAACACTTGGTG
GTGTGTTCTGTTTACTACTTGGAAAGGGCTACTACACTTCCTCTGGCTATTACTTGGATGATCATAT
TCTCAATAGGTGCACAAGCAGCATGTGGTGTAACGTTTGGAAATTATCCCTTTATTTTCGCGAAGAT
CATTAGGTATAATATCAGGTATGACAGGAGCTGGAGGCAATTTTGGTTCCGGATTGACACAACACTAC
TGTTTTTTCACGAGTACAAAGTACTCGACAGGAACAGGACTAACGTATATGGGGATGATGATCATCG
CGTGTAACACTTCCAGTAATGTTAGTTCGTTTTCCACAGTGGGGTAGTATGTTTTTGCCTCCATCTA
AAGATCCTATTAAGGGTACTGAAGAACATTATTTTGGTTCTGAGTATACTGAGGATGAGAAACAAA
AGGGAATGCACCAGAACAGCATCAAGTTCGCGGAAAACAGCAGGACAGAGCGTGGGAAGAAGCGCG
TTGGTTCAGCACCTACTCCGCCTAATGTAACACCAAATCGCGTCTGATGGGGAAAAAAATTAAAT
ACTTACTTCGCAGTTCATGCTCGT

**SEQ ID NO: 96, *Lycopersicon esculentum* putative high-affinity
nitrate transporter (AAK72402)**

MGDIEGSPGSSMHGVTGREPVLAFSVASLIVPTDTSANFKVPVDSEHKAKVFKFYFSKPHGLTFQ
LSWISFCTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSGSILSRAMGAI CDMLGPRYGCA
FLIMLSAPTVLCMSFVSSAGGYVAVRFMIGFSLATFVSCQYWMSTMFNSQII GLVNGTAAGWGNMG
GGATQLIMPLLYDII RRAGATPFTAWRIAFFIPGWLHVIMGILVLTGQDLDPDGNLASLQKKG DVS
KDKFSKILWYAATNYRTWILVLLYGYSMVELTTDNVIAEYFFDRFDLKLHTAGIIAATFGMANLL
ARPFGGWSSDVA AKHFGMRGRLWNSWILQTLGGVFCLLLGRATTLPLAITWMIIFSIGAQAACGVT
FGIIPFISRRSLGII SGMTGAGGNFGSGLTQLLFFTSTKYSTGTGLTYMGMMII IACTLPVMLVRFP
QWGS MFLPPSKDPIKGT EEHYFGSEYTEDEKQKGMHQNSIKFAENS RTERGKKRVGSAPT PPNVTP
NRV

**SEQ ID NO: 97, *Populus tremula* x *Populus tremuloides* mRNA for
nitrate transporter (tNit2.1 gene) (AJ646890)**

CTTCCCTAGTCTGAAACTCCTATCACAATCCGGTTTGGAAAGAGAATAGAGGAAGGGAATGGCTGAC
GTTGAGGGTTCCCCGGGTAGTTCCATGCATGGAGTGACAGGCAGAGAACAAAGCTTTGCCTTTTCG
GTTGCCTCTCCTACAGTCCCGACGGATACAACAGCAAAATTTGCCTTGCCAGTTGATTCTGAGCAC
AAGGCCAAAGTGTTCAAGATTTTCTCTTTTGCTAACCCCTCATATGAGAACATTTACACCTTTCTTGG
ATATCATTCCTTCACTTGTTTTGTCTCCACTTTTGCTGCAGCACCCCTTGTTCTTATCATTTCGGGAC
AACCTCAATTTAACC AAAAGTGACATCGGTAATGCTGGTGTTGCTTCTGTCTCTGGAAGCATCTTC
TCTAGGCTTGTAATGGGTGCAGTTTGTGACCTCTTGGGGCCGCGATATGGGTGTGCGTTTCTGATC
ATGCTCTCAGCCCCAACTGTGTTTTGCATGTCGTTTGTGGACTCAGCTGGAGGATACCTAGCAGTC
CGTTTCATGATTGGATTCTCTCTTGCAACG

FIGURE 8 (continued)

57/104

TTCGTGTCATGCCAGTACTGGATGAGCACAAATGTTTAAACAGCAAGATTATCGGACTCGTCAATGGA
 ACCGCAGCCGGTTGGGGCAATATGGGTGGAGGTGCAACTCAGCTCGTAATGCCCTTGGTCTACGAG
 CTCATTAAGCGAGCTGGTTCAACTTCATTCACTGCTTGGAGGATAGCATTTTTTGTCCCAGGATGG
 CTTTCATGTTATCATGGGAATCTTGGTCTTGAATCTAGGCCAAGACTTGCCTGATGGGAATCTCGGT
 GCCCTAAAGAAGAAGGGTGATGTTGCTAAAGATAAGTTCTCCAAGGTAAGTCTGGTATGCTGTTACA
 AACTATAGGACCTGGATCTTTGTCTTCTCTATGGCTACTCCATGGGAGTTGAATTATCCACCGAC
 AATGTTATCGCCGAGTACTTCTATAACAGGTTTCGATCTAAAGCTTCACACAGCAGGTGTCATTGCT
 GCTACCTTTGGTATGGCTAACCTTGTAGCTCGTCCCTTTGGTGGATATTTTTCTGATGTAGCAGCA
 AGGTACTTCGGGATGAGAGGCAGGTTATGGGTGCTCTGGATTTTACAGACACTTGGAGGAGTTTTC
 TGTACTTGGCTCGGTCGAGCTAATTCACCTTCCCTTGTCTGTACCGCTATGATTCTCTTCTCTATT
 GGAGCGCAAGCCGCATGTGGAGCAACTTTTGGTATCATTCCCTTTATTTCTCGACGATCATTTGGGC
 ATCATATCCGGCCTAACTGGTGCAGGTGGAAATTTTGGGTCCGGATTGACACAACTAGTATTCTTT
 TCGAGCTCAAGTTTGTCCACAGCTGCAGGTCTATCCTGGATGGGTGTCATGATTTGCGGCTGCACT
 CTCCCTGTGACATTGGTTTACTTCCACAATGGGGCGGCATGTTCTTTCCGCCTTCTAAAGACGTA
 GTGAAGTCAACAGAAGAATCCTATTATGCATCAGAGTGGGATGAGGACGAGAAGCAAAGGGGCATG
 CACCAGAAAAGCCTCAAGTTTGGCGAGAACAGCCGATCTGAACGTGGCAAGCGCATTGCCTCTGCA
 CCAACACCACCAAGTACCACACCAAACCGTGTGTAGATCAAAGCGTTGGCCATGCTTCTATAGTGC

SEQ ID NO: 98, *Populus tremula* x *Populus tremuloides* nitrate transporter (CAG26716)

MADVEGSPGSSMHGVTGREQSFAFSVASPTVPTDITAKFALPVDSEHKAKVFKIFSFANPHMRTFH
 LSWISFFTCFVSTFAAAPLVPIIRDNLNLTKSDIGNAGVASVSGSIFSRMLVMGAVCDLLGPRYGCA
 FLIMLSAPTVCMSFVDSAGGYLAVRFMIGFSLATFVSCQYWMSTMFSKIIIGLVNGTAAGWGNMG
 GGATQLVMPLVYELIKRAGSTSFSAWRIAFFVPGWLHVIMGILVLNLGQDLDPGNLGLKKGKDVA
 KDKFSKVLWYAVTNYRTWIFVLLYGYSMGVELSTDNVIAEYFYNRFDLKLHTAGVIAATFGMANLV
 ARPFGGYFSDVAARYFGRMRGLWVLWILQTLGGVFCTWLGRANSLPLAVTAMILFSIGAQAACGAT
 FGIIPFISRRSLGIIISGLTGAGGNFGSGLTQLVFFSSSSLSTAAGLSWMGVMICGCTLPVTLVYFP
 QWGGMFFPPSKDVVKSTEESSYYASEWDEDEKQGRMHQKSLKFAENSRSERGKRIASAPTPPSTTPN
 R

SEQ ID NO: 99, *Nicotiana tabacum* mRNA for high affinity nitrate transporter protein (nrt2.1 gene) (AJ557583)

TTAAAAAAAAAATGGGTGATATTGAGGGCGAACCAGGGAGTTCCATGCATGGAGTCACTGGTAGAG
 AGCCAGTTCTTGCTTTCTCAGTGGCTTCTCCGATGGTGCCAACTGATACCACTGCAAAATTTTTCAG
 TACCAGTTGATACTGAACACAAAGCCAAGATTTTTTAAGTTCTATTCAATTTTCAAAGCCACATGGTC
 TTACTTTCCAGCTCTCCTGGATTTCTTTCTTCACTTGTTTTGTTTCAACTTTTGCCGCTGCCCCTT
 TAGTTCCCTATCATTAGGGACAACCTTAATTTAACCAAAATGGATGTTGGTAATGCCGGAGTTGCTT
 CCGTTTCCGGAAGTATTTTATCTAGGCTTGTTATGGGTGCAGTTTGTGATATGTTAGGGCCAAGAT
 ATGGCTGTGCATTTCTGATTATGTTGTCAGCCCCAACTGTATTTTGCATGTCATTTGTGTCTGTCGG
 CTGGAGGATATGTTGCTGTCCGGTTCATGATCGGATTCTCGCTAGCAACATTTGTGTCTGTCGAAT
 ATTGGATGAGTACTATGTTTAATAGTCAGATTATAGGACTTGTCAATGGGACAGCTGCAGGATGGG
 GAAATATGGGTGGTGGTGGCGACTCAA

FIGURE 8 (continued)

58/104

CTTATTATGCCAATTGTGTATGATATAATAAGAAGAGCAGGAGCAACTCCATTCACTGCTTGGAGA
ATTGCATTTTTTCATTCCTGGCTGGCTTCATATTGTGATGGGTATTTTGGTGTGACTCTTGGCCAA
GATTTGCCTGATGGGAACCGTGGTGATTTACAGAAGAAGGGTGATGTTTCTAAAGATAAATTCTCC
AACATATTGTGGTACGCTGCAACAACTACAGGACGTGGATCTTTGTTCTTCTCTACGGATACTCT
ATGGGAGTTGAACTGTCTACAGACAACGTAATTGCGGAGTACTTCTTCGACAGATTTGATCTAAAG
CTTCACACAGCGGGAATTATTGCAGCGACCTTTGGTATGGCTAATTTATTAGCTCGTCCATTCGGA
GGATTTTCTTCAGATTACGCAGCCAAAAGATTTCGGCATGAGAGGCAGACTTTGGGTCCTTTGGATA
TTACAAACACTGGGAGGAGTATTCTGCGTCCTGTTGGGCCGTTCAAATCCTCTGCCCATAGCCGTC
ACATTCATGATCCTTTTCTCTATTGGTGCTCAAGCTGCATGTGGTGCAACATTCGGTATTATTCCA
TTCATTTCTCGCCGATCCTTAGGTATAATCTCAGGAATGACTGGGGCTGGAGGAAATTTCGGTTCT
GGATTGACACAACACTGTTGTTCTTCACGAGCTCAAATACTCGACAGCAACAGGGCTAACTTACATG
GGACTAATGATCATAGGATGCACTCTTCCAGTGACTTTCTGTCAATTTCCCACAATGGGGAAGTATG
TTTTTCCCACCAACGAAAGACCCTGTTAAGGGAAGTGAGGAACATTATTATGCCGCAGAGTATACC
GAAGCTGAGAGGCAGAAAGGTATGCACCAAAACAGCTTGAAGTTCGCCGAGAACTGCCGATCGGAG
CGTGGCAAGCGCGTGGGATCGGCACCTACTCCTCCAAATTTAACGCCTAATCGTGTCTGAGATCCC
G

SEQ ID NO: 100, *Nicotiana tabacum* high affinity nitrate transporter protein (CAD89798)

MGDIEGEPGSSMHGVTGREPVLAFSVASPMVPTDTTAKFSVPVDTEHKAKIFKFYSFSKPHGLTFQ
LSWISFFTCFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSGSILSRLVMGAVCDMLGPRYGCA
FLIMLSAPTVCMSFVSSAGGYVAVRFMIGFSLATFVSCQYWMSTMFNSQIIGLVNGTAAGWGNMG
GGATQLIMPVYDIIRRAGATPFTAWRIAFFIPGWLHIVMGILVLTGQDLDPGNRGDLQKKGDVS
KDKFSNWLWYAATNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFDLKLHTAGIIAATFGMANLL
ARPFGGFSSDYAAKRFGMRGRLWVLWILQTLGGVFCVLLGRSNPLPIAVTFMILFSIGAQAACGAT
FGIIPFISRRSLGIISGMTGAGGNFGSGLTQLLFFTSSKYSTATGLTYMGLMIIGCTLPVTFCHFP
QWGSMFPPPTKDPVKGSEEHYAAEYTEAERQKGMHQNSLKFAENCRSERGKRVGSAPTPPNLTPN
RV

SEQ ID NO: 101, *N.plumbaginifolia* mRNA for nitrate transporter Nrt2;1Np (Y08210)

TTCACTTTCAACATTTAATCAATCTTAGTGCTATCAGTTTATTTTCCTTAAGAAAAAATGGCTG
ATATTGAGGGAGAACCAGGGAGTTCTATGCATGGAGTCACTGGTAGAGAGCCAGTTCTTGCTTTCT
CAGTGGCTTCTCCAATGGTGCCAACTGATACCACTGCTAAATTTTTCAGTACCAGTTGATACTGAAC
ACAAAGCCAAGGTTTTTAAATTTTATTCATTTTCAAAGCCTCATGGACTTACTTTCCAGCTCTCCT
GGATTTCTTTCTTCACTTGTTTTGTATCAACTTTTGCTGCTGCTCCTTTAGTTCCTCTCATTAGGG
ACAACCTTAATTTAACCAAAATGGATGTTGGTAATGCCGGAGTTGCTTCCGTTTCTGGAAGTATTT
TATCTAGGCTTGTTATGGGTGCAGTTTGTGATATGTTAGGGCCAAGATACGGCTGTGCATTTCTGA
TTATGTTGTCAGCCCCAACTGTATTTTGTATGTCGTTTCGTGTCGTCGGCTGGAGGATATGTTGCTG
TCCGGTTCATGATCGGATTCTCGCTCGCAACATTTGTGTCGTGCCAATATTGGATGAGTACTATGT
TTAATAGTCAGATTATAGGACTTGTCAATGGAACAGCTGCTGGGTGGGGAAATATGGGTGGTGGTG
CGACTCAACTTATTATGCCAATTCTGTATGATATAATAAGAAAAGCAGGAGCAACTCCATTCACTG
CTTGGAGAATTGCATTTTTTCATTCCTGGCTGGCTTCATGTTGTAATGGGTATTTTGGTGTGACTC
TTGGTCAAGATTTG

FIGURE 8 (continued)

59/104

CCTGATGGAAACCGTGGTGATTTACAGAAGAAGGGTGGTGTCTTCTAAAGATAAATTCACCAACATA
TTGTGGTACGCTGCAACAACTACAGGACGTGGATCTTTGTCTTCTCTACGGATACTCTATGGGA
GTTGAACTGTCTACCGACAACGTAATTGCAGAGTACTTCTTCGACAGATTTGATCTAAAGCTTCAC
ACAGCGGGAATCATCGCAGCCACATTTGGTATGGCAAATTTATTAGCTCGTCCATTTCGGAGGGTTT
TCTTCAGATTTTCGACGCCAAAAGATTCGGCATGAGGGGTAGACTTTGGGTCTTTTGGATATTACAA
ACACTTGGAGGAGTATTCTGTGTCTGTGGGCCGTTCAAATCTCTGCCCATAGCTGTCACATTC
ATGATCCTTTTCTCAGTTGGTGCTCAAGCTGCATGTGGTGCAACATTCGGTATTATTCCCTTCATA
TCTCGTCGATCATTAGGTATAATCTCGGGAATGACTGGAGCTGGAGGCAATTTCCGTTCTGGATTG
ACACAACTGCTGTTTTTTCACAAGCTCAAAATACTCGACAGCAACAGGGCTAACTTATATGGGGATG
ATGATCATTGGATGCACTCTTCTGTGACACTATGTCATTTCCACAATGGGGAAGCATGTTTTTC
CCACCAACAAAAGATCCAGTTAAGGGAAGTGAGGAACATTATTATGCCGCAGAGTATACAGAAGCT
GAGAGGCAGAAAGGTATGCATCAAAACAGCTTGAAATTCGCCGAGAACTGTTCGATCGGAGCGTGGC
AAGCGCGTGGGATCGGCACCTACTCCTCCAAATTTAACGCCTAACCGTGTCTGAGTTTCTCAGATT
TGATAATTTTCTCTAAGGGGATGGATCATTGTCAATCTCTGATTGGATGAAGATTCAATGAGCTGA
GTCTCAATAAGCATATTATTTTTTAAAGAATGTATCTTTATTTTTCTTGTCTTTCTTCTTCTTCTT
CTTCTTTTTCTTGAATCTACTTATAAGTTTTATGTTTTTTTTTTTAAATGAAGTATATATATGAC
GCATTGTGTATCTTTCCTCTTGCTTTTTTACATCTGAATATTCGTATGAGCCAATGGGTTGTTGTAG
AATCAAAAGTAATATTAATAAACTTTTGACTTCCAAAAA

SEQ ID NO: 102, *Nicotiana plumbaginifolia* nitrate transporter (CAA69387)

MADIEGEPGSSMHGVTGREPVLAFSVASPMVPTDTTAKFSVPVDTEHKAKVFKFYFSKPHGLTFQ
LSWISFFTCTFVSTFAAAPLVPLIRDNLNLTKMDVGNAGVASVSGSILSRLVMGAVCDMLGPRYGCA
FLIMLSAPTVCMSFVSSAGGYVAVRFMIGFSLATFVSCQYWMSTMFNSQIIGLVNGTAAGWGNMG
GGATQLIMPILYDIIRKAGATPFTAWRIAFFIPGWLHVVMGILVLTGQDLPDGNRGDLQKGGVS
KDKFTNILWYAATNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFDLKLHTAGIIAATFGMANLL
ARPFGGFSSDFAAKRFGMRGRLWVLWILQTLGGVFCVLLGRNSLPIAVTFMILFSVGAQAACGAT
FGIIPFISRRSLGIIISGMTGAGGNFGSGLTQLLFFTSSKYSTATGLTYMGMMIIGCTLPVTLCHFP
QWGSMMFFPPTKDPVKGSEEHYAAEYTEAERQKGMHQNSLKFAENCRSERGKRVGSAPTTPNLT
PNRV

SEQ ID NO: 103, *Lycopersicon esculentum* putative high-affinity nitrate transporter (NRT2;1) mRNA, complete cds (AF092655)

TATTCTCAATACATTTCAAATCAATCATTTATAAAATTAACCAGTTATTTCTCAATTGAAGAAAT
GGCTGATGTAGAAGGATCACCGGGGAGTTCTATGCATGGAGTCACCGGAAGAGAACCTGTTCTCGC
TTTCTCCGTGGCTTCTCCAATGGTGCCTACGGATACCTCCGCCAAATTTTTCAGTACCGGTGGACAC
TGAACACAAGGCTAAACAATTTAAGTTTTATTTCGTTTTTCGAAGCCTCATGGACTTACGTTCCAGCT
CTCCTGGATCTCCTTTTTTCACTTGTTCGTTTCGACTTTTGCTGCTGCACCTTTAGTTCCTATTAT
TAGGGACAATCTTAATTTGACAAAAATGGATGTTGGTAACGCTGGGGTTGCTTCCGTATCCGGAAG
TATTTTATCTAGGCTTACGATGGGTGCGGTTTGTGATTTGTTGGGTCCAAGGTATGGGTGCGCTTT
TCTTATCATGTTGTCAGCGCCAACGTGTTTTTGTATGTCTTTTGTTCATCCGCTGGTGGCTACGT
AGCTGTCCGGTTCATGATTGGGTTTTTCGCT

FIGURE 8 (continued)

60/104

CGCAACGTTTGTGTCTTGTCAATATTGGATGAGTACTATGTTTAAATAGTAAGATCATAGGGCTAGT
GAACGGAACGGCTGCTGGATGGGGTAATATGGGTGGAGGTGCAACTCAACTCATTATGCCACTTTT
GTATGATATAATTCTGAAGGGCGGGTGCAACTCCGTTCACTGCTTGGAGAATTGCATTTTTTATTCC
TGGATGGCTTCATGTGGTGATGGGTATTTTAGTGTTGACTCTTGGCCAAGATTTACCCGACGGAAA
TCGTGGCACTTTACAGAAGACGGGTACTGTTGCTAAAGATAAAATTCGGTAACATATTGTGGTATGC
TGCAACAAACTACAGGACATGGATCTTTGTTCTTCTCTATGGATACTCTATGGGAGTTGAACTGTC
AACAGACAACGTCATTGCTGAGTACTTCTTCGACAGATTTGATCTAAAGCTTAGCACAGCGGGGAT
CATTGCTGCCACATTTGGTATGGCTAACCTTTTGGCTCGACCATTTGGAGGATTTTCTTCTGATTA
CGCAGCAAAGAAATTCGGTATGAGAGGGGAGACTTTGGGTTTTGTGGATTTTACAAACACTTGAGAG
AGTATTTTGTGTTCTTTTGGGTCGTTCTGAATTCTCTACCACTTGCGGTAACCTTTATGATCCTTTT
CTCAATCGGAGCTCAAGCTGCTTGTGGTGCAACTTTTGGTATTATTCCATTCATTTCTCGACGATC
GTTAGGAATTATAAGCGGAATGACAGGGGCAGGTGGAAATTTTGGTTCTGGATTGACTCAATTGTT
GTTTTTTCACGAGCTCAAAGTACTCGACAGCGACAGGGTTAACTTACATGGGATTCATGATCATAGG
ATGCACTCTTCTGTTACATTTTGTCAATTTCCCACAATGGGGAAGCATGTTTTTGCCACCAACAAA
AGATCCAGTCAAGGGAACGGAAGAACATTATTATACTTCAGAGTACACAGAGGCCGAGAGGCAAAA
AGGGATGCACCAAAACAGCTTGAAATTCGCTGAAAATTGCCGATCAGAGCGTGGTAAGCGTGTTGG
TTCCGCACCAACCCACCAAATTTGACACCAAATCGTGTTTGATGATCTTTATGAGGAATGGATAG
TCTTGAATCTGTGATTTAAATTTAAGGTTCAATGTGCTGAGTCGTCTCAATAAGCAAAATCTATCT
TGATTTTTCTTCTTTGTTTTTTTTTATAATGATATTGCTTGTGATCTTTC
CAGACAAATACCTTGAATCCACGAAGGTGTATGCTTTTTTTTTTAATGAAGTATATATAATATATTA
CTCATTGTGTATGTTTTCTATTGCTTTTTTCAAAAGAATATTCTATGGCCAATGGTGGTTGTGTTT
TACTCTGTAGATTCAAAAGTGTATTATAATAAACTCTTGACTTGTAAGAAGGGGACTGATCATTT
ATTCCAGTTGATTTATAGAAAGTTCGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 104, *Lycopersicon esculentum* putative high-affinity nitrate transporter (AAF00053)

MADVEGSPGSSMHGVTGREPVLAFSVASPMVPTDTSKFSVPVDTEHKAKQFKFYSFSKPHGLTFQ
LSWISFFTCTFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSGSILSRLTMGAVCDLLGPRYGCA
FLIMLSAPTVCMSFVSSAGGYVAVRFMIGFSLATFVSCQYWMSTMFSKII GLVNGTAAGWGNMG
GGATQLIMPLLYDIIRRAGATPFTAWRIAFFIPGWLHVVMGILVLTGLQDLDPDGNRGT LQKTGTVA
KDKFGNIIWYAATNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFDLKLSTAGIIAATFGMANLL
ARPFGGFSSDYAAKKFGMRGRLWVLWILQTLGGVFCVLLGRSNSLPLAVTFMILFSIGAQAACGAT
FGIIPFISRRSLGII SGMTGAGGNFGSGLTQLLFFTSSKYSTATGLTYMGFMIIGCTLPVTFCHFP
QWGSMLPPTKDPVKGTEEHYYTSEYTEAERQKGMHQNSLKFAENCRSERGKRVGSAPT PPNLTPN
RV

SEQ ID NO: 105, *Arabidopsis thaliana* trans-membrane nitrate transporter protein AtNRT2:1 mRNA, complete cds (AF093754)

AGTGTGAGTAATTTAGCTTGAATCAAATCTCAAACCTTGCAAAGAACTTGAAATATTTTATAACAA
TGGGTGATTCTACTGGTGAGCCGGGGAGCTCCATGCATGGAGTCACCGGTAGAGAACAAAGCTTTG
CATTCTCGGTGCAATCACCAATTGTGCATACCGACAAGACGGCCAAGTTCGACCTTCCGGTGGACA
CAGAGCATAAGGCAACGGTTTTCAAGCTCTTCTCCTTCGCCAACCTCAC

FIGURE 8 (continued)

61/104

ATGAGAACGTTCCATCTCTCGTGGATCTCTTTCTCCACATGTTTTGTCTCGACTTTCGCAGCTGCA
CCACTTGTCCCTATCATCCGGGAGAATCTCAACCTCACCAAACAAGACATTGGAAACGCCGGAGTT
GCCTCTGTCTCTGGGAGTATCTTCTCTAGGCTCGTGATGGGAGCCGTGTGTGATCTTTTGGGTCCC
CGTTACGGTTGTGCCTTCCTTGTGATGTTGTCTGCCCCAACGGTGTTCTCCATGAGCTTCGTGAGT
GACGCAGCAGGCTTCATAACGGTGAGGTTTCATGATTGGTTTTTGCCTGGCGACGTTTGTGTCTTGT
CAATACTGGATGAGCACTATGTTCAACAGTCAGATCATTGGTCTGGTGAATGGGACAGCAGCCGGA
TGGGGAAACATGGGTGGCGGCATAACGCAGTTGCTCATGCCCATTTGTGTATGAAATCATTAGGCGC
TGCGGTTCCACAGCCTTCACGGCCTGGAGGATCGCCTTCTTTGTACCCGGTTGGTTGCACATCATC
ATGGGAATCTTGGTGCTCAATCTAGGTCAAGATCTGCCAGATGGAAATCGAGCTACCTTGGAGAAA
GCGGGAGAAGTTGCCAAAGACAAATTCGGAAAGATTCTGTGGTATGCCGTTACAACTACAGGACT
TGGATCTTCGTTCTTCTCTACGGATACTCCATGGGAGTTGAGTTGAGCACTGATAATGTTATCGCC
GAGTACTTCTTTGACAGGTTTCACTTGAAGCTCCACACAGCAGGGCTCATAGCAGCATGTTTCGGA
ATGGCCAATTTCTTTGCTCGTCCAGCAGGAGGCTACGCATCTGACTTTGCAGCCAAGTACTTCGGG
ATGAGAGGGAGGTTGTGGACGTTGTGGATCATACAGACGGCTGGTGGCCTCTTCTGTGTGTGGCTC
GGCCGCGCCAACACCCTTGTAAGTCCCGTTGTGGCTATGGTGCTCTTCTCTATGGGGGCACAAGCT
GCTTGCGGAGCCACCTTTGCAATTGTGCCCTTTGTCTCCCGCGAGCTCTAGGCATCATCTCGGGT
TTAACCGGGGCTGGAGGGAACCTTTGGATCAGGGCTCACACAACCTCTTCTTCTCGACCTCACAC
TTCACAACCTGAACAAGGGCTAACGTGGATGGGAGTGATGATAGTCGCTTGCACGTTACCTGTGACC
TTAGTTCACCTTCTCAATGGGGAAGCATGTTCTTGCCCTCTTCCACAGATCCAGTGAAAGGTACA
GAGGCTCATTATTATGTTCTGAGTGGAATGAGCAGGAGAAGCAGAAGAACATGCATCAAGGAAGC
CTCCGGTTTTGCCGAGAACGCCAAGTCAGAGGGTGAGCGCCGCGTCCGCTCTGCTGCTACGCCGCCT
GAGAACACACCCAACAATGTTTGATCATACTTCCACCCACGGTGGAATGGTGAAGGATGATCGCA
TATAAGAATATGTACACAGTGAAAAAATAATGCAAATGTTATCAATGCTTGATAACATTACT
ATCTATCTTTTCACTTACTAAACAAACCTTTTGCTTTTTTGCTTGAAATCTTTTTATTATATATCAA
AATATATCTCTATGTCTTGAGGTTTGATTATTTTGCATATATCATTAAATGATTGATAATATTGGA
ACTG

SEQ ID NO: 106, *Arabidopsis thaliana* trans-membrane nitrate transporter protein AtNRT2:1 (AAC64170)

MGDSTGEPGSSMHGVTGREQSFAFSVQSPIVHTDKTAKFDLPVDTEHKATVFKLFSFAKPHMRTFH
LSWISFSTCFVSTFAAAPLVPIIRENLNLTKQDIGNAGVASVSGSIFSRMLVMGAVCDLLGPRYGCA
FLVMLSAPTIVFSMSFVSDAAGFITVRFMIGFCLATFVSCQYWMSTMFNSQIIIGLVNGTAAGWGNMG
GGITQLLMPIVYEIIIRRCGSTAFTAWRIAFFVPGWLHIIMGILVLNLGQDLDPDGNRATLEKAGEVA
KDKFGKILWYAVTNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFHLKLHTAGLIAACFGMANFF
ARPAGGYASDFAAKYFGMRGRLWTLWIIQTAGGLFCVWLGRANTLVTAVVAMVLFMSGAQAACGAT
FAIVPFSRRALGIIISGLTGAGGNFGSGLTQLLFFSTSHFTTEQGLTWMGVMIVACTLPVTLVHFP
QWGSMLPSTDPVKGTEAHYYGSEWNEQEKQKNMHQGSRLFAENAKSEGRRVRSATPPENTPN
NV

SEQ ID NO: 107, *Lycopersicon esculentum* putative high-affinity nitrate transporter (NRT2;2) mRNA, complete cds (AF092654)

TTTCAAATCAATCATTTATAAAATTAACCAGTTATTTCTCAATTGAAGAAATGACTGATGTAGAA
GGATCACCGGGGAGTTCTATGCATGGAGTCACCGGAAGAGAACCTGTTCTCGCTTTCT

FIGURE 8 (continued)

62/104

CCGTGGCTTCTCCAATGGTGCCTACGGATACCTCCGCCAAGTTTTTCAGTACCGGTGGATACTGAAC
ACAAGGCTAAACAATTTAAGTTTTATTTCGTTTTTCGAAGCCTCATGGACTTACGTTCCAGCTCTCCT
GGATCTCCTTTTTCACTTGTTTCGTTTCGACTTTTGCTGCTGCACCTTTAGTTCCTATTATTAGGG
ACAATCTTAATTTGACAAAAATGGATGTCGGTAACGCTGGGGTTGCTTCCGTATCCGGAAGTATTT
TATCTAGGCTTACGATGGGTGCGGTTTGTGATTTGTTGGGTCCAAGGTATGGGTGCGCTTTTCTTA
TCATGTTGTCGGCCCCAACTGTTTTTTGTATGTCCTTTGTTTCATCCGCTGGTGGCTACGTAGCCG
TCCGGTTCATGATTGGGTTTTCCCTCGCAACGTTTGTGTGCTGTCAATATTGGATGAGTACTATGT
TTAATAGTAAGATCATAGGGCTAGTGAACGGAACGGCTGCTGGATGGGGTAATATGGGTGGAGGTG
CAACTCAACTCATTATGCCACTTTTGTATGATATAATTCGGAGGGCGGGTGCAATTCCGTTCACTG
CTTGGAGAATTGCATTTTTTATTCCCTGGATGGCTTCATGTGGTGATGGGTATTTTAGTGTTGACTC
TTGGCCAAGATTTACCCGACGGAAATCGTGGCACTTTACAGAAGACGGGTACTGTTGCTAAAGATA
AATTCGGTAACATATTGTGGTATGCTGCAACAACTACAGGACATGGATCTTTGTTCTTCTCTATG
GATACTCTATGGGAGTTGAACTGTCAACAGACAACGTCATTGCTGAGTACTTCTTCGACAGATTTG
ATCTAAAGCTTAGCACAGCGGGGATCATTGCTGCCACATTTGGTATGGCTAACCTTTTGGCTCGAC
CATTTGGAGGATTTTCTTCTGATTACGCAGCAAAGAAATTCGGTATGAGAGGGAGACTTTGGGTTT
TGTGGATTTTACAAACACTTGGAGGAGTATTTTGTGTTCTTTTGGGTGCTTCGAATTCTCTACCAC
TTGCTGTAACCTTTATGATCCTTTTCTCAATCGGAGCTCAAGCTGCTTGTGGTGCAACTTTTGGTA
TTATTCCATTCAATTTCTCGACGATCGTTAGGAATTATAAGCGGAATGACAGGGGCAGGTGGAAATT
TTGGTTCTGGATTGACTCAATTGTTGTTTTTACGAGCTCAAAGTACTCGACAGCGACAGGGTTAA
CTTACATGGGATTCATGATCATAGGATGCACTCTTCCTGTTACATTTTGTCAATTTCCCACAATGGG
GAAGCATGTTTCTCCCAACCAACAAAAGATCCAGTCAAGGGAACGGAAGAACATTATTATACTTCAG
AGTACACAGAGGCAGAGAGGCAAAAAGGGATGCACCAAAACAGCTTGAAATTCGCTGAAAATTGCC
GATCGGAGCGTGGTAAGCGCGTTGGTTCCGCACCCACTCCACCAAATTTGACACCAAACCGTGTCT
GATCGGATTGATGATCGTCAATCTTTAGTTCAATGAGCTGAGTTGTTTCAATAAGCAAAATAAGTC
CTGATTTTTTTTTCTTCTTTCTTTTTTTGTTTTTTCTTAAATGATGTTGCTTGTCAATACGCTGGA
ATCTACTAAGGTGTATGTGGTTTTAAATTTACGTATATATAATATATATATATATATATATTACAC
ATTTTAATGTTAAAAAAAAAAAAAAAAAAAAA

**SEQ ID NO: 108, *Lycopersicon esculentum* putative high-affinity
nitrate transporter (AAF00054)**

MTDVEGSPGSSMHGVTGREPVLAFSVASPMVPTDTSAKFSVPVDTEHKAKQFKFYSFSKPHGLTFQ
LSWISFFTCTFVSTFAAAPLVPIIRDNLNLTKMDVGNAGVASVSGSILSRLTMGAVCDLLGPRYGCA
FLIMLSAPTVCMSFVSSAGGYVAVRFMIGFSLATFVSCQYWMSTMFNSKIIGLVNGTAAGWGNMG
GGATQLIMPLLYDIIRRAGAIPTAWRIAFFIPGWLHVVMGILVLTGQDLDPDGNRGTGKTGTVA
KDKFGNILWYAAATNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFDLKLSTAGIIAATFGMANLL
ARPFGGFSSDYAAKKFGMRGRLWVLWILQTLGGVFCVLLGRSNSLPLAVTFMILFSIGAQAACGAT
FGIIPFISRRSLGIIISGMTGAGGNFGSGLTQLLFFTSSKYSTATGLTYMGFMIIGCTLPVTFCHFP
QWGSMLPPTKDPVKGTEEHYYTSEYTEAERQKGMHQNLSLKFAENCRSERGKRVGSAPTPPNLT
PNRV

FIGURE 8 (continued)

63/104

SEQ ID NO: 109, Brassica napus mRNA for high-affinity nitrate transporter (nrt2 gene) (AJ293028)

CACATTCTTGTGAAAGAACTTAAACATTTTGCATCAATGGGTGATTCTACTGGCGAGCCGGGAAGC
TCCATGCATGGAGTGACCGGTAGAGAACAAACATTTGCTTTCTCGGTGGCTTCACCGATTGTCCCA
ACCGACAAGACAGCAAAGTTCGACCTGCCGGTGGACTCGGAGCATAAGGCAACGGTTTTTCAAGCTC
TTCTCCTTCGCCAAACCTCACATGCGAACGTTCCATCTCTCGTGGATCTCTTTCTCCACGTGTTTT
GTCTCGACGTTTGCGGCTGCACCACTTGTCCCCATCATCCGAGAGAATCTCAACCTCACGAAACAA
GACATCGGTAACGCAGGAGTTGCGTCCGTCTCGGGGAGTATCTTCTCTAGGCTGGTGATGGGAGCA
GTGTGTGATCTTCTCGGTCCACGTTACGGCTGTGCCCTTCCTTGTTATGCTTTCCGCACCAACGGTG
TTCTCAATGAGCTTCGTGAGTGGAGCCGCAGGATTCATAACGGTGAGGTTTCATGATTGGGTTCTGT
CTAGCAACGTTTGTGTCTTGTCAATATGGAATGAGTACTATGTTCAATAGTCAGATCATCGGTCTG
GTGAACGGTACAGCCGCCGGGTGGGGAAACATGGGTGGTGGCATAACGCAGTTGCTCATGCCGGTT
GTCTATGAGATCATAAGGCGCTGTGGTGCAACAGCGTTCACGGCCTGGAGGCTTGCCCTTCTTCGTC
CCTGGTTGGTTGCACATCATCATGGGAGTCTTGGTGCTCAATCTAGGTCAAGATTTGCCAGATGGT
AACCGAAGTGCCTTGGAGAAAAAGGGAGAAGTTGCCAAAGACAAATTCGAAAGATTATGTGGTAC
GCCGTCACAACTACAGGACTTGGATCTTTGTTCTTCTCTATGGATACTCCATGGGAGTTGAGCTG
AGCACTGACAATGTTATCGCCGAATACTTCTTTGACAGGTTCCACTTGAAGCTTCACACAGCTGGA
ATCATAGCAGCATGTTTCGGAATGGCCAACTTCTTTGCTCGTCCAGCAGGAGGCTATGCATCTGAC
CTTGACGCCAAATACTTCGGGATGAGAGGGAGGTTATGGGCGTTGTGGATCATTCAGACAGCAGGT
GGTGTCTTCTGCGTGTGGCTCGGCCGTGCCAACACCCTCGTTACTGCCGTTGTAGCTATGGTCCTC
TTCTCTTTAGGAGCACAAGCCGCTTGTGGAGCCACCTTCGCAATCGTTCCCTTTGTTTCTCGGCGA
GCCCTTGGTATCATCTCAGGTTTAACCGGTGCTGGAGGAACTTTGGGTGAGGCTCACACAGCTC
ATCTTCTTCTCGACCTCAAGGTTCAACAACGAACAAGGGCTAACATGGATGGGAGTGATGATAGTT
GCCTGCACGTTGCCTGTGACTTTAATCCACTTCCCTCAGTGGGGAAGCATGTTCTTGCCCTCCTTCT
ACCGATCCAGTCAAAGGTCCGAAGGAGCACTATTATGCTTCAGAGTGGAATGAGCAGGAGAAGGAG
AAGAACATGCATCAGGGAAGCCTCAGGTTTGCTAAGAACGCCAAGTCTGAGGGCGGCCGCCGTGTC
CGTTCTGCTGCTACCCCGCTGAGAACACACCAAACAATGTTTGATCATAACAGCCACAAGGAAAG
TGTGAAGGATGGTCGCAGATAAGAATTTATATGTCCACAGTGAAAACAAATGCGTATGTTATCAA
TGCTTGCTGGACGTTATTTGTTGTGTATCTTTCTTTTTTTTCACTGAAGAAACATTTGTTTTGTTTA
CGGCTTCAAGAAATATTTTTCTAATCAAAATGTCTACCTCTTGCGACATT

SEQ ID NO: 110, Brassica napus high-affinity nitrate transporter (CAC05338)

MGDSTGEPGSSMHGVTGREQTFAFSVASPIVPTDKTAKFDLPVDSEHKATVFKLFSFAKPHMRTFH
LSWISFSTCFVSTFAAAPLVPIIRENLNLTKQDIGNAGVASVSGSIFSR LVMGAVCDLLGPRYGCA
FLVMLSAPT VFSMSFVSGAAGFITVRFMIGFCLATFVSCQYGMSTMFNSQIIIGLVNGTAAGWGNMG
GGITQLLMPVVYEIIIRRCGATAFTAWRLAFFVPGWLHIIMGVLVLNLGQDLDPDGNRSALKKGEVA
KDKFGKIMWYAVTNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFHLKLHTAGIIAACFGMANFF
ARPAGGYASDLAAKYFGMRGRLWALWIIQTAGGVFCVWLGRANTLVTAVVAMVLFSLGAQAACGAT
FAIVPFSRRALGIIISGLTGAGGNFGSGLTQLIFFSTSRFTTEQGLTWMGVMIVACTLPVTLIHFP
QWGSNFLPPSTDPVKGPKEHYAYASEWNEQEKEKNMHQGS LRFKNAKSEGRRVRSAAATPPENTPN
NV

FIGURE 8 (continued)

64/104

SEQ ID NO: 111, Arabidopsis thaliana putative high-affinity nitrate transporter (At5g60770) mRNA, complete cds (DQ056732)

ATG GCCGATGGTTTTGGTGAACCGGGAAGCTCAATGCATGGAGTCACCGGCAGAGAACAAAGCTAT
GCATTCTCTGTGCGAGTCTCCGGCAGTTCCTTCCGACTCATCAGCAAAATTTTCTCTCCCCGTGGAC
ACCGAACACAAAGCCAAAGTCTTCAAACCTTATCCTTTGAAGCTCCACATATGAGAACTTTCCAT
CTTGCTTGATCTCATTTCTTCACTTGCTTCATTTCCACTTTTCGCTGCTGCTCCTCTTGTCCCCATC
ATTAGAGATAACCTTAATCTCACAAGACAAGATGTCGGAAATGCTGGTGTGCTTCTGTCTCTGGC
AGTATCTTCTCTAGGCTTGTTATGGGAGCAGTTTGTGATCTCCTTGGGCCACGTTATGGCTGTGCT
TTCCTCGTCATGCTCTCTGCTCCAACCGTCTTCTCCATGTCTTTCGTTGGTGGTGCCGGAGGGTAC
ATAACGGTGAGGTTTCATGATCGGGTCTGCCTGGCGACTTTCGTGTCATGCCAGTATTGGATGAGC
ACAATGTTCAATGGTCAGATCATAGGTCTAGTGAACGGGACAGCGGCAGGGTGGGGGAACATGGGC
GGTGGGGTCACTCAGTTGCTCATGCCAATGGTCTATGAGATCATCCGACGGTTAGGGTCCACGTCC
TTCACCGCATGGAGGATGGCTTTCTTCGTCCCCGGGTGGATGCACATCATCATGGGGATCTTGGTC
TTGACTCTAGGGCAAGACCTCCCTGATGGTAATAGAAGCACACTCGAGAAGAAAGGTGCAGTTACT
AAAGACAAGTTCTCAAAGGTTTTATGGTACGCGATCACGAACTATAGGACATGGGTTTTCTGTGCTG
CTATATGGATACTCCATGGGAGTAGAGCTCACAACCGATAACGTCATCGCTGAGTACTTTTTCGAC
AGGTTCCATCTTAAGCTTCATACCGCCGGTATAATCGCGGCAAGCTTTGGTATGGCAAACCTTCTTT
GCCCCGTCCTATTGGTGGTTGGGCCTCAGATATTGCGGCTAGACGCTTCGGCATGAGAGGCCGTCTC
TGGACCCATATGGATCATCAAACCTTAGGCGGTTTCTTCTGCCTATGGCTAGGCCGAGCCACCACG
CTCCCGACCGCGGTTGTCTTCATGATCCTCTTCTCTCTCGGCGCTCAAGCCGCTTGTGGAGCTACC
TTTGCTATCATACCTTTCATCTCACGCCGCTCCTTAGGGATCATCTCTGGTCTTACTGGAGCTGGT
GGAAACTTCGGCTCTGTTTTGACCCAACTCGTATTCTTCTCGACCTCAACGTTCTCCACGGAACAA
GGGCTGACATGGATGGGGGTGATGATTATGGCGTGATACATTACCCGTCACCTTAGTGCACCTCCCG
CAATGGGGAAGCATGTTTTTGCCTTCCACGGAAGATGAAGTGAAGTCTACGGAGGAGTATTATTAC
ATGAAAGAGTGACAGAGACCGAGAAGCGAAAGGGTATGCATGAAGGGAGTTTGAAGTTCGCCGTG
AATAGTAGATCGGAGCGTGGACGGCGCGTGGCTTCTGCACCGTCTCCTCCGCCGGAACACGTTTAA

SEQ ID NO: 112, Arabidopsis thaliana putative high-affinity nitrate transporter (AAY78876)

MADGFGEPEGSSMHGVTGREQSYAFSVESPAVPSDSSAKFSLPVDTEHKAKVFKLLSFEAPHMRTFH
LAWISFFTCFISTFAAAPLVPIIRDNLNLTRQDVGNAGVASVSGSIFSR LVMGAVCDLLGPRYGCA
FLVMLSAPT VFSMSFVGGAGGYITVRFMIGFCLATFVSCQYWMSTMFNQI IGLVNGTAAGWGNMG
GGVTQLLMPMVYEIIRRLGSTSFTAWRMAFFVPGWMHIIMGILVLT LGQDLPDGNRSTLEKKGAVT
KDKFSKVLWYAITNYRTWVFVLLYGYSMVELTTDNVIAEYFFDRFHLKLHTAGI IAASFGMANFF
ARPIGGWASDIAARRFGMRGRLWTLWIIQTLGGFFCLWLGRATTLPTAVVFMI LFSLGAQAACGAT
FAIIPFISRRSLGIISGLTGAGGNFGSGLTQLVFFSTSTFSTEQGLTWMGMIMACTLPVTLVHFP
QWGS MFLPSTEDVKSTEEYYYMKEWTETEKRKGMHEGSLKFAVNSRSERGRRVASAPSPPEHV

FIGURE 8 (continued)

65/104

SEQ ID NO: 113, *Arabidopsis thaliana* high-affinity nitrate transporter (ACH2) (At1g08100) mRNA, complete cds (NM_100685)

AAACTTGAATTTTCTCAAAGGAACTTGATACGTTTAAAATACATGGGTTCTACTGATGAGCCCGGA
AGTTCCATGCATGGAGTTACCGGTAGAGAACAGAGCTATGCTTTCTCGGTAGATGGTAGTGAGCCG
ACCAACACAAAGAAAAAGTACAATCTGCCGGTGGACGCGGAGGATAAGGCAACGGTTTTCAAGCTC
TTCTCCTTCGCCAAACCTCACATGAGAACGTTCCACCTCTCGTGGATCTCTTTCTCCACATGTTTT
GTTTCGACGTTTCGACGCTGCACCACTTATCCCGATCATCAGGGAGAATCTTAACCTCACCAAACAT
GACATTGGAAACGCTGGAGTTGCCTCCGTCTCGGGGAGTATCTTCTCTAGGCTCGTGATGGGAGCC
GTGTGTGATCTTTTGGGTCCTCGTTACGGTTGTGCCTTCCTTGTGATGTTGTCTGCCCCAACGGTG
TTCTCCATGAGCTTCGTGAGTGACGCAGCAGGCTTCATAACGGTGAGGTTTCATGATTGGTTTTTGC
CTGGCGACGTTTGTGTCTTGTCAATACTGGATGAGCACTATGTTCAACAGTCAGATCATCGGTCTG
GTGAACGGGACAGCAGCCGGATGGGGAAACATGGGTGGCGGCATAACGCAGTTGCTCATGCCCAT
GTGTATGAAATCATTAGGCGCTGCGGATCAACAGCGTTACGGCCTGGAGGATCGCCTTCTTTGTC
CCCGGTTGGTTGCACATCATCATGGGAATCTTGGTGCTCACGCTAGGTCAAGATCTGCCAGGTGGA
AACAGAGCTGCCATGGAGAAAGCGGGAGAAGTTGCCAAAGACAAATTCGAAAGATTCTATGGTAC
GCCGTTACAAATTACAGGACTTGGATTTTCGTTCTTCTGTATGGATATTCATGGGAGTTGAGTTA
AGCACAGACAATGTTATCGCCGAGTACTTCTTTGATAGGTTTCACTTGAAGCTTCACACAGCGGGG
ATTATAGCAGCATGTTTCGGAATGGCCAATTTCTTTGCTCGTCCAGCAGGAGGCTGGGCATCTGAC
ATTGCAGCCAAGCGCTTCGGAATGCGAGGGAGGTTGTGGACTTTGTGGATCATTCAGACGTCCGGT
GGTCTCTTTTGTGTGTGGCTCGGACGTGCCAACACCCTCGTCACTGCCGTTGTATCTATGGTCCTC
TTCTCTTTAGGAGCACAAGCCGCTTGCGGAGCCACCTTTGCTATCGTGCCCTTTGTCTCCCGGCGA
GCTCTAGGCATTATCTCGGGTTTAAACGGGGCTGGAGGGAACCTTTGGGTGAGGACTCACACAGCTC
GTCTTTTTTCTCGACTTCGCGCTTCACAACCTGAAGAAGGGCTAACGTGGATGGGAGTGATGATAGTT
GCTTGACAGTTGCCTGTTACCTTAATCCACTTTTCCTCAGTGGGGAAGCATGTTCTTCCCTCCTTCC
AACGATTCGGTCGACGCTACGGAGCACTATTATGTTGGCGAATATAGTAAGGAGGAGCAGCAGATT
GGCATGCATTTAAAAGCAAACCTGTTTGCTGATGGAGCCAAGACCGAGGGAGGCAGCAGCGTCCAC
AAAGGGAACGCAACCAACAATGCTTGATCATGTGTGATTGATATCAAGAAATTAATAATTTCACTT
ATGTGAAATGGACATAAACTGTTGGAAAATAAGAACCATTTCTTTCATCATTTGCTTT

SEQ ID NO: 114, *Arabidopsis thaliana* high-affinity nitrate transporter (ACH2) (NP_172289)

MGSTDEPGSSMHGVTGREQSYAFSVDGSEPTNTKKKYNLPVDAEDKATVFKLFSFAKPHMRTFHLS
WISFSTCFVSTFAAAPLIPIIRENLNLTKHDIGNAGVASVSGSIFSRLVMGAVCDLLGPRYGCAFL
VMLSAPT VFSMSFVSDAAGFITVRFMIGFCLATFVSCQYWMSTMFNSQIIGLVNGTAAGWGNMGGG
ITQLLMPIVYEIIRRCGSTAFTAWRIAFFVPGWLHIIMGILVLTGQDLPGGNRAAMEKAGEVAKD
KFGKILWYAVTNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFHLKLHTAGIIAACFGMANFFAR
PAGGWASDIAAKRFGMRGRLWTLWIIQTSGLFCVWLGRANTLVTAVVSMVLFSLGAQAACGATFA
IVPFVSRRALGIISGLTGAGGNFGSGLTQLVFFSTSRFTTEEGLTWMGVMIVACTLPVTLIHFPQW
GSMFFPPSNDSDATEHYVGEYSKEEQQIGMHLKSKLFADGAKTEGGSSVHKGNATNNA

FIGURE 8 (continued)

66/104

SEQ ID NO: 115, *Arabidopsis thaliana* high-affinity nitrate transporter ACH2 variant mRNA, complete cds (AF019749)

AAACTTGAATTTTCTCAAAGGAACTTGATACGTTTAAAATACATGGGTTCTACTGATGAGCCCAGA
AGTTCCATGCATGGAGTTACCGGTAGAGAACAGAGCTATGCTTTCTCGGTAGATGGTAGTGAGCCG
ACCAACACAAAGAAAAAGTACAATCTGCCGGTGGACGCGGAGGATAAGGCAACGGTTTTCAAGCTC
TTCTCCTTCGCCAAACCTCACATGAGAACGTTCCACCTCTCGTGGATCTCTTTCTCCACATGTTTT
GTTTCGACGTTTCGACGCTGCACCACTTATCCCGATCATCAGGGAGAATCTTAACCTCACCAACAT
GACATTGGAAACGCTGGAGTTGCCTCCGTCTCGGGGAGTATCTTCTCTAGGCTCGTGATGGGAGCC
GTGTGTGATCTTTTGGGTCTCGTTACGGTTGTGCCTTCCTTGTGATGTTGTCTGCCCCAACGGTG
TTCTCCATGAGCTTCGTGAGTGACGCAGCAGGCTTCATAACGGTGAGGTTTCATGATTGGTTTTTGC
CTGGCGACGTTTGTGTCTTGTCAATACTGGATGAGCACTATGTTCAACAGTCAGATCATCGGTCTG
GTGAACGGGACAGCAGCCGGATGGGGAAACATGGGTGGCGGCATAACGCAGTTGCTCATGCCATT
GTGTATGAAATCATTAGGCGCTGCGGATCAACAGCGTTACGGCCTGGAGGATCGCCTTCTTTGTC
CCCGGTTGGTTGCACATCATCATGGGAATCTTGGTGCTCACGCTAGGTCAAGATCTGCCAGGTGGA
AACAGAGCTGCCATGGAGAAAGCGGGAGAAGTTGCCAAAGACAAATTCGGAAGATTCTATGGTAC
GCCGTTACAAATTACAGGACTTGGATTTTCGTTCTTCTGTATGGATATTCATGGGAGTTGAGTTA
AGCACAGACAATGTTATCGCCGAGTACTTCTTTGACAGGTTTCACTTGAAGCTTCACACAGCGGGG
ATTATAGCAGCATGTTTCGGAATGGCCAATTTCTTTGCTCGTCCAGCAGGAGGCTGGGCATCTGAC
ATTGCAGCCAAGCGCTTCGGAATGCGAGGGAGGTTGTGGACTTTGTGGATCATTCAGACGTCCGGT
GGTCTCTTTTGTGTGTGGCTCGGACGTGCCAACACCCTCGTCACTGCCGTTGTATCTATGGTCCTC
TTCTCTTTAGGAGACAAGCCGCTTGCGGAGCCACCTTTGCTATCGTGCCCTTTGTCTCCCGGCGA
GCTCTAGGCATTATCTCGGGTTTAACCGGGGCTGGAGGGAAGTTTGGGTGAGGACTCACACAGCTC
GTCTTTTTTCTCGACTTCGCGCTTCACAAGTGAAGAAGGGCTAACGTGGATGGGAGTGATGATAGTT
GCTTGCACGTTGCCTGTTACCTTAATCCACTTTCTCAGTGGGGAAGCATGTTCTTCCCTCCTTCC
AACGATTCGGTCGACGCTACGGAGCACTATTATGTTGGCGAATATAGTAAGGAGGAGCAGCAGATT
GGCATGCATTTAAAAGCAAACGTTTGTGCTGATGGAGCCAAGACCGAGGGAGGCAGCAGCGTCCAC
AAAGGGAACGCAACCAACAATGCTTGATCATGTGTGATTGATATCAAGAAATTAATAATTTCACTT
ATGTGAAATGGACATAAACTGTTGGAAAATAAGAACCATTTCTTTCATCATTTGCTTT

SEQ ID NO: 116, *Arabidopsis thaliana* high-affinity nitrate transporter ACH2 variant (AAC35884)

MGSTDEPRSSMHGVTGREQSYAFSVDGSEPTNTKKKYNLPVDAEDKATVFKLFSFAKPHMRTFHLS
WISFSTCFVSTFAAAPLIPIIRENLNLTKHDIGNAGVASVSGSIFSRLVMGAVCDLLGPRYGCAFL
VMLSAPT VFSMSFVSDAAGFITVRFMIGFCLATFVSCQYWMSTMFNSQIIGLVNGTAAGWGNMGGG
ITQLLMPIVYEIIRRCGSTAFTAWRIAFFVPGWLHIIMGILVLTGQDLPGGNRAAMEKAGEVAKD
KFGKILWYAVTNYRTWIFVLLYGYSMGVELSTDNVIAEYFFDRFHLKLHTAGIIAACFGMANFFAR
PAGGWASDIAAKRFGMRGRLWTLWIIQTSGLFCVWLGRANTLVAVVSMVLFSLGAQAACGATFA
IVPFVSRRALGIISGLTGAGGNFGSGLTQLVFFSTSRFTTEEGLTWMGVMIVACTLPVTLIHFPQW
GSMFFPPSNDSDATEHYVGEYSKEEQQIGMHLKSKLFADGAKTEGSSVHKGNATNNA

FIGURE 8 (continued)

67/104

SEQ ID NO: 117, *Arabidopsis thaliana* high-affinity nitrate transporter, putative (At5g60780) mRNA, complete cds (NM_125471)

ATGACTCACAACCATTCTAATGAAGAAGGCTCCATTGGAACCTCCTTGCATGGAGTTACAGCAAGA
GAACAAGTCTTCTCTTTCTCCGTCGATGCTTCGTCTCAAACAGTCCAATCAGACGATCCAACAGCT
AAATTCGCCCTTCCGGTTGATTCCGAACATCGAGCCAAAGTGTTCAACCCACTCTCTTTTGCTAAA
CCTCACATGAGAGCCTTCCACTTAGGATGGCTCTCATTCTTCACATGCTTCATCTCCACCTTCGCG
GCAGCACCATTAGTCCCCATCATCCGCGACAACCTCGACCTCACTAAAACCGACATTGGAAACGCC
GGAGTCGCATCCGTCTCTGGTGCCATTTTCTCAAGGTTAGCCATGGGAGCGGTTTGTGATCTCCTC
GGTGCACGATATGGGACTGCCTTCTCCCTCATGCTAACCGCCCCAACCGTCTTCTCAATGTCGTTT
GTGGGTGGCCCTAGCGGATACTTAGGCGTCCGGTTCATGATCGGATTCTGTCTCGCCACGTTTGTA
TCATGCCAGTATTGGACCAGCGTTATGTTCAACGGTAAGATCATAGGACTAGTGAACGGCTGTGCA
GGCGGGTGGGGTGATATGGGCGGTGGAGTGACTCAACTCCTAATGCCGATGGTCTTCCACGTCATC
AACTTGCCGGAGCCACTCCGTTTCATGGCCTGGCGGATAGCTTTCTTCGTTCCCGGATTTCTTCAA
GTTGTTATGGGCATTCTCGTCCTCAGTCTCGGCCAAGATCTCCCTGACGGTAACCTAAGTACCCTT
CAGAAGAGTGGTCAAGTCTCTAAAGACAAATTCTCCAAGGTTTTCTGGTTTGTGTGAAGAACTAC
AGAACATGGATTTTATTTCGTTCTTTATGGATCTTCCATGGGAATTGAATTAACATCAACAACGTT
ATCTCCGGATATTTTTACGACAGGTTTAACTTAAGCTTCAAACAGCTGGTATAGTAGCAGCCAGC
TTTGGAATGGCTAACTTCATCGCCCGTCCCTTCGGTGGTTACGCTTCTGATGTAGCGGCTCGGGTT
TTTGGCATGAGAGGCCGGTTATGGACCTTATGGATCTTCAAACCGTAGGAGCTCTTTTCTGTATC
TGGCTAGGTCGAGCTAGTTCACCTCCCATAGCAATCCTAGCAATGATGCTCTTCTCAATCGGTACA
CAAGCAGCTTGCGGAGCCCTCTTCGGAGTTGCACCTTTTGTCTCGCGCCGCTCTCTAGGGCTCATA
TCGGGACTAACCGGCGCAGGAGGAACTTCGGGTCCGGTTTGACTCAACTGCTTTTCTTCTCATCA
GCGAGGTTTATGACAGCTGAGGGACTCTCATTGATGGGCGTTATGGCGGTTTGTGCACACTCCCA
GTTGCGTTTATACATTTTCCGCAATGGGGAAGCATGTTTTTAAGACCGTCGACCGATGGAGAAAGA
TCACAGGAGGAATATTATTACGGTTCTGAGTGGACGGAGAATGAGAAACAACAAGGATTGCACGAA
GGAAGCATCAAATTTGCAGAGAATAGTAGGTCAGAGAGAGGCCGGAAGTAGCTTTGGCTAACATT
CCAACGCCGGAACGGAACCTCCAAGTCATGTTTGA

SEQ ID NO: 118, *Arabidopsis thaliana* high-affinity nitrate transporter, putative (NP_200886)

MTHNHSNEEGSIGTSLHGVTAREQVFSFSVDASSQTVQSDPTAKFALPVDSEHRAKVFNPLSFAK
PHMRAFHGLWLSFFTCFISTFAAAPLVPIIRDNLDTKTIDIGNAGVASVSGAIFSRILAMGAVCDLL
GARYGTAFSLMLTAPT VFSMSFVGGPSGYLGVRFMIGFCLATFVSCQYWT SVMFNKI IGLVNGCA
GGWGDMMGGVTQLLMPMV FHV I KLAGATPFMAWRIAFFVPGFLQVVMGILVLSLGQDLPDGNLSTL
QKSGQVSKDKFSKVFWFAVKNYRTWILFVLYGSSMGIELTINNVISGYFYDRFNLKLQTAGIVAAS
FGMANFIARPFGGYASDVAARVFGMRGRLWTLWIFQTVGALFCIWLGRASSLPAILAMMLFSIGT
QAACGALFGVAPFVSRRSLGLISGLTGAGGNFGSGLTQLLFFSSARFSTAEGLSLMGMAVLCTLP
VAFIHFPQWGSMLRPSTDGERSQEYYYYGSEWTENEKQQGLHEGSIKFAENSRSERGRKVALANI
PTPENGTPSHV

FIGURE 8 (continued)

68/104

SEQ ID NO: 119, *Arabidopsis thaliana* At3g45060 gene, complete cds (BT015382)

ATGGCTCACAAACCATTCTAATGAAGACGGCTCTATTGGAACCTCCTTGCATGGAGTCACGGCAAGG
GAGCAAGTCTTCTCCTTCTCCGTCCAAGAAGATGTCCCTTCATCTCAAGCCGTCCGAACAAACGAT
CCAACGGCTAAGTTTGGCCCTACCAGTGGACTCCGAACATAGGGCAAAGTGTTCAAACCACTATCA
TTCGCTAAACCACATATGAGAGCCTTCCACTTAGGATGGATCTCTTTCTTCACTTGCTTCATCTCC
ACCTTCGCAGCCGCACCTCTAGTCCCCGTCATTCGCGACAATCTCGACCTGACCAAACCGACATC
GGAAATGCTGGAGTTGCATCAGTTTCCGGCGCCATTTTCTCGAGACTCGCTATGGGTGCTGTATGT
GACCTTCTAGGGGCACGTTATGGAACCGCCTTCTCACTTATGCTTACAGCTCCAGCAGTTTTTCTCC
ATGTCGTTCGTAGCTGACGCGGGAAGCTACTTAGCCGTAAGGTTTCATGATCGGTTTTTGGCTTAGCA
ACGTTTCGTATCATGTCACTACTGGACGAGTGTTATGTTCACTGGAAAGATTATCGGACTCGTTAAC
GGATGTGCTGGAGGGTGGGGAGATATGGGAGGAGGAGTGAAGTCACTAATGCCAATGGTCTTC
CACGTCATCAAACCTACCGGAGCCACTCCCTTTCACGGCTTGGAGGTTTCGCTTCTTCATCCCCGGC
ATTCTTCAGATAGTTATGGGTATTCTCGTTCTCACTCTCGGCCAAGATCTTCCCGATGGTAACCTC
AGTACTCTCCAAAAGAGTGGTCAAGTTTCTAAAGACAAATTCTCCAAGGTCTTTTGGTTCGCTGTG
AAAACTATAGAACATGGATCTTATTCATGCTCTATGGATTTTCTATGGGAGTTGAATTAACGATC
AACAACGTTATATCTGGATACTTCTACGATAGGTTTAACTTACGCTTCACACAGCTGGTATTATA
GCAGCCAGCTTTGGTATGGCAAACCTCTTTGCCCCGTCTTTTGGTGGCTACGCTTCAGATGTAGCT
GCACGGCTCTTCGGTATGAGGGGACGGTTATGGATCTTGTGGATCTTACAACTGTTGGAGCTCTC
TTTTGCATCTGGCTTGGTCGTGCTAGTTCACTACCTATAGCTATCTTAGCCATGATGCTTTTTTCC
ATGGGCACACAAGCTGCTTGTGGAGCTCTCTTTGGTGTGCTCCTTTTGTTCCTCCGCGCTTCTCTT
GGACTTATCTCGGGATTAAGTGGTGGTGGGAAATTTGGGTGGGAGTTACTCAACTTCTTTTC
TTCTCTTCTCGAGGTTTAGTACGGCGGAAGGACTATCGTTGATGGGCGTTATGGCTGTTGTGTGC
TCTCTTCCGGTTGCGTTTATACATTTTCCGCAGTGGGGAAGCATGTTCTTGAGGCCATCACAAAGAT
GGAGAGAAATCAAAGGAAGAGCATTACTATGGAGCGGAATGGACAGAGGAAGAGAAGAGCTTAGGA
CTACACGAAGGAAGCATTAATTTGCTGAAAACAGCCGGTCAGAGAGAGGCCGCAAGGCGATGTTG
GCTGATATTCCAACGCCGGAACCGGATCTCCGGCTCATGTCTAG

SEQ ID NO: 120, *Arabidopsis thaliana* At3g45060 (AAU05505)

MAHNHNSNEDGSIGTSLHGVTAREQVFSFSVQEDVPSSQAVRTNDPTAKFALPVDSEHRAKVFKPLS
FAKPHMRAFHLLGWISFFTCFISTFAAAPLPVPIRDNLDLTKTDIGNAGVASVSGAIFSRAMGAVC
DLLGARYGTAFSLMLTAPAVFSMSFVADAGSYLAVRFMIGFCLATFVSCQYWTSVMFTGKIIGLVN
GCAGGWGDMGGGVTTQLLMPMVFHVIKLTGATPFTAWRFAFFIPGILQIVMGILVLTGQDLDPDGNL
STLQKSGQVSKDKFSKVFVFAVKNYRTWILFMLYGFMSGVELTINNVISGYFYDRFNLTHTAGII
AASFGMANFFARPFGGYASDVAARLFGMRGRLWILWILQTVGALFCIWLGRASSLPAILAMMLFS
MGTQAACGALFGVAPFVSRRSLGLISGLTGAGGNFGSGVTQLLFFSSSRFSTAEGLSLMGVMAVVC
SLPVAFIHFPQWGSMLRPSQDGEKSKEEHYYGAEWTEEEKSLGLHEGSIKFAENSRSERGRKAML
ADIPTPETGSPAHV

FIGURE 8 (continued)

69/104

SEQ ID NO: 121, *Daucus carota* high-affinity nitrate transporter mRNA, partial cds (AY081213)

ATGGGTGACATGGAAGGTTCCCCGGGTTCCCTCCATGCACGGTGTTACCGGTCGTGAACCGTCCCTG
GCTTTCTCCGTTGCTTCCCGTATCGACACCTCCGCTGAATTCCACGTTCCGGTTGACTCCGAACAC
AAAGCTAAAGTTTTCAAATTCAAATCCTTCTCCCCGCCGCACGGTCTGCAGTTCAGCTGACCTGG
ATCTCCTTCCCGACCTGCTTCGTTTCCACCTTCGCTGCTCGTCCGCTGGTTGTTATCATCCGTGAC
AACCTGAACCCGACCAAAATGGACGTTGGTAACGCTGGTGGTTGCTTCCGTTACCGGTTCCATCCTG
TCCCGTGGTGCTATGGGTGCTATCTGCGACATGCTGGGTCCGCGTTACGGTTGCGCTTTCCTGATC
ATGCTGTCCGCTCCGAAAGTTCTGTGCATGTCTTCGTTTCCTCCGCTGGTGGTTACGTTGCTGTT
CGTTTCATGATCGGTTTCTCCCTGGCTACCTTCGTTTCCTGCCGTTACTGGATGTCCACCTCCATG
CACTCCGACATCATCGGTCTGGTTAACGGTACCGCTGCTGGTTGGGGTAACATGACCGGTGGTGCT
ACCCAGCTGATCATGCCGCTGCTGTACGACATCATCCGTGAAGCTGGTGCTACCCCGTTCACCGCT
TGGCGTATCGCTCTGTTTCATCCCGGTTGGCTGCACGTTATCTCCGGTATCCTGGTTCTGACCCTG
GGTCAGGACCTGCCGGACGGTAACGCTCAGAACGAAGCTTCCCTGCGTAAAAAAGGTCGTGTTTAC
AAAGACAAATTCTCCAAAATCCTGCGTTACGCTGCTACCAACTACCGTACCTGGATCCTGGTTCTG
CTGTACGGTTACTCCATGGGTGTTGAACTGACCACCGACAACGTTATCGCTGAATACTTCTTCGAC
CGTTTCGACCTGAACTGCACACCCCGGGTATCATCGCTGCTACCTTCGGTATGGCTAACCTGCTG
GCTCGTCCGTTCCGGTGGTTGGTCTCCGACGTTGCTGCTAAACACTTCGGTATGCGTGGTCGTCAC
TGGAACCTCCTGGGACCTGCAGACCCTGGGTGGTGTCTTCTGCCTGCTGCTGGTTTCGTGCTACCACC
TCCCGATCGACGCTCTGGCTATCACCTGGATGATCATCTTCTCCATCGGTGCTCAGGCTGCTACC
GGTGTTACCTTCGGTATCATCCCGTTCATCTCCCGTCGTTACCTGGGTATCATCTCCAGATGACC
GGTGCTAACGGTAACTTCGGTTCCGGTCAGACCCAGCCGCTGGAATTCGACTCCACCAAATACAAC
ACCGGTCTGGGTCTGACCTACATGGGTATGATGATCATCGCTTGCACCCTGCCGCCGATGCTGGTT
TGGTTCTGGCAGGACGGTTCCATGTTCTGCGCCGCTCCAAAGACCCGATCAAAGGTACCGAACCG
GAACACTACTTCGGTTCCGAATACACCGAAGACGAAAAAGTTAAAGGTATGCACCAGAACTCCATC
AAATTCGCTGAAAACTCCCGTACCGAATTCCGGTAAAAAACGTGTTGGTTCCGCTCCGACCCCGCCG
AACGTTTACCCCAACCGTGTT

SEQ ID NO: 122, *Daucus carota* high-affinity nitrate transporter (AAL99362)

MGDMEGSPGSSMHGVTGREPSLAFSVASRIDTSAEFHVPVDSEHKAKVFKFKSFSPPHGLQFQLTW
ISFPTCFVSTFAARPLVVIIRDNLNPTKMDVGNAGVASVTGSILSRGAMGAICDMLGPRYGCAFLI
MLSAPKVLCSFVSSAGGYVAVRFMIGFSLATFVSCRYWMSTSMHSDIIGLVNGTAAGWGNMTGGA
TQLIMPLLYDIIREAGATPFTAWRIALFIPGWLHVISGILVLTGQDLPDGNAQNEASLRKKGRVH
KDKFSKILRYAATNYRTWILVLLYGYSMGVELTTDNVIAEYFFDRFDLKLHTPGIIAATFGMANLL
ARPFGGWSSDVAAKHFGRGRHWNWDLQTLGGVFCLLLVRATTSPIDALAITWMIIFSIGAQAAT
GVTFGIIPFISRRYLGIISQMTGANGNFGSGQTQPLEFDSTKYNTGLGLTYMGMMIIACTLPMLV
WFWQDGSMLPSPKDPKIGTEPEHYFGSEYTEDEKVKGMHQNSIKFAENSRTEFGKKRVGSAPTPP
NVYPNRV

FIGURE 8 (continued)

70/104

SEQ ID NO: 123, Zea mays partial mRNA for high affinity nitrate transporter (nrt2-1 gene) (AJ344451)

CAGCAAGATCATCGGCACCGTCAACGGGCTCGCCGCCGGATGGGGCAACATGGGAGGCGGCGCCAC
GCAGCTCATCATGCCGCTCGTCTACGACGTCATCCGCAAGTGCGGCGCCACGCCATTCACGGCCTG
GCGCCTCGCCTACTTCGTGCCGGGCCTCATGCACGTCGTTCATGGGCGTCCTGGTGCTCACGCTGGG
GCAGGACCTCCCCGACGGCAACCTCAGGTCGCTGCAGAAGAAGGGCAACGTCAACAAGGACAGCTT
CTCCAAGGTCATGTGGTACGCCGTCATCAACTACCGTACCTGGATCTTCGTCTCTCTCTACGGCTA
CTGCATGGGCGTCGAGCTCACCACCGACAACGTTCATCGCCGAGTACATGTACGACCGCTTCGACCT
CGACCTCCGCGTCGCCGGGACCATCGCCGCCTGCTTCGGCATGGCCAACATCGTCGCACGCCCTAT
GGGCGGCATCATGTCCGACATGGGCGCGCGCTACTGGGGCATGCGCGCTCGCCTCTGGAACATCTG
GATCCTCCAGACCGCCGGCGGCGCCTTCTGCCTCTGGCTGGGACGCGCCAGCACCCCTCCCCGTCTC
CGTCGTGCCATGGTGCTCTTCTCCTTCTGCGCGCAGGCGGCCTGCGGCGCCATCTTCGGGGTCAT
CCCCTTCGTCTCCCGCCGCTCCCTCGGCATCATCTCCGGCATGACGGGCGCCGGCGGCAACTTCGG
CGCCGGGCTCACGCAGCTGCTCTTCTTTACCTCCTCGACCTACTCCACGGGCAGGGGGCTGGAGTA
CATGGGCATCATGATCATGGCGTGCACGCTGCCGGTGGTGTTCTGTGCACTTCCCGCAGTGGGGGTC
CATGTTCTTCCCGCCAGCGCCACCGCCGACGAGGAGGGCTACTACGCCTCCGAGTGGAACGACGA
CGAGAAGAGCAAGGGACTCCATAGCGCTAGCCTCAAGTTCGCCGAGAACAGCCGCTCAGAGCGCGG
CAAGCGCAACGTTCATCCAGGCCGACGCCGCCGCCACGCCGGAGCATGTCTAAGTTCACTACTAAGA
TGGATCGATCGACGATCACCTATACCTCTTTGTATGTACGAATATGCCTTGTTATTACTGTGCGCG
CGCATATACAATACAGTGTGCTCCGTTGACATGAGTTATATAGCACTAAAACTTCTTTTGAAAA
AAAAAAAAAAAA

SEQ ID NO: 124, Zea mays high affinity nitrate transporter (CAC87729)

SKIIGTVNGLAAGWGNMGGGATQLIMPLVYDVIRKCGATPFTAWRLAYFVPGLMHVVMGVLVLTGLG
QDLPGDNLRLSLQKKGNVNKDSFSKVMWYAVINYRTWIFVLLYGYCMGVELTTDNVIAEYMYDRFDL
DLRVAGTIAACFGMANIVARPMGGIMSDMGARYWGMRLWNIWILQTAGGAFCLWLGRASLTLPVS
VVAMVLFSCAQAAACGAIFGVIPFVSRRSLGIISGMTGAGGNFGAGLTQLLFFTSSTYSTGRGLEY
MGIMIMACTLPVVFVHFPQWGSMMFFPPSATADEEGYYASEWNDDEKSKGLHSASLKFAENSRSERG
KRNVIQADAAATPEHV

SEQ ID NO: 125, Oryza sativa nitrate transporter (NRT1) mRNA, complete cds (AF140606)

GGTGGAGGAGAGTGAGGACGGCCACGCGGACGAGCAGAGAGTGCGGGGCTCAGTGTCGGGCTCGC
CGGAGTCCGCGCAATCCGGCCGTTTCATGCTTCATTCTCTCGGACATTAACCTGGTTTACTTGTAAG
AAAGTAGAGCCATGGACTCCTCATACCAGCATGACAAGCCTCTGCTGGATGAAGAGAACTCCTCGC
AAGTGACCCTTGAATATACAGGTGATGGATCTGTTTGATCCGTGGGCATCCTGCTTTAAGGAAAC
ATACAGGGAACCTGGAAGGGTTCCTCATTAGCCATCGTTTTTTTCATTCTGCTCTTATCTGGCCTTTA
CTTCAATTGTAAAAAACCTAGTCAGTTATCTCACAAAAGTTCTACATGAAACAAACGTGGCCGCTG
CAAGAGATGTTGCAACTTGGTCAGGAACAAGTTATCTTGACCTCTGGTTGGAGCCTTCTTAGCTG
ATTCATATCTGGGGAAGTACTGTACAATTCTGATCTTCTGCACGATCTTCATTATCGGATTGATGA
TGTTGCTTCTGTGACGAGCAGTTCATTAATCTCTACTGGTCCTCACTCATGGATCATATGGACAG
ATCCAGTCTCTTCTCAGAACATCATA

FIGURE 8 (continued)

71/104

TTCTTTGTCGGTTTGTACATGGTTGCTTTAGGGTATGGTGCACAGTGCCCCTGCATATCATCATTT
GGTGCTGATCAATTTGATGACACTGATGAAAATGAGAGAACAAAAAGAGTTCTTTTTTCAATTGG
ACCTATTTTCGTAGCCAATGCGGGCTCATTGATCTCGGGGACTGTTATTGTGTGGGTGCAAGATCAC
AAAGGTTGGATCTGGGGTTTTACCATTCTGCACTATTTGTGTATTTAGGTTTTGGTACTTTTATC
TTTGGCTCCTCTATGTATGATTTTCAGAAACCTGGAGGAAGCCCCCTCTTGCGAGAATATGCCAGGTT
GTTGTTGCTGCTATTACAAAACGCGATAAAGATTTGCCATGTGATTCTCTCAGTTCTTTATGAGTTT
CTGGGGCAGAGTTTCAGCAATCGAAGGCAGCCGAAAATTGGAGCATACAACCTGGACTTAAGTTCTTT
GATAGAGCTGCAATGGTGACACCATCTGATTTTTGAATCTGATGGCCTACTAAACACATGGAAGATT
TGCACAGTCACTCAAGTGGAGGAACCTGAAGATTTTGATCAGGATGTTCCCCGTTTGGGCAACGATG
ATATTATTTGCTGCAGTTCTGGACAACATGTTTTTCGACATTCATAGAACAGGGGATGGTGATGGAG
AAACACATCGGCTCTTTTCGAAATACCTGCGGCGTCCTTCCAATCCATTGATGTCATTGCTGTCCTT
ATACTAGTTCCAGTCTATGAAAGAGTCCTTGTTCCAGTGTTTCAGAAAATTCAGTGGCAGAGCAAAT
GGCATTACTCCACTGCAGCGAATGGGGATCGGCCTGTTCTTTTCCATGCTCTCCATGGTATCAGCA
GCATTGGTGGAGAGTAATCGGTTGCGGATTGCGCAGGATGAAGGTTTGGTGCACAGGAAGGTGGCT
GTTCCAATGAGCATCCTGTGGCAGGGACCCAGTACTTCCTGATAGGCGTGGGAGAGGTGTTCTCA
AACATTGGGTAACTGAATTTTTCTACCAGGAATCACCGGACGCCATGAGAAGCTTATGTCTCGCA
TTCTCACTTGCTAACGTTTTCGGCAGGAAGTTACCTCAGCTCGTTTATCGTTTCTCTTGTGCCAGTG
TTCACAGCCAGAGAAGGCAGTCCTGGATGGATACCTGATAACTTGAACGAAGGGCATTGGATCGG
TTCTTCTGGATGATGGCTGGCTTGTGTTTCTTGAATATGCTGGCCTTTGTGTTCTGTGCCATGAGG
TACAAATGTAAGAAGGCTTCTGAACCTTGTTAACATTAGCAATATAATGGTGGTGGAAAAGGACA
ATTGTGTTGCAAAAAAAAAAAAAAAAAA

SEQ ID NO: 126, *Oryza sativa* nitrate transporter (NRT1) (AAF07875)

MDSSYQHDKPLLDEENSSQVTLEYTGDSVCIRGHPALRKHTGNWKGSSLAIVFSFCSYLAFTSIV
KNLVSYLTKVLHETNVAAARDVATWSGTSYLAFLVGAFLADSYLGKYCTILIFCTIFIIGLMMLLL
SAAVPLISTGPHSWIIWTDPVSSQNIIFVGLYMVALGYGAQCPCISSFGADQFDDTDENERTKKS
SFFNWTFVANAGSLISGTVIWVQDHKGWIWGFTISALFVYLGFGTFIFGSSMYDFRNLEEAPLA
RICQVVVAAIHKRDKDLPCDSSVLYEFLGQSSAIEGSRKLEHTTGLKFFDRAAMVTPSDFESDGLL
NTWKICTVTQVEELKILIRMFPVWATMILFAAVLDNMFSTFIEQGMVMEKHIGSFEIPAASFQSID
VIAVLILVPVYERVLVPVFRKFTGRANGITPLQRMGIGLFFSMLSMVSAALVESNRLRIAQDEGLV
HRKVAVPMSILWQGPQYFLIGVGEVFSNIGLTEFFYQESPDAMRSLCLAFSLANVSAGSYLSSFIV
SLVPVFTAREGSPGWIPDNLNEGHLDRFFWMMAGLCFLNMLAFVFCAMRYKCKKAS

FIGURE 8 (continued)

72/104

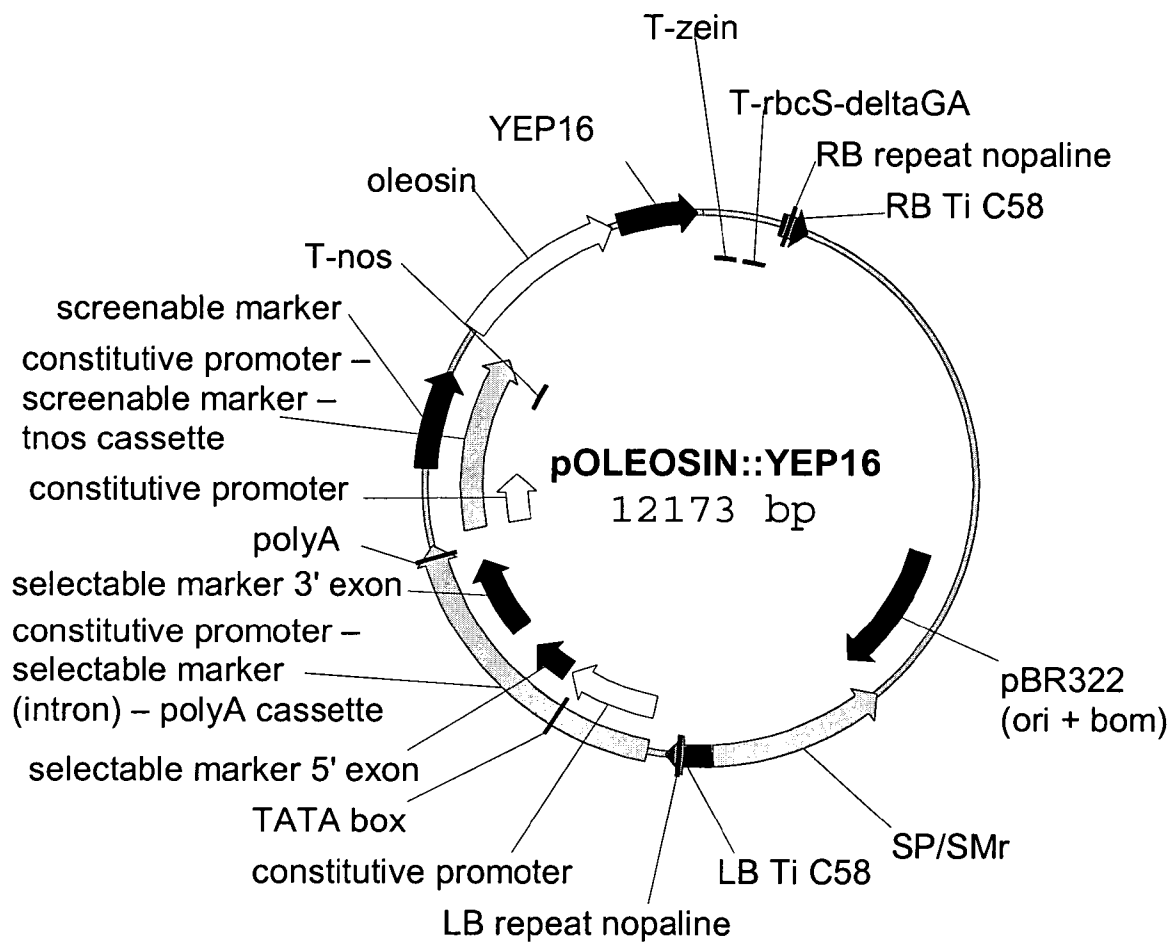


FIGURE 9

73/104**SEQ ID NO 127: Arabidopsis thaliana**

TCATACTCACAGAACAGAAACCCTAATTTCTCCTCAAAGCAATCTCGTTTCATCTTCCGCAAAC
GAAACCCCTCGAGAGTTGTTACTCCTCCTCCTCCTCTGGTGCATGATAAAGCGGCCTCAGGGT
TTGCTGCGGCGCTCGTTAGCGTTTGTCAATCGAAGAATTGTCTTGGTCGGACTCAAGAAGAT
GTCAGAAGATTGATGGAGTTTCTTGTGGGAGAAGAAAAGAAGAGGAACAAGGTCTTAGTCAA
TGATGTTGTTGAGAGAGGTAAATTTGGTAAACACTTCAAGGGCTTGGTCAAGATGTTGATTG
CAAGAGGTAAATCTGGGATTCTGGTGGATGTTTTAATGGAATTTGAGAGAATCTGTAATGAA
TTGGTCTCAAAAAAACTTGTCTGGGTTTCTTGA

SEQ ID NO 128: Arabidopsis thaliana

ASYSQNRNPNFLKAISFHLPPQTKPSRVVTPPPPLVHDKAASGFAAALVSVQCQSKNCLGRITQE
DVRRLMEFLVGEKKRNKVLVNDVVERGKFGKHFKGLVKMLIARGKSGILVDVLMEFERICN
ELVSKKLVWVS

SEQ ID NO 129: Arabidopsis thaliana

ATGGATACTCTCTCAGCATCCGTTTCATCCTTGAACCTCCCTTCTCTTCCCTCCACCACCGCA
GCCACCGTTGAGATCCATCTCCAGCCGCTTTAAATCCACCGTAAACGCCACCACTTCTGCTT
CATCTACCAATCTTTCAAACCAACATCGTCTTCACCTTCTTCAGCATCATACTCACAGAAC
AGAAACCCTAATTTCTCCTCAAAGCAATCTCGTTTCATCTTCCGCAAACGAAACCCTCGAGAGT
TGTTACTCCTCCTCCTCCTCTGGTGCATGATAAAGCGGCCTCAGGGTTTGCTGCGGCGCTCG
TTAGCGTTTGTCAATCGAAGAATTGTCTTGGTCGGACTCAAGAAGATGTCAGAAGATTGATG
GAGTTTCTTGTGGGAGAAGAAAAGAAGAGGAACAAGGTCTTAGTCAATGATGTTGTTGAGAG
AGGTAAATTTGGTAAACACTTCAAGGGCTTGGTCAAGATGTTGATTGCAAGAGGTAAATCTG
GGATTCTGGTGGATGTTTTAATGGAATTTGAGAGAATCTGTAATGAATTGGTCTCAAAAAAA
CTTGTCTGGGTTTCTTGA

SEQ ID NO 130: Arabidopsis thaliana

MDTLSASVSSLNLPSLPPPPQPPLRSISSRFKSTVNATTSASSTNLSKPTSSSPSSASYSQN
RNPFLKAISFHLPPQTKPSRVVTPPPPLVHDKAASGFAAALVSVQCQSKNCLGRITQEDVRRLM
EFLVGEKKRNKVLVNDVVERGKFGKHFKGLVKMLIARGKSGILVDVLMEFERICNELVSKK
LVWVS

SEQ ID NO 131: Arabidopsis thaliana

MDTLSASVSSLNLPSLPPPPQPPLRSISSRFKSTVNATTSASSTNLSKPTSSSPSSS

SEQ ID NO 132: Chlamydomonas

MAMAMRSTFAARVGAKPAVRGARPASRMSCMA

SEQ ID NO 133: Chlamydomonas

MQVTMKSSAVSGQRVGGARVATRSVRRALQV

FIGURE 10

74/104**SEQ ID NO 134: Arabidopsis thaliana**

MASLMLSLGSTSLLPREINKDKLKLGTASNPFLKAKSFSRVMTTVAVKPSR

SEQ ID NO 135: Arabidopsis thaliana

MATQFSASVSLQTSCLATTRISFQKPALISNHGKTNLSFNLRRSIPSRRLSVSC

SEQ ID NO 136: Arabidopsis thalianaMASIAASASISLQARPRQLAIAASQVKSFSNGRRSSLSFNLRQLPTRLTVSCAAKPETVDKV
CAVVRKQL**SEQ ID NO 137: Arabidopsis thaliana**MASIATSASTSLQARPRQLVIGAKQVKSFSYGSRNLSFNLRQLPTRLTVYCAAKPETVDKV
CAVVRKQLSLKE**SEQ ID NO 138: Arabidopsis thaliana**

MASSAAIIVSGSPFRSSPLIHNHSHASRYAPGSISVVSLPRQVSRRGLSVKS

SEQ ID NO 139: Brassica napusMATANALSSPSVLCCSRQGKLSGGSQQKGQRVSYRKANRRFSLRANVKEIAFDQSSRAALQA
GIDKLADAVGLTLGPRGRNVVLDEFGSPKVVNDGVTIA**SEQ ID NO 140: Hordeum vulgare**MAPTVMASATSVAAPFQGLKSTAGLPVSRRSNASSASVSNGGRIRCMQVWPIEGIKKFETLS
YLPPLSTEALLKQVDYLIRSKWVPCLEFSKVGFI FHEH**SEQ ID NO 141: Medicago truncatula**MTTIFRLASSSSPSLRHDATPHNFHIRKTSISNTFSFSSKNSLSFKRILTSGGSRRFIVAAS
PPTEDAVVATEPLTKQDLIDYLASGCKTKDKWRIGTEH**SEQ ID NO 142: Spinacia oleracea**METSMACCSRSIVLPRVSPQHSSALVPSSINLKSLKSSSLFGESLRMTTKSSVRVNKAKNSS
LVTKCELGDSLEEF LAKATTDKGLIRLMMCMGEALRTI**SEQ ID NO 143: Oryza sativa**GGTCAGCCAATACATTGATCCGTTGCCAATCATGCAAAGTATTTTGGCTGTGGCCGAGTGCC
GGAATTGATAATTGTGTTCTGACTAAATTAAATGACCAGAAGTCGCTATCTTCCAATGTATC
CGAAACCTGGATTAAACAATCCTGTTCTGTTCTCTAGCCCCTCCTGCATGGCCGGATTGTTT
TTTTGACATGTTTTCTTGACTGAGGCCTGTTTGTCTAAACTTTTTCTTCAAACCTTTTAACT
TTTTCATCACATCAGAACTTTTCTACACATATAAACTTTTAACTTTTCCGTCACATCGTTCC
AATTTCAATCAAACCTTTCAATTTTGGCGTGAACATAACACACCCTGAGTCTTTTATTGCTCC
TCCGTACGGGTGGCTGGTTGAGAATAGGTATTTTCAGAGAGAAAATCTAGATATTGGGAGG
AACTTGGCATGAATGGCCACTATATTTAGAGCAATTCTACGGTCCTTGAGGAGGTACCATGA**FIGURE 10 (continued)**

75/104

CATCAAACAAGAGTTCACCAAACCGCCCATGCGGCCATGCTGTACGCAACGCACCGCATTG
CCTGATGGCCGCTCGATGCATGCATGCTTCCCCGTGCACATATCCGACAGACGCGCCGTGTC
AGCGAGCTCCTCGACCGACCTGTGTAGCCCATGCAAGCATCCACCCCCGCCACGTACACCCC
GGTACCAAAATTTTAGTGTAATTTTAGTATCTCATTATAACTAGGTATTATGAGGTACCAA
ATTTACAATAGAAAAAATAGTACTTCATGGTACTTTCTTAAGTACCGTAAAATTGCTCCTAT
ATTTAAGGGGATGTTTATATCTATCCATATCCATAATTTGATTTTGATAAGAAAAAATGTGA
GCACACCAAGCATGTCCATGACCTTGCACTCTTGGCTCACTCGTCAACTGTGAAGAACCTCA
AAAATGCTCAATATAGCTACAGGTGCCTGAAAAAATAACTTTAAAGTTTTGAACATCGATTT
CACTAAACAACAATTATTATCTCCCTCTGAAAGATGATAGTTTAGAACTCTAGAATCATTGT
CGGCGGAGAAAGTAAATTATTTTCCCCAAATTTCCAGCTATGAAAAAACCTCACCAAACAC
CTCCTCCTCCCTACGTGTCACCGCTCTCTCCACCTATATATGCCACCTGGCCCCCTCTCCTC
CCATCTCCACTTCACCCGATCGCTTCTTCTTCTTCTTCGTTGCATTTCATCTTGCTAGC

SEQ ID NO 144: Artificial sequence prm00735

GGGGACAAGTTTGTACAAAAAAGCAGGCTTCACAATGGATACTCTCTCAGCATCC

SEQ ID NO 145: Artificial sequence prm00736

GGGGACCACTTTGTACAAGAAAGCTGGGTTGTATCATCAAGAAACCCAGA

FIGURE 10 (continued)

76/104

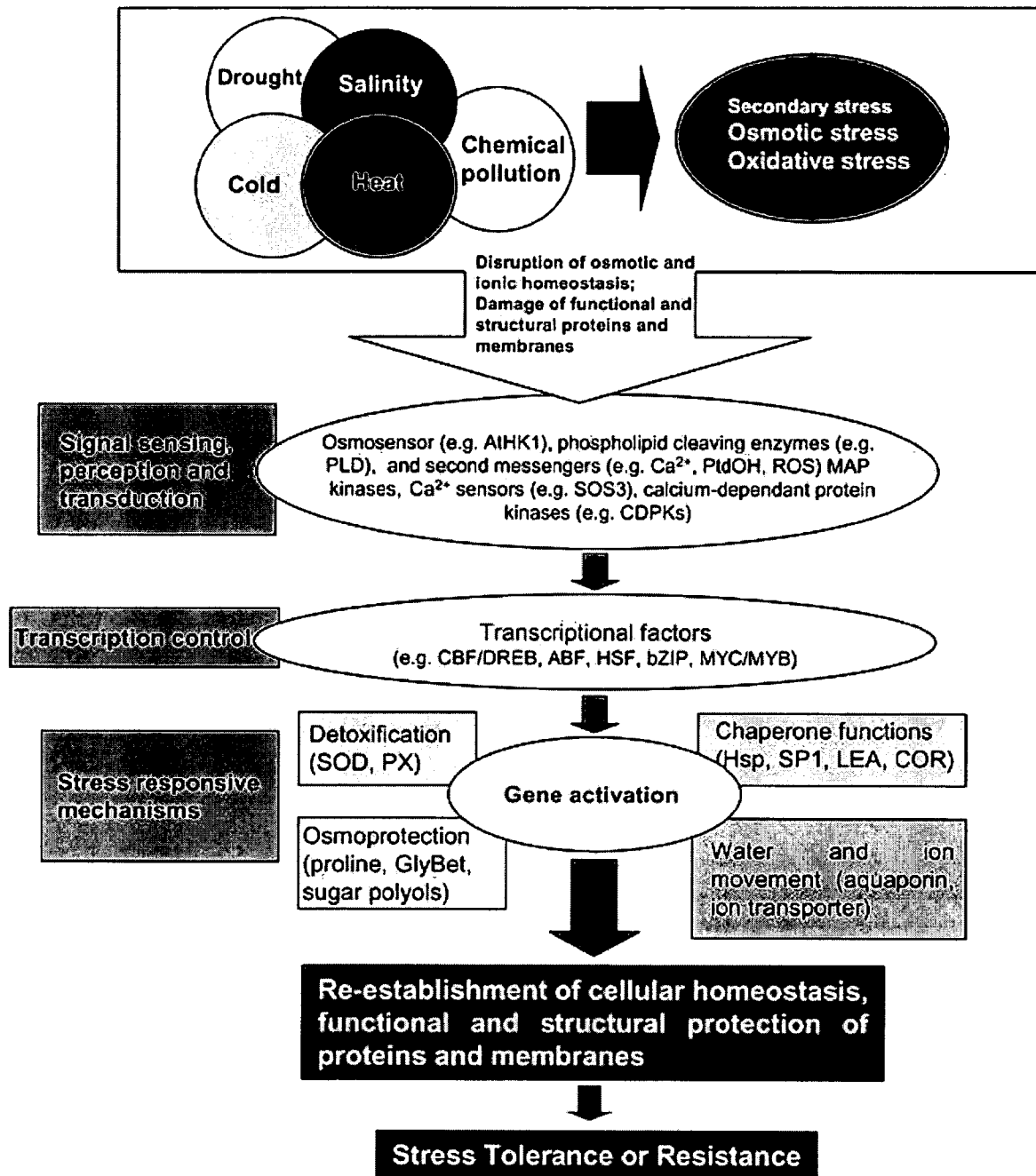


FIGURE 11

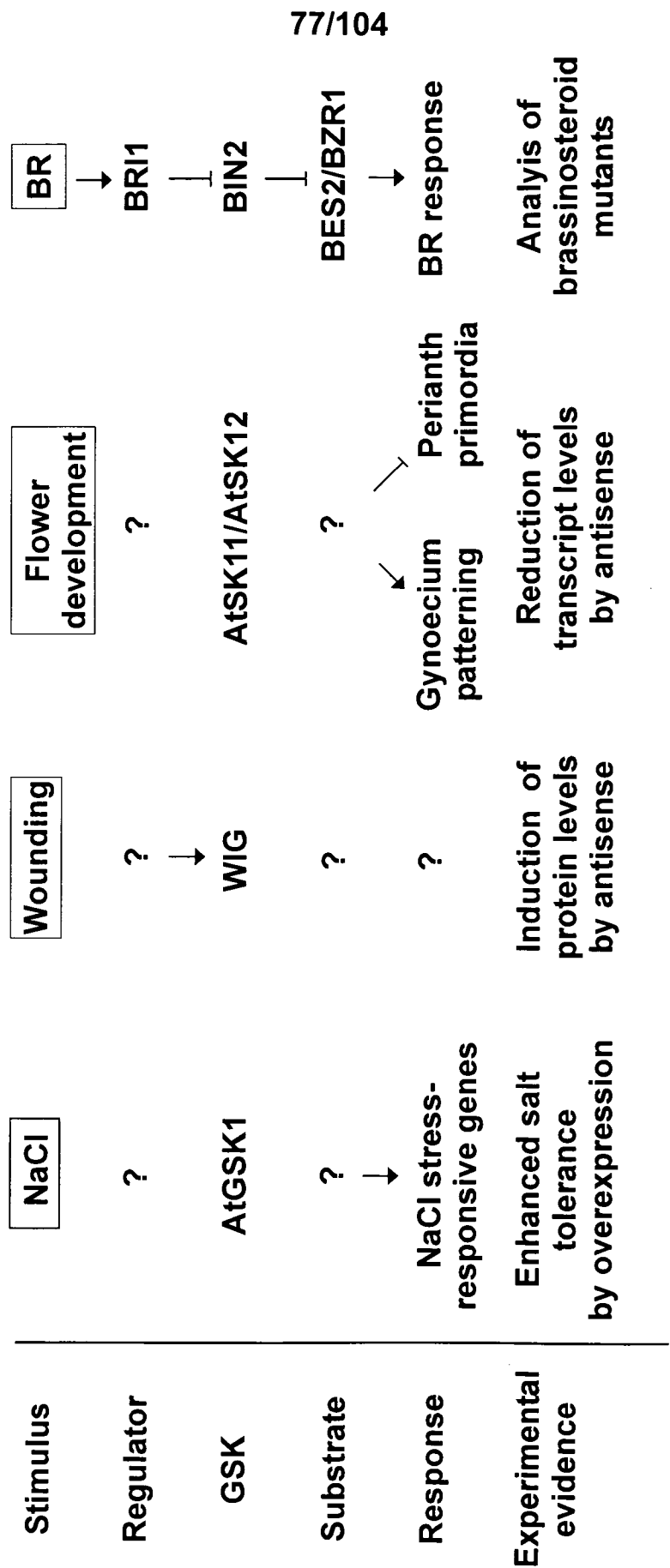


FIGURE 12

78/104

(a)

Arabidopsis GSKS	Group	Gene code	Accession no.	PlantsP ID
AtSK11/ASK α	I	At5g26750	X75432	21309
AtSK12/ASK γ		At3g05840	X75431	21676
ASK ϵ		At5g14640	AL163792	21976
AtGSK1/ASK ι	II	At1g06390	X99696	21488
ASK $\delta\zeta$		At2g30980	X94938	21610
BIN2/UCU1/ASK η		At4g18710	X94939	21835
ASK β	III	At3g61160	AJ002280	21787
ASK θ		At4g00720	Y07822	21794
AtK-1/ASK κ	IV	At1g09840	X79279	21066
ASK δ		At1g57870	AC079732	21176

(b)

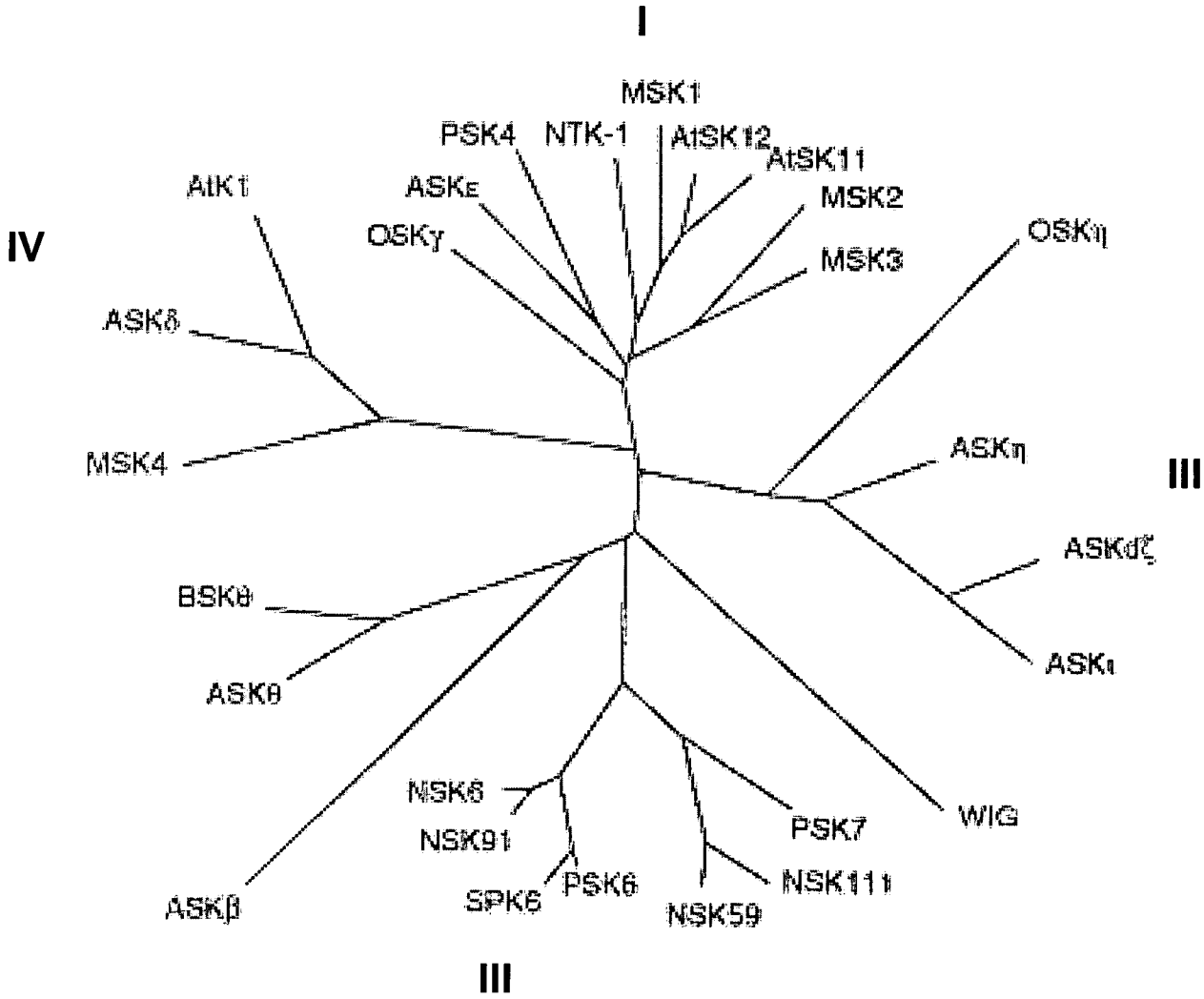


FIGURE 13

79/104

AY108486	-MASVGVAR-SSLGFGQNGTSSSSDPDRPLPNELGSMISIRDD-- --KDVEDI-VVNGNGAEPG	54
AK058276	-MASVGVR-SSLGFGQNETSTSGDADRLPNEMSNMSIRDDN-- --KDIDDI-VVNGNGTEPG	55
AAM77397.1	-----MGNMSIRDD-- --RDPEDI-VVNGNGTEPG	25
BAB40983.1	-MGSVGVP-SGLKNSSSTS-- --MGAEKLPDQMHDLKIRDD-- --KEVEAT-IINGKGTETG	52
AY103545	-MASAGVAP-SGYKNSSSTS-- --IGAELQDHMNLKIRDD-- --KEVEAT-IINGKGTETG	52
AT5g14640	-MASVGLPASSMATKQSNAS-I CAEKLPEGINEMKIKDD-- --KEMEA-VVDGNGTETG	54
CAA58594.1	-MAS-GIMP-- --SAGGKHRTDA-MLVDKLPEEINEMKIRDDKAEKEMEA-VVDGNGTEKG	54
AT5g26750	-MASVGIAPNPGARDSTG-- -- --VDKLPEEMNDMKIRDD-- --KEMEAT-VVDGNGTETG	49
CAA48538.1	-MASVGIAPNPGARDSTG-- -- --VDKLPEEMNDMKIRDD-- --KEMEAT-VVDGNGTETG	49
At3g05840	-MASVGIEPSAAVRESTGN-- --VTDADRLPEEMKDMKIQDD-- --KEMEAT-IVNGNVTTETG	53
CAA73247.1	-MASVGIEPSAAVRESTGN-- --VTDADRLPEEMKDMKIQDD-- --KEMEAT-IVNGNVTTETG	53
CAA48474.1	-MASVGVAPTSGFREVLDGEIGVDDILPEEMSDMKIRDD-- --REMEAT-VVDGNGTETG	55
CAA54803.1	-MTSVGLAPVSGLRESSHS-- --VGVDRLPEEMNDMRIRDD-- --KEIEAA-IVDNGNGTETG	53
CAA48472.1	MMASGGVAPASGFIDKNASS-- --VGVEKLPEEMNDMKIRDD-- --KEMEAATIVDNGNGTETG	55
CAA48473.1	-MATAGVAPASGIVDVNASSA-IAVDKLPEEILGMRIKDD-- --KEMEAH-VVDGNGNSTEAG	54
AK099599	-MTSVGLVDSSSGFPETSTSG-- --ATDRLTDDISEMSIRDK-- --EVEAV-VVSGNSMDIG	52

: : *:* . : : : : * : *

FIGURE 14

80/104

AY108486	HIIVTSIDGRNGQAKQ	TISYMAERVVGHGSFG	TVFQAKCLETGETVA	IKKVLQDKRYKNR	114
AK058276	HVIVTSIDGRNGQAKQ	TISYMAERVVGHGSFG	TVFQAKCLETGETVA	IKKVLQDKRYKNR	115
AAM77397.1	HIIVTSIEGRNGQAKQ	TISYMAERVVGN	SFGTVFQAKCLETGETVA	IKKVLQDKRYKNR	85
BAB40983.1	HIIVTTTGGKNGQPKQ	TVSYMAERIVGQGSFG	IVFQAKCLETGETVA	IKKVLQDKRYKNR	112
AY103545	HIIVTTTGGKNGQPKQ	TVSYMAERIVGQGSFG	IVFQAKCLETGETVA	IKKVLQDKRYKNR	112
AT5g14640	HIIVTTTGGKNGQPKQ	TISYMAERIVGQGSFG	IVFQAKCLETGETVA	IKKVLQDKRYKNR	114
CAA58594.1	HIIVTTTGGKNGEPKQ	TISYMAERVVQGSFG	IVFQAKCLETGETVA	IKKVLQDKRYKNR	114
AT5g26750	HIIVTTIGGRNGQPKQ	TISYMAERVVGHGSFG	VGTVFQAKCLETGETVA	IKKVLQDRRYKNR	109
CAA48538.1	HIIVTTIGGRNGQPKQ	TISYMAERVVGHGSFG	VGTVFQAKCLETGETVA	IKKVLQDRRYKNR	109
At3g05840	HIIVTTIGGRNGQPKQ	TISYMAERVVGHGSFG	VGTVFQAKCLETGETVA	IKKVLQDRRYKNR	113
CAA73247.1	HIIVTTIGGRNGQPKQ	TISYMAERVVGHGSFG	VGTVFQAKCLETGETVA	IKKVLQDRRYKNR	113
CAA48474.1	HIIVTTIGGRNGQPKQ	TISYMAERVVGHGSFG	VGTVFQAKCLETGETVA	IKKVLQDKRYKNR	115
CAA54803.1	HIIVTTIGGRHGQPKQ	TISYMAERIVGQGSFG	VGTVFQAKCLETGETVA	IKKVLQDKRYKNR	113
CAA48472.1	HIIVTTIGGKNGQPKQ	TISYMAERVVGHGSFG	VGTVFQAKCLETGETVA	IKKVLQDKRYKNR	115
CAA48473.1	HVIVTTTGGKNGQPKQ	TISYMAERAVGQGSFG	VGTVFQAKCLETGETVA	IKKVLQDKRYKNR	114
AK099599	HTIVTTVGRNGQPKQ	TISYIAERAVGRGSFG	VGTVFQAKCLETGETVA	IKKVLQDARYKNR	112
	* * * * *	* : : * : *	* : : * : *	* : : * : *	* : : * : *

FIGURE 14 (continued)

81/104

AY108486	ELQTMRVLDHPNVVALKHCFFSKTEKEEELYNLVLLEYVPETAHRVIKHYNKMNQRMPLIY	174
AK058276	ELQTMRVLDHPNVVSLKHCFFSKTEKEEELYNLVLLEYVPETAHRVIKHYNKMNQRMPLIY	175
AAM77397.1	ELQTMRVLDHPNVVALKHCFFSKTEKEEELYNLVLLEYVPETAHRVIKHYNKMNQRMPLIY	145
BAB40983.1	ELQTMRLLDHPNVVALKHCFFSTTEKDELYNLVLLEYVPETVHRVVKHYNKMNQRMPLIY	172
AY103545	ELQTMRLLDHPNVVALKHCFFSTTEKDELYNLVLLEYVPETVHRVVKHHNKMHQRMPLIY	172
AT5g14640	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVYRVSKHYSRANQRMPIY	174
CAA58594.1	ELQTMRLLDHPNVVALRHCFSTTEKDELYNLVLLEYVPETVYRVLRHYSKANQQMPMIY	174
AT5g26750	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVHRVIKHYNKNLQRMPLIY	169
CAA48538.1	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVHRVIKHYNKNLQRMPLIY	169
At3g05840	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVHRVIKHYNKNLQRMPLVY	173
CAA73247.1	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVHRVIKHYNKNLQRMPLVY	173
CAA48474.1	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVHRVIKHYSKLNQRMPIY	175
CAA54803.1	ELQTMRLLDHPNVVCLKHCFFSTTEKDELYNLVLLEYVPETVHRVIKHYNKNLQRMPLIL	173
CAA48472.1	ELQTMRLLDHPNVVSLKHCFFSTTEKDELYNLVLLEYVPETVSRVIRHYNKMNQRMPIY	175
CAA48473.1	ELQTMRLLDHPNVVTLKHCFFSTTEKDELYNLVLLEYVPETVHRVIRHYSKNQRMPLIY	174
AK099599	ELQTMQVLDHPNVACLKHYFCSTTAKEEELYNLVLLEYVPETVHRVIRHYNKMMSQRMPLIY	172
	****:::*****. *: * * * * *:*****:****. ** :*: : *::: *:::	

FIGURE 14 (continued)

82/104

AY108486	AKLYMYQICRALAYIHNSIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	234
AK058276	AKLYMYQICRALAYIHNTIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	235
AAM77397.1	AKLYMYQICRSLAYIHNSIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	205
BAB40983.1	VKLYMYQICRALAYIHNSIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	232
AY103545	VKLYMYQICRALAYIHGTIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	232
AT5g14640	VKLYTYQICRALAYIHGGVGCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	234
CAA58594.1	VKLYTYQIFRALAYIHG-IGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	233
AT5g26750	VKLYTYQIFRALSYIHRCIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	229
CAA48538.1	VKLYTYQIFRALSYIHRCIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	229
At3g05840	VKLYTYQIFRSLSYIHRCIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	233
CAA73247.1	VKLYTYQIFRSLSYIHRCIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	233
CAA48474.1	VKLYTYQIFRALSYIHRCIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	235
CAA54803.1	VKLYTYQIFRALSYIHHTIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	233
CAA48472.1	VKLYSYQICRALAYIHNSIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	235
CAA48473.1	VKLYSYQICRSLAYIHNCVGVSHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISY	234
AK099599	VKLYMYQICRALAYIHNCVGVCHRDIKPQNILVNPHTHQLKLCDFGSAKVLVKGEPNISY	232
	.*** ** * :*:*** :**.*:*****:*****.***:*****:*****	

FIGURE 14 (continued)

83/104

AY108486	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	294
AK058276	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPLFPGDSGVDQLVEIIKVLGTP	295
AAM77397.1	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTP	265
BAB40983.1	ICSRYYRAPELIFGATEYTTAIDWSAGCVLAELMLGQPLFPGESGVDQLVEIIKVLGTP	292
AY103545	ICSRYYRAPELIFGATEYTTAIDWSAGCVLAELMLGQPLFPGESGVDQLVEIIKVLGTP	292
AT5g14640	ICSRYYRAPELIFGATEYTTTIDWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	294
CAA58594.1	ICSRYYRAPELIFGATEYTTAIDWSVGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	293
AT5g26750	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	289
CAA48538.1	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVHIKVLGTP	289
At3g05840	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	293
CAA73247.1	ICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	293
CAA48474.1	ICSRYYRAPELIFGATEYTTAIDVWSVGCVLAELLLGQPLFPGERGVDQLVEIIKVLGTP	295
CAA54803.1	ICSRYYRAPELIFGATEYTTAIDWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTP	293
CAA48472.1	ICSRYYRAPELIFGATEYTTAIDWSAGCVLGELLLGQPLFPGESGVDQLVEIIKVLGTP	295
CAA48473.1	ICSRYYRAPELIFGATEYTTAIDWSAGCVLGELLLGQPLFPGASGVDQLVEIIKVLGTP	294
AK099599	ICSRYYRAPALIFGATEYTTAIDVWSAGCVLAELLLGQVPFPGDSGVDQLVEIIKVLGTP	292
	***** :*:*.****.***:*****:**** *****	

FIGURE 14 (continued)

84/104

AY108486	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPAEAVDLVSRLQYSPKLRSTALEALV	354
AK058276	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPAEAVDLVSRLQYSPYLRSTASEALI	355
AAM77397.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPAEAVDLVSRLQYSPSLRSTALEALI	325
BAB40983.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKVFHKRLPPEAVDLVSRLQYSPNLRCTAVEALV	352
AY103545	TREEIKCMNPNYTEFKFPQIKAHPPWHKVFHKRMPPEAVDLVSRLQYSPNLRCTAMEALV	352
AT5g14640	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRTPPEAVDLVSRLQYSPNLRSTAMEAIV	354
CAA58594.1	TREEIKSMNPNYTEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRSTALEACT	353
AT5g26750	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRSAALDTLV	349
CAA48538.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRSAALDTLV	349
At3g05840	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRCAALDSLV	353
CAA73247.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRCAALDSLV	353
CAA48474.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPAEAVDLVSRLQYSPNLRCAALDCLT	355
CAA54803.1	TREEIKCMNPNYNEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRCTALEAVT	353
CAA48472.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQYSPNLRSTALEALV	355
CAA48473.1	TREEIKCMNPNYTEFKFPQIKAHPPWHKIFRKRMPPEAVDLVSRLQYSPNLRSTALEALV	354
AK099599	TREEIKHMNPNYTEFKFPQIKAHPPWHKIFHKRMPSEAVDLVSRLQYSPHLRCSALEVLI	352
	*****.*****;*:****.***** ***** **.*	

FIGURE 14 (continued)

85/104

[illegible]

FIGURE 14 (continued)

86/104

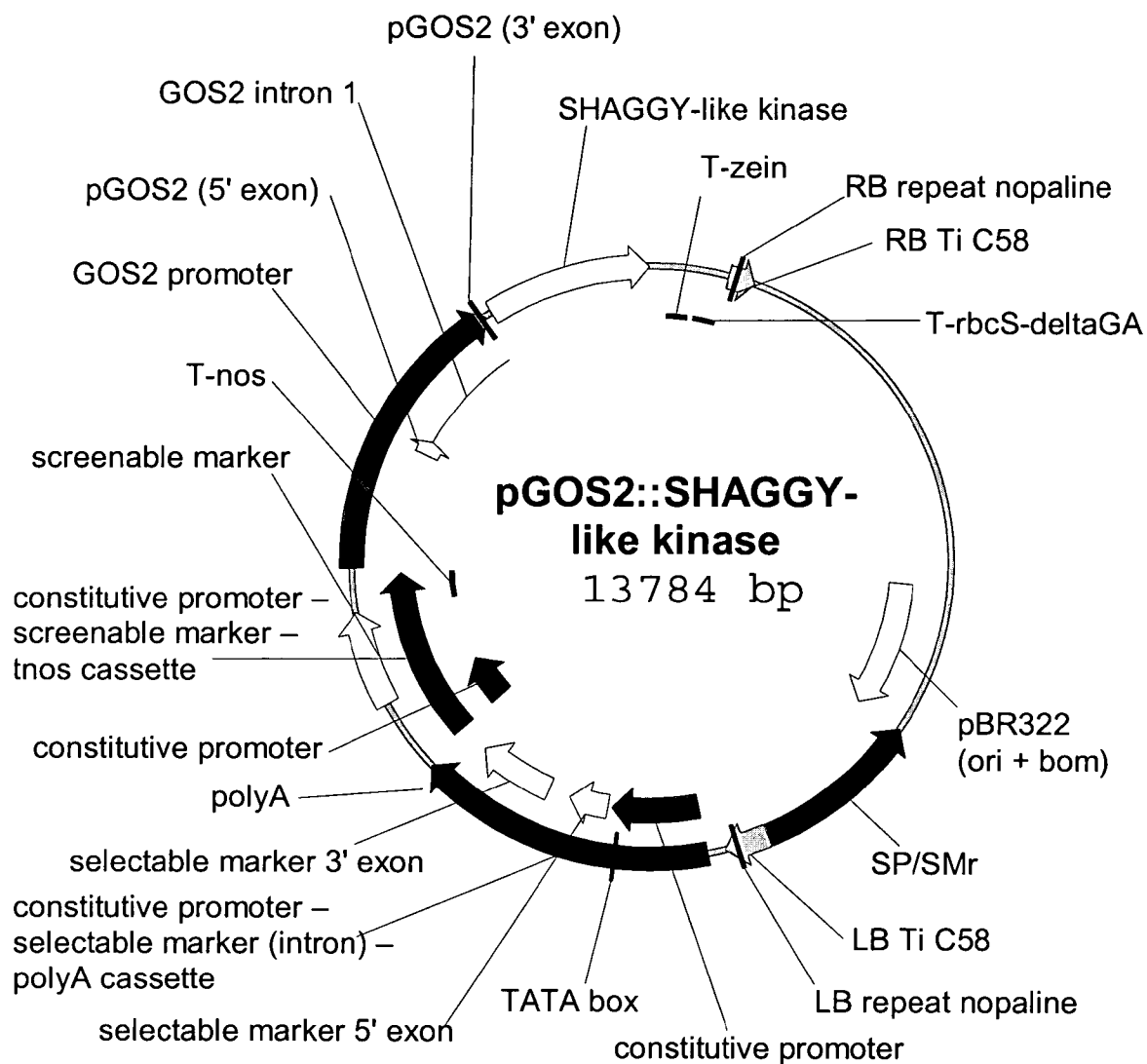


FIGURE 15

87/104

SEQ ID NO 146 - *Oryza sativa* DNA sequence

CAAAAGCAAGAGGAGGAGGCCGCGGCTAGCGAGCGAGCGAGAGAGAGGGGAGAAGAAGAGGT
GGGACAGCCGGGAGATCCATCCCTGTGGAGAGGAGGGAGGGAGGAAGGAGGCGTTGGAGGAG
GAGAGGTTGACCGATAGATCCATTGCGGAGTTGAGTGTGATGCAAAGCTGATTCGCCATCG
TTTAGCTTTTTATAAGAGATGGGTTGAGTAGGGGTTGCGCCGTCTGGGTTAAAGAACAGCAG
TAGCACCAGCATGGGTGCTGAGAAGTTGCCTGATCAGATGCATGATCTGAAGATAAGGGACG
ATAAGGAAGTTGAAGCGACTATTATTAACGGCAAGGGAACAGAAACCGGCCACATAATTGTC
ACAACACTGCTGGTGGCAGAAATGGTCAGCCGAAACAGACAGTTAGCTACATGGCTGAGCGTAT
TGTAGGGCAAGGTTTCAATTTGGGATTGTCTTCCAGGCAAAATGTCTGGAGACAGGTGAGACAG
TTGCTATCAAGAAGGTTCTTCAGGATAAGCGCTACAAGAACCGTGAGCTTCAGACCATGCGC
CTTCTTGACCACCCAAATGTTGTAGCTCTGAAGCACTGTTTCTTCTCTACAACCTGAGAAGGA
TGAAGTGTATCTAAACTTGGTTCTTGAGTATGTGCCTGAAACTGTTTCATCGTGTTGTGAAGC
ATTACAACAAGATGAACCAGCGTATGCCACTTATCTATGTGAAGCTGTATATGTACCAGATT
TGTAGGGCATTAGCTTACATCCATAATAGCATCGGAGTTTGCCACAGAGATATCAAGCCACA
GAATCTTCTGGTAAACCCACATACCCATCAACTCAAGCTATGTGACTTTGGGAGTGCAAAAG
TTCTGGTCAAGGGAGAACCGAACATATCGTACATTTGCTCCCGATACTATAGGGCTCCGGAG
CTCATATTTGGTGGCACCGAATACACTACAGCTATTGACATCTGGTCTGCTGGATGTGTTCT
TGCTGAACTTATGTTAGGGCAGCCTCTGTTTCTGGTGAAAGTGGTGTAGACCAACTTGTGG
AAATCATCAAGGTCCTTGGAACACCTACAAGGGAGGAAATTAAATGCATGAATCCAAACTAT
ACCGAGTTCAGGTTTCCACAGATTAAAGCACACCCATGGCACAAGGTATTCCATAAAAGGTT
GCCTCCAGAAGCTGTTGATCTTGTCTCTAGGCTGCTCCAGTACTACCCCAACCTAAGATGCA
CTGCTGTGGAAGCACTTGTTACCCATTCTTTGATGAGCTTCGAGACCCTAATGCTCGCCTT
CCGAATGGCCGCTTTTTGCCTCCTCTCTTCAACTTCAAGCCTCATGAACTGAAAGGAATCCC
ATCAGATATTATGGCGAAATTGATCCCAGAACATGTGAAGAAGCAATGCTCCTATGCAGGAG
TATGAGACAGCTTCCGCACGACCCCCCTGGAAATTTCCATGACAAGTGCCCATTTCTCTCCC
CCTGGACGACGATGGATCGTCAGCATATGCGTGCATGATGGTTGGTGAGGATGTGAAGTTAC
GTTGTTGTTGTGTGACCACCTAGAGCTTGAACAGAAGGAAAA

SEQ ID NO 147 - *Oryza sativa* - protein sequence

MGSVGVAPSGLKNSSSTSMGAEKLPDQMHD LKIRDDKEVEATIINGKGTETGHIIVTTTGGR
NGQPKQTVSYMAERIVGQGSFGIVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLDHPN
VVALKHCFSTTEKDELYLNLVLEYVPETVHRVVKHYNKMNQRMPLIYVKLYMYQICRALAY
IHNSIGVCHRD IKPQNLLVNPHTHQLKLCDFGSAKVLVKGE PNISYICSRYYRAPELIFGAT
EYTTAIDIWSAGCVLAELMLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNP NYTEFKFP
QIKAH PW HKVFHKRLPPEAVDLVSRLLQYSPNL RCTAVEALVHPFFDEL RDPNARLPNGRFL
PPLFNFKPHELKGI PSDIMAKLIPEHVKKQCSYAGV

FIGURE 16

88/104

SEQ ID NO 148 - *Oryza sativa* - AK058276 DNA sequence

CTCTCCGAATCCTCCCCCGCATTCCGCGCCGGAGCTGAGGAGGGACAGCGAGCCAGCGAGGG
AGGTGGGGCAATCCAGCGAGCGCCAGATCGTGCCGCCAGCCCCGCTCCGTCTCTCTCCGGC
GACCTCCGCCCCCGCTGATCCCGTGGTGGATCAACTACAACATCATCTTTAGGAAAGCCTCT
TGAACATTAGCCTTGTGTGCCTTTCAACAGTATGGCCTCGGTAGGTGTGGTGCCTTCTTCT
TGGGGTTTCAGAACGAAACAAGTACAAGTGGCGATGCCGACCGACTTCCGAATGAGATGAGC
AATATGAGTATAAGGGATGATAATAAGGACATTGACGACATAGTTGTCAATGGCAATGGGAC
AGAACCTGGTCATGTTATTGTGACAAGCATTGATGGAAGAAATGGACAGGCTAAACAGACCA
TTAGCTACATGGCCGAGCGTGTTCGTAGGTCATGGATCCTTTGGAAGTGTTCCTCAGGCCAAG
TGCCTGGAAACCGGTGAGACTGTGGCTATAAAGAAGGTTCTTCAAGACAAGAGATATAAGAA
CCGTGAGCTGCAAACAATGCGAGTTCTTGACCACCCAAATGTGGTGTCACTAAAGCATTGTT
TTTTCTCAAAGACTGAGAAGGAGGAGCTTTACCTCAATTTGGTGTCTGAGTATGTGCCAGAG
ACTGCTCACCGTGTAATTAAACATTACAACAAGATGAACCAACGCATGCCATTGATATATGC
AAAATATACATGTATCAGATATGCAGAGCTTTGGCGTACATTCACAACACCATTTGGCGTGT
GTCACAGGGATATCAAGCCACAAAATCTTCTGGTGAACCCACATACTCATCAGCTGAAATTA
TGTGACTTCGGCAGCGCGAAAGTCTTGGTAAAAGGAGAACCAAATATTTCTTACATCTGTTT
AAGGTACTACAGAGCTCCAGAGCTCATATTTGGTGCTACTGAATACACAACAGCGATTGATG
TTTGGTCTGCCGGTTGTGTGCTTGTGAACTCCTCCTGGGGCAGCCTCTATTCCCTGGCGAC
AGTGGCGTTGATCAGCTTGTGAAATCATCAAGGTTCTGGGTACCCCTACACGAGAGGAGAT
TAAGTGCATGAACCCAAATTACACCGAGTTTAAATTTCCGCAAATCAAAGCTCACCCATGGC
ACAAGATCTTCCATAAAAGAATGCCTGCTGAAGCAGTCGATCTCGTCTCCAGGCTTTTGCAG
TATTCACCATACTCCGGTCCACTGCTTCGGAAGCATTGATCCATCCCTTCTTCGATGAACT
CCGTGATCCAAACACCCGCTTACCGAACGGCCGTTTCCTTCTCCTCTCTTCAACTTCAAGC
CCCATGAACTGAAGGGTATGCCAATGGAATTCCTGGTGAAGCTTATCCCCGAACATGCTCGA
AAGCAATGCGCGTTTGTAGGATGGTGAATTTCTGAGGTCAGCATGAAAAGTGTTCAGAATTT
CTTACCCTCCTCCATTAGAAAGCAGAGATGAACCCTGTGTGCAGCCATTTGGGAAAGCTGG
TGCATATGGAAGTGAAGTACATTTTTTTGTCCGAGATTCTGACGCCGCGTATTCTTTTCCC
CCCTCCCCTTTGCTGCTGCCGGTGTAACCAAAAAATCATCCACGGTTCTGTAAAGTTGATG
AAGAAGAGTGTAATAATCAGGTTGAAAAGTGAATTCGATCGGTTTGTCAAGATTGTAGCAACA
TGCAAGGAAGGATGTTGCACACTTTGTATGGCAATGTTTCGTTCCGTTCCAAATATTTGGACAT
GG

SEQ ID NO 149 - *Oryza sativa* - AK058276 protein sequence

MASVGVRSSLGFQNETSTSGDADRLPNEMSNSIRDDNKDIDDI VVNGNGTEPGHVI VTSI
DGRNGQAKQTI SYMAERVVGHGSFGTVFQAKCLETGETVAI KKV LQDKRYKNRELQ TMRVLD
HPNVVSLKHCFFSKTEKEELYLN LVLEYVPETAHRVI KHYNKMNQRMPLIYAKLYMYQICRA
LAYIHNTIGVCHRD IKPQNLLVNPHTHQLKLCDFGSAKVLVKGE PNISYICSRYYRAPELIF
GATEYTTAIDVWSAGCVLAELL LGQPLFP GDSGVDQLVEI I KVLGTP TREEI KCMNP NYTEF
KFPQIKAH PWHKI FHKRMPAEAVDLVSRL LQYSPYLRSTASEALIHPFFDEL RDPNTRLPNG
RFLPPLFNFKPHELKGMPMEFLVKLI PEHARKQCA FVGW

FIGURE 16 (continued)

89/104

SEQ ID NO 150 - *Oryza sativa* - AK099599 DNA sequence

TTGGGGCGGAGAGACGGGAGAGAGAGGAGAGGAGTCTGAAGTCTAGGGTTAGTGAGGTGAAGGGG
GGCGATTTTGCTCATCGCCCTCCGCCTAGATCGAATCCGAATCCCGCCTCCTCCTCCTCCTC
CTCCTCCCCCGCGCCGATCTTGCCCCGCTCCCTCGCCGCAGCTGCGGGCTTGCCCTAGCCC
GCCGCATCGCCGACGTACTACGCCCCGCTCGGCTCCAGGCTCCAGATCCGGCCTCCAGGGCGT
GCCCCGCTGCTGGACGGCGCTCTCCCGCGTCCGTGGCTACCTCCTCCTCCGGGTTTGCGTTGC
CGTCGCCGAAGCGATCCGTTGGTGGATTGTGTGTAGCTCTGTAACAAAGGATCTTGGTCCAT
AGGAGTGAACCAGAAGGTACAAAACCTTCTTGGCTATTATGACATCGGTGGGTCTAGTAGATT
CTTCATCAGGTTTCCCGGAAACGAGTACTAGTGGAGCCACTGATCGTCTGACAGATGATATC
AGCGAGATGAGCATAAGAGATAAGGAAGTTGAAGCTGTAGTGGTCAGTGGCAATAGTATGGA
CATAGGTCACACTATTGTGACAACTGTTGGTGGAAAGAAATGGGCAGCCAAAGCAGACAATTA
GTTACATCGCAGAGCGTGCTGTTGGGCGTGTTTCATTTGGAGTTGTCTTCCAGGCTAAGTGT
CTAGAAACTGGTGAGAGAGTTGCTGTAAAGAAAGTTCTTCAAGATGCGAGATACAAGAACCG
GGAGCTGCAAACGATGCAAGTTCTCGATCACCCAAATGTTGCATGCTTGAAGCATTACTTTT
GCTCGACTACTGCGAAGGAGGAGCTATACCTCAACTTGGTTCTTGAATATGTGCCAGAACT
GTTTCATCGTGTTATTAGACATTACAATAAGATGAGCCAACGCATGCCATTGATTTATGTTAA
ACTTTATATGTACCAGATTTGTAGGGCTTTGGCATAACATTCATAACTGTGTGGGAGTATGCC
ACAGAGATATAAAGCCACAGAATATATTGGTGAATCCACATAATCATCAGTTGAAATTGTGT
GACTTTGGCAGTGCAAAAGTCTTGGTGAAAGGGGAACCAAATATTTTCATATATCTGTTCTAG
ATACTACAGAGCCCCAGCACTCATATTTGGGGCTACAGAGTACACGACAGCTATTGATGTGT
GGTCTGCTGGCTGTGTTCTTGCTGAACTACTTCTAGGGCAGCCTGTTTTTCTTGGTGACAGT
GGCGTCGACCAACTTGTTGAAATTATCAAGGTACTGGGTACTCCAACAAGGGAAGAAATCAA
ACATATGAATCCGAACCTACACTGAGTTTAAAGTTCCCCCAAATCAAAGCTCACCCATGGCACA
AGATCTTTCATAAAAGAATGCCATCTGAAGCTGTAGATCTTGTGTCTCGGCTTCTGCAGTAC
TCACCACACCTCCGGTGCAGTGCATTGGAGGTGTTAATTCATCCATTCTTCGATGAACTACG
AGATCCAAATGCTCGCTTACCAAATGGCCGTACTCTTCCCCCACTATTCAATTTCAAGCCTC
GTGAGCTGAAAGGAGCATCAATGGAATTTCTTGTGAAGTTGGTTCCACAGCATGCTAAGAAG
CAATGTGCCTTCTTAGGATTATGAGCAGACAGTTTCATACACTAATCGGGTATTACGTTGGTC
TACTTGGTTCCGTAGAACAGCATGGCCTGCAGTATTATTGAATGGGCCCTAATTTTGTCTA
CGTGACCCCTGCTTGGGCATGCCTTCTACCATCATATTCTGTAAAGCAGATGAAGACATGGA
GTGAGTGGTTATTGATTGGGGCTTGATATTGGTCTGCCCTTGACTTGAGAACTTTATTTCAC
TCTGCTGTATCAAGCAAGAAAGAACACGTATGTATGCTTGAGCCATATTTTCATTCCAGAGCC
TCTATCAGGTTTTCACCGACCATCAGATTTAAGTCTTCCAGTTTGTAGGGCTAAGCCAAAAA
GTTCTATGTGTGAAGAGTTGGAGACATCTGTTTGGTTACAAGCTATTTGATTGTATTTGATC
ATTCTTTTGTATTAACACTCTGATAAACTTACATGAGTTAATTCTATTGTTATGTGATATAG
TTGTGTGCCACTTTTAAACACCTAAACAACCTCTGTTCAATGTTGAAATGTTTGGCATGTATC
AACATATCACCTCATTATTTTCGAGGTTGATTTTGTACACCTGATATCTGTTAGCTTGAATGC
TTGATTACAAGCAAATGATTAAATATTTT

FIGURE 16 (continued)

90/104

SEQ ID NO 151 - *Oryza sativa* - AK099599 protein sequence

MTSVGLVDSSSGFPETSTSGATDRLTDDISEMSIRDKEVEAVVVSNGNSMDIGHTIVTTVGGR
NGQPKQTISYIAERAVGRGSFGVVFQAKCLETGERVAVKKVLQDARYKNRELQTMQVLDHPN
VACLKHYFCSTTAKEELYLNLVLEYVPETVHRVIRHYNKMSQRMPLIYVKLYMYQICRALAY
IHNCVGVCHRDIKPQNILVNPHNHQLKLCDFGSAKVLVKGEPNISYICSRYYRAPALIFGAT
EYTTAIDVWSAGCVLAELLLGQPVFPGDSGVDQLVEIIKVLGTPTREEIKHMNPNYTEFKFP
QIKAHPWHKIFHKRMPSEAVDLVSRLLQYSPHLRCSALEVLIHPFFDEL RDPNARLPNGRTL
PPLFNFKPRELKGASMEFLVKLVLPQHAKKQCAFLGL

SEQ ID NO 152 - *Arabidopsis thaliana* - AF428327 - SHAGGY alpha

ACAAAATAATATAAAGTAAAAATATTTTCATAATTCGTCTCTCACCGGAAAAATAAATAAAGT
TAGAGAGAGAGATTTCATAATCATCAAACCCACAAATCCTTTTTTTTTTTTTTTGTTAAACC
CACAAATCCTTACTCGTACGGATCTCTCTCTCTTAATATCCTAATTCTTCTCTTCATCGAT
CTGAGATTTTTACGTTTTTCATCGGCTTGAAAGTTTGAAGAGTTTGTAGCCTGAAAAATGGC
GTCAGTGGGTATAGCTCCTAATCCTGGAGCAAGAGACTCTACTGGTGTGATAAATTGCCTG
AAGAAATGAATGACATGAAAATTCGTGACGATAAAGAAATGGAAGCGACAGTGGTAGATGGA
AATGGAACAGAGACTGGACATATCATTTGTGACTACTATTGGTGGTAGAAATGGCCAACCAAA
ACAGACAATTAGCTACATGGCTGAGCGTGTGTTGGTGCACGGATCTTTTGGTGTGTTGTGTTCC
AAGCGAAATGTCTTGAGACAGGAGAACTGTTGCGATAAAGAAAGTTTTACAAGATAGGAGG
TACAAGAACCGTGAGCTTCAAACCATGAGGCTACTTGACCATCCTAATGTTGTGTCTCTGAA
ACATTGTTTCTTCTCAACCACTGAAAAAGATGAGCTTTACCTCAATCTTGTTCTTGAGTACG
TTCCAGAACTGTTTCATCGTGTTATCAAACACTACAACAACTGAATCAGAGAATGCCTCTT
ATATACGTCAAACCTTTACTATTATCAGATTTTATAGAGCCTTATCTTACATTCACCGATGCAT
TGGTGTGTGTATCGTGACATAAAACCTCAAACTTGTTGGTAAATCCGCACACTCATCAAG
TAAAGCTATGTGATTTTGGAAAGTGCAAAGTATTGGTAAAAGGAGAACCAAAACATTTCTAC
ATCTGCTCGAGGTATTACAGAGCACCTGAACTTATTTTTGGAGCAACCGAGTATACGACAGC
CATTGATGTCTGGTCTGCAGGATGTGTTCTAGCTGAACTATTGCTTGGACAGCCCTTGTTCC
CTGGTGAGAGCGGTGTTGATCAACTTGTAGAGATTATCAAGGTCTTGGGAACGCCTACTAGA
GAAGAAATCAAGTGCATGAACCCAACTACACGGAATTCAAATTCCCTCAGATTAAAGCTCA
TCCATGGCACAAGATTTTCCACAAACGCATGCCTCCAGAAGCTGTTGATTTGGTCTCAAGAC
TTCTTCAATACTCTCCTAATCTACGAAGTGCCGCTCTCGACACATTAGTCCACCCATTCTTT
GATGAGTTAAGAGACCCAAACGCACGTCTACCTAATGGACGTTTCCTTCCACCGCTTTTCAA
CTTCAAGCCTCACGAGCTGAAAGGTGTACCATTGGAGATGGTAGCTAAGTTAGTACCTGAGC
ATGCAAGGAAGCAGTGTCTTGGCTCGGTTTGTGATTTCTCTTAATGTAGCATGAACACAA
CAAACACTTCTTATAAATTACCTCTCTATGTATCAATATGTCACAACTGATATGCACCCTT
TGTTTGTGTATGAGTAGAGAAAAAAGAGTTATTACTATGGTTGGTTGGTTCATAATGTAA
AAGCCACCAAGATTTTTTATC

FIGURE 16 (continued)

91/104

SEQ ID NO 153 - *Arabidopsis thaliana* - At5g26750 - SHAGGY
alpha

MASVGIAPNPGARDSTGVDKLPEEMNDMKIRDDKEMEATVVDGNGTETGHIIVTTIGGRNGQ
PKQTISYMAERVVGHGSFGVVFQAKCLETGETVAIKKVLQDRRYKNRELQTMRLLDHPNVVS
LKHCFFFSTTEKDELYLNLVLEYVPETVHRVIKHYNKLNQRMPLIYVKLYTYQIFRALSIIHR
CIGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFGATEYT
TAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYTEFKFPQIK
AHPWHKIFHKRMPPEAVDLVSRLQYSPNLRSAALDTLVHPFFDEL RDPNARLPNGRFLPPL
FNFKPHELKGVPLEMVAKLVPEHARKQCPWLGL

SEQ ID NO 154 - *Arabidopsis thaliana* - NM_180189 - ASK-gamma

CAGACCAACAACAAAAAGGAGATAAAGAGAAGAGGATTCATCATCATCAATCAATCCTTCAT
TTTATGGATCTACTCATATCTTGATTCTTCCTTCTATCTCTCCCTTTTCTTCCATCTCTTTT
TCTCTGGGTTTCCCCGATTTGAAGAGCGTGACAAAGGAAGAATCTTTTATTAAACAAATTC
TTCTGTTTTAATCTTGGGATGGCCTCGGTGGGCATAGAGCCTAGTGCCGCGGTTAGAGAATC
TACTGGAAACGTTACTGATGCTGATAGATTACCCGAGGAGATGAAGGACATGAAAATTCAAG
ATGATAAAGAAATGGAAGCTACGATTGTTAATGGCAATGTGACTGAGACTGGCCATATAATA
GTAATACTATAGGAGGAAGAAATGGCCAGCCAAAACAGACAATCAGTTACATGGCGGAGCG
AGTTGTTGGACATGGCTCCTTTGGTGTGTGTTCAGGCCAAATGTTTAGAAACAGGAGAAA
CTGTTGCTATAAAGAAAGTTCTACAAGATCGGAGGTACAAGAATCGTGAGCTTCAAACAATG
AGGCTACTTGACCATCCAAATGTTGTGTCTTTGAAACATTGTTTCTTCTCTACAACCGAAAA
AGATGAGCTTTATCTCAACTTGGTTCTGGAATACGTTCCGGAAACTGTGCACCGCGTCATCA
AACACTACAACAACTTAACCAACGAATGCCTCTCGTTTACGTCAAACCTTTACACTTATCAG
ATTTTTAGGTCCTTATCCTACATTACCGATGTATCGGCGTATGTCATCGAGACATCAAACC
TCAAACCTTGTTGGTAAATCCACACACTCATCAAGTGAAACTATGCGATTTTGGAGGTGCGA
AAGTATTGGTTAAAGGAGAGCCAAACATTTTCATACATTTGCTCGAGGTATTACAGAGCACCT
GAGCTCATTTTTTGGAGCCACCGAGTATACTACAGCCATTGATGTCTGGTCTGCAGGATGTGT
TCTCGCCGAGCTTCTTCTCGGGCAGCCATTGTTCCCGGGTGAGAGCGGTGTTGATCAACTTG
TAGAGATTATAAAGGTTTTGGGAACACCAACAAGGGAAGAAATCAAATGCATGAACCCGAAT
TACACAGAGTTCAAATTTCTCTCAGATTAAAGCTCATCCATGGCATAAGATTTTCCACAAGAG
AATGCCTCCAGAAGCTGTTGATTTGGTCTCAAGGCTTCTTCAATACTCTCCCAATCTCCGTT
GTGCTGCTCTTGATTCATTGGTCCACCCATTCTTTGACGAGCTAAGAGATCCGAATGCGCGA
TTACCCAACGGACGTTTCCTTCCACCGCTCTTTAACTTTAAGCCTCATGAACTTAAAGGTGT
GCCTGTGGAGATGGTGGCGAAGTTAGTTCCAGAACATGCGAGGAAGCAATGTCCGTGGCTCA
GTTTGTGATTTGTTCTCACCTGCAAACACGAAAAGTAGAGCAAAGCAGTCGAGATATTCATC
TCTTCTCTCTCTCTCTCTCTGTATTAATATTATTATAATGATCATATCTCAATCTGATG
ATTTAGTAACCCCTTGTGTTGTGATGAGTAGAGAAAGAGTGAATCATTTGTGGGGGTTATG
ATATTGTATAAGCCAACAAAGATTATTTTTTAAAGAGAGTTTCGTGTTTTCTGTCTC

FIGURE 16 (continued)

92/104

SEQ ID NO 155 - *Arabidopsis thaliana* - At3g05840 - ASK-gamma

MASVGIEPSAAVRESTGNVTDADRLPEEMKDMKIQDDKEMEATIVNGNVTETGHIIVTTIGG
RNGQPKQTISYMAERVVGHGSFGVVFQAKCLETGETVAIKKVLQDRRYKNRELQTMRLLDHP
NVVSLKHCFSTTEKDELYLNLVLEYVPETVHRVIKHYNKLNQRMPLVYVKLYTYQIFRSLS
YIHRCIGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFGA
TEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYTEFKF
PQIKAHPWHKIFHKRMPPEAVDLVSRLQYSPNLRCAALDSLHPFFDEL RDPNARLPNGRF
LPPLFNFKPHELKGPVEMVAKLVPEHARKQCPWLSL

SEQ ID NO 156 - *Arabidopsis thaliana* - X68525 - ASK-alpha

CTCAGATCGATGAAGAGAAGAATTAGGATTTTTACGTTTTTCATCGGCTTGAAAGTTTGAAGA
GTTTTGTAGCCTGAAAAATGGCGTCAGTGGGTATAGCTCCTAATCCTGGAGCAAGAGACTCT
ACTGGTGTTGATAAATTGCCTGAAGAAATGAATGACATGAAAATTCGTGACGATAAAGAAAT
GGAAGCGACAGTGGTAGATGGAAATGGAACAGAGACTGGACATATCATTGTGACTACTATTG
GTGGTAGAAATGGCCAACCAAAACAGACAATTAGCTACATGGCTGAGCGTGTTGTTGGTCAC
GGATCTTTTGGTGTTGTGTTCCAAGCGAAATGTCTTGAGACAGGAGAACTGTTGCGATAAA
GAAAGTTTTACAAGATAGGAGGTACAAGAACCGTGAGCTTCAAACCATGAGGCTACTTGACC
ATCCTAATGTTGTGTCTCTGAAACATTGTTTCTTCTCAACCACTGAAAAAGATGAGCTTTAC
CTCAATCTTGTTCTTGAGTACGTTCCAGAACTGTTTCATCGTGTTATCAAACACTACAACAA
ACTGAATCAGAGAATGCCTCTTATATACGTCAAACCTTACACTTATCAGATTTTTAGAGCCT
TATCTTACATTCACCGATGCATTGGTGTGTGTCATCGTGACATAAAACCTCAAACCTTGTTG
GTAAATCCGCACACTCATCAAGTAAAGCTATGTGATTTTGGAAAGTGCAAAAGTATTGGTAAA
AGGAGAACCAACATTTCTACATCTGCTCGAGGTATTACAGAGCACCTGAACTTATTTTTG
GAGCAACCGAGTATACGACAGCCATTGATGTCTGGTCTGCAGGATGTGTTCTAGCTGAACTA
TTGCTTGGACAGCCCTTGTTCCCTGGTGAGAGCGGTGTTGATCAACTTGACACATTATCAA
GGTCTTGGGAACGCCTACTAGAGAAGAAATCAAGTGCATGAACCCAACTACACGGAATTCA
AATTCCTCAGATTAAAGCTCATCCATGGCACAAGATTTTCCACAAACGCATGCCTCCAGAA
GCTGTTGATTTGGTCTCAAGACTTCTTCAATACTCTCCTAATCTACGAAGTGCCGCTCTCGA
CACATTAGTCCACCCATTCTTTGATGAGTTAAGAGACCCAAACGCACGTCTACCTAATGGAC
GTTTCCTTCCACCGGCTTTTCACTTCAAGCCTCACGAGCTGAAAGGTGTACCATTGGAGATG
GTAGCTAAGTTAGTACCTGAGCATGCAAGGAAGCAGTGTCCTTGGCTCGGTTTGTGATTTCC
TCTTAATGTAGCATGAACACAACAAACACTTCTTATAAATTACCTCTCTATGTATCAATATG
TCACAAACTGATATGCACCCTTTGTTTGTGTTGATGAGTAGAGAAAAAAGAGTTATTACTAT
GGTTGGTTGGTTCATAATGTAAAAGCCCACCAAGATTTTTTATCTAGATAAAGAGTTTGCTA
AAAAAAA

FIGURE 16 (continued)

93/104

SEQ ID NO 157 - *Arabidopsis thaliana* - CAA48538 - ASK-alpha

MASVGIAPNPGARDSTGVVDKLPPEEMNDMKIRDDKEMEATVVDGNGTETGHIIVTTIGGRNGQ
PKQTISYMAERVVGHGSFGVVFQAKCLETGETVAIKKVLQDRRYKNRELQTMRLLDHPNVVS
LKHCFSTTEKDELYLNLVLEYVPETVHRVIKHYNKLNQRMPLIYVKLYTYQIFRALSYIHR
CIGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISIYICSRYYRAPELIFGATEYT
TAIDVWSAGCVLAELLLGQPLFPGESGVDQLVHIKVLGTPTREEIKCMNPNYTEFKFPQIK
AHPWHKIFHKRMPPEAVDLVSRLQLQYSPNLRSAALDTLVHPFFDEL RDPNARLPNGRFLPPA
FHKPHELKGVPLEMVAKLVP EHARKQCPWLGL

SEQ ID NO 158 - *Arabidopsis thaliana* - NM_121468 - protein kinase family protein

ATTGGGGTCCGCTCTCTCTCTCTCTGCCATCAGAAGAAAAACCAAACACCGAGACAAAA
CACATCACGAAGAAGAGAGAGATTGCCATTTTCGGCAAGGAAGTGTTTTATTCTAGGGCTT
CTCTAGTTGCTGCGTAGACAAGATGGTGGAGTGAAATTGCGGCGGTGACTTTTCAGATTGAC
AAATTGAATTAAAGATCTTGAATACATATGGCTTCTGTGGGAACATTACCAGCTTCTTCTAT
GGCTACAAAACAAAGCAATGCTTCTATATGCGCTGAAAAATTACCTGAAGGGATTAATGAGA
TGAAGATAAAAGATGATAAGGAAATGGAAGCAGCTGTGGTTGATGGGAATGGAAGTAAACA
GGTCACATTATTGTTACAACCTATTGGTGGTAAAAATGGTCAGCCTAAACAGACCATAAGTTA
TATGGCAGAGCGCATCGTTGGACAAGGTTCTTTTGGAAATCGTTTTTCAGGCCAAGTGTTTAG
AAACGGGGGAAACTGTTGCAATCAAGAAAGTTTTGCAAGACAAGAGATACAAGAATCGGGAG
CTGCAGACAATGCGTCTTCTTGATCACCTAATGTTGTATCCCTCAAGCATTGTTTTTCTC
AACGACTGAAAAAGATGAGCTCTATCTCAATCTGGTCCTTGAATACGTTCTGAGACTGTCT
ATCGCGTCTCAAAGCACTATAGTCGGGCAAACCAGAGGATGCCCATTTATATATGTTAAACTC
TATACTTATCAGATTTGCAGAGCTTTGGCTTATATTCATGGTGGAGTAGGAGTCTGCCACAG
AGACATAAAACCACAGAATCTTCTGGTTAATCCTCATAACGCATCAGGTCAAACCTATGCGATT
TTGGTAGCGCAAAAGTTCTGGTTAAAGGCGAGCCAAACATCTCATAACATCTGCTCCCGTTAC
TATCGAGCACCTGAACTTATATTTGGAGCTACAGAATATACAACAACAATTGACATATGGTC
TGCAGGCTGTGTTCTTGCTGAATTGCTTCTGGGACAGCCTCTATTTCCAGGTGAGAGTGGAG
TTGACCAGCTAGTTGAGATAATAAAGGTTCTTGGAACACCAACACGGGAGGAAATCAAATGC
ATGAATCCAACTACACAGAATTCAAATTCGCGCAATAAAGGCTCATCCTTGGCACAAAAT
ATTCCATAAGCGTACACCTCCAGAAGCTGTAGACCTTGTCTCAAGACTTCTCCAGTATTCTC
CAAACCTCAGATCAACCGCTATGGAGGCGATAGTTCACCCGTTCTTCGATGAGCTACGTGAT
CCCAATACACGTCTTCTTAATGGTCGTGCCTTGCCCTCTCTTCAACTTTAAACCTCAAGA
GCTAAAAGGAGCAAGTTTAGAGTTGTTGTCCAAGCTTATACCTGACCACGCCCCGAAAACAAT
GTTCTCTCCTCGCTCTCTAAATCTCTTCTCTCTCTCTATATATATGTGTGTGTGTGTAT
GTACACATGCATATAATATGCTTATCGTTTCTAAGTAATGGAGATAGCTTCTCAGGATTATC
ATTAGCTTTCATCTTTCATGTATCTTTGTTGTTTATTGTCTTATCACAACCTTTGTACTTTA
TTACATACAATGATTAGTGAATGTATGTGACGGTCTTTGACTCGCCGGTCGCTACAGTTAT
GTTGGATACTAAATTATAAAATAAACTTCTCGCTCGTC

FIGURE 16 (continued)

94/104

SEQ ID NO 159 - *Arabidopsis thaliana* - At5g14640 - protein kinase family protein

MASVGTLPASSMATKQSNASICAELKPEGINEMKIKDDKEMEAADVVDGNGTETGHIIVTTIG
 GKNQPKQQTISYMAERIVGQGSFGIVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLDH
 PNVVSLKHCFSTTEKDELYLNLVLEYVPETVYRVSKHYSRANQRMPIIYVKLYTYQICRAL
 AYIHGGVGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFG
 ATEYTTTIDIWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYTEFK
 FPQIKAHPWHKIFHKRTPPEAVDLVSRLQLQYSPNLRSTAMEAIVHPFFDEL RDPNTRL PNGR
 ALPPLFNFKPQELKGASLELLSKLIPDHARKQCSFLAL

SEQ ID NO 160 - *Arabidopsis thaliana* - Y12710 - shaggy-like kinase gamma

ATGGCCTCGGTGGGCATAGAGCCTAGTGCCGCGGTTAGAGAATCTACTGGAAACGTTACTGA
 TGCTGATAGATTACCCGAGGAGATGAAGGACATGAAAATTCAAGATGATAAAGAAATGGAAG
 CTACGATTGTTAATGGCAATGTGACTGAGACTGGCCATATAATAGTAAC TACTATAGGAGGA
 AGAAATGGCCAGCCAAAACAGACAATCAGTTACATGGCGGAGCGAGTTGTTGGACATGGCTC
 CTTTGGTGTGTGTGTTTCAGGCCAAATGTTTAGAAACAGGAGAAACTGTTGCTATAAAGAAAG
 TTCTACAAGATCGGAGGTACAAGAATCGTGAGCTTCAAACAATGAGGCTACTTGACCATCCA
 AATGTTGTGTCTTTGAAACATTGTTTCTTCTCTACAACCGAAAAAGATGAGCTTTATCTCAA
 CTTGGTTCTGGAATACGTTCCGGAAACTGTGCACCGCGTCATCAAACACTACAACAACTTA
 ACCAACGAATGCCTCTCGTTTACGTCAAAC TTTACACTTATCAGATTTTTAGGTCTCTTATCC
 TACATTACCGATGTATCGGCGTATGTCATCGAGACATCAAACCTCAAACCTTGTGTTGTA
 TCCACACACTCATCAAGTGAAACTATGCGATTTTGGAAGTGCGAAAGTATTGTTTAAAGGAG
 AGCCAAACATTTTATACATTTGCTCGAGGTATTACAGAGCACCTGAGCTCATTTTTTGGAGCC
 ACCGAGTATACTACAGCCATTGATGTCTGGTCTGCAGGATGTGTTCTCGCCGAGCTTCTTCT
 CGGGCAGCCATTGTTCCCGGGTGAGAGCGGTGTTGATCAACTTGTAGAGATTATAAAGGTTT
 TGGGAACACCAACAAGGGAAGAAATCAAATGCATGAACCCGAATTACACAGAGTTCAAATTT
 CCTCAGATTAAAGCTCATCCATGGCATAAGATTTTCCACAAGAGAATGCCTCCAGAAGCTGT
 TGATTTGGTCTCAAGGCTTCTTCAATACTCTCCCAATCTCCGTTGTGCTGCTCTTGATTCAT
 TGGTCCACCCATTCTTTGACGAGCTAAGAGATCCGAATGCGCGATTACCCAACGGACGTTTC
 CTTCCACCGCTCTTTAACTTTAAGCCTCATGAACTTAAAGGTGTGCCTGTGGAGATGGTGGC
 GAAGTTAGTTCCAGAACATGCGAGGAAGCAATGTCCGTGGCTCAGTTTATGA

SEQ ID NO 161 - *Arabidopsis thaliana* - CAA73247 - shaggy-like kinase gamma

MASVGIEPSAAVRESTGNVTDADRLPEEMKDMKIQDDKEMEATIVNGNVTETGHIIVTTIGG
 RNGQPKQQTISYMAERVVGHGSFGVVFQAKCLETGETVAIKKVLQDRRYKNRELQTMRLLDHP
 NVVSLKHCFSTTEKDELYLNLVLEYVPETVHRVIKHYNKLNRMPPLVYVKLYTYQIFRSL
 YIHRICIGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFGA
 TEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYTEFKF
 PQIKAHPWHKIFHKRMPPEAVDLVSRLQLQYSPNLRCAALDSL VHPFFDEL RDPNARLPNGRF
 LPPLFNFKPHELKGVPVEMVAKLVPEHARKQCPWLSL

FIGURE 16 (continued)

95/104

SEQ ID NO 162 - *Zea mays* - AY103545 - DNA sequence

TTGACTGCAGGCCTCGGCACGGTAGGCACAAATCATTTTGGCCGCTGCGTCGCGTTGGGAGC
AGTATTCTACTGTGCCTGCGTCCCGACAAGCGAAAAGAAGAGACGGGGGAGGGTGGGAGAAC
GGATACCGAAAGGGGTAGGAGAGTGAGCAGCCAGAGAACAGGGAGGTAGAGAGGAGGAGGAG
GTAGAAGGCGAAAGAAGGGGAACCAAATCTTGGACGGGAACACATAGATTTCTTTGGTGGAG
GAAGGAGGAGGGCAACAAGAGGAGGTTACAGGTAGCCCAATAGATCTACTGCTGTTGAGGGA
GTTGATGCAAAGCTGAGTTGCTGCGCGTTGGCTTTCTTTAGAGATGGCTTCAGCTGGTGTG
CCCCTTCTGGGTACAAGAACAGCAGCAGCACCAGCATTGGTGCCGAAAAGTTGCAAGATCAC
ATGAACGAGCTAAAGATTAGAGATGATAAGGAAGTTGAAGCAACCATAATTAATGGGAAAGG
GACTGAAACTGGGCACATAATTGTCACCACTACTGGTGGCAAGAATGGTCAACCAAAACAGA
CAGTGAGCTACATGGCTGAGCGCATTGTAGGTCAAGGTTCTTTGGGATCGTCTTCCAGGCC
AAGTGTTTGGAAACGGGTGAGACTGTTGCCATAAAGAAGGTTCTTCAAGACAAGCGTTACAA
GAACCGCGAACTGCAGACCATGCGCCTTCTTGACCACCCTAATGTTGTTGCTTTGAAGCATT
GCTTCTTTTCAACTACTGAGAAGGATGAGCTTTATCTGAACTTGGTCCTTGAGTATGTTCCG
GAGACAGTTCATCGAGTTGTGAAACATCACAAAGATGCACCAACGCATGCCACTTATTTA
TGTGAAGCTTTATATGTACCAGATATGTAGAGCATTGGCTTACATTCATGGTACTATCGGTG
TCTGCCACAGAGATATTAAGCCACAAAATCTTCTGGTGAACCCACACACCCACCAGCTTAAA
ATATGTGACTTTGGTAGTGCAAAAGTTCTGGTCAAGGGGAACCAACATATCATACTCTG
CTCGCGATACTATAGGGCTCCAGAGCTCATATTTGGTGCCACTGAGTATACCACAGCGATTG
ACATTTGGTCTGCTGGATGTGTTCTTGCTGAGCTTATGCTAGGGCAGCCTTTGTTTCCGGGT
GAAAGTGGTGTGGACCAACTTGTGAAATCATCAAGGTCCTCGGTACGCCAACAAGGAAGA
AATTAAATGCATGAACCCAAATTACACAGAGTTTAAGTTCCACAAATCAAAGCACACCCAT
GGCACAAGGTATTCACAAAAGGATGCCGCCAGAAGCTGTTGATCTGGTCTCTCGGCTACTC
CAGTACTCCCCAAATCTGAGATGCACTGCTATGGAGGCACCTTGTTACCCATTCTTTGATGA
GCTTCGAGATCCTAATACTCGCCTTCCAAATGGTCGCTTTTGGCCACCACTATTCAATTTCA
AGCCTCACGAACTTAAAGGAGTCCCATCAGACATTGTTGCGAAATTGGTTCCAGAACATGCG
AAGAAGCAATGCTCTTATGTTGGATTGTGAAATGACCGCGCCTTGGGACTGGAACCTGAGGT
CGCAATCGTGCAATTTCCCCTGGGATGTTGGATGATCTTGAGGCATGCGAGCCTGTTGTTGAA
GATGCAAGGTTACGTACTTGTACGACAATGTGACCTGTGTAGCTGAGTAGTCTATGTCGCAG
TGACATGTAACGGCACCCCCCTTCTACTAACTGACGCTTACTCGAGATTGCCATAGTTGAT
CTTGTAATTTGTTATAGAGCAGTATGAATGTATTTATGGTAGCTTGAATCTATGTATGGATT
CACTTCGTTTTTCCATGTTTCTTGTCTCCAGACCCAGATTGCTACCGTATTGTTTCAGAAT
TCCTAGCTACCTGTTGCCTAAAAAATAAAAAAATCCTCGTGC

SEQ ID NO 163 - *Zea mays* - AY103545 - protein sequence

MASAGVAPSGYKNSSSTSIGAEKLQDHMNELKIRDDKEVEATIINGKGTETGHIIVTTTGGK
NGQPKQTVSYMAERIVGQGSFGIVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLDHPN
VVALKHCFSTTEKDELYLNLVLEYVPETVHRVVKHNMHQRMPLIYVKLYMYQICRALAY
IHGTIGVCHRDIKPQNLLVNPHTHQLKICDFGSAKVLVKGEPNISYICSRYYRAPELIFGAT
EYTTAIDIWSAGCVLAELMLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYTEFKFP
QIKAHPWHKVFHHRMPPEAVDLVSRLQLQYSPNLRCTAMEALVHPFFDEL RDPNTRLPNGRFL
PPLFNFKPHELKGVPSDIVAKLVPEHAKKQCSYVGL

FIGURE 16 (continued)

96/104

SEQ ID NO 164 - *Zea mays* - AY108486 - DNA sequence

GCACGAGCCGCGCCGGAGTTGGAGGAGGGAGAGGGGACAAGCTTTCGGGCGCCGACGCCGAC
 GCGGACCCGCGCCGACACGATCCGGTGGATCAAGTGCATCACACCTTTAGGGAGGCCCCTT
 GGACAGCAGTTTGTGCTGCAAATTCTATATAGCTCTGTGCGAGCATGGCCTCGGTGGGCGTG
 GCACGCTCTTCTTTGGGATTTTCAGAATGGCACAAGTTCTAGCAGTGACCCAGATCGTCTTCC
 CAACGAGTTGGGCAGTATGAGCATAAGGGACGACAAGGACGTTGAAGATATTGTAGTCAATG
 GCAATGGGGCGGAGCCTGGTCATATCATAGTGACCAGCATTGATGGGAGAAAATGGGCAGGCA
 AAGCAGACCATTAGTTACATGGCTGAGCGGGTGGTAGGTCATGGGTCCCTTCGGAACCGTTTTT
 CCAGGCCAAGTGTCTTGAACTGGTGAGACCGTAGCTATAAAAAAGGTTCTTCAAGACAAGA
 GATACAAGAATCGTGAGCTGCAAACCATGCGAGTGCTTGACCACCCAAATGTGGTGGCTCTA
 AAGCACTGTTTCTTCTCAAAGACTGAGAAAGAGGAGCTTTACCTCAATTTGGTGCTTGAGTA
 TGTACCGGAGACTGCTCATCGTGTTCATCAAACATTACAACAAGATGAACCAGCGCATGCCTT
 TGATTTATGCAAACTGTATATGTATCAGATTTGTAGAGCCTTGGCATAACATTCACAACAGC
 ATTGGAGTGTGCCACAGGGACATTAAGCCGCAAAATCTCCTGGTTAATCCTCATACCCATCA
 GCTAAATTTGTGTGACTTTGGCAGCGCGAAAGTTCTGGTAAAAGGCGAACCACAAACATTTCTT
 ACATCTGTTCTAGGTACTACAGAGCTCCAGAGCTCATATTTGGTGCTACTGAATACACAACA
 GCCATTGATGTTTGGTCTGCTGGCTGTGTGCTCGCTGAGCTGCTTCTAGGACAGCCTCTGTT
 CCCTGGAGAAAGCGGTGTTGATCAGCTTGTGAAATCATCAAGGTTCTGGGCACACCCACAC
 GTGAAGAAATTAAGTGCATGAATCCAAATTATACCGAGTTTAAATTTCCCGCAAATCAAAGCT
 CACCCATGGCATAAGATATTCCATAAAAGGATGCCTGCTGAAGCGGTAGATCTCGTGTCCAG
 GCTTCTGCAGTACTACCAAACTTCGGTCGACTGCTTTGGAAGCATTGGTCCATCCGTTCT
 TTGATGAACCTTCGGGATCCAAACACCCGCTTACCGAATGGTCGTTTTCTTCCGCCTCTCTTC
 AATTTTAAGCCCCATGAGCTGAAGAACGTGCCGGCGGATTTTCATGGTGAAATTGGTCCCTGA
 GCATGCACGGAAGCAATGTGCCTTCGTAGGGTGGTGATCTCTGGATAAGAGGATGACGACTC
 GATGATTAGCTGAGGACCAAGTTAATGTCTGTGTTAGAACTGCCGAGATCGACATTGCCAGA
 TGTGGTGTGGTATAAGATAGGCAATATGTGTGATTATTTTTTTGTTTCGAGGTTATCACCCCCC
 TTGCCCCAGAAAAGATGAGAAGATGTCGATGTAACAAGCCCTCTGCGCTTCTGTAAGTAGAT
 GAGTGTGTGCTGCATGCCCCCTGGGTACATGTATCGGTTTGAGCAGAATTCTGTTTGCCTGAA
 TCGTGCCATCACACGCAGGGATCCATCCCTTGTGTGACGATGTTTCAGCCCCAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAA

SEQ ID NO 165 - *Zea mays* - AY108486 - DNA sequence

MASVGVARSSLGFQNGTSSSSDPDRLPNELGSMISIRDDKDVEDIVVNGNGAEPGHIIVTSID
 GRNGQAKQTI SYMAERVVGHGSFGTVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRVLDH
 PNVVALKHCFFSKTEKEELYLNLVLEYVPETAHRVIKHYNKMNQRMPLIYAKLYMYQICRAL
 AYIHNSIGVCHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFG
 ATEYTTAIDVWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYTEFK
 FPQIKAHPPWHKIFHKRMPAEAVDLVSRLQYSPKLRSTALEALVHPFFDEL RDPNTRL PNGR
 FLPLPLFNFKPHELKNVPADFMVKLVPEHARKQCAFGW

FIGURE 16 (continued)

97/104

SEQ ID NO 166 - *Medicago sativa* - X68409 - AMMSK3A

TTTTTTTTTTTTTTTTTTTTTTTTTCAAAATATTTTCCATTTGTCTCTTCTTTCTTCTTTCTTAAT
TCCGAATCCCACGGATTTCACTTCCATTCAAAGTCATAGCTAGATCCAATCCATTCCATTCC
TCTGTTTGAGTTGAAGAGTTGATTGTTGGGGTTGGATGTTTCAGTTTTGAAGCTGTGTATGATC
TGAAAGGAAATAATTAAGTAAAGTGTTTTGCACTTTTTTTAAGAAGATATGATGGCATCAGG
TGGTGTGTCACCTGCTTCTGGATTTATAGATAAGAATGCAAGTTCAGTTGGTGTGAAAAGT
TGCCTGAGGAGATGAATGACATGAAAATTAGGGATGATAAGGAAATGGAAGCCGCTACCATT
GTAGATGGAAATGGGACCGAAACCGGACATATAATTGTCACAACCATTGGTGGTAAAAATGG
CCAGCCAAAGCAGACAATAAGTTACATGGCCGAGCGTGTTGTTGGACATGGATCTTTTGGTG
TAGTTTTTTCAGGCAAAGTGTTTGGAGACTGGAGAACTGTGGCTATAAAGAAGGTTCTTCAA
GATAAGAGGTACAAGAACCGGGAATTGCAAACCTATGCGCCTTCTGGACCACCCTAATGTTGT
ATCTTTGAAGCACTGCTTCTTCTCAACGACTGAAAAGGACGAGCTTTATCTTAACCTGGTG
TTGAATATGTTCTGAGACTGTCAGCCGTGTGATTAGACACTACAACAAAATGAATCAAAGA
ATGCCTATGATATATGTCAAACCTTATTCTTACCAGATTTGCAGGGCACTTGCTTATATTCA
CAACAGTATTGGAGTATGTCACAGGGATATTAAACCTCAAAATTTACTGGTCAATCCTCACA
CCCACCAACTGAAGATATGCGACTTTGGAAGTGCTAAAGTCTTGGTAAAAGGTGAACCAAAC
ATATCTTACATCTGTTCTAGGTACTATAGAGCTCCTGAGCTTATATTCGGTGCAACTGAGTA
CACCACAGCCATTGACATCTGGTCAGCTGGTTGCGTACTTGGTGAACCTTTTGCTTGGCCAGC
CACTGTTTCTGGTGAGAGTGGAGTAGACCAACTTGTGGAAATTATCAAGGTTTTAGGCACC
CCAACAAGGGAAGAAATCAAGTGCATGAATCCTAATTATACAGAGTTTAAATTTCTCTCAAT
CAAAGCTCATCCATGGCATAAGATTTTTTCAACAAGAGAATGCCTCCTGAAGCTGTGGATCTTG
TCTCAAGACTATTGCAATACTCTCAAATCTTTCGAAGCACAGCTTTGGAGGCTTTGGTTTCA
CCATTCTATGATGACGTGCGCGATCCAAACACTCGGTTGCCAAATGGGCGTTTCTCTCCACC
ATTATTTAACTTCAAAGTCAATGAGCTCAAGGGAGTACCTGCAGAGATGCTGGTGAAACTGG
TTCCACCTCATGCAAGAAAGCAATGTGCCTTGTTTCGGGTCATCATGAAGCAGCCTTGTGTAG
TTATTAAGTACTTTCTTCTACCTATGTAAAGGTGTATCTAGTCAAATTTCAAGTGGTTAAAT
AGGTTATTTCTATTTTCTTCTGTTTGATTGTTTCTCACCCAACCTACCATCCAATTTATTA
TTATTTTTCTTCTCGATGTAGAAGAAAGCTGTGCTGTTTAAGAAGCAACTTCAGCTTGATT
ATTACTTTGTAGGATCTGATGTGTTCACTCACCTAACATGAACCATTGTTTATTGAAGTGA
TAGACTTGATCACAACTCACTGAACTAGTAGGAGATGTTTCAAATCTTGAAAAAAAAAAAA
AA

SEQ ID NO 167 - *Medicago sativa* - CAA48472 - AMMSK3A

MMASGGVAPASGFIDKNASSVGVEKLPEEMNDMKIRDDKEMEAATIVDGNGTETGHIIVTTI
GGKNGQPKQTISYMAERVVGHGSFGVVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLD
HPNVVSLKHCFSTTEKDELYLNLVLEYVPETVSRVIRHYNKMNQRMPIYVKLYSYQICRA
LAYIHNSIGVCHRDIKPQNLLVNPHTHQLKICDFGSAKVLVKGEPNISYICSRYYRAPELIF
GATEYTTAIDIWSAGCVLGELLGQPLFPGESGVDQLVEIIKVLGTPTREELKCMNPNYTEF
KFPQIKAHPPWHKIFHKRMPPEAVDLVSRLQLQYSPNLRSTALEALVHPFYDDVRDPNTRL PNG
RFLPPLFNFKVNELKGVPAEMLVKLVPHPHARKQCALFGSS

FIGURE 16 (continued)

98/104

SEQ ID NO 168 - *Medicago sativa* - X68411 - AMMSK1A

GAGCACATGCTTTGGTTTCGTTTCGTTGGTGGATGAGTGGTTAAAATTGAAAGGGTTTCAGT
 GGCAATGGCGTCGGTTGGTGTTCACCAACTTCAGGTTTTAGAGAAGTCCTTGGTGATGGTG
 AAATTGGTGTGATGATATATTGCCAGAGGAAATGAGTGATATGAAAATTAGGGATGATAGA
 GAAATGGAAGCCACCGTTGTTGACGGCAATGGAACGGAGACAGGACATATCATTGTCACTAC
 TATTGGTGGTAGAAATGGTCAGCCAAAGCAGACTATAAGCTATATGGCAGAGCGTGTGTAG
 GACATGGATCATTTGGAGTTGTCTTCCAGGCTAAGTGCTTGGAACTGGTGAAACCGTGGCT
 ATCAAAAAGGTTCTTCAAGACAAGAGGTACAAGAACCGGAATTGCAAACAATGCGACTGCT
 TGATCACCCGAATGTCGTCTCTTTAAAGCATTGTTTCTTTTCAACCACCGAAAAGGATGAAC
 TATACCTGAATTTGGTACTTGAGTATGTTCTTGAAACAGTTCATCGCGTGATTAAGCATTAC
 AGCAAGTTGAACCAAAGGATGCCAATGATTTATGTGAAGCTCTATACATACCAGATCTTTAG
 AGCATTATCTTATATTCATCGTTGCATTGGAGTCTGTCATCGGGATATCAAGCCCCAAAATC
 TATTGGTCAATCCACACACCCACCAGGTTAAATTATGCGACTTTGGAAGTGCGAAAGTCTTG
 GTTAAAGGCGAACCAAATATATCGTATATATGTTCTAGATACTACAGAGCACCCGAGCTTAT
 TTTTGGAGCAACTGAATATACTACTGCTATTGATGTATGGTCTGTTGGTTGTGTTTTGGCTG
 AGCTGCTGCTTGGACAGCCATTGTTCCCAGGTGAGAGAGGAGTTGATCAGCTTGTTGAGATC
 ATCAAGGTTCTGGGAACCTCCGACAAGAGAAGAAATTAAATGCATGAATCCTAATTATACCGA
 ATTTAAATTCCCTCAAATCAAAGCACATCCATGGCACAAGATCTTCCATAAGCGCATGCCTG
 CAGAAGCTGTTGATTTGGTATCAAGATTATTACAATACTCCCCAAACCTGCGGTGCCAAGCT
 TTAGATTGCTTGACCCATCCTTTCTTCGATGAGCTTCGTGACCCAAATGCTCGCTTGCCAAC
 TGGCCGTTTCCTCCCACCACTGTTTAACTTCAAACCTCACGAACTGAAAGGAGTTCCAGTCG
 AGACCTTGATGAACTGGTTCCAGAGCATGCGAGGAAGCAATGCCCGTTTCTTGCTTGTA
 TATGTCGTAAATGTAACAAAACCTGCAAGTGTTGTTTCCATATGAACGTTCTATTTGATGAT
 ATGATATTTATTAGTATCTTTGTTGTATTTCGGTTGCCTGTGATAGAAAATTTAGAGATATAT
 GCTACCCAATATTACCCAAACCCTTATATGGGTATTTCAGAATACCCTTTTCTGTATCACAG
 CAGATTGTAACATGCAATAGAAGACAAGTGTCTACAATTATCTAAATGTTGTATCAGTATTT
 GTACTTGTATTTGTATTTGTGGAGATAATGACGGATTATTGCGTAAAAAAAAAAAAAAAAAAAA
 A

SEQ ID NO 169 - *Medicago sativa* - CAA48474 - AMMSK1A

MASVGVAPTSGFREVLDGEIGVDDILPEEMSDMKIRDDREMEATVVDGNGTETGHIIVTTI
 GGRNGQPKQTI SYMAERVVGHGSFGVVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLD
 HPNVVSLKHCFSTTEKDELYLNLVLEYVPETVHRVIKHYSKLNQRMPIYVKLYTYQIFRA
 LSYIHRICIGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISYICSRYYRAPELIF
 GATEYTTAIDVWSVGCVLAEELLGQPLFPGERGVDQLVEI IKVLGTPTREEIKMNPNYTEF
 KFPQIKAHPPWHKIFHKRMPAEAVDLVSRLQLQYSPNLRCQALDCLTHPFFDEL RDPNARLPTG
 RFLPPLFNFKPHELKGVVPVETLMKLVPEHARKQCPFLGL

FIGURE 16 (continued)

99/104

SEQ ID NO 170 - *Medicago sativa* - X68410 - AMMSK2A

GTTC AATTGAAGCTGCAAAAAAAAAAAAAATCTTGATCTACTTTGGTTGTGATAATGGCAAC
AGCGGGTGTAGCACCTGCTTCTGGAATAGTAGATGTAAATGCAAGTTCAGCTATTGCTGTTG
ATAAGTTACCTGATGAGATTCTTGGCATGAGAATTAAGGATGATAAGGAAATGGAAGCACAT
GTGGTAGATGGAAATAGTACTGAAGCAGGACATGTAATTGTCCTACCATTGGTGGTAAAAA
TGGCCAGCCAAAGCAGACAATAAGCTACATGGCTGAGCGTGCTGTTGGACAGGGATCATTG
GTGTAGTTTTCCAGGCTAAGTGCTTGGAGACAGGTGAACTGTGGCTATAAAAAAGGTTCTT
CAAGACAAGAGGTATAAGAACCGGGAATTGCAAACAATGCGCCTTCTGGACCACCCCAATGT
TGTAAC TTTGAAGCATTGTTTCTTTTCAACAAGTGAAGACGAGCTCTATCTTAAC TTGG
TACTTGAGTTTGTTTCTGAGACTGTCCATCGTGATCAGACACTACAGCAAATGAATCAG
AGGATGCCATTGATATACGTAAACTTTATTCTTACCAGATATGTAGATCACTAGCTTATAT
TCATAACTGTGTTGGAGTGTCTCATAGGGACATAAAACCTCAAAATTTACTGGTCAATCCTC
ACACCCATCAGCTGAAGCTGTGTGACTTTGGGAGTGCAAAAGTCTTGGTCAAGGGTGAACCA
AACATATCTTACATCTGTTTCGAGGTATTATAGAGCTCCTGAGCTTATATTTGGTGCAACTGA
ATACACCTCAGCCATTGACATTTGGTCAGCTGGCTGTGTGCTTGGCGAACTATTGCTTGGCC
AGCCTCTCTTTCCCGGTGCGAGTGGAGTAGACCAGCTCGTTGAAATTATCAAGGTTTTAGGT
ACCCCAACAAGGGAAGAAATAAAGTGTATGAATCCTAATTACACTGAGTTCAAATTCCCACA
AATCAAAGCTCATCCATGGCACAAGATCTTTGCAAGCGTATGCCACCGGAAGCTGTGGATC
TCGTCTCAAGACTACTTCAATACTCTCAAATCTTGAAGCACAGCTTTGGAGGCTCTGGTT
CATCCCTTCTTTGATGAATTGCGTGATCCAAATACCCGCTTACCAAATGGGCGACATCTTCC
TCCTTTATTTAACTTCAAAGCCAACGAGCTTAAGGGAGTGCCTGCTGAAATGCTGGTGAAGT
TGGTTCCGTCTCACGCAAGAAAGCAGTGTCTTTGTTTGCGTCGTATAGACTTAGAATGCT
GTCTTGTGTAAATATTATGGACTCCCTGTTGTAGAAATTGTATGTAGCCTGTTTCATGTTGT
TAATAGTCTCTCTTTTGTATTGTTGTTCCATTAATTTGTTTCTACCAAAGAAAACACCTCAG
TTTATTATAAGTTTCAAGTTGATCTCTCTTACGATTTAATTGTTCTCCTGATCTTCAATTA
TTAACAGATTGTATTAACTATTAATACTATTAATACTAGAACAAATTGTTTATTCTAGCG

SEQ ID NO 171 - *Medicago sativa* - CAA48473 - AMMSK2A

MATAGVAPASGIVDVNASSAIAVDKLPDEILGMRIKDDKEMEAHVVDGNSTEAGHVIIVTTIG
GKNGQPKQTI SYMAERAVGQGSFGVVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLDH
PNVVT LKHCFSTTEKDELYLNLVLEFVPETVHRVIRHYSKMNQRMPLIYVKLYSYQICRSL
AYIHNCVGVSHRDIKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFG
ATEYTS AIDIWSAGCVLGELLLGQPLFP GASGVDQLVEI IKVLGTPTREEIKCMNPNYTEFK
FPQIK AHPWHKIFRKRMPPEAVDLVSRL LQYSPNLRSTALEALVHPFFDEL RDPNTRLPNGR
HLPPLFNFKANELKGVPAEMLVKLVPSHARKQCSLFASS

FIGURE 16 (continued)

100/104

SEQ ID NO 172 - *Nicotiana tabacum* - X77763 - NtK-1

TCTCTCTCATCTTCCCTGCGATTCTCTCTCTCAATTTTCAGGTTTTCTCTGTTTCTGTGCGAG
CCTCTAATGATCGGTGTATTCTCAATATCCTGAAGATTTTCTGATTTTCATCGGTGAATGACT
TTTTGAGGTGATAATAGTTTCGAAAATTTTCAGGAAATGACTTCAGTAGGCTTAGCACCTGTA
TCCGGTTTGAGAGAATCCAGTAGCCATAGTGTTGGTGTAGATAGGCTGCCTGAGGAGATGAA
TGACATGAGAATCAGGGATGATAAGGAAATCGAAGCAGCTATTGTGGATGGTAATGGGACTG
AGACAGGCCATATAATAGTGACAACTATTGGTGGTAGACATGGTCAGCCAAAACAGACTATC
AGTTATATGGCTGAACGTATTGTTGGACAAGGATCATTGGAGTGGTTTTCCAGGCCAAAATG
CTTAGAGACTGGTGAACTGTTGCTATTAAAAAGGTTCTTCAAGACAAGAGATATAAGAACA
GGGAGCTGCAGACCATGCGTCTTCTTGATCACCCAAATGTTGTGTGCCTGAAGCACTGCTTC
TTTTCAACAACTGAGAAGGATGAAGTATATCTTAATTTGGTTCTTGAATACGTCCCTGAAAC
TGTCATCGTGTATTATAACACTACAATAAGTTGAATCAAAGGATGCCATTGATACTAGTGA
AGCTTTATACATATCAGATTTTCAGGGCATTGTCTTACATCCATCACACAATTGGAGTGTGC
CACAGGGACATAAAGCCTCAGAATCTTTTGGTGAATCCACATACTCACCAGGTTAAATTGTG
TGACTTTGGAAGTGCTAAAGTTCTGGTTAAAGGAGAACCAAATATTTCTTACATCTGCTCTA
GGTATTATAGAGCGCCTGAACTTATATTTGGAGCAACAGAGTACACTACCGCTATTGACATC
TGGTCTGCTGGCTGTGTTCTAGCCGAGCTACTTCTTGGGCAGCCTTTGTTTCCGGGTGAAAG
TGGAGTTGATCAGCTTGTGAGATTATTAAGGTCTTGGGTACTCCTACCAGGGAAGAAATTA
AATGCATGAATCCAAATTATAACGAGTTCAAATCCCCCAAATTAAAGCTCATCCGTGGCAC
AAGATATTTCAACAAGCGCATGCCTCCAGAAGCTGTTGATCTGGTTTCAAGACTACTGCAGTA
CTCACCTAACTTGCGTTGCACTGCTTTAGAGGCAGTGACCCATGCCTTCTTCGATGAGCTTC
GTGATCCTAATACACGCCTCCCAAATGGCCGCGTCCTTCCCCCCTTGTTTAACTTTAAGGCC
CATGAGTTAAAGGGTGTGTCTGCAGAGAATCTATTGAAGTTGGTTCCGGAGCATGCCAGGAA
ACAGTGCCCGTCCCTTGGTTTATGAGTTCCCACTGTACGGTAGATATAATTTAAGTGTAAGC
TATGTTATTTCTCTGTATCCATTTTTCCCCCTTTGCTCCCCACATGTACCAGTTGTCTCTTT
GTATTATTATCCTAGTTTGTAAGAGCAGAGGTAGGATGTGGTCTTTAACATTCTTACCTCC
AACACTTTCTTTTACCCTGTTCTTTTATGTCCTACTGTTGTAACCTTTTATGTGGTTAAGG
GTGGACTGCTTTCTATATGAACATTTATTTTATGATGAAATTTCAAAGTGATTTTTTAGTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO 173 - *Nicotiana tabacum* - CAA54803 - NtK-1

MTSVGLAPVSGLRESSSHSVGVDRLEPEEMNDMRIRDDKEIEAAIVDGNGTETGHIIVTTIGG
RHGQPKQTI SYMAERIVGQGSFGVVFQAKCLETGETVAIKKVLQDKRYKNRELQTMRLLDHP
NVVCLKHCFSTTEKDEVYLNLVLEYVPETVHRVIKHYNKLNQRMPLILVKLYTYQIFRALS
YIHHTIGVCHRDIKPQNLLVNPHTHQVKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFGA
TEYTTAIDIWSAGCVLAELLLGQPLFPGESGVDQLVEIIKVLGTPTREEIKCMNPNYNEFKF
PQIKAHPWHKIFHKRMPPEAVDLVSRLQLQSPNLRCTALEAVTHAFFDEL RDPNTRL PNGRV
LPPLFNFKAHKGVSAENLLKLVPEHARKQCP SLGL

FIGURE 16 (continued)

101/104

SEQ ID NO 174 - *Triticum aestivum* - AF525086 - GSK-like kinase

GTGGGTGTGGTGCGTCCTTCCTCGCGCTTTCAGAACGACACGAGTACTAGTGGTGATGCCGA
CCGACTTCCGAACGAGATGGGCAATATGAGCATAAGGGATGACAGGGACCCTGAGGATATAG
TAGTCAACGGCAATGGGACGGAACCAGGCCATATTATAGTCACAAGCATTGAGGGAAGAAAT
GGGCAAGCAAAACAGACCATTAGCTACATGGCTGAGCGTGTGGTTGGTAATGGGTCATTTGG
AACTGTTTTCCAGGCTAAGTGTCTTGAACTGGCGAGACGGTGGCTATAAAGAAGGTTCTTC
AAGACAAGAGATATAAGAACCGTGAGCTGCAAACGATGCGAGTCTTGACCACCCAAATGTT
GTGGCTTTAAAGCATTGTTTTTTCTCAAAGACTGAGAAAGAGGAGCTTTACCTCAACCTGGT
GCTTGAGTATGTGCCGAGACTGCTCATCGTGTCTTAAGCATTATAACAAGATGAACCAAC
GCATGCCATTGATATATGCAAACTGTACATGTATCAGATATGTAGATCTTTGGCATAACATT
CACAACAGCATTGGAGTATGCCACAGAGACATCAAGCCTCAAAATCTTCTGGTGAATCCACA
TACGCACCAATTGAAATTATGTGACTTCGGAAGTGCGAAAGTGTTGGTAAAAGGAGAACCAA
ATATTTCTATATCTGTTCAAGGTACTATAGAGCCCCAGAGCTCATATTTGGTGCTACTGAA
TACACAACGGCAATTGACGTTTGGTCTGCTGGCTGTGTTCTTGCTGAACCTCCTTCTAGGACA
GCCTATATTCCCTGGCGACAGTGGTGTGATCAGCTTGTTGAAATCATCAAGGTTTTAGGTA
CCCCTACAAGAGAAGAAATTAAGTGCATGAATCCAAATTATACGGAGTTTAAATTCCCACAA
ATCAAAGCTCACCCATGGCACAAGATCTTCATAAAAGAATGCCTGCTGAAGCAGTAGATCT
TGTCTCCAGACTCTTGCAATATTCACCAAGCCTGCGTTCAACTGCTTTGGAAGCATTAAATTC
ATCCATTCTTCGATGAACCTCCGGGACCCAAACACCCGTTTGCCGAACGGCCGTTTTCTTCCT
CCCCTCTTTAACTTTAAGCCCCATGAGTTGAAGGGTGTGCCGATGGACATCCTGGTGAAGCT
CATCCCTGAACATGCTCGGAAGAACTGTGCCTTTGTAGGATGGTGATCCGCCAGACGGCTGC
TTGAAGTTTtagttcagaacaaatccagttgttctactagaaaacccaggagtttgagatt
gtctgcagccacacgggatataaggcgatgacacatgtgattattattccttttctcgctccga
gacctcgatgccatgtattctttccccctactgccgatgtaacaaaccacccatgatactgt
aagtagatgagaagtgtttcgaccgttttccccctgagctcatgtgctatgcaatgaaggatg
caccctatgtaccgccaatatTTGGTCCAGTATTGTTCATGGATCGAGGCCCCCAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO 175 - *Triticum aestivum* - AAM77397 - GSK-like kinase

MGNMSIRDDRPEDIVVNGNGTEPGHIIVTSIEGRNGQAKQTISYMAERVVGNNGSFQTVFQA
KCLETGETVAIKKVLQDKRYKNRELQTMRLDHPNVVALKHCFFSKTEKEELYLNLVLEYVP
ETAHRVIKHYNKMNRMP LIYAKLYMYQICRSLAYIHNSIGVCHRD IKPQNLLVNPHTHQLK
LCDFGSAKVLVKGEPNISYICSRYYRAPELIFGATEYTTAIDVWSAGCVLAELLLGQPIFPG
DSGVDQLVEIIKVLGTPTREEIKCMNPNYTEFKFPQIKAHPPWHKIFHKRMPAEAVDLVSRL
QYSPSLRSTALEALIHPPFDELRLDPNTRLPNRFLPPLFNFKPHELKGVPM DILVKLIPEHA
RKNCAFVGW

FIGURE 16 (continued)

102/104

SEQ ID NO 176 - *Petunia hybrida* - X83619 - SHAGGY kinase 4

TCTCTCAGGTTTAGGGTTTCGTATTGTCCGATCGCTATACTTTGAAGCTCTTTCCGATCACT
GTTTTGTGTTTTTGTAATGTGAGCTGTTCTTTAGCTACAGGTTTGAAGCTGTTAATCTGT
CATTTGAGTTGTGCCCACTTACTCAGTAGTATAAGTAAGTTTATTTTTGTTGCTGATATGGCG
TCTGGTATAATGCCTTCGGCTGGTGGAACATCGAACTGATGCCATGCTTGTTGACAACT
TCCCGAAGAAATAAATGAAATGAAGATCAGAGATGATAAAGCAGAAAAGGAAATGGAAGCAG
CTGTAGTGGATGGAAATGGAAGTGAAGGAGCCACATCATCGTGACAACCTATTGGGGGCAAA
AATGGTGAGCCTAAGCAGACCATTAGTTACATGGCCGAGCGTGTGTTGGACAGGGTTCGTT
TGGAATAGTGTTCAGGCCAAATGCCTTGAACTGGAGAACTGTTGCAATAAAAAAGGTTT
TACAGGATAAGAGATACAAGAATCGGGAATTGCAACAATACGCCTTCTAGATCATCCTAAT
GTTGTTGCACTGAGGCACTGCTTCTTTTCAACCACAGAAAAGGATGAGCTTTATCTGAATTT
GGTCCTTGAATATGTACCAGAGACTGTCTACCGTGTCTTGAGACATTACAGCAAAGCAAACC
AACAGATGCCTATGATTTATGTCAAGCTCTACACATATCAGATTTTCAGAGCTTTGGCCTAC
ATACACGGCATAGGAGTCTGCCACAGGGACATCAAGCCTCAGAATCTACTGGTCAACCCCCA
CACCCACCAGCTTAAGCTCTGCGACTTTGGGAGTGCAAAAGTTCTGGTCAAAGGCGAACCA
ATATTTTCATATATTTGTTCTCGTTACTATCGTGCACCCGAACCTATATTCGGAGCAACTGAA
TACACTTTTGCAATTGACATTTGGTCTGTGGGTTGCGTCTTGCCGAAGTCTTCTGGGGCA
GCCCCTCTTTCTGGTGAGAGTGGAGTTGATCAGCTTGTGAAATAATCAAGGTTCTTGAA
CACCAACTCGGGAGGAAATCAAGAGTATGAATCCAAATTACTGAGTTCAAATTTCCACAA
ATCAAAGCTCACCTTGGCACAAAATTTTTCATAAGCGGATGCCTCCAGAAGCTGTGGACCT
TGTGTCAAGGCTTCTCCAATATTCTCCAAATTTGAGGTCCACTGCGTTGGAGGCTTGCACTC
ACACTTTCTTTGATGAACTCCGTGATCCTAAGACTCGCCTCCCTAATGGTTCGGCCATTGCCA
CCTCTTTTCAACTTCAGGCCTCAAGAGCTGAAAGGAGCGTCGGCAGACCTCTTAAACAAGCT
GATACCAGAACATGCTAAGAAGCAGTGTACCTTTCTTGGTGTCTAGGTTTATGAATGTTGTG
TATCTATTGTATACTTGAAATATTTTGCAACCACTGGTTAATTCTCTACTTTGGCTAAACCT
GTTTGACATGTCTTCTTCCATGAAACTTATAACTGAAACCACATTGTGTAAGTTGTTCC
TAGTAGTGCAATGCTATTTACTTGAACTTG

SEQ ID NO 177 - *Petunia hybrida* - CAA58594 - SHAGGY kinase 4

MASGIMPSAGGKHRTDAMLVDKLPEEINEMKIRDDKAEKEMEAAVVDGNGTEKGHIIVTTIG
GKNGEPKQTI SYMAERVVGQGSFGIVFQAKCLETGETVAIKKVLQDKRYKNRELQTI RLLDH
PNVVALRHCFSTTEKDELYLNLVLEYVPETVYRVLRHYSKANQQMPMIYVKLYTYQIFRAL
AYIHGIGVCHRD IKPQNLLVNPHTHQLKLCDFGSAKVLVKGEPNISYICSRYYRAPELIFGA
TEYTF AIDIWSVGCVLAE LLLGQPLFPGESGVDQLVEI IKVLGTPTREEIKSMNPNYTEFKF
PQIK AHPWHKIFHKRMPPEAVDLVSRLLOQYSPNLRSTALEACTHTFFDEL RDPKTRL PNGRP
LPPLFNFRPQELKGASADLLNKLIPEHAKKQCTFLGV

FIGURE 16 (continued)

103/104

SEQ ID NO 178 - *Oryza sativa* - GOS2 promoter

aatccgaaaagtttctgcaccgttttcacccttaactaacaatatagggaacgtgtgctaa
atataaaatgagaccttatatatgttagcgctgataactagaactatgcaagaaaaactcatc
cacctacttttagtggcaatcgggctaaataaaaaagagtcgctacactagtttcgttttcct
tagtaattaagtgggaaaatgaaatcattattgcttagaatatacgttcacatctctgtcat
gaagttaaattattcgaggtagccataattgtcatcaaactcttcttgaataaaaaaatctt
tctagctgaactcaatgggtaaagagagagatttttttaaaaaatagaatgaagatattc
tgaacgtattggcaaagatttaacatataattatataattttatagtttgtgcattcgtca
tatcgcacatcattaaggacatgtcttactccatcccaatttttatttagtaattaaagaca
attgacttatttttattattatcttttttcgattagatgcaagggtacttacgcacacactt
tgtgctcatgtgcatgtgtgagtgacacctcctcaatacacgttcaactagcaacacatctct
aatatcactcgctatttaatacattttaggttagcaatatctgaattcaagcactccaccatc
accagaccacttttaataatatctaaaatacaaaaaataattttacagaatagcatgaaaag
tatgaaacgaactatttaggtttttcacatacaaaaaaaaaaagaattttgctcgtgcgcga
gcgccaatctcccatattgggcacacaggcaacaacagagtggtgcccacagaacaacca
caaaaaacgatgatctaacggaggacagcaagtcgcaacaaccttttaacagcaggctttg
cggccaggagagaggaggagaggcaagaaaaccaagcatcctcctcctcccatctataaat
tcctcccccttttccccctctctatataggaggcatccaagccaagaagaggagagcacca
aggacacgcgactagcagaagccgagcgaccgccttcttcgatccatatcttcgggtcgagt
tcttggtcgatctcttccctcctccacctcctcctcacagggtatgtgcccttcgggtgttc
ttggatttattgttctaggttgtgtagtagcggttgatgttaggaaaggggatctgtatc
tgtgatgattcctgttcttggatttgggatagaggggttcttgatgttgcatgttatcggtt
cggtttgattagtagtatggttttcaatcgtctggagagctctatggaaatgaaatggttta
gggtacggaatcttgcgattttgtgagtaccttttggttgaggtaaaatcagagcacgggtg
attttgcttggtgtaataaaagtacgggtgttttggtcctcgattctggtagtgatgcttctc
gatttgacgaagctatcctttggtttattccctattgaacaaaaataatccaactttgaagac
ggccccgttgatgagattgaatgattgattcttaagcctgtccaaaatttcgcagctggctt
gtttagatacagtagtccccatcacgaaattcatggaaacagttataatcctcaggaacagg
ggattccctgttcttccgatttgcttttagtcccagaatttttttcccaaataatcttaaaaa
gtcactttctggttcagttcaatgaattgattgctacaaataatgctttttatagcgttatcc
tagctgtagttcagttaataggtaataacccttatagtttagtcaggagaagaacttatccga
tttctgatctccatttttaattatatgaaatgaactgtagcataagcagtagttcatttggtat
tattttttttattagctctcacccttcattattctgagctgaaagtctggcatgaactgtc
ctcaattttgttttcaaattcacatcgattatctatgcattatcctcttgatctacctgta
gaagtttctttttgggtattccttgactgcttgattacagaaagaaatttatgaagctgtaa
tcgggatagttatactgcttggttcttatgattcatttcctttgtgcagttcttggtgtagct
tgccactttcaccagcaaagttc

SEQ ID NO 179 - sense primer: prm5797

ggggacaagtttgtacaaaaaagcaggcttaacaatgggttcagtaggggttg

SEQ ID NO 180 - antisense primer: prm5798

ggggaccactttgtacaagaaagctgggtgaagctgtctcatactcctgc

FIGURE 16 (continued)

104/104**SEQ ID NO 181 - *Oryza sativa* - beta-expansin promoter**

aaaaccaccgagggacctgatctgcaccggttttgatagttgagggacccgttggtgtctggt
tttccgatcgagggacgaaaatcggattcgggtgtaaagttaagggacctcagatgaacttat
tccggagcatgattgggaagggaggacataaggcccatgtcgcgatgtgtttggacgggtccag
atctccagatcactcagcaggatcggccgcgttcgcgtagcaccgcggtttgattcggctt
cccgaaggcggcggccggtggccgtgcccgtagcttccgccggaagcgagcacgccgcc
gccgccgaccggctctgcgtttgcaccgccttgcacgcgatacatcgggatagatagctac
tactctctcgtttcacaatgtaaatcattctactattttccacattcatattgatgttaat
gaatatagacatatatatctattttagattcattaacatcaatatgaatgtaggaaatgctag
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FIGURE 16 (continued)

PF57967.ST25.txt
SEQUENCE LISTING

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<130> PF57967

<150> EP 05110413.1
<151> 2005-11-07

<150> EP 05110429.7
<151> 2005-11-07

<150> US 60/736,194
<151> 2005-11-14

<150> EP 05110900.7
<151> 2005-11-17

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<151> 2005-11-23

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<151> 2005-11-24

<150> US 60/742,287
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caccatgccc	tcctctccga	caacgaccgc	ctccgcgcgc	aggtaatctc	attaaccgag	540
aagctgcaag	acaaggagac	gtcgccgtcg	tcggcgacca	tcaccaccgc	ggcgaggag	600
gtcgaccagc	cggacgaaca	cacggaggcc	gcgtcaacca	ccggcttcgc	caccgtcgac	660
ggcgcatgtg	cggcgccacc	gcccggccac	cagcagccgc	cgcataaaga	tgatcttgtg	720
agcagcggcg	gcaccaacga	cgacggcgat	ggcggcgcg	ccgtggtggt	cttcgacgtc	780
accgaggggc	ccaacgaccg	cctcagctgc	gagtcggcgt	acttcgccga	cgccgcggag	840

PF57967.ST25.txt

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atgttcggcg ccgccggagt tgtgcaccac gacgccgcgg acgacgagga ggcgcagctc 1020
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<210> 2
<211> 349
<212> PRT
<213> Oryza sativa

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          20          25          30
Asn Ser GIy GIy Phe Phe Arg GIy VaI Pro Ala Ala VaI Leu GIy Met
          35          40          45
Asp GIu Ser Arg Ser Ser Ser Ser Ala Ala GIy Ala GIy Ala Lys Arg
          50          55          60
Pro Phe Phe Thr Thr His GIu GIu Leu Leu GIu GIu Tyr Tyr Asp
65          70          75          80
GIu GIn Ala Pro GIu Lys Lys Arg Arg Leu Thr Ala GIu GIn VaI GIn
          85          90          95
Met Leu GIu Arg Ser Phe GIu GIu GIu Asn Lys Leu GIu Pro GIu Arg
          100          105          110
Lys Thr GIu Leu Ala Arg Arg Leu GIy Met Ala Pro Arg GIn VaI Ala
          115          120          125
VaI Trp Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr Lys GIn Leu GIu
          130          135          140
His Asp Phe Asp Arg Leu Lys Ala Ala Tyr Asp Ala Leu Ala Ala Asp
145          150          155          160
His His Ala Leu Leu Ser Asp Asn Asp Arg Leu Arg Ala GIn VaI lie
          165          170          175
Ser Leu Thr GIu Lys Leu GIn Asp Lys GIu Thr Ser Pro Ser Ser Ala
          180          185          190
Thr lie Thr Thr Ala Ala GIn GIu VaI Asp GIn Pro Asp GIu His Thr
          195          200          205
GIu Ala Ala Ser Thr Thr GIy Phe Ala Thr VaI Asp GIy Ala Leu Ala
          210          215          220
Ala Pro Pro Pro GIy His GIn GIn Pro Pro His Lys Asp Asp Leu VaI
225          230          235          240
Ser Ser GIy GIy Thr Asn Asp Asp GIy Asp GIy GIy Ala Ala VaI VaI
          245          250          255
VaI Phe Asp VaI Thr GIu GIy Ala Asn Asp Arg Leu Ser Cys GIu Ser
          260          265          270
Ala Tyr Phe Ala Asp Ala Ala GIu Ala Tyr GIu Arg Asp Cys Ala GIy
          275          280          285
His Tyr Ala Leu Ser Ser GIu GIu GIu Asp GIy GIy Ala VaI Ser Asp
290          295          300
GIu GIy Cys Ser Phe Asp Leu Pro Asp Ala Ala Ala Ala Ala Ala
305          310          315          320
Met Phe GIy Ala Ala GIy VaI VaI His His Asp Ala Ala Asp Asp GIu
          325          330          335
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PF57967 . ST25 .txt

340

345

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 <211> 1197
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 <213> Oryza sativa

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 agaccggtgc tcggcatgga ggaaggaggc cgcggcgtca agcggccctt cttcaccacc 180
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 aaatcgttct ctttttcatt tttccgcttc tttgtctgta atgttgagtt tcgatcggct 1140
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 <211> 343
 <212> PRT
 <213> Oryza sativa

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 20 25 30
 GIy Ala Met Phe His Arg GIy Ala Arg Pro VaI Leu GIy Met GIu GIu
 35 40 45
 GIy GIy Arg GIy VaI Lys Arg Pro Phe Phe Thr Thr Pro Asp GIu Leu
 50 55 60
 Leu GIu GIu GIu Tyr Tyr Asp GIu GIn Leu Pro GIu Lys Lys Arg Arg
 65 70 75 80
 Leu Thr Pro GIu GIn Val His Leu Leu GIu Arg Ser Phe GIu GIu GIu
 85 90 95
 Asn Lys Leu GIu Pro GIu Arg Lys Thr GIu Leu Ala Arg Lys Leu GIy
 100 105 110
 Leu GIn Pro Arg GIn VaI Ala VaI Trp Phe GIn Asn Arg Arg Ala Arg
 115 120 125
 Trp Lys Thr Lys GIn Leu GIu Arg Asp Phe Asp Arg Leu Lys Ala Ser
 130 135 140
 Phe Asp Ala Leu Arg Ala Asp His Asp Ala Leu Leu GIn Asp Asn His

PF57967.ST25.txt

145 150 155 160
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 GIu Thr Thr Thr GIu GIy Ser Ala GIy Ala Ala VaI Asp VaI Pro GIy
 180 185 190
 Leu Pro Ala Ala Ala Asp VaI Lys VaI Ala VaI Pro Asp Ala GIu GIu
 195 200 205
 Pro Ala Leu GIu GIu Ala Ala Ala Ala Phe GIu GIu GIn GIn GIu GIn
 210 215 220
 GIn VaI Lys Ala GIu Asp Arg Leu Ser Thr GIy Ser GIy GIy Ser Ala
 225 230 235 240
 VaI VaI Asp Thr Asp Ala GIn Leu VaI VaI GIy Cys GIy Arg GIn His
 245 250 255
 Leu Ala Ala VaI Asp Ser Ser VaI GIu Ser Tyr Phe Pro GIy GIy Asp
 260 265 270
 GIu Tyr His Asp Cys VaI Met GIy Pro Met Asp His Ala Ala GIy GIy
 275 280 285
 H e GIn Ser GIu GIu Asp Asp GIy Ala GIy Ser Asp GIu GIy Cys Ser
 290 295 300
 Tyr Tyr Ala Asp Asp Ala GIy VaI Leu Phe Ala Asp His GIy His His
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 His His His GIn His Ala Asp Asp Asp GIu GIu Asp GIy GIn GIn H e
 325 330 335
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 <213> Zea mays

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 atggcgggtcc tgggcatgga cgacgcgacg cgcgtgggca agcggccctt cttcacgaca 180
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 35 40 45
 Ala Thr Arg VaI GIy Lys Arg Pro Phe Phe Thr Thr His GIu GIu Leu
 50 55 60
 Leu GIu GIu GIu Tyr Tyr Asp GIu GIn Ala Pro GIu Lys Lys Arg Arg
 65 70 75 80
 Leu Thr Ala GIu GIn VaI GIn Leu Leu GIu Arg Ser Phe GIu GIu GIu
 85 90 95
 Asn Lys Leu GIu Pro GIu Arg Lys Thr GIu Leu Ala Arg Arg Leu GIy
 100 105 110
 Met Ala Pro Arg GIn VaI Ala VaI Trp Phe GIn Asn Arg Arg Ala Arg
 115 120 125
 Trp Lys Thr Lys GIn Leu GIu Thr Asp Tyr Asp Arg Leu Lys Ala Ala
 130 135 140
 Tyr Asp Ala Leu Ala Ala Asp His GIn GIy Leu Leu Ala Asp Asn Asp
 145 150 155 160
 Asn Leu Arg Ala GIn VaI lie Ser Leu Thr GIu Lys Leu GIn GIy Lys
 165 170 175
 GIu Thr Ser Pro Ser Ala Thr Thr Ala Ala GIn GIu VaI Asp GIn Pro
 180 185 190
 Asp GIu His Thr Ala VaI Ser GIy Thr GIu GIu Leu Leu Ala GIn GIn
 195 200 205
 Leu Lys Asp Asn Leu His Ser Ser GIy Asp Cys Thr GIy His GIy Thr
 210 215 220
 Leu Ser Ser GIu GIu Asp Asp GIy GIy VaI VaI Ser Asp GIu GIy Cys
 225 230 235 240
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PF57967.ST25.txt

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 35 40 45
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 GIu Tyr Tyr Asp GIu GIn Leu Pro GIu Lys Lys Arg Arg Leu Thr Pro
 65 70 75 80
 GIu GIn VaI Leu Leu GIu Arg Ser Phe GIu GIu GIu Asn Lys Leu
 85 90 95
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 100 105 110
 Arg GIn VaI Ala VaI Trp Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr
 115 120 125
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 Thr Phe GIu VaI Leu GIn GIu VaI Lys Ser GIu Asp Arg Leu Ser Thr
 210 215 220
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 225 230 235 240
 Arg Phe Ala Ala Ala VaI Asp Ser Ser VaI GIu Ser Tyr Phe Pro GIy
 245 250 255
 GIy GIu Asp His Tyr His Asp Cys GIy Thr Met GIy Pro VaI Asn His
 260 265 270
 GIy Ala GIy GIy GIy lie GIn Ser Asp Asp Asp GIy Ala GIy Ser Asp
 275 280 285
 GIu GIy Cys Ser Tyr Tyr Ala Asp GIu Ala Ala Ala Ala Ala Ala
 290 295 300
 Phe Phe Ala GIy His Ala Thr His His His Ala Asp GIu Asp GIu Asp
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 325 330

<210> 9

PF57967.ST25.txt

<211> 825

<212> DNA

<213> Saccharum officinarum

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cacctcaagg	ctgcctacga	cgcgctcgcc	gccgaccacc	agggcctcct	ggccgacaac	480
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agctttgatc	tcccggatgc	catgtttgct	gccgggggtca	cccaccatgg	cgccgacgcc	780
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<211> 274

<212> PRT

<213> Saccharum officinarum

<400> 10

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			20					25					30		
Ser	Asn	GIy	Phe	Phe	Arg	GIy	VaI	Pro	Met	Ala	VaI	Leu	GIy	Met	Asp
		35					40					45			
Asp	Ala	Thr	Arg	VaI	GIy	Lys	Arg	Pro	Phe	Phe	Thr	Thr	His	GIu	GIu
	50					55					60				
Leu	Leu	GIu	GIu	GIu	Tyr	Tyr	Asp	GIu	GIIn	Ala	Pro	GIu	Lys	Lys	Arg
65					70					75				80	
Arg	Leu	Thr	Ala	GIu	GIIn	VaI	GIIn	Leu	Leu	GIu	Arg	Ser	Phe	GIu	GIu
			85					90					95		
GIu	Asn	Lys	Leu	GIu	Pro	GIu	Arg	Lys	Thr	GIu	Leu	Ala	Arg	Arg	Leu
			100					105					110		
GIy	Met	Ala	Pro	Arg	GIIn	VaI	Ala	VaI	Trp	Phe	GIIn	Asn	Arg	Arg	Ala
		115					120					125			
Arg	Trp	Lys	Thr	Lys	GIIn	Leu	GIu	Thr	Asp	Tyr	Asp	His	Leu	Lys	Ala
	130					135					140				
Ala	Tyr	Asp	Ala	Leu	Ala	Ala	Asp	His	GIIn	GIy	Leu	Leu	Ala	Asp	Asn
145				150						155				160	
Asp	Ser	Leu	Arg	Ala	GIIn	VaI	VaI	Ser	Leu	Thr	GIu	Lys	Leu	GIIn	GIy
			165					170						175	
Lys	GIu	Thr	Ser	Pro	Ser	Ala	Thr	Thr	Ala	Ala	GIIn	GIu	VaI	Asp	GIIn
			180					185					190		
Pro	Asp	GIu	His	Thr	Ala	Ala	Ser	GIy	Thr	GIu	Lys	Leu	Leu	Ala	GIIn
		195					200					205			
GIIn	Leu	Lys	Asp	Asp	Leu	His	Ser	Ser	GIy	Asp	Cys	Thr	GIy	His	GIy
	210					215					220				

PF57967.ST25.txt

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 Ser Phe Asp Leu Pro Asp Ala Met Phe Ala Ala GIy VaI Thr His His
 245 250 255
 GIy Ala Asp Ala GIu GIu Ala GIn Leu Ala Asn Trp Thr Ser Trp Phe
 260 265 270
 Trp Asn

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 <211> 828
 <212> DNA
 <213> Sorghum bicolor

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<210> 12
 <211> 275
 <212> PRT
 <213> Sorghum bicolor

<400> 12
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 1 5 10 15
 GIy GIy GIy GIy Ala GIn Met Leu Phe GIy GIy GIy GIy Ser
 20 25 30
 Ala Asn Ser Asn GIy Phe Phe Arg GIy VaI Pro Met Ala VaI Leu GIy
 35 40 45
 Met Asp Asp Ala Thr Arg VaI GIy Lys Arg Pro Phe Phe Thr Thr His
 50 55 60
 GIu GIu Leu Leu GIu GIu GIu Tyr Tyr Asp GIu GIn Ala Pro GIu Lys
 65 70 75 80
 Lys Arg Arg Leu Thr Ala GIu GIn VaI GIn Leu Leu GIu Arg Ser Phe
 85 90 95
 GIu GIu GIu Asn Lys Leu GIu Pro GIu Arg Lys Thr GIu Leu Ala Arg
 100 105 110
 Arg Leu GIy Met Ala Pro Arg GIn VaI Ala VaI Trp Phe GIn Asn Arg
 115 120 125
 Arg Ala Arg Trp Lys Thr Lys GIn Leu GIu Thr Asp Tyr Asp Arg Leu
 130 135 140

PF57967.ST25.txt

Lys Ala Ala Tyr Asp Ala Leu Ala Ala Asp His GIn GIy Leu Leu Ala
 145 150 155 160
 Asp Asn Asp Ser Leu Arg Ala GIn VaI lie Ser Leu Thr Asp Lys Leu
 165 170 175
 GIn Arg Lys GIu Thr Ser Pro Ser Ala Thr Thr Ala Ala GIn GIu VaI
 180 185 190
 Asp GIn Pro Asp GIu His Thr Ala Ala Ser GIy Thr GIu Lys Leu Leu
 195 200 205
 VaI GIn GIn Leu Lys Asp Asp Leu His Ser Ser GIy Asp Phe Thr GIy
 210 215 220
 His GIy Ala Leu Ser Ser GIu GIu GIu Asp GIy VaI VaI Ser Asp
 225 230 235 240
 GIu GIy Cys Ser Phe Asp Leu Pro Asp Ala Met Phe Ala Ala GIy VaI
 245 250 255
 Thr His His GIy Ala GIu GIu Ala GIn Leu Ala Asn Trp Thr Ser Trp
 260 265 270
 Phe Trp Asn
 275

<210> 13
 <211> 1023
 <212> DNA
 <213> Triticum aestivum

<400> 13
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 atggactcgc gcgcgggscgc catcgccggc gcggccggca tgttccatcg aggggtgaga 120
 ccggtcctcg gcggcatgga agaagggcgc ggcgtgaagc ggcccttctt cacctcgccg 180
 gatgacatgc tcgaggagga gtactacgac gagcagctcc cggagaagaa gcggcgcttc 240
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 gagaggaaga cggagctggc ccgcaagctc gggctgcagc cagccagggt ggccgtctgg 360
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 aaggcgtcct tcgacgccct ccggggccgac cagcagcccc tcctccagga caaccaccgg 480
 ctccggtcac aggtggtaac gtgaccgag aagatgcaag ataaggaggc gccggaaggc 540
 agcttcggtg cagccgccga cgctcggag ccggagcagg cggcggcgga ggcgaaggct 600
 tccttgcccg acgcccagga gcaggccgcg gcagcggagg cgttcgagggt ggtgcagcag 660
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 tgcagctact accccgacga cgccgccgtc ttcttcgccg ccgcgcaagg gcacggccac 960
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 tag 1023

<210> 14
 <211> 340
 <212> PRT
 <213> Triticum aestivum

<400> 14
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 GIn Met Leu Phe Met Asp Cys GIy Ala GIy GIy lie Ala GIy Ala Ala
 20 25 30

PF57967.ST25.txt

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

<210> 15
 <211> 819
 <212> DNA
 <213> Arabidopsis thaliana

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 gaaacttcga agcgaaggcc cttcttttagc tcccctgagg atctctacga cgatgacttt 180
 tacgacgacc agttgcctga aaagaagcgt cgcctcacta ccgaacaagt gcatctgctg 240
 gagaaaagct tcgagacaga gaacaagcta gagcctgaac gcaagactca gcttgccaag 300
 aagcttggtc tacagccaag gcaagtggct gtctggtttc agaatcgccg agctcgttgg 360
 aaaacaaaac agcttgagag agactacgat cttctcaagt ccacttacga ccaacttctt 420

PF57967.ST25.txt

tctaactacg	actccatcgt	catggacaac	gataagctca	gatccgaggt	tacttcctg	480
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ccaaaccaac	ttgatccggt	ttacattaat	gcggcagcaa	tcaaaaccga	ggaccgggta	600
agttcaggga	gcgttgggag	cgcggtacta	gacgacgacg	cacctcaact	actagacagc	660
tgtgactctt	acttcccaag	catcgtaccc	atccaagaca	acagcaacgc	cagtgatcat	720
gacaatgacc	ggagctgttt	cgccgacgtc	tttgtgcca	ccacttcacc	gtcgcacgat	780
catcacggtg	aatcattggc	tttctgggga	tggccttag			819

<210> 16
 <211> 272
 <212> PRT
 <213> Arabidopsis thaliana

<400> 16

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

<210> 17
 <211> 969
 <212> DNA
 <213> Daucus carota

PF57967.ST25.txt

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tcaaatcca tgggttagctt tcaagatgct aagcgaaaaa atccctacga tgggttcttt      180
atgcggtcat atgatgaaga agaaattggg gatgaagaat atgatgaata ctttcagcag      240
cctgagaaga agaggaggct caaggctgat caaatccagt ttcttgagaa aagttttgag      300
actgataaca agcttgagcc tgaaagaaaa gttcagcttg caaaagaact cggcttgcag      360
ccaagacagg ttgcgatatg gtttcagaac cgtcgagcac ggtggaagac caaaacacta      420
gaaaaagatt atgatgtatt gcaaaatagc tacaacagcc tcaaggctga ctatgacaat      480
ctacttgccg agaaagaaaa acttaaagcc gaggttctcg acctgacaga caagctactt      540
ctcaaagaag ataaggggag caagacagta gtttttgata agcaaaagggt gtctgcagca      600
ttccaacaag aacgtgttag taatgacata tctgtgggtg aagtactcag taactcagtt      660
atggactgca agcaagaaga tcataactct gtgaaaagtg atgcagttga ttctgacagt      720
ccacactaca gtgatgaagt ctactccagt tttatggagc cagtggatcg ctcttatgtt      780
tttgaacctg ctcagtcgga tatactctca gatgaagaag atgacatggg gaacaactta      840
tttctcccat catatcatgt tttctcaaag actgaagacg gtagttactc cgaccagcct      900
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gaattataa

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<210>  18
<211>  322
<212>  PRT
<213>  Daucus carota

```

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<400>  18
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Ala Ser Leu Leu Phe His Ser GIn Arg Pro GIu Pro Phe Phe Leu Ser
          20          25          30
Ala Pro Ser Pro Ser Leu lie GIy Ser Lys Ser Met VaI Ser Phe GIn
          35          40          45
Asp Ala Lys Arg Lys Asn Pro Tyr Asp GIy Phe Phe Met Arg Ser Tyr
          50          55          60
Asp GIu GIu GIu H e GIy Asp GIu GIu Tyr Asp GIu Tyr Phe GIn GIn
          65          70          75          80
Pro GIu Lys Lys Arg Arg Leu Lys Ala Asp GIn lie GIn Phe Leu GIu
          85          90          95
Lys Ser Phe GIu Thr Asp Asn Lys Leu GIu Pro GIu Arg Lys VaI GIn
          100          105          H O
Leu Ala Lys GIu Leu GIy Leu GIn Pro Arg GIn VaI Ala H e Trp Phe
          115          120          125
GIn Asn Arg Arg Ala Arg Trp Lys Thr Lys Thr Leu GIu Lys Asp Tyr
          130          135          140
Asp VaI Leu GIn Asn Ser Tyr Asn Ser Leu Lys Ala Asp Tyr Asp Asn
          145          150          155          160
Leu Leu Ala GIu Lys GIu Lys Leu Lys Ala GIu VaI Leu Asp Leu Thr
          165          170          175
Asp Lys Leu Leu Lys GIu Asp Lys GIy Ser Lys Thr VaI VaI Phe
          180          185          190
Asp Lys GIn Lys VaI Ser Ala Ala Phe GIn GIn GIu Arg VaI Ser Asn
          195          200          205
Asp H e Ser VaI GIy GIu VaI Leu Ser Asn Ser VaI Met Asp Cys Lys
          210          215          220
GIn GIu Asp His Asn Ser VaI Lys Ser Asp Ala VaI Asp Ser Asp Ser

```

PF57967.ST25.txt

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225          230          235          240
Pro His Tyr Ser Asp GIu VaI Tyr Ser Ser Phe Met GIu Pro VaI Asp
          245          250          255
Arg Ser Tyr VaI Phe GIu Pro Ala GIn Ser Asp lie Ser GIn Asp GIu
          260          265          270
GIu Asp Asp Met GIy Asn Asn Leu Phe Leu Pro Ser Tyr His VaI Phe
          275          280          285
Ser Lys Thr GIu Asp GIy Ser Tyr Ser Asp GIn Pro Ser Asn Ser Ser
          290          295          300
Tyr Phe GIy Phe Pro VaI GIu Asp His Thr Phe GIy Phe Trp GIy Thr
305          310          315          320
GIu Leu

```

```

<210> 19
<211> 1038
<212> DNA
<213> Glycine max

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<400> 19
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ttccaagggt caaaacccgt ggttgathtt gagaatgtaa gtgggagcag gatgacggat 180
aggcctttct ttcaagcgtt ggagaaggaa gagaactgtg atgaggatta cgagggtgt 240
ttccaccaac cggggaagaa aaggaggctc acaagcgaac aagttcagtt ccttgaaagg 300
aactttgagg tagagaacaa gcttgaacc gaaaggaaag tccaacttgc aaaagagctt 360
ggcttgacagc caaggcaagt tgctatatgg ttccaaaacc gaagggaag gttcaagacc 420
aagcagctag aaaaagacta tggcgtgttg aaagctagtt atgacagact caaaagtgc 480
tatgaaagtc ttgttcaaga gaatgacaag ttaaaagcag aggtgaattc tctggagagc 540
aaattgattc ttagagataa agagaaggag gagaattcgg atgacaagtc atctcctgat 600
gatgctgtca attcttcttc accccacaac aacaaggagc ctatggattt attaattatt 660
tcaaaaaatg caacaacaac aacaacatct gaaaatggga ccaaagtgtt gtcaccactc 720
ccactcccta ttatggtaac atgctgcaag caagaagatg ccaactcagc caaaagtgat 780
gtccttgatt cggatagccc acattgcact tcattcgtgg agcctgctga ttcctctcat 840
gcctttgaac cagaagacca ctcagaagac ttctcccaag atgaagagga taaccttagt 900
gaaaaccttt tgatgacctt cccttcttct tgttgcttac ctaagggtga agaactgc 960
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<210> 20
<211> 345
<212> PRT
<213> Glycine max

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<400> 20
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GIn Asn GIu Arg Leu Pro Cys Ser Ser GIu VaI Leu GIu Ser Leu Trp
          20          25          30
Ala GIn Thr Ser Asn Pro Ala Ser Phe GIn GIy Ser Lys Pro VaI VaI
          35          40          45
Asp Phe GIu Asn VaI Ser GIy Ser Arg Met Thr Asp Arg Pro Phe Phe
          50          55          60
GIn Ala Leu GIu Lys GIu GIu Asn Cys Asp GIu Asp Tyr GIu GIy Cys

```

PF57967.ST25.txt

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

<210> 21
 <211> 858
 <212> DNA
 <213> Craterostigma plantagineum

<400> 21															
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gacgaggaat	actacgacga	gcagttgttg	cctgagaaga	agcgccgact	caccgccgag										240
caggttcact	tgcttgagaa	gagcttcgag	gctgagaaca	agcttgagcc	tgagcgaaag										300
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tatgattctc	ttctctcaac	ctacgactct	attcgccagg	aaaacgacaa	gctcaaagcc										480
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aagctgacgg	tgaaggtgga	ggaccgcctg	agcacgggga	gcaacggcag	cgcagtaatg										660
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PF57967.ST25.txt

gaggaatacgc actgcgccgc cgcaagtttg gctgctgcga aggaggacga cggcagcgat 780
 gagggcggggt gttactttcac cgaggctctc gcggcggagg aggaggaggc gccgtttgct 840
 tgggtgtattt ggtcttaa 858

<210> 22
 <211> 285
 <212> PRT
 <213> Craterostigma plantagineum

<400> 22
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 20 25 30
 Thr Arg Ser Ser Ser VaI Leu Asn Met GIU GIU Ser Ser Leu Lys Arg
 35 40 45
 GIn lie Phe Ser GIY GIY GIY GIY Asp GIU Phe Tyr Asp GIU GIU Tyr
 50 55 60
 Tyr Asp GIU GIn Leu Leu Pro GIU Lys Lys Arg Arg Leu Thr Ala GIU
 65 70 75 80
 GIn VaI His Leu Leu GIU Lys Ser Phe GIU Ala GIU Asn Lys Leu GIU
 85 90 95
 Pro GIU Arg Lys Ala GIU Leu Ala Lys Lys Leu GIY Leu GIn Pro Arg
 100 105 110
 GIn VaI Ala lie Trp Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr Lys
 115 120 125
 GIn Leu GIU Arg Asp Tyr Asp Lys Leu Lys Ser Ser Tyr Asp Ser Leu
 130 135 140
 Leu Ser Thr Tyr Asp Ser lie Arg GIn GIU Asn Asp Lys Leu Lys Ala
 145 150 155 160
 GIU Leu Leu Ser Leu Asn GIU Lys Leu GIn Pro Lys Asp Asp Asp Asp
 165 170 175
 Pro Ser Ala GIU lie GIY Arg Asn Leu Ser Ser Ser Ser Pro Pro VaI
 180 185 190
 Asp Ala Ala GIU Pro Pro Cys Leu Lys Leu Thr VaI Lys VaI GIU Asp
 195 200 205
 Arg Leu Ser Thr GIY Ser Asn GIY Ser Ala VaI Met Asp GIY Asp GIY
 210 215 220
 Pro GIn GIn Leu Leu Asp Asp Ser GIY Asp Ser Tyr Phe GIU Asn Asp
 225 230 235 240
 GIU GIU Tyr Asp Cys Ala Ala Ala Ser Leu Ala Ala Ala Lys GIU Asp
 245 250 255
 Asp GIY Ser Asp GIU GIY GIY Cys Tyr Phe Thr GIU Ala Leu Ala Ala
 260 265 270
 GIU GIU GIU GIU Ala Pro Phe Ala Trp Cys lie Trp Ser
 275 280 285

<210> 23
 <211> 813
 <212> DNA
 <213> Gossypium hirsutum

<220>
 <221> variation

PF57967.ST25.txt

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aagaagcgac	tgttcttcag	ctcgccggag	gatttgtacg	acgaagagta	ctacgacgag	180
cagttgcccg	agaaaaagcg	tcgccttacg	tcggagcagg	tgtatctgct	agagaagagc	240
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ctgcaaccaa	ggcaggtggc	ggtatggttc	cagaaccgcc	gtgcaagggtg	gaagacaaa	360
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gacactattc	tcaaagaaaa	tgagaagctc	aatctgagg	tagcttcctt	gactgaaaaa	480
ctacaagcca	aagatgtggc	aacagaagca	atagcaggtg	aaaaggatga	agggttagca	540
gctgagatgg	cctccgcctt	ccaattcagt	atgaagggtg	aggaccgtct	tagtagcggc	600
agtgtcggaa	gcgcggtggt	ggatgaggat	gccccacagc	tggtggacag	cggcaattcc	660
tactttccaa	gcgatgaata	ctccagaggc	attggccctt	tcgatggggt	tcagtcggaa	720
gatgaggatg	gcagtataaa	ttgcgggagt	tacttctccg	atgtgttcgc	aaccacagag	780
cagggagcat	taggattgtg	ggcctggatc	taa			813

<210> 24

<211> 270

<212> PRT

<213> Gossypium hirsutum

<220>

<221> UNSURE

<222> (270) .. (270)

<223> Xaa can be any naturally occurring amino acid

<400> 24

Met	GIu	Ser	GIy	Arg	Leu	Phe	Phe	Asn	Pro	Ser	Thr	Thr	His	Arg	Asn
1				5				10						15	
Met	Leu	Leu	Leu	GIy	Asn	Thr	GIu	Pro	lie	Phe	Arg	GIy	Ala	Arg	Thr
			20					25					30		
Met	VaI	Ser	Met	GIu	GIu	Asn	Pro	Lys	Lys	Arg	Leu	Phe	Phe	Ser	Ser
			35				40					45			
Pro	GIu	Asp	Leu	Tyr	Asp	GIu	GIu	Tyr	Tyr	Asp	GIu	GIn	Leu	Pro	GIu
	50				55					60					
Lys	Lys	Arg	Arg	Leu	Thr	Ser	GIu	GIn	VaI	Tyr	Leu	Leu	GIu	Lys	Ser
65				70					75					80	
Phe	GIu	Ala	GIu	Asn	Lys	Leu	GIu	Pro	GIu	Arg	Lys	Ser	GIn	Leu	Ala
			85				90						95		
Lys	Lys	Leu	GIy	Leu	GIn	Pro	Arg	GIn	VaI	Ala	VaI	Trp	Phe	GIn	Asn
			100				105						110		
Arg	Arg	Ala	Arg	Trp	Lys	Thr	Lys	GIn	Leu	GIu	Arg	Asp	Tyr	Asp	Leu
		115				120						125			
Leu	Lys	Ser	Ser	Phe	Asp	Ser	Leu	GIn	Ser	Asn	Tyr	Asp	Thr	lie	Leu
	130				135						140				
Lys	GIu	Asn	GIu	Lys	Leu	Lys	Ser	GIu	VaI	Ala	Ser	Leu	Thr	GIu	Lys
145				150					155						160
Leu	GIn	Ala	Lys	Asp	VaI	Ala	Thr	GIu	Ala	H e	Ala	GIy	GIu	Lys	Asp
			165				170						175		
GIu	GIy	Leu	Ala	Ala	GIu	Met	Ala	Ser	Ala	Leu	GIn	Phe	Ser	Met	Lys
		180					185						190		

PF57967.ST25.txt

```

VaI  GIu  Asp  Arg  Leu  Ser  Ser  GIy  Ser  VaI  GIy  Ser  Ala  VaI  VaI  Asp
      195      200      205
GIu  Asp  Ala  Pro  GIn  Leu  VaI  Asp  Ser  GIy  Asn  Ser  Tyr  Phe  Pro  Ser
      210      215      220
Asp  GIu  Tyr  Ser  Arg  GIy  lie  GIy  Pro  Phe  Asp  GIy  VaI  GIn  Ser  GIu
      225      230      235      240
Asp  GIu  Asp  GIy  Ser  Asp  Asn  Cys  GIy  Ser  Tyr  Phe  Ser  Asp  VaI  Phe
      245      250      255
Ala  Thr  Thr  GIu  GIn  GIy  Ala  Leu  GIy  Leu  Trp  Ala  Trp  Xaa
      260      265      270

```

```

<210> 25
<211> 858
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> variation
<222> (294) .. (294)
<223> /replace="c" /replace="g" /replace="t"

```

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<400> 25
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tcgaagaggc gacccttctt tagctcgccg gaggatctat atgacgagga atactacgac 180
gagcagtcac cggagaagaa gcgccgtctc actcctgagc aggtgcactt gttggagaag 240
agctttgaga cagaaaacaa gctggagccc gagcgcaaaa ccagctggc ctaaaagctg 300
gggctgcagc ccagacaggt ggctgtatgg ttccaaaacc gccgtgccg gtggaagacc 360
aagcagctcg agagggatta tgatcagctc aaatcctctt atgactccct tctctctgat 420
tttgactccg ttcgcaaaga taacgataag ctcaaactcg aggttgtttc attgatggaa 480
aagttacagg ggaaagtggg tggaggagca gggggaaatg aaaaatctga catcttgag 540
gtggatgcta tgacgatcct tcaagtgaag gtgaaggctg gggaccggtt gagcagtggc 600
agtgggtgga gcgcggtggg agatgagcat agttcacagc tgggtggacag tggggactca 660
tattttcaca ctgatcatga ggagtatcca gggcctggag gatgcaatgt tcctccaccc 720
atggatgggt tacaatcgga ggaagatgat ggtagtgtat atcatggcag ttgccatggc 780
tacttctcta acgtctttgt ggcagaagag cagcaccatg aacaaggaga agagcctatt 840
ggatggttct ggtcttaa
858

```

```

<210> 26
<211> 285
<212> PRT
<213> Lycopersicon esculentum

<220>
<221> UNSURE
<222> (98) .. (98)
<223> Xaa can be any naturally occurring amino acid

```

```

<400> 26
Met Gly Ser Gly His H e Phe Phe Asp Pro Ser Ser Cys His GIy Asn
1      5      10      15
Met Leu Phe Leu GIy Ser GIy A&p Pro VaI Phe Arg GIy Pro Arg Ser
      20      25      30
Thr Met Met Lys Met GIu Asp Ser Ser Lys Arg Arg Pro Phe Phe Ser

```

PF57967 .ST25 .txt

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

<210> 27
 <211> 972
 <212> DNA
 <213> Lycopersicon esculentum

<400> 27
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 cagagagacg tgttttcttc atctactgca ccgaaagggc atcttggttc ctttttgcc 120
 cctgcctctt cttcttctaa tttcttgga tccagttcta tggtaggttt tcgcggtgtt 180
 aatggaggga agagatcatt ctttgattcg ttcgatcagg atgacaatga agctgatgaa 240
 ttgggggaat atcttcatca agcggagaag aagaggcgac ttactgacaa ccaagttcag 300
 tttcttgaga agagttttgg ggaagagaac aaacttgaac cagaaagaaa agttcagctt 360
 gctaaagaac ttggtctgca gcctcgccaa attgcaattt gggttcagaa tcgtcgtgcg 420
 cgatggaaga ctaagcagct cgagaaagat tatgatgaat tgaggaatag atacgatact 480
 ctgaaatcaa attacaataa tcttctcaag gaaaaagaag atcttcgaac tgaagttttc 540
 cgtctcaccg gtaagctgtt tatcaaagag aaaggaaatg ggcaattgga ttgctgcgat 600
 gaacacaaac actccaatgc attggcaaaa gaaaccgtgg ttgatccaat gtccaatgta 660
 ccagctctgg ttgttaagca ccagcaggaa gatttaagct ctgctaagag tgatgttttc 720
 gactcagaaa gccacgttta caccagtaga atgcattcct cagtcgtaga tcaggatgat 780
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 agcaagaata tgctttctac tgccaaccta cttggcaaa acgcggatga tgattatccc 900
 gcgacatcat caaatttgag ttactttgga tttccagttg aagaccaagg ttttggtttc 960

PF57967.ST25.txt

tggacttatt aa

972

<210> 28
 <211> 323
 <212> PRT
 <213> Lycopersicon esculentum

<400> 28
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 Phe Thr GIn Lys GIn Arg Asp VaI Phe Ser Ser Ser Thr Ala Pro Lys
 20 25 30
 GIy His Leu GIy Ser Leu Phe Ala Pro Ala Ser Ser Ser Ser Asn Phe
 35 40 45
 Leu GIy Ser Ser Ser Met VaI Ser Phe Arg GIy VaI Asn GIy GIy Lys
 50 55 60
 Arg Ser Phe Phe Asp Ser Phe Asp GIn Asp Asp Asn GIu Ala Asp GIu
 65 70 75 80
 Leu GIy GIu Tyr Leu His GIn Ala GIu Lys Lys Arg Arg Leu Thr Asp
 85 90 95
 Asn GIn VaI GIn Phe Leu GIu Lys Ser Phe GIy GIu GIu Asn Lys Leu
 100 105 H O
 GIu Pro GIu Arg Lys VaI GIn Leu Ala Lys GIu Leu GIy Leu GIn Pro
 115 120 125
 Arg GIn H e Ala lie Trp Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr
 130 135 140
 Lys GIn Leu GIu Lys Asp Tyr Asp GIu Leu Arg Asn Arg Tyr Asp Thr
 145 150 155 160
 Leu Lys Ser Asn Tyr Asn Asn Leu Leu Lys GIu Lys GIu Asp Leu Arg
 165 170 175
 Thr GIu VaI Phe Arg Leu Thr GIy Lys Leu Phe H e Lys GIu Lys GIy
 180 185 190
 Asn GIy GIn Leu Asp Leu Arg Asp GIu His Lys His Ser Asn Ala Leu
 195 200 205
 Ala Lys GIu Thr VaI VaI Asp Pro Met Ser Asn VaI Pro Ala Leu VaI
 210 215 220
 VaI Lys His GIn GIn GIu Asp Leu Ser Ser Ala Lys Ser Asp VaI Phe
 225 230 235 240
 Asp Ser GIu Ser Pro Arg Tyr Thr Ser Arg Met His Ser Ser VaI VaI
 245 250 255
 Asp GIn Asp Asp Ser Ala Arg Ala Phe GIu Thr Asp GIn Ser Asp Ser
 260 265 270
 Ser GIn Asp Asp Asp GIu Asn Phe Ser Lys Asn Met Leu Ser Thr Ala
 275 280 285
 Asn Leu Leu GIy Lys Asp Ala Asp Asp Asp Tyr Pro Ala Thr Ser Ser
 290 295 300
 Asn Leu Ser Tyr Phe GIy Phe Pro VaI GIu Asp GIn GIy Phe GIy Phe
 305 310 315 320
 Trp Thr Tyr

<210> 29
 <211> 1014
 <212> DNA

PF57967.ST25.txt

<213> Medicago sat iva

<400> 29

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tctcttttcc	tttcttcttc	tgcttctttc	tttggttcaa	gatctatggt	gagttttgaa	180
gatgttcaag	gaagggaaaag	gcgcaacagg	tctttctttg	gaggatttga	tcttgacgaa	240
aacggagagg	atgagatgga	tgagtacttt	catcaatccg	agaagaaacg	gcgtctctca	300
gtggatcaag	ttcagtttct	tgagaaaagc	tttgaggagg	acaacaaact	tgaaccagag	360
agggaaacca	agctagctaa	agaccttggt	ttgcagccac	ggcaagttgc	tatttggttt	420
caaaaccgtc	gtgcaagggtg	gaagactaaa	cagcttgaga	aggattatga	ttctcttaat	480
gatggttatg	agtctcttaa	gacagagtat	gacaaccttc	tcaaagagaa	agataggtta	540
caatctgagg	tggcaagcct	aactgaaaag	gtacttgaaa	gagagaaaca	agagggaaaa	600
ttcaaacaag	gtgaaagtga	aacaaaggaa	ttcttgaagg	aaccaacaat	taataagcct	660
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aataataata	ataataacaa	acttgaagat	attagttcag	caaggagtga	catattggat	780
tgtgaaagtc	cacgctacac	tgatggagtg	ttagagacat	gtgattcttc	ctatgtattt	840
gaacctgaat	atcaatcgga	cctatcacaa	gatgaagaag	atcacaattt	attgcctcct	900
tacatcttta	caaaacttga	agatgtgaat	tactccgacc	cgccacataa	ttcaacaagt	960
tatggatttc	aagaggaaga	tcatcatcaa	gctctttggc	cttgggtctta	ttag	1014

<210> 30

<211> 337

<212> PRT

<213> Medicago sativa

<400> 30

Met	Ala	GIy	GIy	Arg	VaI	Phe	Ser	Asn	GIy	Pro	Ala	Asn	lie	Ser	Asn
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lie	Asn	Met	Asn	lie	Leu	Leu	GIn	Asn	GIn	GIn	Thr	Pro	Arg	GIy	
			20					25				30			
Asn	Ser	Ser	GIn	GIn	Pro	Leu	Asp	Ser	Leu	Phe	Leu	Ser	Ser	Ser	Ala
		35					40				45				
Ser	Phe	Phe	GIy	Ser	Arg	Ser	Met	VaI	Ser	Phe	GIu	Asp	VaI	GIn	GIy
	50					55					60				
Arg	Lys	Arg	Arg	Asn	Arg	Ser	Phe	Phe	GIy	GIy	Phe	Asp	Leu	Asp	GIu
65				70					75				80		
Asn	GIy	GIu	Asp	GIu	Met	Asp	GIu	Tyr	Phe	His	GIn	Ser	GIu	Lys	Lys
			85					90					95		
Arg	Arg	Leu	Ser	VaI	Asp	GIn	VaI	GIn	Phe	Leu	GIu	Lys	Ser	Phe	GIu
			100					105					110		
GIu	Asp	Asn	Lys	Leu	GIu	Pro	GIu	Arg	Lys	Thr	Lys	Leu	Ala	Lys	Asp
		115					120					125			
Leu	GIy	Leu	GIn	Pro	Arg	GIn	VaI	Ala	H e	Trp	Phe	GIn	Asn	Arg	Arg
	130					135					140				
Ala	Arg	Trp	Lys	Thr	Lys	GIn	Leu	GIu	Lys	Asp	Tyr	Asp	Ser	Leu	Asn
145					150					155					160
Asp	GIy	Tyr	GIu	Ser	Leu	Lys	Thr	GIu	Tyr	Asp	Asn	Leu	Leu	Lys	GIu
			165					170						175	
Lys	Asp	Arg	Leu	GIn	Ser	GIu	VaI	Ala	Ser	Leu	Thr	GIu	Lys	VaI	Leu
			180					185					190		
GIu	Arg	GIu	Lys	GIn	GIu	GIy	Lys	Phe	Lys	GIn	GIy	GIu	Ser	GIu	Thr
		195					200					205			
Lys	GIu	Phe	Leu	Lys	GIu	Pro	Thr	H e	Asn	Lys	Pro	Leu	VaI	Asp	Ser

PF57967.ST25.txt

```

      210              215              220
VaI Ser GIu GIy GIu GIy Ser Lys Leu Ser H e VaI GIu Ala Ser Asn
225              230              235              240
Asn Asn Asn Asn Asn Asn Lys Leu GIu Asp H e Ser Ser Ala Arg Ser
      245              250              255
Asp H e Leu Asp Cys GIu Ser Pro Arg Tyr Thr Asp GIy VaI Leu GIu
      260              265              270
Thr Cys Asp Ser Ser Tyr VaI Phe GIu Pro GIu Tyr GIn Ser Asp Leu
      275              280              285
Ser GIn Asp GIu GIu Asp His Asn Leu Leu Pro Pro Tyr H e Phe Thr
      290              295              300
Lys Leu GIu Asp VaI Asn Tyr Ser Asp Pro Pro His Asn Ser Thr Ser
305              310              315              320
Tyr GIy Phe GIn GIu GIu Asp His His GIn Ala Leu Trp Pro Trp Ser
      325              330              335
Tyr

```

```

<210> 31
<211> 843
<212> DNA
<213> Aquilegia formosa x Aquilegia pubescens

```

```

<400> 31
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ttgaaaagac gtccttttta tagttcaaca gatgaactaa ttgaagagga gttttatgat 180
gaacagctac ctgaaaagaa acgtcgtctt acttctgagc aggttcatct attggagaag 240
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gggttgcaac cgagacaagt tgcagtttgg tttcagaata gacgagctcg ttggaagact 360
aagcaactag agagagatta tgatcttctt aaagcttctt atgattccct tcgttctgat 420
tacgatgaca ttgttaaaga gaatgagaag ctcaaactctg aggtgggttc cttactggg 480
aagttgcagg tcaaggaggg agctgggatg gagttaaatc agatatctga cccaccactc 540
tccactgaag aaaatgttta tgtaactacg atgcaattta atgttaaggt tgaggatcgc 600
ttgagctctg gcagtggggt aagtgtgtgt gttgatgagg aatgtcgaca gcttgttgac 660
agtgttgatt cctatttccc tggcgatgac tatgggtcaat gcataggccc agtagatgga 720
gtccagtcag aagaagatga cattagtgtgac gacagccgga gctatttctc agatgtcttt 780
ccagctgcac cagagcagaa ccaccaggag agtgagacat tgggttggtg ggactgggct 840
taa 843

```

```

<210> 32
<211> 280
<212> PRT
<213> Aquilegia formosa x Aquilegia pubescens

```

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<400> 32
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20 25 30
Ser Phe H e Asn Met GIu Asp Ser Leu Lys Arg Arg Pro Phe Tyr Ser
35 40 45
Ser Thr Asp GIu Leu H e GIu GIu GIu Phe Tyr Asp GIu GIn Leu Pro
50 55 60

```

PF57967.ST25.txt

GIu Lys Lys Arg Arg Leu Thr Ser GIu GIn VaI His Leu Leu GIu Lys
65 70 75 80
Ser Phe GIu Thr GIu Asn Lys Leu GIu Pro Asp Arg Lys Thr GIn Leu
85 90 95
Ala Lys Lys Leu GIy Leu GIn Pro Arg GIn VaI Ala VaI Trp Phe GIn
100 105 110
Asn Arg Arg Ala Arg Trp Lys Thr Lys GIn Leu GIu Arg Asp Tyr Asp
115 120 125
Leu Leu Lys Ala Ser Tyr Asp Ser Leu Arg Ser Asp Tyr Asp Asp lie
130 135 140
VaI Lys GIu Asn GIu Lys Leu Lys Ser GIu VaI VaI Ser Leu Thr GIy
145 150 155 160
Lys Leu GIn VaI Lys GIu GIy Ala GIy Met GIu Leu Asn GIn lie Ser
165 170 175
Asp Pro Pro Leu Ser Thr GIu GIu Asn VaI Asp VaI Thr Thr Met GIn
180 185 190
Phe Asn VaI Lys VaI GIu Asp Arg Leu Ser Ser GIy Ser GIy VaI Ser
195 200 205
Ala VaI VaI Asp GIu GIu Cys Arg GIn Leu VaI Asp Ser VaI Asp Ser
210 215 220
Tyr Phe Pro GIy Asp Asp Tyr GIy GIn Cys lie GIy Pro VaI Asp GIy
225 230 235 240
VaI GIn Ser GIu GIu Asp Asp lie Ser Asp Asp Ser Arg Ser Tyr Phe
245 250 255
Ser Asp VaI Phe Pro Ala Ala Pro GIu GIn Asn His GIn GIu Ser GIu
260 265 270
Thr Leu GIy Trp Trp Asp Trp Ala
275 280

<210> 33
<211> 2193
<212> DNA
<213> Oryza satrva

<400> 33
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catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
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aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360
atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420
ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480
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gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600
tcaactagca acacatctct aatatcactc gcctatttta tacatttagg tagcaatatc 660
tgaattcaag cactccacca tcaccagacc acttttaata atatctaaaa tacaaaaaat 720
aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa 780
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ggaggcatcc aagccaagaa gagggagagc accaaggaca cgcgactagc agaagccgag 1080
cgaccgcctt cttcgatcca tatcttccgg tcgagttcct ggtcgatctc ttccctcctc 1140

PF57967.ST25.txt

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gatttgggat	agaggggttc	ttgatgttgc	atgttatcgg	ttcgggttga	ttagtagtat	1320
ggttttcaat	cgtctggaga	gctctatgga	aatgaaatgg	tttagggtag	ggaatcttgc	1380
gattttgtga	gtaccttttg	tttgaggtaa	aatcagagca	ccggtgattt	tgcttggtgt	1440
aataaaagta	cggttggttg	gtcctcgatt	ctggtagtga	tgcttctcga	tttgacgaag	1500
ctatcctttg	tttattccct	attgaacaaa	aataatccaa	cttgaagac	ggccccgttg	1560
atgagattga	atgattgatt	cttaagcctg	tccaaaattt	cgcagctggc	ttgttttagat	1620
acagtagtcc	ccatcacgaa	attcatggaa	acagttataa	tcctcaggaa	caggggattc	1680
cctgttcttc	cgatttgctt	tagtcccaga	atttttttct	ccaaatatct	taaaaagtca	1740
ctttctgggt	cagttcaatg	aattgattgc	tacaaataat	gcttttatag	cgttatccta	1800
gctgtagtgc	agttaatagg	taatacccct	atagtttagt	caggagaaga	acttatccga	1860
tttctgatct	ccatttttaa	ttatatgaaa	tgaactgtag	cataagcagt	attcatttgg	1920
attatttttt	ttattagctc	tcacccttct	attattctga	gctgaaagtc	tggcatgaac	1980
tgtcctcaat	tttgttttca	aattcacatc	gattatctat	gcattatcct	cttgtatcta	2040
cctgtagaag	tttctttttg	gtatttcctt	gactgcttga	ttacagaaag	aaatttatga	2100
agctgtaatc	gggatagtta	tactgcttgt	tcttatgatt	catttccttt	gtgcagttct	2160
tggtgtagct	tgccactttc	accagcaaag	ttc			2193

<210> 34
 <211> 49
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm6000

<400>	34					
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<210> 35
 <211> 48
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prmβ001

<400>	35					
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<210> 36
 <211> 834
 <212> DNA
 <213> Oryza sativa

<400>	36					
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aattctagt	atgatggata	tggaggggtt	gggatggagg	cggaggggga	cgtggaggag	120
gagatgatgg	cgtgcggcgg	cggcggggag	aagaagcggc	ggctgagcgt	ggagcaggtt	180
cgcgcgctgg	agcggagctt	cgagggtggag	aacaagcttg	agcctgagcg	gaaggcgagg	240
ctggcgcgcg	acctcgccct	gcagccgcgc	caggtcgccg	tctggttcca	gaaccgccc	300
gcgcggtgga	agaccaagca	gctcgagcgc	gactacgccg	cgctccgcca	ttcctacgac	360
tccctgcgcc	tcgatcacga	cgcgctccgc	cgcgacaagg	acgccctcct	cgccgagatc	420

PF57967.ST25.txt

aaggagctga	aggcgaagct	cggggacgag	gaggcgccgg	cgagcttcac	gtcgggtgaag	480
gaggagccgg	cggcctccga	cgggccaccg	gcggcgggat	ttgggtcgtc	cgacagcgac	540
tcaagcgccg	tgctgaacga	cgtggacgcg	gccggcgccg	cgcccgcggc	gacggacgcg	600
ctggctccgg	aggcgtgcac	gtttctcgg	gcgccgcccg	ccgcgggccc	gggcgcgggc	660
gcagcgccgg	cggcgagcca	cgaggagggtg	ttcttccacg	gcaatttcct	caagggtggag	720
gaggacgaga	cggggttcct	cgacgacgac	gagccgtgcg	gcgggttctt	cgccgacgat	780
cagccccgc	cgctctcgtc	gtggtggggc	gaaccacg	agcactggaa	ctga	834

<210> 37
 <211> 277
 <212> PRT
 <213> Oryza sativa

<400> 37

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

<210> 38
 <211> 750
 <212> DNA

PF57967.ST25.txt

<213> Oryza sat iva

<400> 38

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tcgctggagt	ccatgttcgc	gacgcagacc	aagctggagc	cgaggcagaa	gctgcagctc	180
gccagggagc	tcggcctgca	gcctcgccag	gtcgccatct	ggttccagaa	caagcgcgcg	240
cggtggaagt	ccaagcagct	cgagcgcgag	tactccgccc	tccgcgacga	ctacgacgcc	300
ctcctctgca	gctacgagtc	cctcaagaag	gagaagctcg	ccctcatcaa	gcagctggag	360
aagctggcgg	agatgctgca	ggagccacgg	gggaagtacg	gcgataatgc	cggggacgac	420
gcgcggtcgg	gcggcgctgc	cgcatgaag	aaggaggagt	tcgtcggcgc	gggcggcgcc	480
gccacgctct	actcgtcggc	cgagggtggc	gggacgacga	cgacgacgac	ggccaagttg	540
atgccccact	tcggcagcga	cgacgtcgac	gcggggctct	tcctccggcc	gtcgtcgag	600
catcatccgc	cgccgccgca	cgccggtgcc	ggcttcacgt	cctccgagcc	ggccgccgac	660
caccagtcct	tcaacttcca	ctcgagctgg	ccgtcgtcca	cggagcagac	ctgcagcagc	720
acgccatggt	gggaattcga	gagcgagtga				750

<210> 39

<211> 249

<212> PRT

<213> Oryza sativa

<400> 39

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Lys	GIy	GIy	Lys	GIy	GIy	GIy	GIy	GIy	GIy	Ala	Ala	Asp	Arg	Lys	Lys	
			20					25					30			
Arg	Phe	Ser	GIu	GIu	GIn	H e	Lys	Ser	Leu	GIu	Ser	Met	Phe	Ala	Thr	
		35					40					45				
GIn	Thr	Lys	Leu	GIu	Pro	Arg	GIn	Lys	Leu	GIn	Leu	Ala	Arg	GIu	Leu	
		50				55					60					
GIy	Leu	GIn	Pro	Arg	GIn	VaI	Ala	lie	Trp	Phe	GIn	Asn	Lys	Arg	Ala	
65				70					75						80	
Arg	Trp	Lys	Ser	Lys	GIn	Leu	GIu	Arg	GIu	Tyr	Ser	Ala	Leu	Arg	Asp	
			85					90						95		
Asp	Tyr	Asp	Ala	Leu	Leu	Cys	Ser	Tyr	GIu	Ser	Leu	Lys	Lys	GIu	Lys	
			100					105					H O			
Leu	Ala	Leu	H e	Lys	GIn	Leu	GIu	Lys	Leu	Ala	GIu	Met	Leu	GIn	GIu	
		115						120				125				
Pro	Arg	GIy	Lys	Tyr	GIy	Asp	Asn	Ala	GIy	Asp	Asp	Ala	Arg	Ser	GIy	
		130				135					140					
GIy	VaI	Ala	GIy	Met	Lys	Lys	GIu	GIu	Phe	VaI	GIy	Ala	GIy	GIy	Ala	
145				150					155						160	
Ala	Thr	Leu	Tyr	Ser	Ser	Ala	GIu	GIy	GIy	GIy	Thr	Thr	Thr	Thr	Thr	
			165					170						175		
Thr	Ala	Lys	Leu	Met	Pro	His	Phe	GIy	Ser	Asp	Asp	VaI	Asp	Ala	GIy	
			180					185					190			
Leu	Phe	Leu	Arg	Pro	Ser	Ser	GIn	His	His	Pro	Pro	Pro	Pro	His	Ala	
		195					200					205				
GIy	Ala	GIy	Phe	Thr	Ser	Ser	GIu	Pro	Ala	Ala	Asp	His	GIn	Ser	Phe	
	210					215					220					
Asn	Phe	His	Ser	Ser	Trp	Pro	Ser	Ser	Thr	GIu	GIn	Thr	Cys	Ser	Ser	
225					230					235					240	
Thr	Pro	Trp	Trp	GIu	Phe	GIu	Ser	GIu								

PF57967 .ST25 .txt

245

<210> 40
 <211> 945
 <212> DNA
 <213> Populus tremuloides

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 ggcccttggt ctgttcacaca acctcttgaa tcttttttcc tttctggctc ttctccttct 120
 tttcttggtt caagatccat gatgagtttt gaagatgttc atcaagcaaa cggatcaacc 180
 aggccttttt tccgctcgtt tgatcacgaa gacaatggag acgatgatct ggatgaatat 240
 tttcatcaac ctgaaaagaa gaggagactt actgttgatc aagttcagtt tcttgaaaag 300
 agttttgagc ttgagaacaa gcttgaacct gaaaggaaaa tccagcttgc aaaggatctt 360
 ggcccttcagc cgcgtcaggt tgctatatgg tttcaaaacc gccgagcaag atggaagact 420
 aaacagctgg aaaaggatta tgacgttttg caatctagct acaatagcct taaggctgac 480
 tatgacaacc tcctcaagga gaaggagaaa ctaaaagctg aggttaatct tctcaccgac 540
 aagttgctcc tcaaagagaa agagaaggga atctcagaat tgtctgataa agatgcatta 600
 tcgcaagagc cacctaaaag ggctatagct gattcagctt ccgaggggtga agtgtcgaaa 660
 atctcaacag tggcctgtaa gcaggaagat atcagctcag ccaaaagcga catatttgat 720
 tcagacagcc cacattacgc tgatgggggtg cattcctcac tcttagaggc aggagattct 780
 tcatatgttt tcgaaccgga tcaatcagat ttgtcacaa atgaagaaga taactttagc 840
 aagagcttat tgcctccata cgtctttccg aagcttgaag atgacgatta ctctgacccg 900
 cctgcaagtt ttgaagatca tgccttttgg tcctgggtcat actaa 945

<210> 41
 <211> 314
 <212> PRT
 <213> Populus tremuloides

<400> 41
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 1 5 10 15
 GIn Ser GIn Arg GIy Pro Cys Ala Ala Ser GIn Pro Leu GIu Ser Phe
 20 25 30
 Phe Leu Ser GIy Ser Ser Pro Ser Phe Leu GIy Ser Arg Ser Met Met
 35 40 45
 Ser Phe GIu Asp VaI His GIn Ala Asn GIy Ser Thr Arg Pro Phe Phe
 50 55 60
 Arg Ser Phe Asp His GIu Asp Asn GIy Asp Asp Asp Leu Asp GIu Tyr
 65 70 75 80
 Phe His GIn Pro GIu Lys Lys Arg Arg Leu Thr VaI Asp GIn VaI GIn
 85 90 95
 Phe Leu GIu Lys Ser Phe GIu Leu GIu Asn Lys Leu GIu Pro GIu Arg
 100 105 110
 Lys lie GIn Leu Ala Lys Asp Leu GIy Leu GIn Pro Arg GIn VaI Ala
 115 120 125
 lie Trp Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr Lys GIn Leu GIu
 130 135 140
 Lys Asp Tyr Asp VaI Leu GIn Ser Ser Tyr Asn Ser Leu Lys Ala Asp
 145 150 155 160
 Tyr Asp Asn Leu Leu Lys GIu Lys GIu Lys Leu Lys Ala GIu VaI Asn
 165 170 175
 Leu Leu Thr Asp Lys Leu Leu Leu Lys GIu Lys GIu Lys GIy lie Ser

PF57967.ST25.txt

180 185 190
 GIu Leu Ser Asp Lys Asp Ala Leu Ser GIn GIu Pro Pro Lys Arg Ala
 195 200 205
 H e Ala Asp Ser Ala Ser GIu GIy GIu VaI Ser Lys H e Ser Thr VaI
 210 215 220
 Ala Cys Lys GIn GIu Asp H e Ser Ser Ala Lys Ser Asp H e Phe Asp
 225 230 235 240
 Ser Asp Ser Pro His Tyr Ala Asp GIy VaI His Ser Ser Leu Leu GIu
 245 250 255
 Ala GIy Asp Ser Ser Tyr VaI Phe GIu Pro Asp GIn Ser Asp Leu Ser
 260 265 270
 GIn Asp GIu GIu Asp Asn Phe Ser Lys Ser Leu Leu Pro Pro Tyr VaI
 275 280 285
 Phe Pro Lys Leu GIu Asp Asp Asp Tyr Ser Asp Pro Pro Ala Ser Phe
 290 295 300
 GIu Asp His Ala Phe Trp Ser Trp Ser Tyr
 305 310

<210> 42
 <211> 954
 <212> DNA
 <213> Populus tremuloides

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 tctccttctt ttcttgggtc aagatccatg atgagttttg cagatgttca ccaagcaaat 180
 ggatcaacta gaccgttttt ccgcccataat gatcacgaag acaacggcga cgatgatttg 240
 gatgaatatt ttcatcaacc tgaaaagaag aggagactta ctgttgatca agttcagttt 300
 cttgaaagaa gttttgaggt tgagaacaag cttgaaccgg aaaggaaaat ccagctggcg 360
 aaggatcttg gcttgcagcc tcggcagggt gccatatggt ttcaaaaccg ccgggcaaga 420
 tggaagacga aacagcttga aaaagattat gaggttctgc aatctagcta caatggcctt 480
 aaggctgact acgacaacct cttcaaggag aaggagaaac taaaagctga ggttaatctt 540
 ctcaccaacg agttgtctct taaagagaaa gagaaaggaa gctcagaatt gtctgataaa 600
 gatgcattat ctcaagagcc acccaaaaag gcaatagccg attcagcttc agagggtgaa 660
 gtgtcgaaaa cttcaaccgt ggcctgccag caggaagata ttagctcagc caaaagtgat 720
 atgtttgatt cagacagccc acatttttgcg gatgggggtac attcctcact cttagaggca 780
 ggtgattctt cacatgtctt cgagcccgtac caatcggatt tatcacaaga tgaagaagat 840
 aacttgagca agagtctttt gcctccgtac gtctttccaa agcttgaaga tggtgattac 900
 tctgacccgc cagcaagttt tgaagatcat gccttttggg gctggtcata ctaa 954

<210> 43
 <211> 317
 <212> PRT
 <213> Populus tremuloides

<400> 43
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 VaI Leu VaI GIn Ser GIn Arg GIy Pro Cys Ala Ala Ser GIn Pro Leu
 20 25 30
 GIu Ala Phe Phe Leu Ser GIy Ser Ser Pro Ser Phe Leu GIy Ser Arg
 35 40 45
 Ser Met Met Ser Phe Ala Asp VaI His GIn Ala Asn GIy Ser Thr Arg

PF57967 .ST25 .txt

50 55 60
 Pro Phe Phe Arg Pro Tyr Asp His GIu Asp Asn GIy Asp Asp Asp Leu
 65 70 75 80
 Asp GIu Tyr Phe His GIn Pro GIu Lys Lys Arg Arg Leu Thr VaI Asp
 85 90 95
 GIn VaI GIn Phe Leu GIu Arg Ser Phe GIu VaI GIu Asn Lys Leu GIu
 100 105 110
 Pro GIu Arg Lys H e GIn Leu Ala Lys Asp Leu GIy Leu GIn Pro Arg
 115 120 125
 GIn VaI Ala H e Trp Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr Lys
 130 135 140
 GIn Leu GIu Lys Asp Tyr GIu VaI Leu GIn Ser Ser Tyr Asn GIy Leu
 145 150 155 160
 Lys Ala Asp Tyr Asp Asn Leu Phe Lys GIu Lys GIu Lys Leu Lys Ala
 165 170 175
 GIu VaI Asn Leu Leu Thr Asn GIu Leu Leu Leu Lys GIu Lys GIu Lys
 180 185 190
 GIy Ser Ser GIu Leu Ser Asp Lys Asp Ala Leu Ser GIn GIu Pro Pro
 195 200 205
 Lys Lys Ala H e Ala Asp Ser Ala Ser GIu GIy GIu VaI Ser Lys Thr
 210 215 220
 Ser Thr VaI Ala Cys GIn GIn GIu Asp H e Ser Ser Ala Lys Ser Asp
 225 230 235 240
 Met Phe Asp Ser Asp Ser Pro His Phe Ala Asp GIy VaI His Ser Ser
 245 250 255
 Leu Leu GIu Ala GIy Asp Ser Ser His VaI Phe GIu Pro Asp GIn Ser
 260 265 270
 Asp Leu Ser GIn Asp GIu GIu Asp Asn Leu Ser Lys Ser Leu Leu Pro
 275 280 285
 Pro Tyr VaI Phe Pro Lys Leu GIu Asp GIy Asp Tyr Ser Asp Pro Pro
 290 295 300
 Ala Ser Phe GIu Asp His Ala Phe Trp Cys Trp Ser Tyr
 305 310 315

<210> 44
 <211> 909
 <212> DNA
 <213> Populus tremuloides

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 tctatggtta attttaggaa tgatggagga gacactgtag acatgtcttt tttccaacca 180
 catgtcaaag aagaaagtag cgatgaggat tatgatgcgc acctaaagcc atctgaaaag 240
 aaaaggcggc ttacagctgc tcaagtccag tttcttgaga agagctttga ggcggagaat 300
 aagcttgaac cagagaggaa gatgcagctt gctaaagaac tcggcttgca gcctcgccag 360
 gttgcaatat ggtttcaaaa ccgtagagct cggttcaaga acaagcagct ggaaagggac 420
 tacgactcct tgagaatcag ctttgacaaa ctcaaggctg attatgacaa actcctcctc 480
 gagaagcaga atttgaaaaa cgagcttctt tctactgaaag aaaaattgct tagcagagag 540
 gaaagtatgg aaagttcaga accatttgat gtcattccatt caccggatgc agaacttgag 600
 cctatttctg atacagtgtc tgaaaatggt tccgccattg tgccaatggt gacacccaaa 660
 caagaagaaa gttcagctaa aaatgatggt ttcaactcag acagcccacg ttcatttttg 720
 gagccccgtg attgttatcg tgttttcgag tcagaccaac cagatttttc ccaagttgaa 780
 gaagataatc tcaccaggag ctttctaccc cctccgtact ttccaaaact ctaccgagag 840

PF57967.ST25.txt

ccacctgcaa gttcacgtaa ttttgaattc tcagcggaag atcagccctt ttggtcctgg 900
atttactga 909

<210> 45
<211> 302
<212> PRT
<213> Populus tremuloides

<400> 45
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20 25 30
Phe Ser Thr Leu His GIy Ala Lys Ser Met VaI Asn Phe Arg Asn Asp
35 40 45
GIy GIy Asp Thr VaI Asp Met Ser Phe Phe GIn Pro Hxs VaI Lys GIu
50 55 60
GIu Ser Ser Asp GIu Asp Tyr Asp Ala His Leu Lys Pro Ser GIu Lys
65 70 75 80
Lys Arg Arg Leu Thr Ala Ala GIn VaI GIn Phe Leu GIu Lys Ser Phe
85 90 95
GIu Ala GIu Asn Lys Leu GIu Pro GIu Arg Lys Met GIn Leu Ala Lys
100 105 110
GIu Leu GIy Leu GIn Pro Arg GIn VaI Ala lie Trp Phe GIn Asn Arg
115 120 125
Arg Ala Arg Phe Lys Asn Lys GIn Leu GIu Arg Asp Tyr Asp Ser Leu
130 135 140
Arg lie Ser Phe Asp Lys Leu Lys Ala Asp Tyr Asp Lys Leu Leu Leu
145 150 155 160
GIu Lys GIn Asn Leu Lys Asn GIu Leu Leu Ser Leu Lys GIu Lys Leu
165 170 175
Leu Ser Arg GIu GIu Ser Met GIu Ser Ser GIu Pro Phe Asp VaI lie
180 185 190
His Ser Pro Asp Ala GIu Leu GIu Pro lie Pro Asp Thr VaI Ser GIu
195 200 205
Asn VaI Ser Ala lie VaI Pro Met VaI Thr Pro Lys GIn GIu GIu Ser
210 215 220
Ser Ala Lys Asn Asp VaI Phe Asn Ser Asp Ser Pro Arg Ser Phe Leu
225 230 235 240
GIu Pro Arg Asp Cys Tyr Arg VaI Phe GIu Ser Asp GIn Pro Asp Phe
245 250 255
Ser GIn VaI GIu GIu Asp Asn Leu Thr Arg Ser Phe Leu Pro Pro Pro
260 265 270
Tyr Phe Pro Lys Leu Tyr Arg GIu Pro Pro Ala Ser Ser Arg Asn Phe
275 280 285
GIu Phe Ser Ala GIu Asp GIn Pro Phe Trp Ser Trp lie Tyr
290 295 300

<210> 46
<211> 975
<212> DNA
<213> Medicago truncatula

<400> 46

PF57967.ST25.txt

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ggttcaaatt cagtgggttaa ttttgagaat ggtgggtgga gcaacagagt ggtaacagat      180
agacccttct ttcaacaact tgagaaagaa gagaattgtg gtgatgaaga ttatgaagca      240
tgctaccatc aacaaggaaa gaaaaggagg ctttcaagtg aacaagttca atttcttgaa      300
aagagttttg aggtagaaaa caagcttgaa cctgatagga aagttcaact tgcaaaagag      360
cttgggtttg aaccaagaca agttgctata tggtttcaaa acagaagggc aaggttcaaa      420
actaaacagc ttgaaaaaga ttatggcaca ttgaaagcta gctttgatag tctcaaagat      480
gattatgata atcttcttca agagaatgac aagttaaaag aagaggtgaa ttctctcaag      540
aacaaattga tccaagaga taaagaaaaa gtgaattcag aagacaaatc atcaccagaa      600
gcaatcaatt cacctcataa caacatagat ccaatggata taatttcaat tacaatttca      660
gaaaatgggt ccaaaatgtc actccctaata atggtactaa aatgtaagca agaagatgcc      720
aattcagcta aaagtgatgt gcttgattct gatagccac attgcaatga tgggaacaat      780
ctttcttctt tcatagagcc tacagattca gatttctcac aagatgaaga ggataatgat      840
aacttgagtc ataatctttt gactcttctt tgcttaccaa aagttgaaga tgtttgctat      900
gatgaccac atgaaaattc ttgtaatttt gggttcctg ttgaagatca aaccttttgt      960
ttctggcctt attga                                     975

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<210> 47
<211> 324
<212> PRT
<213> Medicago truncatula

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

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PF57967.ST25.txt

Asn	Ser	Ala	Lys	Ser	Asp	VaI	Leu	Asp	Ser	Asp	Ser	Pro	His	Cys	Asn
				245					250					255	
Asp	GIy	Asn	Asn	Leu	Ser	Ser	Phe	lie	GIu	Pro	Thr	Asp	Ser	Asp	Phe
			260					265					270		
Ser	GIn	Asp	GIu	GIu	Asp	Asn	Asp	Asn	Leu	Ser	His	Asn	Leu	Leu	Thr
		275				280					285				
Leu	Pro	Cys	Leu	Pro	Lys	VaI	GIu	Asp	VaI	Cys	Tyr	Asp	Asp	Pro	His
	290				295					300					
GIu	Asn	Ser	Cys	Asn	Phe	GIy	Phe	Pro	VaI	GIu	Asp	GIn	Thr	Phe	Cys
305					310					315					320
Phe	Trp	Pro	Tyr												

<210> 48
 <211> 984
 <212> DNA
 <213> Phaseolus vulgaris

<400> 48

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aggccctttt	ttcaagcggt	ggagaaggaa	gataactgtg	atgatgatta	tgagggttgc	240
ttccatcaac	cgggtaagaa	aaggaggctc	acaagcgaac	aagttcagtt	ccttgaaagg	300
aactttgagg	tcgagaacaa	gcttgaacct	gaaaggaagg	tccaacttgc	aaaggagctt	360
ggcttgcagc	caaggcaagt	ggctatatgg	ttccaaaacc	gaagggcaag	gttcaagacc	420
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aaattgattc	ttagagataa	agagaaggag	aattcggacg	acaagtcac	tcctgatgct	600
gtcaattcac	cccacaagaa	gcctatggat	ttaatttcaa	attcaacatc	tgaaaatggg	660
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gaagaggata	atcttagtga	aagccttttg	accctccctt	gcttaccaa	ggttgaagaa	900
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<-210> 49
 <211> 327
 <212> PRT
 <213> Phaseolus vulgaris

<400> 49

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GIn	Asn	Asp	Arg	Leu	Pro	Cys	Ser	Ser	GIu	VaI	Leu	GIu	Ser	Leu	Trp
		20					25					30			
Ala	His	Thr	Ser	Asn	Ala	Ala	Ser	Phe	GIn	GIy	Ser	Lys	Ser	Met	VaI
		35					40				45				
Asp	Phe	GIu	Asn	VaI	Ser	GIy	GIy	Arg	VaI	Thr	Asp	Arg	Pro	Phe	Phe
	50				55					60					
GIn	Ala	Leu	GIu	Lys	GIu	Asp	A&n	Cys	Asp	Asp	Asp	Tyr	GIu	GIy	Cys
65				70					75					80	
Phe	His	GIn	Pro	GIy	Lys	Lys	Arg	Arg	Leu	Thr	Ser	GIu	GIn	VaI	GIn

PF57967.ST25.txt

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

<210> 50
 <211> 957
 <212> DNA
 <213> Lotus corniculatus

<400> 50
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 agtcttttgc ttcagaatca acctcctgat tcttctctct tcctctctac ctctgcttct 120
 tttctcggtt caagatccat ggtgagcttc gcagataata aattagggca aacgcggtcg 180
 ttcttctccg cgtttgacct cgatgagaac ggcgatgagg tcatggacga gtactttcac 240
 caatcggaga agaagcgccg tctctctggt gaccaagttc agtttctgga gaagagcttc 300
 gaggtggata acaagctcga acctgacagg aaaaccaaga ttgccaagga ccttggtttg 360
 cagccacgcc aagtcgcaat ctgggtccag aaccgccgtg cacggtggaa gacgaaacag 420
 cttgagaagg attatgattc tctgcatagt agctttgaga gtctcaaadc caactatgat 480
 aatcttctca aggagaaaga catgttaaaa gctgaggtgg caagtctcac tgagaagggtg 540
 cttgcaagag agaatttgaa acaagttgaa agtgaaacaa agggattggt tgaaccaccc 600
 caaaggcctt tacttgattc agtttcagag agtgagaagt ctaaagtctc tgttggggct 660
 tgtaaacatg aggatatcag ttcagccagg agtgagagtt tggattctga tagcccacgt 720
 tacagggatg gatatggagt taactcagca gtgctagaga catgtgattc ttcttatgtg 780
 gttgaacctg atcaatcgga tatgtcacag gatgaggaag acaacctgac caagaccctg 840
 ttgcctccat acatgttttc caaacttgga gatatggatt actccgacct gcctgaaagt 900
 tcatgtaatt tcggatttcc ggaggaagat catgcccttt ggtcatggtc ttactga 957

PF57967.ST25.txt

<210> 51
 <211> 318
 <212> PRT
 <213> Lotus corniculatus

<400> 51
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 VaI Ser Asp Thr Ser Leu Leu Leu GIn Asn GIn Pro Pro Asp Ser Ser
 20 25 30
 Leu Phe Leu Ser Thr Ser Ala Ser Phe Leu GIy Ser Arg Ser Met VaI
 35 40 45
 Ser Phe Ala Asp Asn Lys Leu GIy GIn Thr Arg Ser Phe Phe Ser Ala
 50 55 60
 Phe Asp Leu Asp GIu Asn GIy Asp GIu VaI Met Asp GIu Tyr Phe His
 65 70 75 80
 GIn Ser GIu Lys Lys Arg Arg Leu Ser VaI Asp GIn VaI GIn Phe Leu
 85 90 95
 GIu Lys Ser Phe GIu VaI Asp Asn Lys Leu GIu Pro Asp Arg Lys Thr
 100 105 110
 Lys lie Ala Lys Asp Leu GIy Leu GIn Pro Arg GIn VaI Ala lie Trp
 115 120 125
 Phe GIn Asn Arg Arg Ala Arg Trp Lys Thr Lys GIn Leu GIu Lys Asp
 130 135 140
 Tyr Asp Ser Leu His Ser Ser Phe GIu Ser Leu Lys Ser Asn Tyr Asp
 145 150 155 160
 Asn Leu Leu Lys GIu Lys Asp Met Leu Lys Ala GIu VaI Ala Ser Leu
 165 170 175
 Thr GIu Lys VaI Leu Ala Arg GIu Asn Leu Lys GIn VaI GIu Ser GIu
 180 185 190
 Thr Lys GIy Leu VaI GIu Pro Pro GIn Arg Pro Leu Leu Asp Ser VaI
 195 200 205
 Ser GIu GIy GIu GIu Ser Lys VaI Ser VaI GIy Ala Cys Lys His GIu
 210 215 220
 Asp lie Ser Ser Ala Arg Ser GIu Ser Leu Asp Ser Asp Ser Pro Arg
 225 230 235 240
 Tyr Arg Asp GIy Tyr GIy VaI Asn Ser Ala VaI Leu GIu Thr Cys Asp
 245 250 255
 Ser Ser Tyr VaI VaI GIu Pro Asp GIn Ser Asp Met Ser GIn Asp GIu
 260 265 270
 GIu Asp Asn Leu Thr Lys Thr Leu Leu Pro Pro Tyr Met Phe Ser Lys
 275 280 285
 Leu GIy Asp Met Asp Tyr Ser Asp Pro Pro GIu Ser Ser Cys Asn Phe
 290 295 300
 GIy Phe Pro GIu GIu Asp His Ala Leu Trp Ser Trp Ser Tyr
 305 310 315

<210> 52
 <211> 1602
 <212> DNA
 <213> Oryza sativa

<400> 52

PF57967.ST25.txt

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ccggcggttcg cgttctcgcac ggaggtgggc ggcgaggacg cggcggcggc gagcaagttc 120
gacttgccgg tggactcgga gcacaaggcg aagacgatca ggttgctgtc gttcgcgaac 180
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atccccctcg tctcccgcgg ctcgctcggc atcatctccg gcatgaccgg cgccggcggc 1260
aacttcggcg ccgggctcac gcagctgctc ttcttcacgt cgtcgaggta ctccacgggc 1320
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aagttcgccg agaactcccg ctccgagcgt ggccgcccga acgtcatcaa cgccgccgcg 1560
gccgccgcca cgccgcccaa caactcgccg gacgacgcct aa 1602

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<210> 53
 <211> 533
 <212> PRT
 <213> Oryza sativa

<400> 53
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 20 25 30
 Asp Ala Ala Ala Ser Lys Phe Asp Leu Pro Val Asp Ser Glu His
 35 40 45
 Lys Ala Lys Thr Ile Arg Leu Leu Ser Phe Ala Asn Pro His Met Arg
 50 55 60
 Thr Phe His Leu Ser Trp Ile Ser Phe Phe Ser Cys Phe Val Ser Thr
 65 70 75 80
 Phe Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn Leu
 85 90 95
 Thr Lys Ala Asp H e Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser
 100 105 H O
 Ile Phe Ser Arg Leu Ala Met Gly Ala Ile Cys Asp Met Leu Gly Pro
 115 120 125
 Arg Tyr Gly Cys Ala Phe Leu H e Met Leu Ala Ala Pro Thr Val Phe
 130 135 140
 Cys Met Ser Leu Ile Asp Ser Ala Ala Gly Tyr H e Ala Val Arg Phe
 145 150 155 160

PF57967.ST25.txt

```

Leu lie GIy Phe Ser Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met
      165      170
Ser Thr Met Phe Asn Ser Lys lie lie GIy Leu VaI Asn GIy Leu Ala
      180      185      190
Ala GIy Trp GIy Asn Met GIy GIy GIy Ala Thr GIn Leu lie Met Pro
      195      200      205
Leu VaI Tyr Asp VaI lie Arg Lys Cys GIy Ala Thr Pro Phe Thr Ala
      210      215      220
Trp Arg Leu Ala Tyr Phe VaI Pro GIy Thr Leu Hrs VaI VaI Met GIy
      225      230      235
VaI Leu VaI Leu Thr Leu GIy GIn Asp Leu Pro Asp GIy Asn Leu Arg
      245      250      255
Ser Leu GIn Lys Lys GIy Asp VaI Asn Arg Asp Ser Phe Ser Arg VaI
      260      265      270
Leu Trp Tyr Ala VaI Thr Asn Tyr Arg Thr Trp lie Phe VaI Leu Leu
      275      280      285
Tyr GIy Tyr Ser Met GIy VaI GIu Leu Thr Thr Asp Asn VaI lie Ala
      290      295      300
GIu Tyr Phe Tyr Asp Arg Phe Asp Leu Asp Leu Arg VaI Ala GIy lie
      305      310      315
H e Ala Ala Ser Phe GIy Met Ala Asn H e VaI Ala Arg Pro Thr GIy
      325      330      335
GIy Leu Leu Ser Asp Leu GIy Ala Arg Tyr Phe GIy Met Arg Ala Arg
      340      345      350
Leu Trp Asn H e Trp H e Leu GIn Thr Ala GIy GIy Ala Phe Cys Leu
      355      360      365
Leu Leu GIy Arg Ala Ser Thr Leu Pro Thr Ser VaI VaI Cys Met VaI
      370      375      380
Leu Phe Ser Phe Cys Ala GIn Ala Ala Cys GIy Ala H e Phe GIy VaI
      385      390      395
H e Pro Phe VaI Ser Arg Arg Ser Leu GIy H e H e Ser GIy Met Thr
      405      410      415
GIy Ala GIy GIy Asn Phe GIy Ala GIy Leu Thr GIn Leu Leu Phe Phe
      420      425      430
Thr Ser Ser Arg Tyr Ser Thr GIy Thr GIy Leu GIu Tyr Met GIy H e
      435      440      445
Met H e Met Ala Cys Thr Leu Pro VaI VaI Leu VaI His Phe Pro GIn
      450      455      460
Trp GIy Ser Met Phe Leu Pro Pro Asn Ala GIy Ala GIu GIu GIu Hrs
      465      470      475
Tyr Tyr GIy Ser GIu Trp Ser GIu GIn GIu Lys Ser Lys GIy Leu Hrs
      485      490      495
GIy Ala Ser Leu Lys Phe Ala GIu Asn Ser Arg Ser GIu Arg GIy Arg
      500      505      510
Arg Asn VaI H e Asn Ala Ala Ala Ala Ala Thr Pro Pro Asn Asn
      515      520      525
Ser Pro GIu His Ala
      530

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<210> 54

<211> 53

<212> DNA

<213> Artificial sequence

PF57 967 . ST25 . txt

<220>

<223> primer: prm07061

<400> 54

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<210> 55

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> primer: prm07062

<400> 55

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<210> 56

<211> 3848

<212> DNA

<213> Artificial sequence

<220>

<223> expression cassette

<400> 56

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catccacctta	cttttagtgcc	aatcgggcta	aataaaaaag	agtcgctaca	ctagtttcgt	180
tttccttagt	aattaagtgg	gaaaatgaaa	tcattattgc	ttagaatata	cgttcacatc	240
tctgtcatga	agttaaatta	ttcgaggtag	ccataattgt	catcaaactc	ttcttgaata	300
aaaaaatctt	tctagctgaa	ctcaatgggt	aaagagagag	atTTTTTTta	aaaaaataga	360
atgaagatat	tctgaacgta	ttggcaaaga	tttaaacata	taattatata	attttatagt	420
ttgtgcattc	gtcatatcgc	acatcattaa	ggacatgtct	tactccatcc	caatttttat	480
ttagtaatta	aagacaattg	acttattttt	attattttatc	ttttttcgat	tagatgcaag	540
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aaccaagcat	cctcctcctc	ccatctataa	attcctcccc	ccttttcccc	tctctatata	1020
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PF57967.ST25.txt

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acgcctaa 3848

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<210> 57
<211> 27
<212> PRT
<213> Artificial sequence

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<220>
<223> signature sequence 1

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<220>
<221> VARIANT
<222> (1) .. (1)
<223> /replace="Ser"

```

```

<220>
<221> VARIANT
<222> (2) .. (2)

```

PF57967.ST25.txt

```
<223> /replace= "Pro"

<220>
<221> VARIANT
<222> (3) .. (3)
<223> /replace="Gly" /replace="Ser" /replace="Ala"

<220>
<221> VARIANT
<222> (5) .. (5)
<223> /replace="Val" /replace="Leu"

<220>
<221> VARIANT
<222> (6) .. (6)
<223> /replace="Leu" /replace="Thr"

<220>
<221> VARIANT
<222> (7) .. (7)
<223> /replace="Ala" /replace="Phe" /replace="Leu"

<220>
<221> VARIANT
<222> (8) .. (8)
<223> /replace="Val" /replace="Met" /replace="Ile"

<220>
<221> VARIANT
<222> (9) .. (9)
<223> /replace="Thr" /replace="Ile" /replace="Ala" /replace="Asn"

<220>
<221> VARIANT
<222> (12) .. (12)
<223> /replace="Phe"

<220>
<221> VARIANT
<222> (13) .. (13)
<223> /replace="Cγ s" /replace="Thr"

<220>
<221> VARIANT
<222> (14) .. (14)
<223> /replace="Phe" /replace="Tγ r"

<220>
<221> VARIANT
<222> (16) .. (16)
<223> /replace="Ile"

<220>
<221> VARIANT
```

PF57967.ST25.txt

```

<222> (19) .. (19)
<223> /replace="Ser"

<220>
<221> VARIANT
<222> (20) .. (20)
<223> /replace="Ile" /replace="Val"

<220>
<221> VARIANT
<222> (21) .. (21)
<223> /replace="Gly" /replace="Asn"

<220>
<221> VARIANT
<222> (23) .. (23)
<223> /replace="Ile" /replace="Asn"

<220>
<221> VARIANT
<222> (24) .. (24)
<223> /replace="Val"

<220>
<221> VARIANT
<222> (25) .. (25)
<223> /replace="Ser" /replace="His" /replace="Val"

<220>
<221> VARIANT
<222> (26) .. (26)
<223> /replace="Gln" /replace="Gly"

<400> 57
Asn Tyr Thr Trp lie Phe VaI Leu Leu Tyr GIy Tyr Ser Met GIy VaI
1      5      10      15
GIu Leu Thr Thr Asp Asn VaI lie Ala GIu Tyr
      20      25

<210> 58
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> signature sequence 2

<220>
<221> VARIANT
<222> (3) .. (3)
<223> /replace="Ala"

<220>
<221> VARIANT

```

PF57967 .ST25 .txt

<222> (7) .. (7)
 <223> /replace="Thr"

<220>
 <221> VARIANT
 <222> (10) .. (10)
 <223> /replace="Ser"

<400> 58
 Leu GIy Pro Arg Tyr GIy Cys Ala Phe Leu
 1 5 10

<210> 59
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> signature sequence 3

<220>
 <221> VARIANT
 <222> (6) .. (6)
 <223> /replace="Arg"

<220>
 <221> VARIANT
 <222> (9) .. (9)
 <223> /replace="Ile"

<220>
 <221> VARIANT
 <222> (10) .. (10)
 <223> /replace="Val"

<220>
 <221> VARIANT
 <222> (11) .. (11)
 <223> /replace="Leu" /replace="Val"

<220>
 <221> VARIANT
 <222> (14) .. (14)
 <223> /replace="Glu"

<220>
 <221> VARIANT
 <222> (17) .. (17)
 <223> /replace="Asp"

<220>
 <221> VARIANT
 <222> (18) .. (18)
 <223> /replace="Pro"

PF57967.ST25.txt

<400> 59
Ser Thr Phe Ala Ala Pro Leu Val Pro lie lie Arg Asp Asn Leu
1 5 10 15
Asn Leu

<210> 60
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> signature sequence 4

<220>
<221> VARIANT
<222> (4) ..(4)
<223> /replace="Met"

<220>
<221> VARIANT
<222> (8) ..(8)
<223> /replace="Cys"

<400> 60
Val Arg Phe Leu lie GIy Phe Ser Leu Ala
1 5 10

<210> 61
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> signature sequence 5

<220>
<221> VARIANT
<222> (5) ..(5)
<223> /replace="Arg"

<220>
<221> VARIANT
<222> (8) ..(8)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (10) ..(10)
<223> /replace="Val"

<220>
<221> VARIANT

PF57967 .ST25 .txt

<222> (11) .. (11)
 <223> /replace="Ser"

<220>
 <221> VARIANT
 <222> (12) .. (12)
 <223> /replace="Ser"

<400> 61
 Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe
 1 5 10

<210> 62
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> signature sequence 6

<220>
 <221> VARIANT
 <222> (2) .. (2)
 <223> /replace="Gln" /replace="Ser" /replace="Met " /replace="His"
 /replace="Thr"

<220>
 <221> VARIANT
 <222> (4) .. (4)
 <223> /replace="Val"

<220>
 <221> VARIANT
 <222> (13) .. (13)
 <223> /replace="Thr"

<220>
 <221> VARIANT
 <222> (15) .. (15)
 <223> /replace="Ala"

<220>
 <221> VARIANT
 <222> (17) .. (17)
 <223> /replace="Leu"

<220>
 <221> VARIANT
 <222> (20) .. (20)
 <223> /replace="Gly"

<400> 62
 Lys Ala Asp He Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser He
 1 5 10 15

PF57967.ST25.txt

Phe Ser Arg Leu
20

<210> 63
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> signature sequence 7

<220>
<221> VARIANT
<222> (3) .. (3)
<223> /replace="Thr" /replace="Cys"

<220>
<221> VARIANT
<222> (5) .. (5)
<223> /replace="Gly"

<400> 63
Asn GIy Leu Ala Ala GIy Trp GIy
1 5

<210> 64
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> signature sequence 8

<220>
<221> VARIANT
<222> (2) .. (2)
<223> /replace="Ser"

<220>
<221> VARIANT
<222> (4) .. (4)
<223> /replace="Val" /replace="Gln"

<220>
<221> VARIANT
<222> (7) .. (7)
<223> /replace="Pro"

<220>
<221> VARIANT
<222> (8) .. (8)
<223> /replace="Val" /replace="Ile"

<220>

PF57967 .ST25 .txt

<221> VARIANT
 <222> (9) .. (9)
 <223> /replace="Glu"

<220>
 <221> VARIANT
 <222> (11) .. (11)
 <223> /replace="Ser" /replace="Asp"

<220>
 <221> VARIANT
 <222> (12) .. (12)
 <223> /replace="Thr"

<220>
 <221> VARIANT
 <222> (13) .. (13)
 <223> /replace="Ala" /replace="Thr"

<400> 64
 GIy Ala GIy Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser
 1 5 10

<210> 65
 <211> 1858
 <212> DNA
 <213> Phragmites australis

<400> 65
 acaacagctc agatcaagca cctgcatttg cataagagct agcaagcaag caagtccaag 60
 aaagaagcta gctagcttgt atcagatcaa gactcgagag gccagctatg gaggttggcg 120
 cgccggggag ctgctgacac ggcgtcacgg ggcgcgagcc ggcgttcgcc ttctcgacgt 180
 ctgcggtgcc cgacgacgat gcagcgagca agttcgacct gccggtggac tcggagcaca 240
 aggccaagag catccggctc ttctccttcg ccaacccgca catgcgcacc ttccatctct 300
 cgtggatctc ctctctcacc tgcttcgtct ccaccttcgc cgccgcgccg ctgctcccca 360
 tcatccgga caacctcaac ctccaccaagg ccgacatcgg caacgccggc gtggcctccg 420
 tctcgggatc catcttctcc cgtctcgcca tgggcgccat ctgcgacctc ctgcggccgc 480
 gctacggctg cgcttctctc atcatgctca cggcgccac cgtcttctgc atgtccctca 540
 tcgacgacgc agccggctac atcgtcgtca ggttcttgat cggcttctct ctggccacgt 600
 tcgtgtcgtg ccagtactgg atgagcacca tgttcaatag caagatcatc gggacggtga 660
 acgggctggc ggctgggtgg gggaacatgg gcggcgccgc cacgcagctc cccatgccgc 720
 tcgtctacga cgtcatccgc aagtgcggcg cgacgccctt cacggcgtgg cgcacgcct 780
 acttcgtgcc ggggctaata cacgtggtga tgggcacctt ggtgctcacg ctggggcagg 840
 acctccccga cggcaacctg aggagcctcc agaagaaggc cgacgccaac aaggacaagt 900
 tctccaaggt gctctggtac gccgtcacca actatcgac ctggatcttc gtgctgctct 960
 acggctactg catgggctg gagctgacca ccgacaacgt catcgccgag tactactacg 1020
 accacttcga cctagacctc cgcgtcgccg gcacatcgc cgttgcttc ggaatggcca 1080
 acatcgtggc acggcccttg ggcggcatcc tctccgacat cggcgcgcgc tactggggca 1140
 tgccgcgcgc cctct ggaac atctggatgc tccagactgc tggcggcgcc ttctgcctct 1200
 ggctcgccgc cgccagcacg ctctctgcct ccattaccgc catgggtgctc ttctccttct 1260
 gcgcccaggc cgcttgcggc gccattttcg gcgtcacccc ttctgctacc cgccgctccc 1320
 tcggcatcat gtccgggatg acgggggctg gcggcaactt cggcgcgggg ctcacgcagc 1380
 tgctcttctt cacctcgtcc aagtactcca cgggcatggg gctggagtac atgggcatca 1440
 tgatcatggc gtgcacgctg cccgtggtgt tcgtgcactt cccgcaatgg ggatccatgc 1500

PF57967.ST25.txt

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tcctcccgcc cagcgccggc gccgtcgagg agcactacta cagctcggag tggagtgagg 1560
aggagaagag caaggggctc cacagctcca gcctcaagtt ttcagagAAC tgccgttcag 1620
agcgcggaac ccgcaacgtc atcctcgcgg caccaaacag cagccccgag caggtataag 1680
acgcacgtat atgtccgcat tcgtaccctt gtgcgcgtat acgcatacgc cagcggtttg 1740
tttaataagg tgcgcatata tatatatgta actagctata atgcgtatca ccgttatgcg 1800
cacgcacacg aaatatatat aattcgatgt tgacgcatat acaaaaaaaaa aaaaaaaaa 1858

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<210> 66
 <211> 523
 <212> PRT
 <213> Phragmites australis

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<400> 66
Met GIu VaI GIy Ala Pro GIy Ser Ser Leu His GIy VaI Thr GIy Arg
1      5      10      15
GIu Pro Ala Phe Ala Phe Ser Thr Ser Ala VaI Pro Asp Asp Asp Ala
      20      25      30
Ala Ser Lys Phe Asp Leu Pro VaI Asp Ser GIu His Lys Ala Lys Ser
      35      40      45
lie Arg Leu Phe Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu
      50      55      60
Ser Trp lie Ser Phe Phe Thr Cys Phe VaI Ser Thr Phe Ala Ala Ala
      65      70      75      80
Pro Leu VaI Pro lie lie Arg Asp Asn Leu Asn Leu Thr Lys Ala Asp
      85      90      95
lie GIy Asn Ala GIy VaI Ala Ser VaI Ser GIy Ser H e Phe Ser Arg
      100      105      H O
Leu Ala Met GIy Ala lie Cys Asp Leu Leu GIy Pro Arg Tyr GIy Cys
      115      120      125
Ala Phe Leu lie Met Leu Thr Ala Pro Thr VaI Phe Cys Met Ser Leu
      130      135      140
lie Asp Asp Ala Ala GIy Tyr lie VaI VaI Arg Phe Leu H e GIy Phe
      145      150      155      160
Ser Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met Ser Thr Met Phe
      165      170      175
Asn Ser Lys lie lie GIy Thr VaI Asn GIy Leu Ala Ala GIy Trp GIy
      180      185      190
Asn Met GIy GIy GIy Ala Thr GIn Leu Pro Met Pro Leu VaI Tyr Asp
      195      200      205
VaI lie Arg Lys Cys GIy Ala Thr Pro Phe Thr Ala Trp Arg H e Ala
      210      215      220
Tyr Phe VaI Pro GIy Leu Met His VaI VaI Met GIy H e Leu VaI Leu
      225      230      235      240
Thr Leu GIy GIn Asp Leu Pro Asp GIy Asn Leu Arg Ser Leu GIn Lys
      245      250      255
Lys GIy Asp Ala Asn Lys Asp Lys Phe Ser Lys VaI Leu Trp Tyr Ala
      260      265      270
VaI Thr Asn Tyr Arg Thr Trp lie Phe VaI Leu Leu Tyr GIy Tyr Cys
      275      280      285
Met GIy VaI GIu Leu Thr Thr Asp Asn VaI H e Ala GIu Tyr Tyr Tyr
      290      295      300
Asp His Phe Asp Leu Asp Leu Arg VaI Ala GIy H e H e Ala Ala Cys
      305      310      315      320
Phe GIy Met Ala Asn H e VaI Ala Arg Pro Leu GIy GIy H e Leu Ser

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PF57967.ST25.txt

325 330 335
 Asp lie GIy Ala Arg Tyr Trp GIy Met Arg Ala Arg Leu Trp Asn lie
 340 345 350
 Trp lie Leu GIn Thr Ala GIy GIy Ala Phe Cys Leu Trp Leu GIy Arg
 355 360 365
 Ala Ser Thr Leu Pro Ala Ser lie Thr Ala Met VaI Leu Phe Ser Phe
 370 375 380
 Cys Ala GIn Ala Ala Cys GIy Ala lie Phe GIy VaI Thr Pro Phe VaI
 385 390 395 400
 Thr Arg Arg Ser Leu GIy lie Met Ser GIy Met Thr GIy Ala GIy GIy
 405 410 415
 Asn Phe GIy Ala GIy Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser Lys
 420 425 430
 Tyr Ser Thr GIy Met GIy Leu GIu Tyr Met GIy H e Met H e Met Ala
 435 440 445
 Cys Thr Leu Pro VaI VaI Phe VaI Hxs Phe Pro GIn Trp GIy Ser Met
 450 455 460
 Leu Leu Pro Pro Ser Ala GIy Ala VaI GIu GIu His Tyr Tyr Ser Ser
 465 470 475 480
 GIu Trp Ser GIu GIu Lys Ser Lys GIy Leu Hrs Ser Ser Ser Leu
 485 490 495
 Lys Phe Ser GIu Asn Cys Arg Ser GIu Arg GIy Asn Arg Asn VaI H e
 500 505 510
 Leu Ala Ala Pro Asn Ser Thr Pro GIu His VaI
 515 520

<210> 67
 <211> 1691
 <212> DNA
 <213> Zea mays

<400> 67
 ccaagggaaa gggatacatc acctgctgct ctagctctgc tatagcgcta gcagcaatat 60
 aatggcggcc gtcggcgctc cggggagctc tctgcacgga gtcacggggc gcgagccggc 120
 gttcgcatc tccacggagc acgaggagc ggcgagcaat ggcggcaagt tgcacctgcc 180
 ggtggactcg gagcacaagg cgaagagcgt ccggctcttc tccgtggcga acccgcacat 240
 gcgcacctc cacctctcct ggatctcctt ctacacctgc ttcgtgtcca ccttcgccgc 300
 cgcgccgctg gtcccatca tccgcgacaa cctcaacctc accaaggccg acatcgccaa 360
 cgcgggcgctg gcctccgtgt cgggctccat ctctctccgc ctaccatgg gcgccgtctg 420
 cgacctgctg ggcccgct acggctgcgc ctctctcatc atgctgtccg cgccaccgt 480
 gttctgcatg tcgctcatcg acgacgccgc gggctacatc accgtcaggt tcctcatcgg 540
 ctctctccctc gccaccttcg tctcctgccg gtactggatg agcaccatgt tcagcagcaa 600
 gatcatcggc accgtcaacg ggctcgccgc cggatggggc aacatgggag gcggcgccac 660
 gcagctcatc atgccgctcg tctacgacgt catccgcaag tgcggcgcca cgcccttcac 720
 ggcgtggcgc ctgcctact tcgtgccggg cctcatgcac gtcgtcatgg gcgtcctggt 780
 gtcacgctg gggcaggacc tccccgacgg caacctcagg tcgctgcaga agaagggcaa 840
 cgtcaacaag gacagcttct ccaaggctcat gtggtacgcc gtcatcaact accgcacctg 900
 gatcttcgct ctctctacg gctactgcat gggcgctcag ctaccaccg acaacgtcat 960
 cgccaggtac atgtacgacc gcttcgacct cgacctccgc gtcgccggga ccatcgccgc 1020
 ctgcttcggc atggccaaca tcgtcgcgcg ccccatgggc ggcatcatgt ccgacatggg 1080
 cgcgcgctac tggggcatgc gcgctcgctt ctggaacatc tggatcctcc agaccgccgg 1140
 cgggcgcttc tgctcttgcc tgggacgcgc cagcacctc cccgtctccg tcgtcgccat 1200
 ggtgctcttc tcttctgctg cgcaggcggc ctgcggcgcc atcttcgggg tcatcccctt 1260
 cgtctcccgc cgctccctcg gcatcatctc cgcatgacg ggcgccggcg gcaacttcgg 1320

PF57967.ST25.txt

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cgcgggggctc acgcagctgc tcttcttcac ctcctcaacc tactccacgg gcaggggggct 1380
agagtacatg ggcacatga tcatggcgtg cacgctacct gtggtgttcg tgcacttccc 1440
gcagtggggg tccatgttct tccgcccag cgccaccgcc gacgaggagg gctactacgc 1500
ctccgagtgg aacgacgacg agaagagcaa gggactccat agcgccagcc tcaagtttgc 1560
cgagaacagc cgctcagagc gcggcaagcg aaacgtcatc caggccgatg ccgccgccac 1620
gccggagcat gtctaagtct actactaata agatggatcg atccatcatc catgttcacc 1680
tgctacctac c 1691

```

<210> 68
 <211> 524
 <212> PRT
 <213> Zea mays

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<400> 68
Met Ala Ala VaI GIy Ala Pro GIy Ser Ser Leu His GIy VaI Thr GIy
1 5 10 15
Arg GIu Pro Ala Phe Ala Phe Ser Thr GIu His GIu GIu Ala Ala Ser
20 25 30
Asn GIy GIy Lys Phe Asp Leu Pro VaI Asp Ser GIu His Lys Ala Lys
35 40 45
Ser VaI Arg Leu Phe Ser VaI Ala Asn Pro His Met Arg Thr Phe His
50 55 60
Leu Ser Trp lie Ser Phe Phe Thr Cys Phe VaI Ser Thr Phe Ala Ala
65 70 75 80
Ala Pro Leu VaI Pro lie lie Arg Asp Asn Leu Asn Leu Thr Lys Ala
85 90 95
Asp lie GIy Asn Ala GIy VaI Ala Ser VaI Ser GIy Ser H e Phe Ser
100 105 110 H O
Arg Leu Thr Met GIy Ala VaI Cys Asp Leu Leu GIy Pro Arg Tyr GIy
115 120 125
Cys Ala Phe Leu H e Met Leu Ser Ala Pro Thr VaI Phe Cys Met Ser
130 135 140
Leu lie Asp Asp Ala Ala GIy Tyr H e Thr VaI Arg Phe Leu H e GIy
145 150 155 160
Phe Ser Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met Ser Thr Met
165 170 175
Phe Ser Ser Lys H e H e GIy Thr VaI Asn GIy Leu Ala Ala GIy Trp
180 185 190
GIy Asn Met GIy GIy GIy Ala Thr GIn Leu H e Met Pro Leu VaI Tyr
195 200 205
Asp VaI H e Arg Lys Cys GIy Ala Thr Pro Phe Thr Ala Trp Arg Leu
210 215 220
Ala Tyr Phe VaI Pro GIy Leu Met His VaI VaI Met GIy VaI Leu VaI
225 230 235 240
Leu Thr Leu GIy GIn Asp Leu Pro Asp GIy Asn Leu Arg Ser Leu GIn
245 250 255
Lys Lys GIy Asn VaI Asn Lys Asp Ser Phe Ser Lys VaI Met Trp Tyr
260 265 270
Ala VaI H e Asn Tyr Arg Thr Trp H e Phe VaI Leu Leu Tyr GIy Tyr
275 280 285
Cys Met GIy VaI GIu Leu Thr Thr Asp Asn VaI H e Ala GIu Tyr Met
290 295 300
Tyr Asp Arg Phe Asp Leu Asp Leu Arg VaI Ala GIy Thr H e Ala Ala
305 310 315 320

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PF57967.ST25. txt

Cys Phe GIy Met Ala Asn H e VaI Ala Arg Pro Met GIy GIy H e Met
 325 330 335
 Ser Asp Met GIy Ala Arg Tyr Trp GIy Met Arg Ala Arg Leu Trp Asn
 340 345 350
 lie Trp lie Leu GIn Thr Ala GIy GIy Ala Phe Cys Leu Trp Leu GIy
 355 360 365
 Arg Ala Ser Thr Leu Pro VaI Ser VaI VaI Ala Met VaI Leu Phe Ser
 370 375 380
 Phe Cys Ala GIn Ala Ala Cys GIy Ala H e Phe GIy VaI H e Pro Phe
 385 390 395 400
 VaI Ser Arg Arg Ser Leu GIy H e H e Ser GIy Met Thr GIy Ala GIy
 405 410 415
 GIy Asn Phe GIy Ala GIy Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser
 420 425 430
 Thr Tyr Ser Thr GIy Arg GIy Leu GIu Tyr Met GIy H e Met H e Met
 435 440 445
 Ala Cys Thr Leu Pro VaI VaI Phe VaI His Phe Pro GIn Trp GIy Ser
 450 455 460
 Met Phe Phe Pro Pro Ser Ala Thr Ala Asp GIu GIu GIy Tyr Tyr Ala
 465 470 475 480
 Ser GIu Trp Asn Asp Asp GIu Lys Ser Lys GIy Leu His Ser Ala Ser
 485 490 495
 Leu Lys Phe Ala GIu Asn Ser Arg Ser GIu Arg GIy Lys Arg Asn VaI
 500 505 510
 H e GIn Ala Asp Ala Ala Ala Thr Pro GIu His VaI
 515 520

<210> 69
 <211> 1789
 <212> DNA
 <213> Zea mays

<400> 69
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 ctagcagcaa tggcggccgt cgcgctccg ggcagctctc tgcacggagt cacggggcgc 120
 gagccggcgt tcgccttctc cacggagcac gaggaggcgg cgagcaatgg tggcaagtgc 180
 gacctgccgg tggactcaga gcacaaggcg aagagcgctc gtctcttctc cgtggcgaac 240
 ccacacatgc gcaccttcca cctctcctgg atctccttct tcacctgctt cgtgtccacc 300
 ttcgccgccg cgccgctggt ccccatcatc cgcgacaacc tcaacctcac caaggccgac 360
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 cccaccgtgt tctgcatgtc gctcatcgac gacgccgcgg gctacatcac cgtcagggtc 540
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 agcagcaaga tcatcggcac cgtcaacggg ctgcgccggg gatggggcac aatgggaagg 660
 cggcgccacg cagctcatat gccgctcgtc tacgacgtca tccgcaagtg cggcgccacg 720
 ccattcacgg cctggcgcct cgcctacttc gtgccgggcc tcatgcacgt cgtcatgggc 780
 gtctgtgtgc tcacgtggg gcaggacctc cccgacggca acctcagggtc gctgcagaag 840
 aagggcaacg tcaacaagga cagcttctcc aaggtcatgt ggtacgccgt catcaactac 900
 cgtacctgga tctttgtcct cctctacggc tactgcatgt gcgtcgagct caccaccgac 960
 aacgtcatcg ccgagtagat gtacgaccgc ttgcacctcg acctccgcgt cgctggggacc 1020
 atcgccgcct gcttcggcat ggccaacatc gtcgcacgcc ccatgggcgg catcatgtcc 1080
 gacatgggcg cgcgctactg gggcatgcgc gctgcctctt ggaacatctg gatcctccag 1140
 accgccggcg gcgccttctg cctctggctg gggcgcgcca gcaccctcc cgtctccgtc 1200
 gtcgccatgg tgctcttctc cttctgcgcg caggcgccat gcggcgccat cttcgggggt 1260

PF57967.ST25.txt

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atccccctttg tctcccgccg ctccctcggc atcatctccg gcatgacggg cgccggcgcc 1320
aacttcggcg ccgggctcac gcagctgctc ttctttacct cctcgacctt ctccacgggc 1380
agggggctgg agtacatggg catcatgatc atggcggtgca cgctgcccgt ggtgttcgtg 1440
cacttccctc agtgggggtc catgttcttt ccgccagcg ccaccgccga cgaggagggc 1500
tactacgcct ccgagtggaa cgacgacgag aagagcaagg gactccatag cgccagcctc 1560
aagttcgccg agaacagccg ctcagagcgc ggcaagcgaa acgtcatcca ggccgacgcc 1620
gccgccacgc cggagcatgt ctaagtctac tactaagatg gatcgatcga cgatcaccta 1680
tacctctttg tatgtacgaa tatgccttgt tattactgcg cgcgcgcata tacaatacac 1740
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<210> 70
 <211> 524
 <212> PRT
 <213> Zea mays

<400> 70

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

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PF57967.ST25. txt

Tyr Asp Arg Phe Asp Leu Asp Leu Arg Val Ala GIY Thr H e Ala Ala
 305 310 315 320
 Cys Phe GIY Met Ala Asn H e Val Ala Arg Pro Met GIY GIY H e Met
 325 330 335
 Ser Asp Met GIY Ala Arg Tyr Trp GIY Met Arg Ala Arg Leu Trp Asn
 340 345 350
 H e Trp H e Leu GIn Thr Ala GIY GIY Ala Phe Cys Leu Trp Leu GIY
 355 360 365
 Arg Ala Ser Thr Leu Pro Val Ser Val Val Ala Met Val Leu Phe Ser
 370 375 380
 Phe Cys Ala GIn Ala Ala Cys GIY Ala H e Phe GIY Val H e Pro Phe
 385 390 395 400
 Val Ser Arg Arg Ser Leu GIY H e H e Ser GIY Met Thr GIY Ala GIY
 405 410 415
 GIY Asn Phe GIY Ala GIY Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser
 420 425 430
 Thr Tyr Ser Thr GIY Arg GIY Leu GIU Tyr Met GIY H e Met H e Met
 435 440 445
 Ala Cys Thr Leu Pro Val Val Phe Val His Phe Pro GIn Trp GIY Ser
 450 455 460
 Met Phe Phe Pro Pro Ser Ala Thr Ala Asp GIU GIU GIY Tyr Tyr Ala
 465 470 475 480
 Ser GIU Trp Asn Asp Asp GIU Lys Ser Lys GIY Leu His Ser Ala Ser
 485 490 495
 Leu Lys Phe Ala GIU Asn Ser Arg Ser GIU Arg GIY Lys Arg Asn Val
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 H e GIn Ala Asp Ala Ala Ala Thr Pro GIU His Val
 515 520

<210> 71
 <211> 1837
 <212> DNA
 <213> Hordeum vulgare

<400;> 71
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 actgccgca gcaagttcac gctgccggtg gactccgagc acaaggccaa gtccttcagg 180
 ctcttctcct tcgccaaccc gcacatgcgc accttccatc tctcgtggat ctccttcttc 240
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 tggggcaaca tgggtgggtg cgccacgcag ctcatcatgc cgctcgtctt ccatgcaatc 660
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PF57967.ST25.txt

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tctgaattta caacagcttt gaggcggccg cgaatttc 1837

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<210> 72
 <211> 507
 <212> PRT
 <213> Hordeum vulgare

<400> 72
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 Thr Leu Pro VaI Asp Ser GIu His Lys Ala Lys Ser Phe Arg Leu Phe
 20 25 30
 Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp H e Ser
 35 40 45
 Phe Phe Thr Cys Phe lie Ser Thr Phe Ala Ala Ala Pro Leu VaI Pro
 50 55 60
 lie lie Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp H e GIy Asn Ala
 65 70 75 80
 GIy VaI Ala Ser VaI Ser GIy Ser H e Phe Ser Arg Leu Ala Met GIy
 85 90 95
 Ala lie Cys Asp Leu Leu GIy Pro Arg Tyr GIy Cys Ala Phe Leu VaI
 100 105 H O
 Met Leu Ser Ala Pro Thr VaI Phe Cys Met Ala VaI H e Asp Asp Ala
 115 120 125
 Ser GIy Tyr H e Ala VaI Arg Phe Leu H e GIy Phe Ser Leu Ala Thr
 130 135 140
 Phe VaI Ser Cys GIn Tyr Trp Met Ser Thr Met Phe Asn Ser Lys H e
 145 150 155 160
 lie GIy Thr VaI Asn GIy Leu Ala Ala GIy Trp GIy Asn Met GIy GIy
 165 170 175
 GIy Ala Thr GIn Leu H e Met Pro Leu VaI Phe His Ala H e GIn Lys
 180 185 190
 Cys GIy Ala Thr Pro Phe VaI Ala Trp Arg H e Ala Tyr Phe VaI Pro
 195 200 205
 GIy Met Met His H e VaI Met GIy Leu Leu VaI Leu Thr Met GIy GIn
 210 215 220
 Asp Leu Pro Asp GIy Asn Leu Ala Ser Leu GIn Lys Lys GIy Asp Met
 225 230 235 240
 Ala Lys Asp Lys Phe Ser Lys VaI Leu Trp GIy Ala VaI Thr Asn Tyr
 245 250 255
 Arg Thr Trp H e Phe VaI Leu Leu Tyr GIy Tyr Cys Met GIy VaI GIu
 260 265 270
 Leu Thr Thr Asp Asn VaI H e Ala GIu Tyr Tyr Phe Asp His Phe His

PF57967 . ST25 .txt

275 280 285
 Leu Asp Leu Arg Ala Ala GIy Thr lie Ala Ala Cys Phe Gly Met Ala
 290 295 300
 Asn lie VaI Ala Arg Pro Thr GIy GIy Tyr Leu Ser Asp Leu GIy Ala
 305 310 315 320
 Arg Tyr Phe GIy Met Arg Ala Arg Leu Trp Asn lie Trp lie Leu GIn
 325 330 335
 Thr Ala GIy GIy Ala Phe Cys lie Trp Leu GIy Arg Ala Ser Ala Leu
 340 345 350
 Pro Ala Ser VaI Thr Ala Met VaI Leu Phe Ser lie Cys Ala GIn Ala
 355 360 365
 Ala Cys GIy Ala H e Phe GIy VaI Ala Pro Phe VaI Ser Arg Arg Ser
 370 375 380
 Leu GIy lie H e Ser GIy Leu Thr GIy Ala GIy GIy Asn VaI GIy Ala
 385 390 395 400
 GIy Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser GIn Tyr Ser Thr GIy
 405 410 415
 Arg GIy Leu GIu Tyr Met GIy H e Met lie Met Ala Cys Thr Leu Pro
 420 425 430
 VaI Ala Leu VaI His Phe Pro GIn Trp GIy Ser Met Phe Phe Pro Ala
 435 440 445
 Ser Ala Asp Ala Thr GIu GIu GIu Tyr Tyr Ala Ser GIu Trp Ser GIu
 450 455 460
 GIu GIu Lys Ala Lys GIy Leu His H e Ala GIy GIn Lys Phe Ala GIu
 465 470 475 480
 Asn Ser Arg Ser GIu Arg GIy Arg Arg Asn VaI H e Leu Ala Thr Ser
 485 490 495
 Ala Thr Pro Pro Asn Asn Thr Pro GIn His VaI
 500 505

<210> 73
 <211> 1750
 <212> DNA
 <213> Triticum aestivum

<220>
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<400> 73
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PF57967.ST25.txt

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ccgattgttt	tttcatatac	tatgtacaag	tactgaacat	cggctgtaat	aagggtgtacg	1620
catttatatt	tccagtgtag	acttgtgtaa	tgcgtttctt	acgcacgaaa	tgttttggtg	1680
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aaaaaaaaaa						1750

<210> 74
 <211> 507
 <212> PRT
 <213> π ticum aestivum

<400> 74
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 Thr Leu Pro VaI Asp Ser GIu His Lys Ala Lys Ser Phe Arg Leu Phe
 20 25 30
 Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp H e Ser
 35 40 45
 Phe Phe Thr Cys Phe VaI Ser Thr Phe Ala Ala Ala Pro Leu VaI Pro
 50 55 60
 H e H e Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp H e GIy Asn Ala
 65 70 75 80
 GIy VaI Ala Ser VaI Ser GIy Ser H e Phe Ser Arg Leu Ala Met GIy
 85 90 95
 Ala H e Cys Asp Leu Leu GIy Pro Arg Tyr GIy Cys Ala Phe Leu VaI
 100 105 H O
 Met Leu Ser Ala Pro Thr VaI Phe Cys Met Ala VaI H e Asp Asp Ala
 115 120 125
 Ser GIy Tyr H e Ala VaI Arg Phe Leu H e GIy Phe Ser Leu Ala Thr
 130 135 140
 Phe VaI Ser Cys GIn Tyr Trp Met Ser Thr Met Phe Asn Ser Lys H e
 145 150 155 160
 lie GIy Thr VaI Asn GIy Leu Ala Ala GIy Trp GIy Asn Met GIy GIy
 165 170 175
 GIy Ala Thr GIn Leu H e Met Pro Leu VaI Phe His Ala H e GIn Lys
 180 185 190
 Cys GIy Ala Thr Pro Phe VaI Ala Trp Arg H e Ala Tyr Phe VaI Pro
 195 200 205
 GIy Met Met His H e VaI Met GIy Leu Leu VaI Leu Thr Met GIy GIn
 210 215 220
 Asp Leu Pro Asp GIy Asn Leu Ala Ser Leu GIn Lys Lys GIy Asp Met
 225 230 235 240

PF57967.ST25.txt

Ala Lys Asp Lys Phe Ser Lys Val Leu Trp GIY Ala Val Thr Asn Tyr
 245 250 255
 Arg Thr Trp lie Phe Val Leu Leu Tyr GIY Tyr Cys Met GIY Val GIU
 260 265 270
 Leu Thr Thr Asp Asn Val lie Ala GIU Tyr Tyr Tyr Asp His Phe His
 275 280 285
 Leu Asp Leu Arg Ala Ala GIY Thr lie Ala Ala Cys Phe GIY Met Ala
 290 295 300
 Asn lie Val Ala Arg Pro Met GIY GIY Tyr Leu Ser Asp Leu GIY Ala
 305 310 315 320
 Arg Tyr Phe GIY Met Arg Ala Arg Leu Trp Asn lie Trp lie Leu GIn
 325 330 335
 Thr Ala GIY GIY Ala Phe Cys lie Trp Leu GIY Arg Ala Ser Ala Leu
 340 345 350
 Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser H e Cys Ala GIn Ala
 355 360 365
 Ala Cys GIY Ala Val Phe GIY Val Ala Pro Phe Val Ser Arg Arg Ser
 370 375 380
 Leu GIY H e H e Ser GIY Leu Thr GIY Ala GIY GIY Asn Val GIY Ala
 385 390 395 400
 GIY Leu Thr GIn Leu Phe Phe Thr Ser Ser GIn Tyr Ser Thr GIY
 405 410 415
 Arg GIY Leu GIU Tyr Met GIY H e Met H e Met Ala Cys Thr Leu Pro
 420 425 430
 Val Ala Leu Val His Phe Pro GIn Trp GIY Ser Met Phe Phe Pro Ala
 435 440 445
 Ser Ala Asp Ala Thr GIU GIU GIU Tyr Tyr Ala Ser GIU Trp Ser GIU
 450 455 460
 GIU GIU Lys Asn Lys GIY Leu His H e Ala GIY GIn Lys Phe Ala GIU
 465 470 475 480
 Asn Ser Arg Ser GIU Arg GIY Arg Arg Asn Val H e Leu Ala Thr Ser
 485 490 495
 Ala Thr Pro Pro Asn Asn Thr Pro GIn His Val
 500 505

<210> 75
 <211> 1741
 <212> DNA
 <213> Hordeum vulgare

<400> 75
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 acgaggctgc gagcaagttc tcgctgcccg tggactcgga gcacaaggcc aagtccatca 180
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PF57967.ST25.txt

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cgagcttttc	tttacctgtg	tacacgtaca	gtgcgcgtat	tatacacaca	tcgatcgtgt	1680
atatacgct	ggaatccgca	agcagtatgt	tttttgaaaa	aaaaaaagcg	gccgcgaatt	1740
c						1741

<210> 76
 <211> 509
 <212> PRT
 <213> Hordeum vulgare

<400> 76

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			20					25					30		
Leu	Phe	Ser	Phe	Ala	Asn	Pro	His	Met	Arg	Thr	Phe	His	Leu	Ser	Trp
		35					40					45			
lie	Ser	Phe	Phe	Thr	Cys	Phe	VaI	Ser	Thr	Phe	Ala	Ala	Ala	Pro	Leu
	50					55					60				
VaI	Pro	lie	H e	Arg	Asp	Asn	Leu	Asn	Leu	Ala	Lys	Ala	Asp	H e	GIy
65					70				75					80	
Asn	Ala	GIy	VaI	Ala	Ser	VaI	Ser	GIy	Ser	H e	Phe	Ser	Arg	Leu	Ala
				85				90						95	
Met	GIy	Ala	H e	Cys	Asp	Leu	Leu	GIy	Pro	Arg	Tyr	GIy	Cys	Ala	Phe
		100						105					H O		
Leu	VaI	Met	Leu	Ala	Ala	Pro	Thr	VaI	Phe	Cys	Met	Ser	Leu	H e	Asp
		115					120					125			
Asp	Ala	Ala	GIy	Tyr	H e	Thr	VaI	Arg	Phe	Leu	H e	GIy	Phe	Ser	Leu
	130					135					140				
Ala	Thr	Phe	VaI	Ser	Cys	GIn	Tyr	Trp	Met	Ser	Thr	Met	Phe	Asn	Ser
145					150					155					160
Lys	H e	H e	GIy	Thr	VaI	Asn	GIy	Leu	Ala	Ala	GIy	Trp	GIy	Asn	Met
				165				170						175	
GIy	GIy	GIy	Ala	Thr	GIn	Leu	H e	Met	Pro	Leu	VaI	Phe	His	Ala	H e
			180					185					190		
GIn	Lys	Cys	GIy	Ala	Thr	Pro	Phe	VaI	Ala	Trp	Arg	H e	Ala	Tyr	Phe
		195					200					205			
VaI	Pro	GIy	Met	Met	His	VaI	VaI	Met	GIy	Leu	Leu	VaI	Leu	Thr	Met
	210					215					220				
GIy	GIn	Asp	Leu	Pro	Asp	GIy	Asn	Leu	Ala	Ser	Leu	GIn	Lys	Lys	GIy
225					230					235					240

PF57967.ST25.txt

GIu Met Ala Lys Asp Lys Phe Ser Lys Val Val Trp GIy Ala Val Thr
 245 250 255
 Asn Tyr Arg Thr Trp lie Phe Val Leu Leu Tyr GIy Tyr Cys Met GIy
 260 265 270
 Val GIu Leu Thr Thr Asp Asn Val lie Ala GIu Tyr Tyr Phe Asp His
 275 280 285
 Phe His Leu Asp Leu Arg Thr Ser GIy Thr lie Ala Ala Cys Phe GIy
 290 295 300
 Met Ala Asn lie Val Ala Arg Pro Ala GIy GIy Tyr Leu Ser Asp Leu
 305 310 315 320
 GIy Ala Arg Tyr Phe GIy Met Arg Ala Arg Leu Trp Asn lie Trp lie
 325 330 335
 Leu GIn Thr Ala GIy GIy Ala Phe Cys Leu Trp Leu GIy Arg Ala Lys
 340 345 350
 Ala Leu Pro GIu Ser H e Thr Ala Met Val Leu Phe Ser H e Cys Ala
 355 360 365
 GIn Ala Ala Cys GIy Ala Val Phe GIy Val H e Pro Phe Val Ser Arg
 370 375 380
 Arg Ser Leu GIy lie H e Ser GIy Leu Ser GIy Ala GIy GIy Asn Phe
 385 390 395 400
 GIy Ala GIy Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser Lys Tyr GIy
 405 410 415
 Thr GIy Arg GIy Leu GIu Tyr Met GIy H e Met H e Met Ala Cys Thr
 420 425 430
 Leu Pro Val Ala Leu Val His Phe Pro GIn Trp GIy Ser Met Leu Leu
 435 440 445
 Pro Pro Asn Ala Asn Ala Thr GIu GIu GIu Phe Tyr Ala Ala GIu Trp
 450 455 460
 Ser GIu GIu GIu Lys Lys Lys GIy Leu Hxs H e Pro GIy GIn Lys Phe
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 485 490 495
 Thr Ala Ala Thr Pro Pro Asn Asn Thr Pro GIn His Ala
 500 505

<210> 77
 <211> 1796
 <212> DNA
 <213> Triticum aestivum

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PF57967.ST25.txt

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<211> 507

<212> PRT

<213> T π ticum aestivum

<400> 78

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			85					90						95	
Ala	H e	Cys	Asp	Leu	Leu	GIy	Pro	Arg	Tyr	GIy	Cys	Ala	Phe	Leu	VaI
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Phe	VaI	Ser	Cys	GIn	Tyr	Trp	Met	Ser	Thr	Met	Phe	Asn	Ser	Lys	H e
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lie	GIy	Thr	VaI	Asn	GIy	Leu	Ala	Ala	GIy	Trp	GIy	Asn	Met	GIy	GIy
			165					170					175		
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PF57967.ST25.txt

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 Arg Thr Trp lie Phe Val Leu Leu Tyr GIY Tyr Cys Met GIY Val GIU
 260 265 270
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 275 280 285
 Leu Asp Leu Arg Ala Ala GIY Thr lie Ala Ala Cys Phe GIY Met Ala
 290 295 300
 Asn lie Val Ala Arg Pro Met GIY GIY Tyr Leu Ser Asp Leu GIY Ala
 305 310 315 320
 Arg Tyr Phe GIY Met Arg Ala Arg Leu Trp Asn lie Trp lie Leu GIn
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 Thr Ala GIY GIY Ala Phe Cys lie Trp Leu GIY Arg Ala Ser Ala Leu
 340 345 350
 Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser H e Cys Ala GIn Ala
 355 360 365
 Ala Cys GIY Ala Val Phe GIY Val Ala Pro Phe Val Ser Arg Arg Ser
 370 375 380
 Leu GIY H e H e Ser GIY Leu Thr GIY Ala GIY GIY Asn Val GIY Ala
 385 390 395 400
 GIY Leu Thr GIn Leu Phe Phe Thr Ser Ser GIn Tyr Ser Thr GIY
 405 410 415
 Arg GIY Leu GIU Tyr Met GIY H e Met H e Met Ala Cys Thr Leu Pro
 420 425 430
 Val Ala Leu Val His Phe Pro GIn Trp GIY Ser Met Phe Phe Pro Ala
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 Ser Ala Asp Ala Thr GIU GIU GIU Tyr Tyr Ala Ser GIU Trp Ser GIU
 450 455 460
 GIU GIU Lys GIY Lys GIY Leu His H e Thr GIY GIn Lys Phe Ala GIU
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 <212> DNA
 <213> Triticuin aestivum

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PF57967.ST25.txt

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gtac 1744

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 <212> PRT
 <213> π ticum aestivum

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35 40 45
Phe Phe Thr Cys Phe VaI Ser Thr Phe Ala Ala Ala Pro Leu VaI Pro
50 55 60
H e H e Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp H e GIy Asn Ala
65 70 75 80
GIy VaI Ala Ser VaI Ser GIy Ser H e Phe Ser Arg Leu Ala Met GIy
85 90 95
Ala VaI Cys Asp Leu Leu GIy Pro Arg Tyr GIy Cys Ala Phe Leu VaI
100 105 H O
Met Leu Ser Ala Pro Thr VaI Phe Cys Met Ala VaI H e Asp Asp Ala
115 120 125
Ser GIy Tyr H e Ala VaI Arg Phe Leu H e GIy Phe Ser Leu Ala Ala
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GIy Ala Thr GIn Leu H e Met Pro Leu VaI Phe His Ala H e GIn Lys
180 185 190
Cys GIy Ala Thr Pro Phe VaI Ala Trp Arg H e Ala Tyr Phe VaI Pro
195 200 205
GIy Met Met His H e VaI Met GIy Leu Leu VaI Leu Thr Met GIy GIn
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Asp Leu Pro Asp GIy Asn Leu Ala Ser Leu GIn Lys Lys GIy Asp Met
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PF57967.ST25.txt

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 275 280 285
 Leu His Leu Arg Ala Ala GIY Thr lie Ala Ala Cys Phe GIY Met Ala
 290 295 300
 Asn lie Val Ala Arg Pro Met GIY GIY Tyr Leu Ser Asp Leu GIY Ala
 305 310 315 320
 Arg Tyr Phe GIY Met Arg Ala Arg Leu Trp Asn lie Trp lie Leu GIn
 325 330 335
 Thr Ala GIY GIY Ala Phe Cys lie Trp Leu GIY Arg Ala Ser Ala Leu
 340 345 350
 Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser H e Cys Ala GIn Ala
 355 360 365
 Ala Cys GIY Ala Val Phe GIY Val Ala Pro Phe Val Ser Arg Arg Ser
 370 375 380
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 385 390 395 400
 GIY Leu Thr GIn Leu Phe Phe Thr Ser Ser GIn Tyr Ser Thr GIY
 405 410 415
 Arg GIY Leu GIU Tyr Met GIY H e Met H e Met Ala Cys Thr Leu Pro
 420 425 430
 H e Thr Leu Val His Phe Pro GIn Trp GIY Ser Met Phe Phe Pro Ala
 435 440 445
 Ser Ala Asp Ala Thr GIU GIU GIU Tyr Tyr Ala Ser GIU Trp Ser GIU
 450 455 460
 GIU GIU Lys GIY Lys GIY Leu His H e Ala GIY GIn Lys Phe Ala GIU
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 485 490 495
 Ala Thr Pro Pro Asn Asn Thr Pro GIn His Val
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<210> 81
 <211> 1704
 <212> DNA
 <213> Hordeum vulgare

<400> 81
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 <211> 507
 <212> PRT
 <213> Hordeum vulgare

<400> 82

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Ser	Phe	Ala	Asn	Pro	His	Met	Arg	Thr	Phe	His	Leu	Ser	Trp	H e	Ser
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Phe	Phe	Thr	Cys	Phe	VaI	Ser	Thr	Phe	Ala	Ala	Ala	Pro	Leu	VaI	Pro
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Ala	lie	Cys	Asp	Leu	Leu	GIy	Pro	Arg	Tyr	GIy	Cys	Ala	Phe	Leu	VaI
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Met	Leu	Ser	Ala	Pro	Thr	VaI	Phe	Cys	Met	Ala	VaI	H e	Asp	Asp	Ala
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Ser	GIy	Tyr	H e	Ala	VaI	Arg	Phe	Leu	H e	GIy	Phe	Ser	Leu	Ala	Thr
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Phe	VaI	Ser	Cys	GIn	Tyr	Trp	Met	Ser	Thr	Met	Phe	Asn	Ser	Lys	H e
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GIy	Ala	Thr	GIn	Leu	H e	Met	Pro	Leu	VaI	Phe	His	Ala	H e	GIn	Lys
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Asp	Leu	Pro	Asp	GIy	Asn	Leu	Ala	Ser	Leu	GIn	Lys	Lys	GIy	Asp	Met
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PF57967.ST25.txt

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 275 280 285
 Leu Asn Leu Arg Ala Ala GIy Thr lie Ala Ala Cys Phe GIy Met Ala
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 Asn lie VaI Ala Arg Pro Met GIy GIy Tyr Leu Ser Asp Leu GIy Ala
 305 310 315 320
 Arg Tyr Phe GIy Met Arg Ala Arg Leu Trp Asn lie Trp lie Leu GIn
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 Thr Ala GIy GIy Ala Phe Cys lie Trp Leu GIy Arg Ala Ser Ala Leu
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 Pro Ala Ser VaI Thr Ala Met VaI Leu Phe Ser H e Cys Ala GIn Ala
 355 360 365
 Ala Cys GIy Ala H e Phe GIy VaI GIu Pro Phe VaI Ser Arg Arg Ser
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 Arg GIy Leu GIu Tyr Met GIy H e Met H e Met Ala Cys Thr Leu Pro
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 VaI Ala Leu VaI His Phe Pro GIn Trp GIy Ser Met Phe Leu Ala Ala
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 <212> DNA
 <213> Hordeum vulgare

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PF57967.ST25.txt

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gtttgcagcc ccagcgtaat aagttgtatg ggggtttatc tttttactat ggtaaacctta 1740
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atgcttgaaa aaaaaaaaaa aaaaa 1825

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<210> 84
 <211> 506
 <212> PRT
 <213> Hordeum vulgare

<400> 84
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 Thr Leu Pro VaI Asp Ser GIu His Lys Ala Lys Ser Phe Arg Leu Phe
 20 25 30
 Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp lie Ser
 35 40 45
 Phe Phe Thr Cys Phe VaI Ser Thr Phe Ala Ala Ala Pro Leu VaI Pro
 50 55 60
 lie lie Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp lie GIy Asn Ala
 65 70 75 80
 GIy VaI Ala Ser VaI Ser GIy Ser H e Phe Ser Arg Leu Ala Met GIy
 85 90 95
 Ala lie Cys Asp Leu Leu GIy Pro Arg Tyr GIy Cys Ala Phe Leu VaI
 100 105 H O
 Met Leu Ser Ala Pro Thr VaI Phe Cys Met Ala VaI H e Asp Asp Ala
 115 120 125
 Ser GIy Tyr H e Ala VaI Arg Phe Leu H e GIy Phe Ser Leu Ala Thr
 130 135 140
 Phe VaI Ser Cys GIn Tyr Trp Met Ser Thr Met Phe Asn Ser Lys H e
 145 150 155 160
 H e GIy Thr VaI Asn GIy Leu Ala Ala GIy Trp GIy Asn Met GIy GIy
 165 170 175
 GIy Ala Thr GIn Leu H e Met Pro Leu VaI Phe His Ala H e GIn Lys
 180 185 190
 Cys GIy Ala Thr Pro Phe VaI Ala Trp Arg H e Ala Tyr Phe VaI Pro
 195 200 205
 GIy Met Met His H e VaI Met GIy Leu Leu VaI Leu Thr Met GIy GIn
 210 215 220
 Asp Leu Pro Asp GIy Asn Leu Ala Ser Leu GIn Lys Arg GIy Asp Met
 225 230 235 240

PF57967.ST25.txt

Ala Lys Asp Lys Phe Ser Lys Val Leu Trp GIY Ala Val Thr Asn Tyr
 245 250 255
 Arg Thr Trp lie Phe Val Leu Leu Tyr GIY Tyr Cys Met GIY Val GIU
 260 265 270
 Leu Thr Thr Asp Asn Val lie Ala GIU Tyr Tyr Phe Asp His Phe His
 275 280 285
 Leu Asp Leu Arg Ala Ala GIY Thr lie Ala Ala Cys Phe GIY Met Ala
 290 295 300
 Asn lie Val Ala Arg Pro Met GIY GIY Tyr Leu Ser Asp Leu GIY Ala
 305 310 315 320
 Arg Tyr Phe GIY Met Arg Ala Leu Trp Asn lie Trp lie Leu GIn Thr
 325 330 335
 Ala GIY GIY Ala Phe Cys lie Trp Leu GIY Arg Ala Ser Ala Leu Pro
 340 345 350
 Ala Ser Val Thr Ala Met Val Leu Phe Ser H e Cys Ala GIn Ala Ala
 355 360 365
 Cys GIY Ala lie Phe GIY Val Ala Pro Phe Val Ser Arg Arg Ser Leu
 370 375 380
 GIY H e H e Ser GIY Leu Thr GIY Ala GIY GIY Asn Val GIY Ala GIY
 385 390 395 400
 Leu Thr GIn Leu Leu Phe Phe Thr Ser Ser GIn Tyr Ser Thr GIY Arg
 405 410 415
 GIY Leu GIU Tyr Met GIY H e Met H e Met Ala Cys Thr Leu Pro Val
 420 425 430
 Ala Leu Val His Phe Pro GIn Trp GIY Ser Met Phe Phe Pro Ala Ser
 435 440 445
 Ala Asp Ala Thr GIU GIU GIU Tyr Tyr Ala Ser GIU Trp Ser GIU GIU
 450 455 460
 GIU Lys GIY Lys GIY Leu His H e Ala GIY GIn Lys Phe Ala GIU Asn
 465 470 475 480
 Ser Arg Ser GIU Arg GIY Arg Arg Asn Val H e Phe Ala Thr Ser Ala
 485 490 495
 Thr Pro Pro Asn Asn Thr Pro GIn GIn Val
 500 505

<210> 85
 <211> 1885
 <212> DNA
 <213> Prunus persica

<400> 85
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 gtgtcatgcc agtattggat gagtaccatg tttaacagta agattattgg gctggttaat 660
 gggacagctg ctgggtgggg aaacatgggt ggtggggcca cccagctctt gatgccattg 720
 gtgtttgata taattggaag agttgggtgca actcctttca ctgcttgag aattgccttt 780

PF57967.ST25.txt

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tttttcttt attattatca gtttttccc aagcatataa gtgaactgat gattattttt 1860
atttcagaaa aaaaaaaaaa aaaaa 1885

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<210> 86
 <211> 530
 <212> PRT
 <213> Prunus persica

```

<400> 86
Met Ala GIu VaI GIu GIy GIu Pro GIy Ser Ser Met His GIy VaI Thr
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GIy Arg GIu GIn Thr Phe Ala Phe Ser VaI Ala Ser Pro lie VaI Pro
20 25 30
Thr Asp Pro Thr Ala Lys Phe Asp Leu Pro VaI Asp Ser GIu His Lys
35 40 45
Ala Lys VaI Phe Lys lie Phe Ser Leu Ala Asn Pro His Met Arg Thr
50 55 60
Phe His Leu Ser Trp lie Ser Phe Phe Thr Cys Phe VaI Ser Thr Phe
65 70 75 80
Ala Ala Ala Pro Leu VaI Pro lie lie Arg Asp Asn Leu Asn Leu Thr
85 90 95
Lys GIn Asp lie GIy Asn Ala GIy VaI Ala Ser VaI Ser GIy Ser lie
100 105 110
Phe Ser Arg Leu VaI Met GIy Ala VaI Cys Asp Leu Leu GIy Pro Arg
115 120 125
Tyr GIy Cys Ala Phe Leu lie Met Leu Ser Ala Pro Thr VaI Phe Cys
130 135 140
Met Ser Phe VaI Ser Asp Ala GIy GIy Tyr Leu Ala VaI Arg Phe Met
145 150 155 160
H e GIy Phe Ser Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met Ser
165 170 175
Thr Met Phe Asn Ser Lys H e H e GIy Leu VaI Asn GIy Thr Ala Ala
180 185 190
GIy Trp GIy Asn Met GIy GIy GIy Ala Thr GIn Leu Leu Met Pro Leu
195 200 205
VaI Phe Asp H e H e GIy Arg VaI GIy Ala Thr Pro Phe Thr Ala Trp
210 215 220

```

PF57967.ST25.txt

Arg lie Ala Phe Phe lie Pro GIY Trp Leu His VaI lie Met GIY lie
 225 230 235 240
 Met VaI Leu Thr Leu GIY GIn Asp Leu Pro Asp GIY Asn Leu Ala Ala
 245 250 255
 Leu GIn Lys Lys GIY Asp VaI Ala Lys Asp GIn Phe Ser Lys VaI Leu
 260 265 270
 Trp His Ala VaI Thr Asn Tyr Arg Thr Trp lie Phe VaI Leu Leu Tyr
 275 280 285
 GIY Tyr Ser Met GIY VaI GIU Leu Ser Thr Asp Asn VaI H e Ala GIU
 290 295 300
 Tyr Phe Tyr Asp Arg Phe Asn Leu Lys Leu His Thr Ala GIY H e H e
 305 310 315 320
 Ala Ala Thr Phe GIY Met Ala Asn Leu VaI Ala Arg Pro Phe GIY GIY
 325 330 335
 Phe Ala Ser Asp Arg Ala Ala Arg Tyr Phe GIY Met Arg GIY Arg Leu
 340 345 350
 Trp Thr Leu Trp H e Leu GIn Thr Leu GIY GIY VaI Phe Cys H e Trp
 355 360 365
 Leu GIY Arg Ala Asn Ser Leu Pro H e Ala VaI Phe Ala Met H e Leu
 370 375 380
 Phe Ser VaI GIY Ala GIn Ala Ala Cys GIY Ala Thr Phe GIY VaI H e
 385 390 395 400
 Pro Phe H e Ser Arg Arg Ser Leu GIY H e H e Ser GIY Leu Thr GIY
 405 410 415
 Ala GIY GIY Asn Phe GIY Ser GIY Leu Thr GIn Leu VaI Phe Phe Ser
 420 425 430
 Ser Ser Ala Phe Ser Thr Ala Thr GIY Leu Ser Leu Met GIY VaI Met
 435 440 445
 H e VaI Cys Cys Thr Leu Pro VaI Thr Leu VaI His Phe Pro GIn Trp
 450 455 460
 GIY Ser Met Phe Leu Pro Pro Ser Lys Asp VaI VaI Lys Ser Thr GIU
 465 470 475 480
 GIU Phe Tyr Tyr GIY Ala GIU Trp Asn GIU GIU GIU Lys GIn Lys GIY
 485 490 495
 Leu His GIn GIn Ser Leu Arg Phe Ala GIU Asn Ser Arg Ser GIU Arg
 500 505 510
 GIY Arg Arg VaI Ala Ser Ala Pro Thr Pro Pro Asn Thr Thr Pro Ser
 515 520 525
 His VaI
 530

<210> 87
 <211> 1962
 <212> DNA
 <213> Prunus persica

<400> 87
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 cttcacttgc tttgtctcaa cttttgcagc ggccccactt gtccctataa tccgagacaa 360
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PF57967.ST25.txt

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gaaatacaag agatgatcag ttgagttgat acaagtagtt ttatttgtaa tgaaaataga 1860
gttgccatat agcgtgtgcc tctatatatg tatctgttac acaaatgttt ttactttcaa 1920
ggtttaaact tatgataatt ttcaaaaaaa aaaaaaaaaa aa 1962

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<210> 88
 <211> 530
 <212> PRT
 <213> Prunus persica

<400> 88
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 GIy Arg GIu GIn Thr Phe Ala Phe Ser VaI Ala Ser Pro lie VaI Pro
 20 25 30
 Thr Asp Pro Thr Ala Lys Phe Asp Leu Pro VaI Asp Ser GIu His Lys
 35 40 45
 Ala Lys VaI Phe Lys lie Phe Ser Leu Ala Asn Pro His Met Arg Thr
 50 55 60
 Phe His Leu Ser Trp lie Ser Phe Phe Thr Cys Phe VaI Ser Thr Phe
 65 70 75 80
 Ala Ala Ala Pro Leu VaI Pro lie H e Arg Asp Asn Leu Asn Leu Thr
 85 90 95
 Lys GIn Asp H e GIy Asn Ala GIy VaI Ala Ser VaI Ser GIy Ser H e
 100 105 110
 Phe Ser Arg Leu VaI Met GIy Ala VaI Cys Asp Leu Leu GIy Pro Arg
 115 120 125
 Tyr GIy Cys Ala Phe Leu H e Met Leu Ser Ala Pro Thr VaI Phe Cys
 130 135 140
 Met Ser Phe VaI Ser Asp Ala GIy GIy Tyr Leu Ala VaI Arg Phe Met
 145 150 155 160
 H e GIy Phe Ser Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met Ser

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

<400> 89

PF57967.ST25.txt

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<210> 90
<211> 530
<212> PRT
<213> Glycine max

```

```

<400> 90
Met Ala GIu lie GIu GIy Ser Pro GIy Ser Ser Met His GIy VaI Thr
1      5      10      15
GIy Arg GIu GIn Thr Phe VaI Ala Ser VaI Ala Ser Pro lie VaI Pro
      20      25      30
Thr Asp Thr Thr Ala Lys Phe Ala Leu Pro VaI Asp Ser GIu His Lys
      35      40      45
Ala Lys VaI Phe Lys Leu Phe Ser Leu Ala Asn Pro His Met Arg Thr
      50      55      60
Phe His Leu Ser Trp lie Ser Phe Phe Thr Cys Phe VaI Ser Thr Phe
65      70      75      80
Ala Ala Ala Pro Leu VaI Pro lie lie Arg Asp Asn Leu Asn Leu Thr
      85      90      95
Lys Ser A&p H e GIy Asn Ala GIy VaI Ala Ser VaI Ser GIy Ser H e
      100      105      H O
Phe Ser Arg Leu Ala Met GIy Ala VaI Cys Asp Met Leu GIy Pro Arg

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PF57967 .ST25 .txt

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

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PF57967 .ST25 .txt

<210> 91
 <-211> 1990
 <212> DNA
 <213> Lotus ^apomcus

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 ggaggggaaca aaccttcata tcctcagttt ctccccaat ggtcccaaca gacaccacag 180
 ccaaattcga tttaccagtt gattcacagc acaaagccaa agttttcaaa ctgttctcat 240
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 ccatgggtgt aatttgtgac ctcttaggcc cacgttacgg gtgtgccttc ctgatcatgc 480
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 ttcggttcat gatcggttcc tcattggcca cggttggttc gtgccagtag tggatgagta 600
 ccatgtttaa cagtaagatt attgggcttg ttaatggaac tgcagctggg tggggttaaca 660
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 ctcttggtca ctccacacag tggggtagca tgttccttcc tccttcaaaa gacatcaaca 1500
 agtccagtga ggaacactat tacactgctg aatgggatga ggaagagagg aagaaggggt 1560
 tgcactctca aagtcttaag tttgcagaga atagtcgctc tgagagagga aaacgtgttt 1620
 cctctgtccc aactcctcca aacacaaccc ctacccatgt ctaagatgga tggatgatca 1680
 ccacagtgga aagctaataa ggaagagagt atatggatcc cttgattgaa taatttatcc 1740
 ttaagccttt aaagataact tggcatccag aaatttggtg ttgccccttc aaattctact 1800
 tgttatagaa atttgggtgt attttctata agggactttg gtgtctgtgg gagtgtgggt 1860
 ctatcagtta attatacaaa caggtggtgt acaaaaaataa tatattgagt tttttaattt 1920
 tgggtgtgata tatattaatg aatgttactc aaaaaaaaaa aaaaaaaaaa actcgagggg 1980
 gggcccggtg 1990

<210> 92
 <211> 530
 <212> PRT
 <213> Lotus]apomcus

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 GIy Arg GIu GIn Thr Phe H e Ser Ser Val Ser Ser Pro Met Val Pro
 20 25 30
 Thr Asp Thr Thr Ala Lys Phe Asp Leu Pro Val Asp Ser GIn Hxs Lys
 35 40 45
 A Ia Lys Val Phe Lys Leu Phe Ser Leu Ala Asn Pro His Met Thr Thr

	50					55					60					
Phe 65	His	Leu	Ser	Trp	lie 70	Ser	Phe	Phe	Thr	Cys 75	Phe	VaI	Ser	Thr	Phe 80	
Ala	Ala	Ala	Pro	Leu 85	VaI	Pro	lie	lie	Arg 90	Asp	Asn	Leu	Asn	Leu 95	Thr	
Lys	Ser	Asp	H e 100	GIy	Asn	Ala	GIy	VaI 105	Ala	Ser	VaI	Ser	GIy 110	Ser	H e	
Phe	Ser	Arg 115	Leu	Thr	Met	GIy	VaI 120	H e	Cys	Asp	Leu	Leu 125	GIy	Pro	Arg	
Tyr	GIy 130	Cys	Ala	Phe	Leu	H e 135	Met	Leu	Ser	Ala	Pro 140	Thr	VaI	Phe	Cys	
Met 145	Ser	Phe	VaI	Asn	Asp 150	Ala	Ala	GIy	Tyr	H e 155	VaI	VaI	Arg	Phe	Met 160	
H e	GIy	Phe	Ser	Leu 165	Ala	Thr	Phe	VaI	Ser 170	Cys	GIn	Tyr	Trp	Met 175	Ser	
Thr	Met	Phe 180	Asn	Ser	Lys	H e	H e	GIy 185	Leu	VaI	Asn	GIy	Thr 190	Ala	Ala	
GIy	Trp	GIy 195	Asn	Met	GIy	GIy	GIy 200	Ala	Thr	GIn	Leu	H e 205	Met	Pro	H e	
VaI	Tyr 210	GIu	Leu	H e	Arg	Arg	Ala 215	GIy	Ser	Thr	GIy	Phe	Thr	Ala	Trp	
Arg 225	H e	Ala	Phe	Phe	H e 230	Pro	GIy	Phe	Met	Hrs 235	VaI	Phe	Met	GIy	H e 240	
Leu	VaI	Leu	Thr	Leu 245	GIy	GIn	Asp	Leu	Pro 250	Asp	GIy	Asn	Leu	Ser 255	Ala	
Leu	GIn	Lys 260	Lys	GIy	Asp	VaI	Ala	Lys 265	Asp	Lys	Phe	Ser	Lys 270	VaI	Leu	
Trp	Tyr	Ala 275	H e	Thr	Asn	Tyr	Arg	Thr 280	Trp	H e	Phe	Ala	Leu	Leu	Tyr	
GIy	Tyr 290	Ser	Met	GIy	VaI	GIu 295	Leu	Thr	Thr	Asp	Asn 300	VaI	H e	Ala	GIu	
Tyr 305	Phe	Tyr	Asp	Arg	Phe	Asn	Leu	Lys	Leu	Hrs 315	Thr	VaI	GIy	H e	H e 320	
Ala	Ala	Ser	Phe	GIy 325	Met	Ala	Asn	Leu	VaI 330	Ala	Arg	Pro	Phe	GIy 335	GIy	
Tyr	VaI	Ser	Asp	VaI 340	Ala	Ala	Arg	Leu	Phe 345	GIy	Met	Arg	GIy	Arg	Leu	
Trp	Thr	Leu 355	Trp	H e	Leu	GIn	Thr	Leu	GIy	GIy	VaI	Phe	Cys	H e	Trp	
Leu	GIy 370	Arg	Ala	Asn	Ser	Leu	Pro	H e	Ala	VaI	Leu	Ala	Met	H e	Leu	
Phe 385	Ser	VaI	GIy	Ala	GIn 390	Ala	Ala	Cys	GIy	Ala	Thr	Phe	GIy	H e	H e 400	
Pro	Phe	H e	Ser	Lys 405	Arg	Ser	Leu	GIy	H e 410	H e	Ser	GIy	Leu	Thr	GIy	
Ala	GIy	GIy	Asn	Phe 420	GIy	Ser	GIy	Leu	Thr	GIn	Leu	VaI	Phe	Phe	Ser	
Thr	Ser	Arg 435	Phe	Ser	Thr	GIy	Ala	GIy	Leu	Ser	Trp	Met	GIy	VaI	Met	
H e	VaI 450	GIy	Cys	Thr	Leu	Pro	VaI	Thr	Leu	VaI	Hrs 460	Phe	Pro	GIn	Trp	
GIy 465	Ser	Met	Phe	Leu	Pro 470	Pro	Ser	Lys	Asp	H e	Asn	Lys	Ser	Ser	GIu	
GIu	Hrs	Tyr	Tyr	Thr	Ala	GIu	Trp	Asp	GIu	GIu	GIu	Arg	Lys	Lys	GIy 480	

PF57967.ST25.txt

485 490 495
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 500 505 510
 GIy Lys Arg Val Ser Ser Ala Pro Thr Pro Pro Asn Thr Thr Pro Thr
 515 520 525
 His Val
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 <211> 1838
 <212> DNA
 <213> Nicotiana tabacum

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 ggaaatatgg ggggtggagc tactcagctt attatgccta ttctctatga tattattaga 660
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 gcttccctac agaagaaagg cgatgtttct aaagataagt tctctaagat atttgtggtat 840
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<210> 94
 <211> 530
 <212> PRT
 <213> Nicotiana tabacum

<400> 94
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PF57967.ST25.txt

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			20					25					30		
Thr	Asp	Thr	Thr	Ala	His	Phe	Lys	VaI	Pro	VaI	Asp	Ser	GIu	His	Lys
		35					40					45			
Ala	Lys	VaI	Phe	Lys	Phe	Tyr	Ser	Phe	Ser	Lys	Pro	His	GIy	Leu	Thr
	50					55					60				
Phe	GIn	Leu	Ser	Trp	lie	Ser	Phe	Phe	Thr	Cys	Phe	VaI	Ser	Thr	Phe
65					70					75					80
Ala	Ala	Ala	Pro	Leu	VaI	Pro	lie	lie	Arg	Asp	Asn	Leu	Asn	Leu	Thr
			85						90					95	
Lys	Met	Asp	VaI	GIy	Asn	Ala	GIy	VaI	Ala	Ser	VaI	Ser	GIy	Ser	H e
		100						105					H O		
Leu	Ser	Arg	Leu	Ala	Met	GIy	Ala	H e	Cys	Asp	Met	Leu	GIy	Pro	Arg
		115				120						125			
Tyr	GIy	Cys	Ala	Phe	Leu	H e	Met	Leu	Ser	Ala	Pro	Thr	VaI	Phe	Cys
	130					135					140				
Met	Ser	Phe	VaI	Ser	Ser	Ala	GIy	GIy	Tyr	VaI	Ala	VaI	Arg	Phe	Met
145					150					155					160
H e	GIy	Phe	Ser	Leu	Ala	Thr	Phe	VaI	Ser	Cys	GIn	Tyr	Trp	Met	Ser
			165						170					175	
Thr	Met	Phe	Asn	Ser	GIn	H e	H e	GIy	Leu	VaI	Asn	GIy	Thr	Ala	Ala
			180					185					190		
GIy	Trp	GIy	Asn	Met	GIy	GIy	GIy	Ala	Thr	GIn	Leu	H e	Met	Pro	H e
		195				200						205			
Leu	Tyr	Asp	H e	H e	Arg	Arg	Ala	GIy	Ala	Thr	Pro	Phe	Thr	Ala	Trp
	210				215						220				
Arg	H e	Ala	Phe	Phe	H e	Pro	GIy	Trp	Leu	His	VaI	H e	Met	GIy	H e
225					230					235					240
Leu	VaI	Leu	Thr	Leu	GIy	GIn	Asp	Leu	Pro	Asp	GIy	Asn	Leu	Ala	Ser
			245						250					255	
Leu	GIn	Lys	Lys	GIy	Asp	VaI	Ser	Lys	Asp	Lys	Phe	Ser	Lys	H e	Leu
		260						265					270		
Trp	Tyr	Ala	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	H e	Phe	VaI	Leu	Leu	Tyr
		275				280						285			
GIy	Tyr	Ser	Met	GIy	VaI	GIu	Leu	Thr	Thr	Asp	Asn	VaI	H e	Ala	GIu
	290					295					300				
Tyr	Phe	Phe	Asp	Arg	Phe	Asp	Leu	Lys	Leu	His	Thr	Ala	GIy	H e	H e
305					310					315					320
Ala	Ala	Thr	Phe	GIy	Met	Ala	A&n	Leu	Leu	Ala	Arg	Pro	Phe	GIy	GIy
			325						330					335	
Trp	Ser	Ser	Asp	H e	Ala	Ala	Lys	His	Phe	GIy	Met	Arg	GIy	Arg	Leu
			340					345					350		
Trp	Asn	Leu	Trp	H e	Leu	GIn	Thr	Leu	GIy	GIy	VaI	Phe	Cys	Phe	Leu
		355				360						365			
Leu	GIy	Lys	Ala	Asn	Thr	Leu	Pro	Met	Ala	H e	Ala	Trp	Met	H e	H e
	370					375					380				
Phe	Ser	Leu	GIy	Ala	GIn	Ala	Ala	Cys	GIy	Ala	Thr	Phe	GIy	H e	H e
385					390					395					400
Pro	Phe	H e	Ser	Arg	Arg	Ser	Leu	GIy	H e	H e	Ser	GIy	Met	Thr	GIy
			405						410					415	
Ala	GIy	GIy	Asn	Phe	GIy	Ser	GIy	Leu	Thr	GIn	Leu	Leu	Phe	Phe	Thr
			420					425					430		
Thr	Thr	Lys	Trp	Ser	Thr	GIu	Thr	GIy	Leu	Ser	Tyr	Met	GIy	H e	Met
		435				440						445			

PF57967.ST25.txt

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GIy Ser Met Phe Leu Pro Thr Lys Asp Pro Val Lys Ser Thr GIu
465          470          475          480
GIu His Tyr Phe Thr Ser GIu Tyr Thr GIu Ala GIu Lys Gln Lys GIy
          485          490          495
Met His Gln Asn Ser lie Lys Phe Ala GIu Asn Cys Arg Ser GIu Arg
          500          505          510
GIy Lys Arg Val GIy Ser Ala Leu Thr Pro Pro Asn Val Thr Pro Asn
          515          520          525
Arg Val
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<210> 95
<211> 1646
<212> DNA
<213> Lycopersicon esculentum

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tttcaaagtc cctgttgatt ctgaacataa agctaaagtt tttaaatttt attcgttttc 180
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<210> 96
<211> 531
<212> PRT
<213> Lycopersicon esculentum

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<400> 96

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PF57967 .ST25 .txt

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

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PF57967.ST25. txt

Ser Thr Lys Tyr Ser Thr GIy Thr GIy Leu Thr Tyr Met GIy Met Met
 435 440 445
 H e H e Ala Cys Thr Leu Pro VaI Met Leu VaI Arg Phe Pro GIn Trp
 450 455 460
 GIy Ser Met Phe Leu Pro Pro Ser Lys Asp Pro H e Lys GIy Thr GIu
 465 470 475 480
 GIu His Tyr Phe GIy Ser GIu Tyr Thr GIu Asp GIu Lys GIn Lys GIy
 485 490 495
 Met His GIn Asn Ser H e Lys Phe Ala GIu Asn Ser Arg Thr GIu Arg
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 GIy Lys Lys Arg VaI GIy Ser Ala Pro Thr Pro Pro Asn VaI Thr Pro
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 Asn Arg VaI
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<210> 97

<211> 1680

<212> DNA

<213> Populus tremula x Populus tremuloides

<400> 97

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<210> 98

<211> 529

<212> PRT

<213> Populus tremula x Populus tremuloides

PF57967 .ST25 .txt

<-400> 98

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Thr Asp Thr Thr Ala Lys Phe Ala Leu Pro Val Asp Ser GIu His Lys
      35      40      45
Ala Lys Val Phe Lys lie Phe Ser Phe Ala Asn Pro His Met Arg Thr
      50      55      60
Phe His Leu Ser Trp lie Ser Phe Phe Thr Cys Phe Val Ser Thr Phe
65      70      75      80
Ala Ala Ala Pro Leu Val Pro lie lie Arg Asp Asn Leu Asn Leu Thr
      85      90      95
Lys Ser Asp H e GIy Asn Ala GIy Val Ala Ser Val Ser GIy Ser H e
      100      105      H O
Phe Ser Arg Leu Val Met GIy Ala Val Cys Asp Leu Leu GIy Pro Arg
      115      120      125
Tyr GIy Cys Ala Phe Leu H e Met Leu Ser Ala Pro Thr Val Phe Cys
      130      135      140
Met Ser Phe Val Asp Ser Ala GIy GIy Tyr Leu Ala Val Arg Phe Met
145      150      155      160
H e GIy Phe Ser Leu Ala Thr Phe Val Ser Cys GIn Tyr Trp Met Ser
      165      170      175
Thr Met Phe Asn Ser Lys H e H e GIy Leu Val Asn GIy Thr Ala Ala
      180      185      190
GIy Trp GIy Asn Met GIy GIy GIy Ala Thr GIn Leu Val Met Pro Leu
      195      200      205
Val Tyr GIu Leu H e Lys Arg Ala GIy Ser Thr Ser Phe Ser Ala Trp
      210      215      220
Arg H e Ala Phe Phe Val Pro GIy Trp Leu His Val H e Met GIy H e
225      230      235      240
Leu Val Leu Asn Leu GIy GIn Asp Leu Pro Asp GIy Asn Leu GIy Ala
      245      250      255
Leu Lys Lys Lys GIy Asp Val Ala Lys Asp Lys Phe Ser Lys Val Leu
      260      265      270
Trp Tyr Ala Val Thr Asn Tyr Arg Thr Trp H e Phe Val Leu Leu Tyr
      275      280      285
GIy Tyr Ser Met GIy Val GIu Leu Ser Thr Asp Asn Val H e Ala GIu
      290      295      300
Tyr Phe Tyr Asn Arg Phe Asp Leu Lys Leu His Thr Ala GIy Val H e
305      310      315      320
Ala Ala Thr Phe GIy Met Ala Asn Leu Val Ala Arg Pro Phe GIy GIy
      325      330      335
Tyr Phe Ser Asp Val Ala Ala Arg Tyr Phe GIy Met Arg GIy Arg Leu
      340      345      350
Trp Val Leu Trp H e Leu GIn Thr Leu GIy GIy Val Phe Cys Thr Trp
      355      360      365
Leu GIy Arg Ala Asn Ser Leu Pro Leu Ala Val Thr Ala Met H e Leu
      370      375      380
Phe Ser H e GIy Ala GIn Ala Ala Cys GIy Ala Thr Phe GIy H e H e
385      390      395      400
Pro Phe H e Ser Arg Arg Ser Leu GIy H e H e Ser GIy Leu Thr GIy
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PF57967.ST25. txt

Ala GIy GIy Asn Phe GIy Ser GIy Leu Thr GIn Leu VaI Phe Phe Ser
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 435 440 445
 H e Cys GIy Cys Thr Leu Pro VaI Thr Leu VaI Tyr Phe Pro GIn Trp
 450 455 460
 GIy GIy Met Phe Phe Pro Pro Ser Lys Asp VaI VaI Lys Ser Thr GIu
 465 470 475 480
 GIu Ser Tyr Tyr Ala Ser GIu Trp Asp GIu Asp GIu Lys GIn Arg GIy
 485 490 495
 Met His GIn Lys Ser Leu Lys Phe Ala GIu Asn Ser Arg Ser GIu Arg
 500 505 510
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 515 520 525
 Arg

<210> 99
 <211> 1611
 <212> DNA
 <213> Nicotiana tabacum

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<210> 100
 <211> 530
 <212> PRT

PF57967 .ST25 .txt

<213> Nicotiana tabacum

<400> 100

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

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PF57967.ST25. txt

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 Ser Ser Lys Tyr Ser Thr Ala Thr GIy Leu Thr Tyr Met GIy Leu Met
 435 440 445
 H e H e GIy Cys Thr Leu Pro VaI Thr Phe Cys His Phe Pro GIn Trp
 450 455 460
 GIy Ser Met Phe Phe Pro Pro Thr Lys Asp Pro VaI Lys GIy Ser GIu
 465 470 475 480
 GIu Hls Tyr Tyr Ala Ala GIu Tyr Thr GIu Ala GIu Arg GIn Lys GIy
 485 490 495
 Met His GIn Asn Ser Leu Lys Phe Ala GIu Asn Cys Arg Ser GIu Arg
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 GIy Lys Arg VaI GIy Ser Ala Pro Thr Pro Pro Asn Leu Thr Pro Asn
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 Arg VaI
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<210> 101

<211> 1992

<212> DNA

<213> Nicotiana plumbaginifolia

<400> 101

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PF57967.ST25. txt

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<211> 530
<212> PRT
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35 40 45
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50 55 60
Phe Gln Leu Ser Trp lie Ser Phe Phe Thr Cys Phe Val Ser Thr Phe
65 70 75 80
Ala Ala Ala Pro Leu Val Pro Leu lie Arg Asp Asn Leu Asn Leu Thr
85 90 95
Lys Met Asp Val GIY Asn Ala GIY Val Ala Ser Val Ser GIY Ser H e
100 105 H O
Leu Ser Arg Leu Val Met GIY Ala Val Cys Asp Met Leu GIY Pro Arg
115 120 125
Tyr GIY Cys Ala Phe Leu H e Met Leu Ser Ala Pro Thr Val Phe Cys
130 135 140
Met Ser Phe Val Ser Ser Ala GIY GIY Tyr Val Ala Val Arg Phe Met
145 150 155 160
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165 170 175
Thr Met Phe Asn Ser Gln H e H e GIY Leu Val Asn GIY Thr Ala Ala
180 185 190
GIY Trp GIY Asn Met GIY GIY GIY Ala Thr Gln Leu H e Met Pro H e
195 200 205
Leu Tyr Asp H e H e Arg Lys Ala GIY Ala Thr Pro Phe Thr Ala Trp
210 215 220
Arg H e Ala Phe Phe H e Pro GIY Trp Leu His Val Val Met GIY H e
225 230 235 240
Leu Val Leu Thr Leu GIY Gln Asp Leu Pro Asp GIY Asn Arg GIY Asp
245 250 255
Leu Gln Lys Lys GIY GIY Val Ser Lys Asp Lys Phe Thr Asn H e Leu
260 265 270
Trp Tyr Ala Ala Thr Asn Tyr Arg Thr Trp H e Phe Val Leu Leu Tyr
275 280 285
GIY Tyr Ser Met GIY Val GIU Leu Ser Thr Asp Asn Val H e Ala GIU
290 295 300
Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu His Thr Ala GIY H e H e
305 310 315 320
Ala Ala Thr Phe GIY Met Ala Asn Leu Leu Ala Arg Pro Phe GIY GIY
325 330 335
Phe Ser Ser Asp Phe Ala Ala Lys Arg Phe GIY Met Arg GIY Arg Leu

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PF57967.ST25. txt

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 370 375 380
 Phe Ser Val GIY Ala Gln Ala Ala Cys GIY Ala Thr Phe GIY H e H e
 385 390 395 400
 Pro Phe H e Ser Arg Arg Ser Leu GIY H e H e Ser GIY Met Thr GIY
 405 410 415
 Ala GIY GIY Asn Phe GIY Ser GIY Leu Thr Gln Leu Leu Phe Phe Thr
 420 425 430
 Ser Ser Lys Tyr Ser Thr Ala Thr GIY Leu Thr Tyr Met GIY Met Met
 435 440 445
 H e H e GIY Cys Thr Leu Pro Val Thr Leu Cys His Phe Pro Gln Trp
 450 455 460
 GIY Ser Met Phe Phe Pro Pro Thr Lys Asp Pro Val Lys GIY Ser GIU
 465 470 475 480
 GIU Hrs Tyr Tyr Ala Ala GIU Tyr Thr GIU Ala GIU Arg Gln Lys GIY
 485 490 495
 Met His Gln Asn Ser Leu Lys Phe Ala GIU Asn Cys Arg Ser GIU Arg
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 Arg Val
 530

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 <211> 2060
 <212> DNA
 <213> Lycopersicon esculentum

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PF57967.ST25.txt

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gacaaatacc ttgaatccac gaagggtgat gctTTTTTTT taatgaagta tatataatat 1860
attactcatt gtgtatgttt tctattgctt ttttcaaaag aatattctat ggccaatggt 1920
ggttgtgttt tactctgtag attcaaaagt gtattataat aaaactcttg acttgaaga 1980
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<210> 104
<211> 530
<212> PRT
<213> Lycopersicon esculentum

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<400> 104
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GIy Arg GIu Pro Val Leu Ala Phe Ser Val Ala Ser Pro Met Val Pro
20 25 30
Thr Asp Thr Ser Ala Lys Phe Ser Val Pro Val Asp Thr GIu His Lys
35 40 45
Ala Lys GIn Phe Lys Phe Tyr Ser Phe Ser Lys Pro His GIy Leu Thr
50 55 60
Phe GIn Leu Ser Trp lie Ser Phe Phe Thr Cys Phe Val Ser Thr Phe
65 70 75 80
Ala Ala Ala Pro Leu Val Pro lie lie Arg Asp Asn Leu Asn Leu Thr
85 90 95
Lys Met Asp Val GIy Asn Ala GIy Val Ala Ser Val Ser GIy Ser H e
100 105 110
Leu Ser Arg Leu Thr Met GIy Ala Val Cys Asp Leu Leu GIy Pro Arg
115 120 125
Tyr GIy Cys Ala Phe Leu lie Met Leu Ser Ala Pro Thr Val Phe Cys
130 135 140
Met Ser Phe Val Ser Ser Ala GIy GIy Tyr Val Ala Val Arg Phe Met
145 150 155 160
H e GIy Phe Ser Leu Ala Thr Phe Val Ser Cys GIn Tyr Trp Met Ser
165 170 175
Thr Met Phe Asn Ser Lys H e H e GIy Leu Val Asn GIy Thr Ala Ala
180 185 190
GIy Trp GIy Asn Met GIy GIy GIy Ala Thr GIn Leu H e Met Pro Leu
195 200 205
Leu Tyr Asp H e H e Arg Arg Ala GIy Ala Thr Pro Phe Thr Ala Trp
210 215 220
Arg H e Ala Phe Phe H e Pro GIy Trp Leu His Val Val Met GIy H e
225 230 235 240
Leu Val Leu Thr Leu GIy GIn Asp Leu Pro Asp GIy Asn Arg GIy Thr
245 250 255
Leu GIn Lys Thr GIy Thr Val Ala Lys Asp Lys Phe GIy Asn H e Leu
260 265 270

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PF57967.ST25.txt

Trp Tyr Ala Ala Thr Asn Tyr Arg Thr Trp lie Phe VaI Leu Leu Tyr
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 GIy Tyr Ser Met GIy VaI GIu Leu Ser Thr Asp Asn VaI lie Ala GIu
 290 295 300
 Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu Ser Thr Ala GIy lie lie
 305 310 315 320
 Ala Ala Thr Phe GIy Met Ala Asn Leu Leu Ala Arg Pro Phe GIy GIy
 325 330 335
 Phe Ser Ser Asp Tyr Ala Ala Lys Lys Phe GIy Met Arg GIy Arg Leu
 340 345 350
 Trp VaI Leu Trp lie Leu GIn Thr Leu GIy GIy VaI Phe Cys VaI Leu
 355 360 365
 Leu GIy Arg Ser Asn Ser Leu Pro Leu Ala VaI Thr Phe Met lie Leu
 370 375 380
 Phe Ser H e GIy Ala GIn Ala Ala Cys GIy Ala Thr Phe GIy H e H e
 385 390 395 400
 Pro Phe H e Ser Arg Arg Ser Leu GIy H e H e Ser GIy Met Thr GIy
 405 410 415
 Ala GIy GIy Asn Phe GIy Ser GIy Leu Thr GIn Leu Leu Phe Phe Thr
 420 425 430
 Ser Ser Lys Tyr Ser Thr Ala Thr GIy Leu Thr Tyr Met GIy Phe Met
 435 440 445
 H e H e GIy Cys Thr Leu Pro VaI Thr Phe Cys His Phe Pro GIn Trp
 450 455 460
 GIy Ser Met Phe Leu Pro Pro Thr Lys Asp Pro VaI Lys GIy Thr GIu
 465 470 475 480
 GIu His Tyr Tyr Thr Ser GIu Tyr Thr GIu Ala GIu Arg GIn Lys GIy
 485 490 495
 Met His GIn Asn Ser Leu Lys Phe Ala GIu Asn Cys Arg Ser GIu Arg
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 GIy Lys Arg VaI GIy Ser Ala Pro Thr Pro Pro Asn Leu Thr Pro Asn
 515 520 525
 Arg VaI
 530

<210> 105

<211> 1902

<212> DNA

<213> Arabidopsis thaliana

<400> 105

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aacctcacat	gagaacgttc	catctctcgt	ggatctcttt	ctccacatgt	tttgtctcga	300
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gcggcataac	gcagttgctc	atgcccattg	tgtatgaaat	cattaggcgc	tcggtttcca	720
cagccttcac	ggcctggagg	atcgccctct	ttgtaccggt	ttggttgac	atcatcatgg	780

PF57967.ST25.txt

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gttatcaatg cttgcataac attactatct atctttcatt tactaaacaa accttttgct 1800
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<210> 106

<211> 530

<212> PRT

<213> Arabidopsis thaliana

<400> 106

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Thr Asp Lys Thr Ala Lys Phe Asp Leu Pro VaI Asp Thr GIU His Lys
35 40 45
Ala Thr VaI Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr
50 55 60
Phe His Leu Ser Trp H e Ser Phe Ser Thr Cys Phe VaI Ser Thr Phe
65 70 75 80
Ala Ala Ala Pro Leu VaI Pro H e H e Arg GIU Asn Leu Asn Leu Thr
85 90 95
Lys GIn A&p H e GIY Asn Ala GIY VaI Ala Ser VaI Ser GIY Ser H e
100 105 H O
Phe Ser Arg Leu VaI Met GIY Ala VaI Cys Asp Leu Leu GIY Pro Arg
115 120 125
Tyr GIY Cys Ala Phe Leu VaI Met Leu Ser Ala Pro Thr VaI Phe Ser
130 135 140
Met Ser Phe VaI Ser Asp Ala Ala GIY Phe H e Thr VaI Arg Phe Met
145 150 155 160
H e GIY Phe Cys Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met Ser
165 170 175
Thr Met Phe Asn Ser GIn H e H e GIY Leu VaI Asn GIY Thr Ala Ala
180 185 190
GIY Trp GIY Asn Met GIY GIY GIY H e Thr GIn Leu Leu Met Pro H e
195 200 205
VaI Tyr GIU H e H e Arg Arg Cys GIY Ser Thr Ala Phe Thr Ala Trp
210 215 220

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PF57967.ST25.txt

Arg lie Ala Phe Phe VaI Pro GIY Trp Leu His lie lie Met GIY lie
 225 230 235 240
 Leu VaI Leu Asn Leu GIY GIn Asp Leu Pro Asp GIY Asn Arg Ala Thr
 245 250 255
 Leu GIU Lys Ala GIY GIU VaI Ala Lys Asp Lys Phe GIY Lys lie Leu
 260 265 270
 Trp Tyr Ala VaI Thr Asn Tyr Arg Thr Trp lie Phe VaI Leu Leu Tyr
 275 280 285
 GIY Tyr Ser Met GIY VaI GIU Leu Ser Thr Asp Asn VaI H e Ala GIU
 290 295 300
 Tyr Phe Phe Asp Arg Phe His Leu Lys Leu His Thr Ala GIY Leu H e
 305 310 315 320
 Ala Ala Cys Phe GIY Met Ala Asn Phe Phe Ala Arg Pro Ala GIY GIY
 325 330 335
 Tyr Ala Ser Asp Phe Ala Ala Lys Tyr Phe GIY Met Arg GIY Arg Leu
 340 345 350
 Trp Thr Leu Trp H e H e GIn Thr Ala GIY GIY Leu Phe Cys VaI Trp
 355 360 365
 Leu GIY Arg Ala Asn Thr Leu VaI Thr Ala VaI VaI Ala Met VaI Leu
 370 375 380
 Phe Ser Met GIY Ala GIn Ala Ala Cys GIY Ala Thr Phe Ala H e VaI
 385 390 395 400
 Pro Phe VaI Ser Arg Arg Ala Leu GIY H e H e Ser GIY Leu Thr GIY
 405 410 415
 Ala GIY GIY Asn Phe GIY Ser GIY Leu Thr GIn Leu Leu Phe Phe Ser
 420 425 430
 Thr Ser His Phe Thr Thr GIU GIn GIY Leu Thr Trp Met GIY VaI Met
 435 440 445
 H e VaI Ala Cys Thr Leu Pro VaI Thr Leu VaI His Phe Pro GIn Trp
 450 455 460
 GIY Ser Met Phe Leu Pro Pro Ser Thr Asp Pro VaI Lys GIY Thr GIU
 465 470 475 480
 Ala His Tyr Tyr GIY Ser GIU Trp Asn GIU GIn GIU Lys GIn Lys Asn
 485 490 495
 Met His GIn GIY Ser Leu Arg Phe Ala GIU Asn Ala Lys Ser GIU GIY
 500 505 510
 GIY Arg Arg VaI Arg Ser Ala Ala Thr Pro Pro GIU Asn Thr Pro Asn
 515 520 525
 Asn VaI
 530

<210> 107

<211> 1870

<212> DNA

<213> Lycopersicon esculentum

<400> 107

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ttctccgtgg	cttctccaat	ggtgcctacg	gatacctccg	ccaagttttc	agtaccggtg	180
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acgttccagc	tctcctggat	ctcctttttc	acttgtttcg	tttcgacttt	tgctgctgca	300
cctttagttc	ctattattag	ggacaatcct	aatttgacaa	aaatggatgt	cggtaacgct	360
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PF57967.ST25.txt

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tggggaagca	tgtttctccc	accaacaaaa	gatccagtca	aggaacgga	agaacattat	1500
tatacttcag	agtacacaga	ggcagagagg	caaaaaggga	tgacacaaaa	cagcttgaaa	1560
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tgagttgttt	caataagcaa	aataagtcct	gatttttttt	tcttctttct	tttttggttt	1740
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atttacgtat	atataatata	tatatatata	tatattacac	attttaatgt	taaaaaaaa	1860
aaaaaaaaaa						1870

<210> 108

<211> 530

<212> PRT

<213> Lycopersicon esculentum

<400> 108

Met	Thr	Asp	VaI	GIu	GIy	Ser	Pro	GIy	Ser	Ser	Met	His	GIy	VaI	Thr
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			20					25					30		
Thr	Asp	Thr	Ser	Ala	Lys	Phe	Ser	VaI	Pro	VaI	Asp	Thr	GIu	His	Lys
		35					40					45			
Ala	Lys	GIn	Phe	Lys	Phe	Tyr	Ser	Phe	Ser	Lys	Pro	Hxs	GIy	Leu	Thr
	50					55					60				
Phe	GIn	Leu	Ser	Trp	H e	Ser	Phe	Phe	Thr	Cys	Phe	VaI	Ser	Thr	Phe
65					70				75					80	
Ala	Ala	Ala	Pro	Leu	VaI	Pro	H e	H e	Arg	Asp	Asn	Leu	Asn	Leu	Thr
			85						90					95	
Lys	Met	Asp	VaI	GIy	Asn	Ala	GIy	VaI	Ala	Ser	VaI	Ser	GIy	Ser	H e
		100					105					110			
Leu	Ser	Arg	Leu	Thr	Met	GIy	Ala	VaI	Cys	Asp	Leu	Leu	GIy	Pro	Arg
		115				120					125				
Tyr	GIy	Cys	Ala	Phe	Leu	H e	Met	Leu	Ser	Ala	Pro	Thr	VaI	Phe	Cys
	130					135					140				
Met	Ser	Phe	VaI	Ser	Ser	Ala	GIy	GIy	Tyr	VaI	Ala	VaI	Arg	Phe	Met
145					150				155					160	
H e	GIy	Phe	Ser	Leu	Ala	Thr	Phe	VaI	Ser	Cys	GIn	Tyr	Trp	Met	Ser
				165				170						175	

PF57967.ST25.txt

Thr Met Phe Asn Ser Lys lie lie GIY Leu Val Asn GIY Thr Ala Ala
 180 185 190
 GIY Trp GIY Asn Met GIY GIY GIY Ala Thr GIn Leu lie Met Pro Leu
 195 200 205
 Leu Tyr Asp lie lie Arg Arg Ala GIY Ala lie Pro Phe Thr Ala Trp
 210 215 220
 Arg H e Ala Phe Phe H e Pro GIY Trp Leu His Val Val Met GIY H e
 225 230 235 240
 Leu Val Leu Thr Leu GIY GIn Asp Leu Pro Asp GIY Asn Arg GIY Thr
 245 250 255
 Leu GIn Lys Thr GIY Thr Val Ala Lys Asp Lys Phe GIY Asn H e Leu
 260 265 270
 Trp Tyr Ala Ala Thr Asn Tyr Arg Thr Trp H e Phe Val Leu Leu Tyr
 275 280 285
 GIY Tyr Ser Met GIY Val GIU Leu Ser Thr Asp Asn Val H e Ala GIU
 290 295 300
 Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu Ser Thr Ala GIY H e H e
 305 310 315 320
 Ala Ala Thr Phe GIY Met Ala Asn Leu Leu Ala Arg Pro Phe GIY GIY
 325 330 335
 Phe Ser Ser Asp Tyr Ala Ala Lys Lys Phe GIY Met Arg GIY Arg Leu
 340 345 350
 Trp Val Leu Trp H e Leu GIn Thr Leu GIY GIY Val Phe Cys Val Leu
 355 360 365
 Leu GIY Arg Ser Asn Ser Leu Pro Leu Ala Val Thr Phe Met H e Leu
 370 375 380
 Phe Ser H e GIY Ala GIn Ala Ala Cys GIY Ala Thr Phe GIY H e H e
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 Pro Phe H e Ser Arg Arg Ser Leu GIY H e H e Ser GIY Met Thr GIY
 405 410 415
 Ala GIY GIY Asn Phe GIY Ser GIY Leu Thr GIn Leu Leu Phe Phe Thr
 420 425 430
 Ser Ser Lys Tyr Ser Thr Ala Thr GIY Leu Thr Tyr Met GIY Phe Met
 435 440 445
 H e H e GIY Cys Thr Leu Pro Val Thr Phe Cys His Phe Pro GIn Trp
 450 455 460
 GIY Ser Met Phe Leu Pro Pro Thr Lys Asp Pro Val Lys GIY Thr GIU
 465 470 475 480
 GIU His Tyr Tyr Thr Ser GIU Tyr Thr GIU Ala GIU Arg GIn Lys GIY
 485 490 495
 Met His GIn Asn Ser Leu Lys Phe Ala GIU Asn Cys Arg Ser GIU Arg
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 GIY Lys Arg Val GIY Ser Ala Pro Thr Pro Pro Asn Leu Thr Pro Asn
 515 520 525
 Arg Val
 530

<210> 109
 <211> 1832
 <212> DNA
 <213> Brassica napus

<400> 109
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PF57967.ST25.txt

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<210> 110

<211> 530

<212> PRT

<213> Brassica napus

<400> 110

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Thr Asp Lys Thr Ala Lys Phe Asp Leu Pro VaI Asp Ser GIU His Lys
35 40 45
Ala Thr VaI Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr
50 55 60
Phe His Leu Ser Trp lie Ser Phe Ser Thr Cys Phe VaI Ser Thr Phe
65 70 75 80
Ala Ala Ala Pro Leu VaI Pro lie lie Arg GIU Asn Leu Asn Leu Thr
85 90 95
Lys GIn Asp H e GIY Asn Ala GIY VaI Ala Ser VaI Ser GIY Ser H e
100 105 110
Phe Ser Arg Leu VaI Met GIY Ala VaI Cys Asp Leu Leu GIY Pro Arg
115 120 125
Tyr GIY Cys Ala Phe Leu VaI Met Leu Ser Ala Pro Thr VaI Phe Ser

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[illegible]

91/147

PF57967 .ST25 .txt

<212> DNA

<213> Arabidopsis thaliana

<400> 111

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atcgggttct	gcctggcgac	tttcgtgtca	tgccagtatt	ggatgagcac	aatgttcaat	540
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gtcactcagt	tgctcatgcc	aatggtctat	gagatcatcc	gacggttagg	gtccacgtcc	660
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ttggtcttga	ctctagggca	agacctccct	gatggtaata	gaagcacact	cgagaagaaa	780
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acatgggttt	tcgtgctgct	atatggatac	tccatgggag	tagagctcac	aaccgataac	900
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gcggcaagct	ttggtatggc	aaacttcttt	gcccgtccta	ttggtggttg	ggcctcagat	1020
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ttcatgatcc	tcttctctct	cggcgtctca	gccgcttggt	gagctacctt	tgctatcata	1200
cctttcatct	cacgccgctc	cttagggatc	atctctggtc	ttactggagc	tggtggaaac	1260
ttcggctctg	gtttgaccca	actcgtattc	ttctcgacct	caacgttctc	cacggaacaa	1320
gggctgacat	ggatgggggt	gatgattatg	gcgtgtacat	taccgcgtcac	tttagtgcac	1380
ttcccgaat	ggggaagcat	gtttttgcct	tccacggaag	atgaagtga	gtctacggag	1440
gagtattatt	acatgaaaga	gtggacagag	accgagaagc	gaaagggtat	gcatgaaggg	1500
agtttgaagt	tcgccgtgaa	tagtagatcg	gagcgtggac	ggcgcgtggc	ttctgcaccg	1560
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<210> 112

<211> 527

<212> PRT

<213> Arabidopsis thaliana

<-400> 112

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			20					25					30		
Ser	Asp	Ser	Ser	Ala	Lys	Phe	Ser	Leu	Pro	VaI	Asp	Thr	GIu	His	Lys
			35				40					45			
Ala	Lys	VaI	Phe	Lys	Leu	Leu	Ser	Phe	GIu	Ala	Pro	His	Met	Arg	Thr
			50			55					60				
Phe	His	Leu	Ala	Trp	lie	Ser	Phe	Phe	Thr	Cys	Phe	H e	Ser	Thr	Phe
65				70					75					80	
Ala	Ala	Ala	Pro	Leu	VaI	Pro	H e	H e	Arg	Asp	Asn	Leu	Asn	Leu	Thr
			85					90						95	
Arg	GIn	Asp	VaI	GIy	Asn	Ala	GIy	VaI	Ala	Ser	VaI	Ser	GIy	Ser	H e
			100				105						H O		
Phe	Ser	Arg	Leu	VaI	Met	GIy	Ala	VaI	Cys	Asp	Leu	Leu	GIy	Pro	Arg
			115				120					125			

PF57967 .ST25 .txt

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145      150      155      160
lie GIY Phe Cys Leu Ala Thr Phe Val Ser Cys GIn Tyr Trp Met Ser
165      170      175
Thr Met Phe Asn GIY GIn H e H e GIY Leu Val Asn GIY Thr Ala Ala
180      185      190
GIY Trp GIY Asn Met GIY GIY GIY Val Thr GIn Leu Leu Met Pro Met
195      200      205
Val Tyr GIU H e H e Arg Arg Leu GIY Ser Thr Ser Phe Thr Ala Trp
210      215      220
Arg Met Ala Phe Phe Val Pro GIY Trp Met His H e H e Met GIY H e
225      230      235      240
Leu Val Leu Thr Leu GIY GIn Asp Leu Pro Asp GIY Asn Arg Ser Thr
245      250      255
Leu GIU Lys Lys GIY Ala Val Thr Lys Asp Lys Phe Ser Lys Val Leu
260      265      270
Trp Tyr Ala H e Thr Asn Tyr Arg Thr Trp Val Phe Val Leu Leu Tyr
275      280      285
GIY Tyr Ser Met GIY Val GIU Leu Thr Thr Asp Asn Val H e Ala GIU
290      295      300
Tyr Phe Phe Asp Arg Phe His Leu Lys Leu His Thr Ala GIY H e H e
305      310      315      320
Ala Ala Ser Phe GIY Met Ala Asn Phe Phe Ala Arg Pro H e GIY GIY
325      330      335
Trp Ala Ser Asp H e Ala Ala Arg Arg Phe GIY Met Arg GIY Arg Leu
340      345      350
Trp Thr Leu Trp H e H e GIn Thr Leu GIY GIY Phe Phe Cys Leu Trp
355      360      365
Leu GIY Arg Ala Thr Thr Leu Pro Thr Ala Val Val Phe Met H e Leu
370      375      380
Phe Ser Leu GIY Ala GIn Ala Ala Cys GIY Ala Thr Phe Ala H e H e
385      390      395      400
Pro Phe H e Ser Arg Arg Ser Leu GIY H e H e Ser GIY Leu Thr GIY
405      410      415
Ala GIY GIY Asn Phe GIY Ser GIY Leu Thr GIn Leu Val Phe Phe Ser
420      425      430
Thr Ser Thr Phe Ser Thr GIU GIn GIY Leu Thr Trp Met GIY Val Met
435      440      445
H e Met Ala Cys Thr Leu Pro Val Thr Leu Val His Phe Pro GIn Trp
450      455      460
GIY Ser Met Phe Leu Pro Ser Thr GIU Asp GIU Val Lys Ser Thr GIU
465      470      475      480
GIU Tyr Tyr Tyr Met Lys GIU Trp Thr GIU Thr GIU Lys Arg Lys GIY
485      490      495
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<210> 113
 <211> 1709
 <212> PRT

PF57967.ST25.txt

<213> Arabidops is thaliana

<400> 113

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Thr Thr Thr Ala Ala Ala Ala Thr Ala Cys Ala Thr GIY GIY GIY Thr
      35      40      45
Thr Cys Thr Ala Cys Thr GIY Ala Thr GIY Ala GIY Cys Cys Cys GIY
      50      55      60
GIY Ala Ala GIY Thr Thr Cys Cys Ala Thr GIY Cys Ala Thr GIY GIY
65      70      75      80
Ala GIY Thr Thr Ala Cys Cys GIY GIY Thr Ala GIY Ala GIY Ala Ala
      85      90      95
Cys Ala GIY Ala GIY Cys Thr Ala Thr GIY Cys Thr Thr Thr Cys Thr
      100     105     110
Cys GIY GIY Thr Ala GIY Ala Thr GIY GIY Thr Ala GIY Thr GIY Ala
      115     120     125
GIY Cys Cys GIY Ala Cys Cys Ala Ala Cys Ala Cys Ala Ala Ala GIY
130     135     140
Ala Ala Ala Ala Ala GIY Thr Ala Cys Ala Ala Thr Cys Thr GIY Cys
145     150     155     160
Cys GIY GIY Thr GIY GIY Ala Cys GIY Cys GIY GIY Ala GIY GIY Ala
      165     170     175
Thr Ala Ala GIY GIY Cys Ala Ala Cys GIY GIY Thr Thr Thr Thr Cys
      180     185     190
Ala Ala GIY Cys Thr Cys Thr Thr Cys Thr Cys Cys Thr Thr Cys GIY
      195     200     205
Cys Cys Ala Ala Ala Cys Cys Thr Cys Ala Cys Ala Thr GIY Ala GIY
210     215     220
Ala Ala Cys GIY Thr Thr Cys Cys Ala Cys Cys Thr Cys Thr Cys GIY
225     230     235     240
Thr GIY GIY Ala Thr Cys Thr Cys Thr Thr Thr Cys Thr Cys Cys Ala
      245     250     255
Cys Ala Thr GIY Thr Thr Thr Thr GIY Thr Thr Thr Cys GIY Ala Cys
      260     265     270
GIY Thr Thr Cys GIY Cys Ala GIY Cys Thr GIY Cys Ala Cys Cys Ala
      275     280     285
Cys Thr Thr Ala Thr Cys Cys Cys GIY Ala Thr Cys Ala Thr Cys Ala
290     295     300
GIY GIY GIY Ala GIY Ala Ala Thr Cys Thr Thr Ala Ala Cys Cys Thr
305     310     315     320
Cys Ala Cys Cys Ala Ala Ala Cys Ala Thr GIY Ala Cys Ala Thr Thr
      325     330     335
GIY GIY Ala Ala Ala Cys GIY Cys Thr GIY GIY Ala GIY Thr Thr GIY
      340     345     350
Cys Cys Thr Cys Cys GIY Thr Cys Thr Cys GIY GIY GIY Ala GIY
      355     360     365
Thr Ala Thr Cys Thr Thr Cys Thr Cys Thr Ala GIY GIY Cys Thr Cys
370     375     380
GIY Thr GIY Ala Thr GIY GIY GIY Ala GIY Cys Cys GIY Thr GIY Thr
385     390     395     400
GIY Thr GIY Ala Thr Cys Thr Thr Thr Thr Thr GIY GIY GIY Thr Cys Cys

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PF57967.ST25.txt

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      420      425      430
Thr Thr Cys Cys Thr Thr GIy Thr GIy Ala Thr GIy Thr Thr GIy Thr
      435      440      445
Cys Thr GIy Cys Cys Cys Cys Ala Ala Cys GIy GIy Thr GIy Thr Thr
      450      455      460
Cys Thr Cys Cys Ala Thr GIy Ala GIy Cys Thr Thr Cys GIy Thr GIy
465      470      475      480
Ala GIy Thr GIy Ala Cys GIy Cys Ala GIy Cys Ala GIy GIy Cys Thr
      485      490      495
Thr Cys Ala Thr Ala Ala Cys GIy GIy Thr GIy Ala GIy GIy Thr Thr
      500      505      510
Cys Ala Thr GIy Ala Thr Thr GIy GIy Thr Thr Thr Thr Thr GIy Cys
      515      520      525
Cys Thr GIy GIy Cys GIy Ala Cys GIy Thr Thr Thr GIy Thr GIy Thr
      530      535      540
Cys Thr Thr GIy Thr Cys Ala Ala Thr Ala Cys Thr GIy GIy Ala Thr
545      550      555      560
GIy Ala GIy Cys Ala Cys Thr Ala Thr GIy Thr Thr Cys Ala Ala Cys
      565      570      575
Ala GIy Thr Cys Ala GIy Ala Thr Cys Ala Thr Cys GIy GIy Thr Cys
      580      585      590
Thr GIy GIy Thr GIy Ala Ala Cys GIy GIy GIy Ala Cys Ala GIy Cys
      595      600      605
Ala GIy Cys Cys GIy GIy Ala Thr GIy GIy GIy GIy Ala Ala Ala Cys
      610      615      620
Ala Thr GIy GIy GIy Thr GIy GIy Cys GIy GIy Cys Ala Thr Ala Ala
625      630      635      640
Cys GIy Cys Ala GIy Thr Thr GIy Cys Thr Cys Ala Thr GIy Cys Cys
      645      650      655
Cys Ala Thr Thr GIy Thr GIy Thr Ala Thr GIy Ala Ala Ala Thr Cys
      660      665      670
Ala Thr Thr Ala GIy GIy Cys GIy Cys Thr GIy Cys GIy GIy Ala Thr
      675      680      685
Cys Ala Ala Cys Ala GIy Cys GIy Thr Thr Cys Ala Cys GIy GIy Cys
      690      695      700
Cys Thr GIy GIy Ala GIy GIy Ala Thr Cys GIy Cys Cys Thr Thr Cys
705      710      715      720
Thr Thr Thr GIy Thr Cys Cys Cys GIy GIy Thr Thr GIy GIy Thr
      725      730      735
Thr GIy Cys Ala Cys Ala Thr Cys Ala Thr Cys Ala Thr GIy GIy GIy
      740      745      750
Ala Ala Thr Cys Thr Thr GIy GIy Thr GIy Cys Thr Cys Ala Cys GIy
      755      760      765
Cys Thr Ala GIy GIy Thr Cys Ala Ala GIy Ala Thr Cys Thr GIy Cys
      770      775      780
Cys Ala GIy GIy Thr GIy GIy Ala Ala Ala Cys Ala GIy Ala GIy Cys
785      790      795      800
Thr GIy Cys Cys Ala Thr GIy GIy Ala GIy Ala Ala Ala GIy Cys GIy
      805      810      815
GIy GIy Ala GIy Ala Ala GIy Thr Thr GIy Cys Cys Ala Ala Ala GIy
      820      825      830
Ala Cys Ala Ala Ala Thr Thr Cys GIy GIy Ala Ala Ala GIy Ala Thr

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Thr	Cys	835	Thr	Ala	Thr	Gly	Gly	840	Thr	Ala	Cys	Gly	Cys	845	Cys	Gly	Thr	Thr
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Gly	Gly	Ala	Thr	Thr	Thr	Cys	Gly	Thr	Thr	Cys	Thr	Thr	Cys	Thr	Thr	Cys	Thr	Thr
Gly	Thr	Ala	Thr	Gly	Gly	Ala	Thr	Ala	Thr	Thr	Cys	Cys	Ala	Thr	Gly	Thr	Gly	Thr
Gly	Gly	Ala	Gly	Thr	Thr	Gly	Ala	Gly	Thr	Thr	Ala	Ala	Gly	Cys	Ala	Cys	Ala	Ala
Cys	Ala	Gly	Ala	Cys	Ala	Ala	Thr	Gly	Thr	Thr	Ala	Thr	Cys	Gly	Cys	Cys	Cys	Cys
Cys	Gly	Ala	Gly	Thr	Ala	Cys	Thr	Thr	Cys	Thr	Thr	Thr	Gly	Ala	Thr	Ala	Thr	Thr
Ala	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Cys	Thr	Thr	Gly	Ala	Ala	Gly	Cys	Ala	Thr	Thr
Thr	Thr	Cys	Ala	Cys	Ala	Cys	Ala	Gly	Cys	Gly	Gly	Gly	Gly	Ala	Thr	Ala	Thr	Thr
Thr	Ala	Thr	Ala	Gly	Cys	Ala	Gly	Cys	Ala	Thr	Gly	Thr	Thr	Thr	Thr	Cys	Cys	Cys
Gly	Gly	Ala	Ala	Thr	Gly	Gly	Gly	Cys	Cys	Ala	Ala	Thr	Thr	Thr	Cys	Cys	Cys	Cys
Thr	Thr	Thr	Gly	Cys	Thr	Cys	Gly	Thr	Cys	Cys	Ala	Ala	Gly	Cys	Ala	Cys	Ala	Ala
Gly	Gly	Ala	Gly	Gly	Cys	Thr	Gly	Gly	Gly	Gly	Cys	Ala	Thr	Cys	Thr	Cys	Thr	Thr
Gly	Ala	Cys	Ala	Thr	Thr	Gly	Cys	Ala	Gly	Cys	Cys	Ala	Ala	Gly	Ala	Ala	Gly	Gly
Cys	Gly	Cys	Thr	Thr	Cys	Gly	Gly	Ala	Ala	Thr	Gly	Cys	Gly	Cys	Gly	Gly	Ala	Ala
Gly	Gly	Gly	Ala	Gly	Gly	Thr	Thr	Gly	Thr	Gly	Gly	Gly	Ala	Cys	Thr	Thr	Thr	Thr
Thr	Thr	Gly	Thr	Gly	Gly	Ala	Thr	Cys	Ala	Thr	Thr	Thr	Cys	Ala	Gly	Ala	Gly	Gly
Ala	Cys	Gly	Thr	Cys	Cys	Gly	Gly	Thr	Gly	Gly	Gly	Thr	Cys	Thr	Cys	Thr	Cys	Cys
Thr	Thr	Thr	Thr	Gly	Thr	Gly	Thr	Gly	Thr	Gly	Thr	Gly	Gly	Cys	Thr	Cys	Cys	Cys
Gly	Gly	Ala	Cys	Gly	Thr	Gly	Cys	Cys	Ala	Ala	Cys	Ala	Cys	Ala	Cys	Cys	Cys	Cys
Cys	Thr	Cys	Gly	Thr	Cys	Ala	Cys	Thr	Gly	Cys	Cys	Gly	Gly	Thr	Thr	Thr	Thr	Thr
Gly	Thr	Ala	Thr	Cys	Thr	Ala	Thr	Gly	Gly	Thr	Cys	Cys	Cys	Cys	Thr	Cys	Cys	Cys
Thr	Thr	Cys	Thr	Cys	Thr	Thr	Thr	Ala	Gly	Gly	Ala	Gly	Gly	Cys	Gly	Cys	Ala	Ala
Cys	Ala	Ala	Gly	Cys	Cys	Gly	Cys	Thr	Thr	Gly	Cys	Gly	Gly	Gly	Gly	Gly	Ala	Ala
Gly	Cys	Cys	Ala	Cys	Cys	Thr	Thr	Thr	Gly	Cys	Thr	Ala	Thr	Ala	Thr	Cys	Cys	Cys
Gly	Thr	Gly	Cys	Cys	Cys	Thr	Thr	Thr	Gly	Thr	Cys	Thr	Cys	Thr	Cys	Cys	Cys	Cys
Cys	Gly	Gly	Cys	Gly	Ala	Gly	Cys	Thr	Cys	Thr	Cys	Thr	Ala	Gly	Gly	Cys	Cys	Cys

PF57967.ST25.txt

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1265	1270	12-75
Ala Cys Cys GIy GIy GIy	GIy Cys Thr GIy GIy	Ala GIy GIy GIy
1280	1285	1290
Ala Ala Cys Thr Thr Thr	GIy GIy GIy Thr Cys	Ala GIy GIy Ala
1295	1300	1305
Cys Thr Cys Ala Cys Ala	Cys Ala GIy Cys Thr	Cys GIy Thr Cys
1310	1315	1320
Thr Thr Thr Thr Thr Cys	Thr Cys GIy Ala Cys	Thr Thr Cys GIy
1325	1330	1335
Cys GIy Cys Thr Thr Cys	Ala Cys Ala Ala Cys	Thr GIy Ala Ala
1340	1345	1350
GIy Ala Ala GIy GIy GIy	Cys Thr Ala Ala Cys	GIy Thr GIy GIy
1355	1360	1365
Ala Thr GIy GIy GIy Ala	GIy Thr GIy Ala Thr	GIy Ala Thr Ala
1370	1375	1380
GIy Thr Thr GIy Cys Thr	Thr GIy Cys Ala Cys	GIy Thr Thr GIy
1385	1390	1395
Cys Cys Thr GIy Thr Thr	Ala Cys Cys Thr Thr	Ala Ala Thr Cys
1400	1405	1410
Cys Ala Cys Thr Thr Thr	Cys Cys Thr Cys Ala	GIy Thr GIy GIy
1415	1420	1425
GIy GIy Ala Ala GIy Cys	Ala Thr GIy Thr Thr	Cys Thr Thr Cys
1430	1435	1440
Cys Cys Thr Cys Cys Thr	Thr Cys Cys Ala Ala	Cys GIy Ala Thr
1445	1450	1455
Thr Cys GIy GIy Thr Cys	GIy Ala Cys GIy Cys	Thr Ala Cys GIy
1460	1465	14-70
GIy Ala GIy Cys Ala Cys	Thr Ala Thr Thr Ala	Thr GIy Thr Thr
1475	1480	1485
GIy GIy Cys GIy Ala Ala	Thr Ala Thr Ala GIy	Thr Ala Ala GIy
1490	1495	1500
GIy Ala GIy GIy Ala GIy	Cys Ala GIy Cys Ala	GIy Ala Thr Thr
1505	1510	1515
GIy GIy Cys Ala Thr GIy	Cys Ala Thr Thr Thr	Ala Ala Ala Ala
1520	1525	1530
Ala GIy Cys Ala Ala Ala	Cys Thr GIy Thr Thr	Thr GIy Cys Thr
1535	1540	1545
GIy Ala Thr GIy GIy Ala	GIy Cys Cys Ala Ala	GIy Ala Cys Cys
1550	1555	1560
GIy Ala GIy GIy GIy Ala	GIy GIy Cys Ala GIy	Cys Ala GIy Cys
1565	1570	15-75
GIy Thr Cys Cys Ala Cys	Ala Ala Ala GIy GIy	GIy Ala Ala Cys
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GIy Cys Ala Ala Cys Cys	Ala Ala Cys Ala Ala	Thr GIy Cys Thr
1595	1600	1605
Thr GIy Ala Thr Cys Ala	Thr GIy Thr GIy Thr	Cys Ala Thr Thr
1610	1615	1620
GIy Ala Thr Ala Thr Cys	Ala Ala GIy Ala Ala	Ala Thr Thr Ala
1625	1630	1635
Ala Thr Ala Ala Thr Thr	Thr Cys Ala Cys Thr	Thr Ala Thr GIy
1640	1645	1650
Thr GIy Ala Ala Ala Thr	GIy GIy Ala Cys Ala	Thr Ala Ala Ala

PF57967.ST25.txt

1655		1660		1665
Cys Thr GIy Thr Thr GIy	GIy Ala Ala Ala Ala	Thr Ala Ala Ala		
1670		1675		1680
GIy Ala Ala Cys Cys Ala	Thr Thr Thr Cys Thr	Thr Thr Cys Ala		
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<210> 114
 <211> 522
 <212> PRT
 <213> Arabidopsis thaliana

<400> 114

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Thr Lys Lys Lys Tyr Asn Leu Pro VaI Asp Ala GIu Asp Lys Ala Thr		
	35 40 45	
VaI Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr Phe His		
	50 55 60	
Leu Ser Trp lie Ser Phe Ser Thr Cys Phe VaI Ser Thr Phe Ala Ala		
65	70 75 80	
Ala Pro Leu lie Pro lie lie Arg GIu Asn Leu Asn Leu Thr Lys His		
	85 90 95	
Asp lie GIy Asn Ala GIy VaI Ala Ser VaI Ser GIy Ser lie Phe Ser		
	100 105 110	
Arg Leu VaI Met GIy Ala VaI Cys Asp Leu Leu GIy Pro Arg Tyr GIy		
	115 120 125	
Cys Ala Phe Leu VaI Met Leu Ser Ala Pro Thr VaI Phe Ser Met Ser		
	130 135 140	
Phe VaI Ser Asp Ala Ala GIy Phe H e Thr VaI Arg Phe Met H e GIy		
145	150 155 160	
Phe Cys Leu Ala Thr Phe VaI Ser Cys GIn Tyr Trp Met Ser Thr Met		
	165 170 175	
Phe Asn Ser GIn H e H e GIy Leu VaI Asn GIy Thr Ala Ala GIy Trp		
	180 185 190	
GIy Asn Met GIy GIy GIy H e Thr GIn Leu Leu Met Pro H e VaI Tyr		
	195 200 205	
GIu H e H e Arg Arg Cys GIy Ser Thr Ala Phe Thr Ala Trp Arg H e		
	210 215 220	
Ala Phe Phe VaI Pro GIy Trp Leu His H e H e Met GIy H e Leu VaI		
225	230 235 240	
Leu Thr Leu GIy GIn Asp Leu Pro GIy GIy Asn Arg Ala Ala Met GIu		
	245 250 255	
Lys Ala GIy GIu VaI Ala Lys Asp Lys Phe GIy Lys H e Leu Trp Tyr		
	260 265 270	
Ala VaI Thr Asn Tyr Arg Thr Trp H e Phe VaI Leu Leu Tyr GIy Tyr		
	275 280 285	
Ser Met GIy VaI GIu Leu Ser Thr Asp Asn VaI H e Ala GIu Tyr Phe		
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Phe Asp Arg Phe His Leu Lys Leu His Thr Ala GIy H e H e Ala Ala		
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<210> 115
<211> 1709
<212> DNA
<213> Arabidopsis thaliana
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99/147

PF57967.ST25.txt

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attgatatca  agaaattaat  aatttcactt  atgtgaaatg  gacataaact  gttggaaaat  1680
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<210> 116

<211> 522

<212> PRT

<213> Arabidopsis thaliana

<400> 116

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

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<210> 117
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<212> DNA
<213> Arabidopsis thaliana
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101/147

PF57967.ST25.txt

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gcgagggtta gtacagctga gggactctca ttgatggcg ttatggcggg tttgtgcaca 1380
ctcccagttg cgtttataca ttttccgcaa tggggaagca tgtttttaag accgtcgacc 1440
gatggagaaa gatcacagga ggaatattat tacggttctg agtggacgga gaatgagaaa 1500
caacaaggat tgcacgaagg aagcatcaaa tttgcagaga atagtaggtc agagagaggc 1560
cggaagtag ctttggctaa cattccaacg ccggagaacg gaactccaag tcatgtttga 1620

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<210> 118

<211> 539

<212> PRT

<213> Arabidopsis thaliana

<400> 118

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

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PF57967.ST25.txt

Leu GIn Thr Ala GIY H e VaI Ala Ala Ser Phe GIY Met Ala Asn Phe
 325 330 335
 lie Ala Arg Pro Phe GIY GIY Tyr Ala Ser Asp VaI Ala Ala Arg VaI
 340 345 350
 Phe GIY Met Arg GIY Arg Leu Trp Thr Leu Trp H e Phe GIn Thr VaI
 355 360 365
 GIY Ala Leu Phe Cys H e Trp Leu GIY Arg Ala Ser Ser Leu Pro H e
 370 375 380
 Ala H e Leu Ala Met Met Leu Phe Ser H e GIY Thr GIn Ala Ala Cys
 385 390 395 400
 GIY Ala Leu Phe GIY VaI Ala Pro Phe VaI Ser Arg Arg Ser Leu GIY
 405 410 415
 Leu H e Ser GIY Leu Thr GIY Ala GIY GIY Asn Phe GIY Ser GIY Leu
 420 425 430
 Thr GIn Leu Leu Phe Phe Ser Ser Ala Arg Phe Ser Thr Ala GIU GIY
 435 440 445
 Leu Ser Leu Met GIY VaI Met Ala VaI Leu Cys Thr Leu Pro VaI Ala
 450 455 460
 Phe H e His Phe Pro GIn Trp GIY Ser Met Phe Leu Arg Pro Ser Thr
 465 470 475 480
 Asp GIY GIU Arg Ser GIn GIU GIU Tyr Tyr GIY Ser GIU Trp Thr
 485 490 495
 GIU Asn GIU Lys GIn GIn GIY Leu His GIU GIY Ser H e Lys Phe Ala
 500 505 510
 GIU Asn Ser Arg Ser GIU Arg GIY Arg Lys VaI Ala Leu Ala Asn H e
 515 520 525
 Pro Thr Pro GIU Asn GIY Thr Pro Ser His VaI
 530 535

<210> 119

<211> 1629

<212> DNA

<213> Arabidopsis thaliana

<400> 119

atggctcaca	accatttctaa	tgaagacggc	tctatttgaa	cctccttgca	tggagtcacg	60
gcaagggagc	aagtcttctc	cttctccgtc	caagaagatg	tcccttcac	tcaagccgtc	120
cgaacaaacg	atccaacggc	taagtttgcc	ctaccagtgg	actccgaaca	tagggcaaaa	180
gtgttcaaac	cactatcatt	cgctaaacca	catatgagag	ccttcactt	aggatggatc	240
tctttcttca	cttgcttcat	ctccaccttc	gcagccgcac	ctctagtccc	cgtcattcgc	300
gacaatctcg	acctgaccaa	aaccgacatc	ggaaatgctg	gagttgcatc	agtttccggc	360
gccattttct	cgagactcgc	tatgggtgct	gtatgtgacc	ttctaggggc	acgttatgga	420
accgccttct	cacttatgct	tacagctcca	gcagttttct	ccatgtcggt	cgtagctgac	480
gcggaagct	acttagccgt	aaggttcatg	atcggttttt	gcttagcaac	gttcgtatca	540
tgctcagtact	ggacgagtgt	tatgttcact	ggaaagatta	tcggactcgt	taacggatgt	600
gctggagggt	ggggagatat	gggaggagga	gtgactcagc	tactaatgcc	aatggtcttc	660
cacgtcatca	aactcaccgg	agccactccc	ttcacggcct	ggaggttcgc	cttcttcac	720
ccgggcattc	ttcagatagt	tatgggtatt	ctcgtttctc	ctctcggcca	agatcttccc	780
gatggttaacc	tcagactctc	cctaaagagt	gggtcaagttt	ctaaagacaa	attctccaag	840
gtcttttggg	tcgctgtgaa	aaactataga	acatggatct	tattcatgct	ctatggattt	900
tctatgggag	ttgaattaac	gatcaacaac	gttatatctg	gataacttcta	cgatagggtt	960
aaccttacgc	ttcacacagc	tggtattata	gcagccagct	ttggtatggc	aaacttcttt	1020
gcccgtcctt	ttggtggcta	cgcttcagat	gtagctgcac	ggctcttcgg	tatgagggga	1080
cggttatgga	tcttgtggat	cttacaact	gttggagctc	tcttttgcac	ctggcttggt	1140

PF57967.ST25.txt

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cgtgctagtt cactacctat agctatctta gccatgatgc ttttttccat gggcacacaa 1200
gctgcttggt gagctctctt tgggtgttgct ccttttgttt cccgccgttc tcttggaatt 1260
atctcgggat taactgggtgc tgggtggaat tttgggtcgg gagttactca acttcttttc 1320
ttctcttcct cgagggttag tacggcggaa ggactatcgt tgatgggctg tatggctggt 1380
gtgtgctctc ttccggttgc gtttatacat tttccgcagt ggggaagcat gttcttgagg 1440
ccatcacaag atggagagaa atcaaaggaa gagcattact atggagcgga atggacagag 1500
gaagagaaga gcttaggact acacgaagga agcattaaat ttgctgaaaa cagccggtca 1560
gagagaggcc gcaaggcgat gttggctgat attccaacgc cggaaaccgg atctccggct 1620
catgtctag 1629

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<210> 120

<211> 542

<212> PRT

<213> Arabidopsis thaliana

<400> 120

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

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PF57967.ST25. txt

GIu Leu Thr lie Asn Asn VaI lie Ser GIy Tyr Phe Tyr Asp Arg Phe
 305 310 315 320
 Asn Leu Thr Leu His Thr Ala GIy lie lie Ala Ala Ser Phe GIy Met
 325 330 335
 Ala Asn Phe Phe Ala Arg Pro Phe GIy GIy Tyr Ala Ser Asp VaI Ala
 340 345 350
 Ala Arg Leu Phe GIy Met Arg GIy Arg Leu Trp H e Leu Trp H e Leu
 355 360 365
 GIn Thr VaI GIy Ala Leu Phe Cys lie Trp Leu GIy Arg Ala Ser Ser
 370 375 380
 Leu Pro lie Ala H e Leu Ala Met Met Leu Phe Ser Met GIy Thr GIn
 385 390 395 400
 Ala Ala Cys GIy Ala Leu Phe GIy VaI Ala Pro Phe VaI Ser Arg Arg
 405 410 415
 Ser Leu GIy Leu lie Ser GIy Leu Thr GIy Ala GIy GIy Asn Phe GIy
 420 425 430
 Ser GIy VaI Thr GIn Leu Leu Phe Phe Ser Ser Ser Arg Phe Ser Thr
 435 440 445
 Ala GIu GIy Leu Ser Leu Met GIy VaI Met Ala VaI VaI Cys Ser Leu
 450 455 460
 Pro VaI Ala Phe H e His Phe Pro GIn Trp GIy Ser Met Phe Leu Arg
 465 470 475 480
 Pro Ser GIn Asp GIy GIu Lys Ser Lys GIu GIu His Tyr Tyr GIy Ala
 485 490 495
 GIu Trp Thr GIu GIu GIu Lys Ser Leu GIy Leu His GIu GIy Ser H e
 500 505 510
 Lys Phe Ala GIu Asn Ser Arg Ser GIu Arg GIy Arg Lys Ala Met Leu
 515 520 525
 Ala Asp lie Pro Thr Pro GIu Thr GIy Ser Pro Ala His VaI
 530 535 540

<210> 121
 <211> 1605
 <212> DNA
 <213> Daucus carota

<400> 121
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 tccctggctt tctccgttgc ttcccgtatc gacacctccg ctgaattcca cgttccgggtt 120
 gactccgaac acaaagctaa agttttcaaa ttcaaatacct tctccccgcc gcacgggtctg 180
 cagttccagc tgacctggat ctcccttccc acctgcttcg tttccacctt cgctgctcgt 240
 ccgctgggtg ttatcatccg tgacaacctg aacccgacca aaatggacgt tggtaacgct 300
 ggtgttgctt ccgttaccgg ttccatcctg tcccgtgggtg ctatgggtgc tatctgcgac 360
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 tgcattgtcct tcgtttcctc cgctgggtgt tacgttgctg ttcgtttcat gatcgggtttc 480
 tccctggcta ccttcgtttc ctgccgttac tggatgtcca cctccatgca ctccgacatc 540
 atcgggtctgg ttaacggtac cgctgctggt tggggtaaca tgaccggtgg tgctaccag 600
 ctgatcatgc cgtgtctgta cgacatcatc cgtgaagctg gtgctacccc gttcaccgct 660
 tggcgtatcg ctctgttcat cccgggttgg ctgcacgtta tctccggtat cctggttctg 720
 accctgggtc aggacctgcc ggacggtaac gctcagaacg aagcttccct gcgtaaaaaa 780
 ggtcgtgttc acaaagacaa attctccaaa atcctgcgtt acgctgctac caactaccgt 840
 acctggatcc tggttctgct gtacggttac tccatgggtg ttgaactgac caccgacaac 900
 gttatcgtcg aatacttctt cgaccgtttc gacctgaaac tgcacacccc gggtatcatc 960
 gctgctacct tcggtatggc taacctgctg gctcgtccgt tcggtgggtg gtcctccgac 1020

PF57967.ST25.txt

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gttgctgcta aacacttcgg tatgctgggt cgtcactgga actcctggga cctgcagacc 1080
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gctatcacct ggatgatcat cttctccatc ggtgctcagg ctgctaccgg tgttaccttc 1200
ggatcatccc cgttcatctc ccgctcgttac ctgggtatca tctcccagat gaccgggtgct 1260
aacggtaact tcggttccgg tcagaccag ccgctggaat tcgactccac caaatacaac 1320
accggtctgg gtctgaccta catgggtatg atgatcatcg cttgcaccct gccgccgatg 1380
ctggtttggg tctggcagga cggttccatg ttctgcccgc cgtccaaaga cccgatcaaa 1440
ggtaccgaac cggaacacta cttcggttcc gaatacaccg aagacgaaaa agttaaggt 1500
atgcaccaga actccatcaa attcgctgaa aactcccgta ccgaattcgg taaaaaacgt 1560
gttggttccg ctccgacccc gccgaacgtt tacccaacc gtgtt 1605

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<210> 122
<211> 535
<212> PRT
<213> Daucus carota

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<400> 122
Met GIy Asp Met GIu GIy Ser Pro GIy Ser Ser Met His GIy VaI Thr
1 5 10 15
GIy Arg GIu Pro Ser Leu Ala Phe Ser VaI Ala Ser Arg H e Asp Thr
20 25 30
Ser Ala GIu Phe His VaI Pro VaI Asp Ser GIu His Lys Ala Lys VaI
35 40 45
Phe Lys Phe Lys Ser Phe Ser Pro Pro His GIy Leu GIn Phe GIn Leu
50 55 60
Thr Trp lie Ser Phe Pro Thr Cys Phe VaI Ser Thr Phe Ala Ala Arg
65 70 75 80
Pro Leu VaI VaI lie lie Arg Asp Asn Leu Asn Pro Thr Lys Met Asp
85 90 95
VaI GIy Asn Ala GIy VaI Ala Ser VaI Thr GIy Ser H e Leu Ser Arg
100 105 110
GIy Ala Met GIy Ala lie Cys Asp Met Leu GIy Pro Arg Tyr GIy Cys
115 120 125
Ala Phe Leu lie Met Leu Ser Ala Pro Lys VaI Leu Cys Met Ser Phe
130 135 140
VaI Ser Ser Ala GIy GIy Tyr VaI Ala VaI Arg Phe Met H e GIy Phe
145 150 155 160
Ser Leu Ala Thr Phe VaI Ser Cys Arg Tyr Trp Met Ser Thr Ser Met
165 170 175
His Ser Asp lie lie GIy Leu VaI Asn GIy Thr Ala Ala GIy Trp GIy
180 185 190
Asn Met Thr GIy GIy Ala Thr GIn Leu H e Met Pro Leu Leu Tyr Asp
195 200 205
H e H e Arg GIu Ala GIy Ala Thr Pro Phe Thr Ala Trp Arg H e Ala
210 215 220
Leu Phe H e Pro GIy Trp Leu His VaI H e Ser GIy H e Leu VaI Leu
225 230 235 240
Thr Leu GIy GIn Asp Leu Pro Asp GIy Asn Ala GIn Asn GIu Ala Ser
245 250 255
Leu Arg Lys Lys GIy Arg VaI His Lys Asp Lys Phe Ser Lys H e Leu
260 265 270
Arg Tyr Ala Ala Thr Asn Tyr Arg Thr Trp H e Leu VaI Leu Leu Tyr
275 280 285
GIy Tyr Ser Met GIy VaI GIu Leu Thr Thr Asp Asn VaI H e Ala GIu

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PF57967.ST25.txt

290 295 300
 Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu His Thr Pro GIY lie lie
 305 310 315 320
 Ala Ala Thr Phe GIY Met Ala Asn Leu Leu Ala Arg Pro Phe GIY GIY
 325 330 335
 Trp Ser Ser Asp Val Ala Ala Lys His Phe GIY Met Arg GIY Arg His
 340 345 350
 Trp Asn Ser Trp Asp Leu Gln Thr Leu GIY GIY Val Phe Cys Leu Leu
 355 360 365
 Leu Val Arg Ala Thr Thr Ser Pro lie Asp Ala Leu Ala lie Thr Trp
 370 375 380
 Met H e H e Phe Ser H e GIY Ala Gln Ala Ala Thr GIY Val Thr Phe
 385 390 395 400
 GIY H e H e Pro Phe H e Ser Arg Arg Tyr Leu GIY H e H e Ser Gln
 405 410 415
 Met Thr GIY Ala Asn GIY Asn Phe GIY Ser GIY Gln Thr Gln Pro Leu
 420 425 430
 GIU Phe Asp Ser Thr Lys Tyr Asn Thr GIY Leu GIY Leu Thr Tyr Met
 435 440 445
 GIY Met Met H e H e Ala Cys Thr Leu Pro Pro Met Leu Val Trp Phe
 450 455 460
 Trp Gln Asp GIY Ser Met Phe Leu Pro Pro Ser Lys Asp Pro H e Lys
 465 470 475 480
 GIY Thr GIU Pro GIU His Tyr Phe GIY Ser GIU Tyr Thr GIU Asp GIU
 485 490 495
 Lys Val Lys GIY Met His Gln Asn Ser H e Lys Phe Ala GIU Asn Ser
 500 505 510
 Arg Thr GIU Phe GIY Lys Lys Arg Val GIY Ser Ala Pro Thr Pro Pro
 515 520 525
 Asn Val Tyr Pro Asn Arg Val
 530 535

<210> 123
 <211> 1200
 <212> DNA
 <213> Zea mays

<400> 123
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 cgccacgcag ctcatcatgc cgctcgtcta cgacgtcatc cgcaagtgcg gcgccacgcc 120
 attcacggcc tggcgccctcg cctacttcgt gccgggcctc atgcacgtcg tcatgggcgt 180
 cctggtgctc acgctggggc aggacctccc cgacggcaac ctcaggtcgc tgcagaagaa 240
 gggcaacgtc aacaaggaca gcttctccaa ggtcatgtgg tacgccgtca tcaactaccg 300
 tacctggatc ttcgtcctcc tctacggcta ctgcatgggc gtcgagctca ccaccgaaa 360
 cgtcatcgcc gagtacatgt acgaccgctt cgacctcgac ctccgcgtcg ccgggaccat 420
 cgccgcctgc ttcggcatgg ccaacatcgt cgacgcctt atggggcgga tcatgtcgga 480
 catgggcgcg cgctactggg gcatgcgcgc tcgcctctgg aacatctgga tcctccagac 540
 cgccggcggc gccttctgcc tctggctggg acgcgccagc accctccccg tctccgtcgt 600
 cgccatggtg ctcttctcct tctgcgcgca catctccggc ggcgccatct tcggggtcgt 660
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 cttcccgcag tgggggtcca tgttcttccc gcccagcgcc accgccgacg aggagggcta 900
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PF57967.ST25.txt

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cctcttttga tgtacgaata tgccttgta ttactgtgcg cgccatata caatacacgt 1140
gtgctccggt gacatgagtt atatagcact aaaaacttct ttgaaaaaa aaaaaaaaaa 1200

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<210> 124
<211> 346
<212> PRT
<213> Zea mays

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<400> 124
Ser Lys H e H e Gly Thr Val Asn Gly Leu Ala Ala GIY Trp GIY Asn
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Met GIY GIY GIY Ala Thr Gln Leu H e Met Pro Leu Val Tyr Asp Val
20 25 30
H e Arg Lys Cys GIY Ala Thr Pro Phe Thr Ala Trp Arg Leu Ala Tyr
35 40 45
Phe Val Pro GIY Leu Met His Val Val Met GIY Val Leu Val Leu Thr
50 55 60
Leu GIY Gln Asp Leu Pro Asp GIY Asn Leu Arg Ser Leu Gln Lys Lys
65 70 75 80
GIY Asn Val Asn Lys Asp Ser Phe Ser Lys Val Met Trp Tyr Ala Val
85 90 95
H e Asn Tyr Arg Thr Trp H e Phe Val Leu Leu Tyr GIY Tyr Cys Met
100 105 H O
GIY Val GIU Leu Thr Thr Asp Asn Val H e Ala GIU Tyr Met Tyr Asp
115 120 125
Arg Phe Asp Leu Asp Leu Arg Val Ala GIY Thr H e Ala Ala Cys Phe
130 135 140
GIY Met Ala Asn H e Val Ala Arg Pro Met GIY GIY H e Met Ser Asp
145 150 155 160
Met GIY Ala Arg Tyr Trp GIY Met Arg Ala Arg Leu Trp Asn H e Trp
165 170 L 7 5
H e Leu Gln Thr Ala GIY GIY Ala Phe Cys Leu Trp Leu GIY Arg Ala
180 185 190
Ser Thr Leu Pro Val Ser Val Val Ala Met Val Leu Phe Ser Phe Cys
195 200 205
Ala Gln Ala Ala Cys GIY Ala H e Phe GIY Val H e Pro Phe Val Ser
210 215 220
Arg Arg Ser Leu GIY H e H e Ser GIY Met Thr GIY Ala GIY GIY Asn
225 230 235 240
Phe GIY Ala GIY Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser Thr Tyr
245 250 255
Ser Thr GIY Arg GIY Leu GIU Tyr Met GIY H e Met H e Met Ala Cys
260 265 270
Thr Leu Pro Val Val Phe Val His Phe Pro Gln Trp GIY Ser Met Phe
275 280 285
Phe Pro Pro Ser Ala Thr Ala Asp GIU GIU GIY Tyr Tyr Ala Ser GIU
290 295 300
Trp Asn Asp Asp GIU Lys Ser Lys GIY Leu Hrs Ser Ala Ser Leu Lys
305 310 315 320
Phe Ala GIU Asn Ser Arg Ser GIU Arg GIY Lys Arg Asn Val H e Gln
325 330 335
Ala Asp Ala Ala Ala Thr Pro GIU His Val

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PF57967.ST25.txt

340

345

<210> 125
 <211> 1965
 <212> DNA
 <213> Oryza sativa

<400> 125
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 ttactttgta agaaagtaga gccatggact cctcatacca gcatgacaag cctctgctgg 180
 atgaagagaa ctccctcgaa gtgacccttg aatatacagg tgatggatct gtttgcattc 240
 gtgggcatcc tgctttaagg aaacatacag ggaactggaa gggttcctca ttagccatcg 300
 ttttttcatt ctgctcttat ctggccttta cttcaattgt aaaaaaccta gtcagttatc 360
 tcacaaaagt tctacatgaa acaaacgtgg ccgctgcaag agatgttgca acttggtcag 420
 gaacaagtta tcttgacact ctggttggag ccttcttagc tgattcatat ctggggaagt 480
 actgtacaat tctgatcttc tgcacgatct tcattatcgg attgatgatg ttgcttctgt 540
 cagcagcagt tccattaatc tctactggtc ctactcatg gatcatatgg acagatccag 600
 tctcttctca gaacatcata ttctttgtcg gtttgtacat ggttgcttta ggggatgggtg 660
 cacagtggcc ctgcatatca tcatttgggt ctgatcaatt tgatgacact gatgaaaatg 720
 agagaacaaa aaagagttct tttttcaatt ggacctattt cgtagccaat gcgggctcat 780
 tgatctcggg gactgttatt gtgtgggtgc aagatcacia aggttggatc tggggtttta 840
 ccatttctgc actatttgtg tatttaggtt ttgggtacttt tatctttggc tcctctatgt 900
 atgatttcag aaacctggag gaagcccctc ttgcgagaat atgccagggt gttgttgctg 960
 ctattcacia acgcgataaa gatttgccat gtgattcctc agttctttat gagtttctgg 1020
 ggcagagttc agcaatcgaa ggcagccgaa aattggagca tacaactgga cttaaagtct 1080
 ttgatagagc tgcaatggtg acaccatctg attttgaatc tgatggccta ctaaacacat 1140
 ggaagatttg cacagtcact caagtggagg aactgaagat ttgatcagg atgttccccg 1200
 tttgggcaac gatgatatta ttgtctgcag ttctggacaa catgttttcg acattcatag 1260
 aacaggggat ggtgatggag aaacacatcg gctctttcga aatacctgcg gcgtccttcc 1320
 aatccattga tgtcattgct gtcccttatac tagttccagt ctatgaaaga gtccttggtc 1380
 cagtgttcag aaaattcact ggcagagcaa atggcattac tccactgcag cgaatgggga 1440
 tcggcctgtt cttttccatg ctctccatgg tatcagcagc attggtggag agtaatcggg 1500
 tgccgattgc gcaggatgaa ggtttggtgc acaggaaggt ggctgttcca atgagcatcc 1560
 tgtggcaggg accccagtac ttctgatag gcgtgggaga ggtgttctca aacattgggt 1620
 taactgaatt tttctaccag gaatcaccgg acgccatgag aagcttatgt ctcgcattct 1680
 cacttgctaa cgtttcggca ggaagttacc tcagctcgtt tatcgtttct cttgtgccag 1740
 gtgtcacagc cagagaaggc agtcctggat ggatacctga taactgaac gaagggcatt 1800
 tggatcggtt cttctggatg atggctggct tgtgtttctt gaatatgctg gcctttgtgt 1860
 tctgtgccat gaggtacaaa tgtaagaagg ctctctgaac cttgttaaca ttagcaatat 1920
 aatggtggtg gaaaaggaca attgtgttgc aaaaaaaaaa aaaaaa 1965

<210> 126
 <211> 584
 <212> PRT
 <213> Oryza sativa

<400> 126
 Met Asp Ser Ser Tyr Gln His Asp Lys Pro Leu Leu Asp Glu Glu Asn
 1 5 10 15
 Ser Ser Gln Val Thr Leu Glu Tyr Thr Gly Asp Gly Ser Val Cys lie
 20 25 30
 Arg Gly His Pro Ala Leu Arg Lys His Thr Gly Asn Trp Lys Gly Ser
 35 40 45

PF57967 .ST25 .txt

```

Ser  Leu  Ala  lie  VaI  Phe  Ser  Phe  Cys  Ser  Tyr  Leu  Ala  Phe  Thr  Ser
50      55      60
lie  VaI  Lys  Asn  Leu  VaI  Ser  Tyr  Leu  Thr  Lys  VaI  Leu  His  GIu  Thr
65      70      75      80
Asn  VaI  Ala  Ala  Ala  Arg  Asp  VaI  Ala  Thr  Trp  Ser  GIy  Thr  Ser  Tyr
85      90      95
Leu  Ala  Pro  Leu  VaI  GIy  Ala  Phe  Leu  Ala  Asp  Ser  Tyr  Leu  GIy  Lys
100     105     110
Tyr  Cys  Thr  lie  Leu  lie  Phe  Cys  Thr  lie  Phe  lie  lie  GIy  Leu  Met
115     120     125
Met  Leu  Leu  Leu  Ser  Ala  Ala  VaI  Pro  Leu  lie  Ser  Thr  GIy  Pro  Hrs
130     135     140
Ser  Trp  lie  lie  Trp  Thr  Asp  Pro  VaI  Ser  Ser  GIn  Asn  lie  lie  Phe
145     150     155     160
Phe  VaI  GIy  Leu  Tyr  Met  VaI  Ala  Leu  GIy  Tyr  GIy  Ala  GIn  Cys  Pro
165     170     175
Cys  lie  Ser  Ser  Phe  GIy  Ala  Asp  GIn  Phe  Asp  Asp  Thr  Asp  GIu  Asn
180     185     190
GIu  Arg  Thr  Lys  Lys  Ser  Ser  Phe  Phe  Asn  Trp  Thr  Tyr  Phe  VaI  Ala
195     200     205
Asn  Ala  GIy  Ser  Leu  H e  Ser  GIy  Thr  VaI  H e  VaI  Trp  VaI  GIn  Asp
210     215     220
His  Lys  GIy  Trp  H e  Trp  GIy  Phe  Thr  H e  Ser  Ala  Leu  Phe  VaI  Tyr
225     230     235     240
Leu  GIy  Phe  GIy  Thr  Phe  H e  Phe  GIy  Ser  Ser  Met  Tyr  Asp  Phe  Arg
245     250     255
Asn  Leu  GIu  GIu  Ala  Pro  Leu  Ala  Arg  H e  Cys  GIn  VaI  VaI  VaI  Ala
260     265     270
Ala  H e  His  Lys  Arg  Asp  Lys  Asp  Leu  Pro  Cys  Asp  Ser  Ser  VaI  Leu
275     280     285
Tyr  GIu  Phe  Leu  GIy  GIn  Ser  Ser  Ala  H e  GIu  GIy  Ser  Arg  Lys  Leu
290     295     300
GIu  His  Thr  Thr  GIy  Leu  Lys  Phe  Phe  Asp  Arg  Ala  Ala  Met  VaI  Thr
305     310     315     320
Pro  Ser  Asp  Phe  GIu  Ser  Asp  GIy  Leu  Leu  Asn  Thr  Trp  Lys  H e  Cys
325     330     335
Thr  VaI  Thr  GIn  VaI  GIu  GIu  Leu  Lys  H e  Leu  H e  Arg  Met  Phe  Pro
340     345     350
VaI  Trp  Ala  Thr  Met  H e  Leu  Phe  Ala  Ala  VaI  Leu  Asp  Asn  Met  Phe
355     360     365
Ser  Thr  Phe  H e  GIu  GIn  GIy  Met  VaI  Met  GIu  Lys  His  H e  GIy  Ser
370     375     380
Phe  GIu  H e  Pro  Ala  Ala  Ser  Phe  GIn  Ser  H e  Asp  VaI  H e  Ala  VaI
385     390     395     400
Leu  H e  Leu  VaI  Pro  VaI  Tyr  GIu  Arg  VaI  Leu  VaI  Pro  VaI  Phe  Arg
405     410     415
Lys  Phe  Thr  GIy  Arg  Ala  Asn  GIy  H e  Thr  Pro  Leu  GIn  Arg  Met  GIy
420     425     430
H e  GIy  Leu  Phe  Phe  Ser  Met  Leu  Ser  Met  VaI  Ser  Ala  Ala  Leu  VaI
435     440     445
GIu  Ser  Asn  Arg  Leu  Arg  H e  Ala  GIn  Asp  GIu  GIy  Leu  VaI  His  Arg
450     455     460
Lys  VaI  Ala  VaI  Pro  Met  Ser  H e  Leu  Trp  GIn  GIy  Pro  GIn  Tyr  Phe
465     470     475     480

```

PF57967.ST25.txt

Leu H e GIY VaI GIU GIU VaI Phe Ser Asn H e GIY Leu Thr GIU Phe
 485 490 495
 Phe Tyr GIn GIU Ser Pro Asp Ala Met Arg Ser Leu Cys Leu Ala Phe
 500 505 510
 Ser Leu Ala Asn VaI Ser Ala GIY Ser Tyr Leu Ser Ser Phe lie VaI
 515 520 525
 Ser Leu VaI Pro VaI Phe Thr Ala Arg GIU GIY Ser Pro GIY Trp H e
 530 535 540
 Pro Asp Asn Leu Asn GIU GIY His Leu Asp Arg Phe Phe Trp Met Met
 545 550 555 560
 Ala GIY Leu Cys Phe Leu Asn Met Leu Ala Phe VaI Phe Cys Ala Met
 565 570 575
 Arg Tyr Lys Cys Lys Lys Ala Ser
 580

<210> 127

<211> 405

<212> DNA

<213> Arabidopsis thaliana

<400> 127

tcatactcac	agaacagaaa	ccctaatttc	ctcaaagcaa	tctcgtttca	tcttccgcaa	60
acgaaaccct	cgagagttgt	tactcctcct	cctcctctgg	tgcatgataa	agcggcctca	120
gggtttgctg	cggcgctcgt	tagcgtttgt	caatcgaaga	attgtcttgg	tcggactcaa	180
gaagatgtca	gaagattgat	ggagtttctt	gtgggagaag	aaaagaagag	gaacaagggtc	240
ttagtcaatg	atgttggtga	gagaggtaaa	tttggtaaac	acttcaaggg	cttgggtcaag	300
atgttgattg	caagaggtaa	atctgggatt	ctggtggatg	ttttaatgga	atttgagaga	360
atctgtaatg	aattgggtctc	aaaaaaactt	gtctgggttt	cttga		405

<210> 128

<211> 135

<212> PRT

<213> Arabidopsis thaliana

<400> 128

Ala Ser Tyr Ser GIn Asn Arg Asn Pro Asn Phe Leu Lys Ala H e Ser
 1 5 10 15
 Phe His Leu Pro GIn Thr Lys Pro Ser Arg VaI VaI Thr Pro Pro
 20 25 30
 Pro Leu VaI His Asp Lys Ala Ala Ser GIY Phe Ala Ala Ala Leu VaI
 35 40 45
 Ser VaI Cys GIn Ser Lys Asn Cys Leu GIY Arg Thr GIn GIU Asp VaI
 50 55 60
 Arg Arg Leu Met GIU Phe Leu VaI GIY GIU GIU Lys Lys Arg Asn Lys
 65 70 75 80
 VaI Leu VaI Asn Asp VaI VaI GIU Arg GIY Lys Phe GIY Lys His Phe
 85 90 95
 Lys GIY Leu VaI Lys Met Leu H e Ala Arg GIY Lys Ser GIY H e Leu
 100 105 110
 VaI Asp VaI Leu Met GIU Phe GIU Arg H e Cys Asn GIU Leu VaI Ser
 115 120 125
 Lys Lys Leu VaI Trp VaI Ser
 130 135

PF57967 .ST25 .txt

<210> 129
 <211> 576
 <212> DNA
 <213> Arabidopsis thaliana

<400> 129
 atggatactc tctcagcatc cgtttcatcc ttgaacctcc cttctcttcc tccaccaccg 60
 cagccaccgt tgagatccat ctccagccgc tttaaatcca ccgtaaacgc caccacttct 120
 gcttcatcta ccaatctttc aaaaccaaca tcgtcttcac cttcttcagc atcataactca 180
 cagaacagaa accctaattt cctcaaagca atctcgtttc atcttccgca aacgaaaccc 240
 tcgagagttg ttactcctcc tcctcctctg gtgcatgata aagcggcctc agggtttgct 300
 gcggcgctcg ttagcgtttg tcaatcgaag aattgtcttg gtcggactca agaagatgtc 360
 agaagattga tggagtttct tgtgggagaa gaaaagaaga ggaacaaggc cttagtcaat 420
 gatgttggtg agagaggtaa atttggtaaa cacttcaagg gcttgggtcaa gatgttgatt 480
 gcaagaggta aatctgggat tctggtggat gttttaatgg aatttgagag aatctgtaat 540
 gaattggtct caaaaaaact tgtctggggt tcttga 576

<210> 130
 <211> 191
 <212> PRT
 <213> Arabidopsis thaliana

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

<210> 131
 <211> 57
 <212> PRT
 <213> Arabidopsis thaliana

<400> 131

PF57967 .ST25 .txt

```

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

```

```

<210> 132
<211> 32
<212> PRT
<213> Chlamydomonas

```

```

<400> 132
Met Ala Met Ala Met Arg Ser Thr Phe Ala Ala Arg Val GIY Ala Lys
1      5      10      15
Pro Ala Val Arg GIY Ala Arg Pro Ala Ser Arg Met Ser Cys Met Ala
      20      25      30

```

```

<210> 133
<211> 32
<212> PRT
<213> Chlamydomonas

```

```

<400> 133
Met Gln Val Thr Met Lys Ser Ser Ala Val Ser GIY Gln Arg Val GIY
1      5      10      15
GIY Ala Arg Val Ala Thr Arg Ser Val Arg Arg Ala Gln Leu Gln Val
      20      25      30

```

```

<210> 134
<211> 52
<212> PRT
<213> Arabidopsis thaliana

```

```

<400> 134
Met Ala Ser Leu Met Leu Ser Leu GIY Ser Thr Ser Leu Leu Pro Arg
1      5      10      15
Glu lie Asn Lys Asp Lys Leu Lys Leu GIY Thr Ser Ala Ser Asn Pro
      20      25      30
Phe Leu Lys Ala Lys Ser Phe Ser Arg Val Thr Met Thr Val Ala Val
      35      40      45
Lys Pro Ser Arg
      50

```

```

<210> 135
<211> 54
<212> PRT
<213> Arabidopsis thaliana

```

```

<400> 135
Met Ala Thr Gln Phe Ser Ala Ser Val Ser Leu Gln Thr Ser Cys Leu
1      5      10      15

```

PF57967.ST25.txt

Ala Thr Thr Arg lie Ser Phe GIn Lys Pro Ala Leu lie Ser Asn His
 20 25 30
 GIy Lys Thr Asn Leu Ser Phe Asn Leu Arg Arg Ser lie Pro Ser Arg
 35 40 45
 Arg Leu Ser VaI Ser Cys
 50

<210> 136

<211> 70

<212> PRT

<213> Arabidopsis thaliana

<400> 136

Met Ala Ser lie Ala Ala Ser Ala Ser lie Ser Leu GIn Ala Arg Pro
 1 5 10 15
 Arg GIn Leu Ala lie Ala Ala Ser GIn VaI Lys Ser Phe Ser Asn GIy
 20 25 30
 Arg Arg Ser Ser Leu Ser Phe Asn Leu Arg GIn Leu Pro Thr Arg Leu
 35 40 45
 Thr VaI Ser Cys Ala Ala Lys Pro GIu Thr VaI Asp Lys VaI Cys Ala
 50 55 60
 VaI VaI Arg Lys GIn Leu
 65 70

<210> 137

<211> 74

<212> PRT

<213> Arabidopsis thaliana

<400> 137

Met Ala Ser lie Ala Thr Ser Ala Ser Thr Ser Leu GIn Ala Arg Pro
 1 5 10 15
 Arg GIn Leu VaI lie GIy Ala Lys GIn VaI Lys Ser Phe Ser Tyr GIy
 20 25 30
 Ser Arg Ser Asn Leu Ser Phe Asn Leu Arg GIn Leu Pro Thr Arg Leu
 35 40 45
 Thr VaI Tyr Cys Ala Ala Lys Pro GIu Thr VaI Asp Lys VaI Cys Ala
 50 55 60
 VaI VaI Arg Lys GIn Leu Ser Leu Lys GIu
 65 70

<210> 138

<211> 51

<212> PRT

<213> Arabidopsis thaliana

<400> 138

Met Ala Ser Ser Ala Ala Ala lie VaI Ser GIy Ser Pro Phe Arg Ser
 1 5 10 15
 Ser Pro Leu lie His Asn His His Ala Ser Arg Tyr Ala Pro GIy Ser
 20 25 30
 lie Ser VaI VaI Ser Leu Pro Arg GIn VaI Ser Arg Arg GIy Leu Ser
 35 40 45
 VaI Lys Ser

PF57967 .ST25 .txt

50

<210> 139

<211> 100

<212> PRT

<213> Brassica napus

<400> 139

```

Met Ala Thr Ala Asn Ala Leu Ser Ser Pro Ser Val Leu Cys Ser Ser
1      5      10      15
Arg Gln GIY Lys Leu Ser GIY GIY Ser Gln Gln Lys GIY Gln Arg Val
20      25      30
Ser Tyr Arg Lys Ala Asn Arg Arg Phe Ser Leu Arg Ala Asn Val Lys
35      40      45
GIU lie Ala Phe Asp Gln Ser Ser Arg Ala Ala Leu Gln Ala GIY lie
50      55      60
Asp Lys Leu Ala Asp Ala Val GIY Leu Thr Leu GIY Pro Arg GIY Arg
65      70      75      80
Asn Val Val Leu Asp GIU Phe GIY Ser Pro Lys Val Val Asn Asp GIY
85      90      95
Val Thr H e Ala
100

```

<210> 140

<211> 100

<212> PRT

<213> Hordeum vulgare

<400> 140

```

Met Ala Pro Thr Val Met Ala Ser Ser Ala Thr Ser Val Ala Pro Phe
1      5      10      15
Gln GIY Leu Lys Ser Thr Ala GIY Leu Pro Val Ser Arg Arg Ser Asn
20      25      30
Ala Ser Ser Ala Ser Val Ser Asn GIY GIY Arg H e Arg Cys Met Gln
35      40      45
Val Trp Pro H e GIU GIY H e Lys Lys Phe GIU Thr Leu Ser Tyr Leu
50      55      60
Pro Pro Leu Ser Thr GIU Ala Leu Leu Lys Gln Val Asp Tyr Leu H e
65      70      75      80
Arg Ser Lys Trp Val Pro Cys Leu GIU Phe Ser Lys Val GIY Phe H e
85      90      95
Phe Arg GIU His
100

```

<210> 141

<211> 100

<212> PRT

<213> Medicago truncatula

<400> 141

```

Met Thr Thr H e Phe Arg Leu Ala Ser Ser Ser Ser Pro Ser Leu Arg
1      5      10      15
His Asp Ala Thr Pro His Asn Phe His H e Arg Lys Thr Ser H e Ser
20      25      30

```

PF57967.ST25.txt

Asn Thr Phe Ser Phe Ser Ser Lys Asn Ser Leu Ser Phe Lys Arg lie
 35 40 45
 Leu Thr Ser GIY GIY Ser Arg Arg Phe lie VaI Ala Ala Ser Pro Pro
 50 55 60
 Thr GIU Asp Ala VaI VaI Ala Thr GIU Pro Leu Thr Lys GIn Asp Leu
 65 70 75 80
 lie Asp Tyr Leu Ala Ser GIY Cys Lys Thr Lys Asp Lys Trp Arg lie
 85 90 95
 GIY Thr GIU His
 100

<210> 142
 <211> 100
 <212> PRT
 <213> Spinacia oleracea

<400> 142
 Met GIU Thr Ser Met Ala Cys Cys Ser Arg Ser lie VaI Leu Pro Arg
 1 5 10 15
 VaI Ser Pro GIn His Ser Ser Ala Leu VaI Pro Ser Ser lie Asn Leu
 20 25 30
 Lys Ser Leu Lys Ser Ser Ser Leu Phe GIY GIU Ser Leu Arg Met Thr
 35 40 45
 Thr Lys Ser Ser VaI Arg VaI Asn Lys Ala Lys Asn Ser Ser Leu VaI
 50 55 60
 Thr Lys Cys GIU Leu GIY Asp Ser Leu GIU GIU Phe Leu Ala Lys Ala
 65 70 75 80
 Thr Thr Asp Lys GIY Leu lie Arg Leu Met Met Cys Met GIY GIU Ala
 85 90 95
 Leu Arg Thr lie
 100

<210> 143
 <211> 1236
 <212> DNA
 <213> Oryza sativa

<400> 143
 ggtcagccaa tacattgatc cgttgccaat catgcaaagt attttggctg tggccgagtg 60
 ccggaattga taattgtgtt ctgactaaat taaatgacca gaagtcgcta tcttccaatg 120
 tatccgaaac ctggattaaa caatcctgtt ctgttctcta gccctcctg catggccgga 180
 ttgttttttt gacatgtttt cttgactgag gcctgtttgt tctaaacttt ttcttcaaac 240
 ttttaacttt ttcacacat cagaactttt ctacacatat aaacttttaa cttttccgtc 300
 acatcgttcc aatttcaatc aaactttcaa ttttggcgtg aactaaacac accctgagtc 360
 ttttattgct cctccgtacg ggttggctgg ttgagaatag gtattttcag agagaaaatc 420
 tagatattgg gaggaacttg gcatgaatgg ccactatatt tagagcaatt ctacggtcct 480
 tgaggaggta ccatgaggta ccaaaatttt agtgtaaatt ttagtatctc attataacta 540
 ggtattatga ggtaccaaatt ttacaataga aaaaatagta cttcatggta ctttcttaag 600
 taccgtataaa ttgctcctat atttaagggg atgtttatat ctatccatat ccataatttg 660
 attttgataa gaaaaaatgt gagcacacca agcatgtcca tgaccttgca ctcttggctc 720
 actcgtcaac tgtgaagaac ctcaaaaatg ctcaatatag ctacagggtc ctgaaaaaat 780
 aacttttaag ttttgaacat cgatttcact aaacaacaat tattatctcc ctctgaaaga 840
 tgatagttta gaactctaga atcattgtcg gcggagaaag taaattatct tccccaat 900
 tccagctatg aaaaaaccct caccaaacac catcaaacaa gagttcacca aaccgcccatt 960

PF57967.ST25.txt

gcggccatgc	tgtcacgcaa	cgcaccgcat	tgctgatgg	ccgctcgatg	catgcatgct	1020
tccccgtgca	catatccgac	agacgcgccg	tgtcagcgag	ctcctcgacc	gacctgtgta	1080
gcccatgcaa	gcatccaccc	ccgccacgta	caccccctcc	tcctccctac	gtgtcaccgc	1140
tctctccacc	tatatatgcc	cacctggccc	ctctcctccc	atctccactt	caccgatcg	1200
cttcttcttc	ttcttcgttg	cattcatctt	gctagc			1236

<210> 144
 <211> 55
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm00735

<400> 144						
ggggacaagt	ttgtacaaaa	aagcaggctt	cacaatggat	actctctcag	catcc	55

<210> 145
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm00736

<400> 145						
ggggaccact	ttgtacaaga	aagctgggtt	gtatcatcaa	gaaacccaga		50

<210> 146
 <211> 1592
 <212> DNA
 <213> Oryza sativa

<400> 146						
caaaagcaag	aggaggaggc	cgcggctagc	gagcgcgca	gagagagggg	agaagaagag	60
gtgggacagc	cgggagatcc	atccctgtgg	agaggaggga	gggagggaag	aggcgttgga	120
ggaggagagg	ttgaccgata	gatccattgc	ggagttgagt	gttgatgcaa	agctgattcg	180
ccatcgttta	gctttttata	agagatgggt	tcagtagggg	ttgcgccgtc	tgggttaaag	240
aacagcagta	gcaccagcat	gggtgctgag	aagttgcctg	atcagatgca	tgatctgaag	300
ataagggacg	ataaggaagt	tgaagcgact	attattaacg	gcaagggaac	agaaaccggc	360
cacataattg	tcacaactac	tggtggcaga	aatggtcagc	cgaaacagac	agttagctac	420
atggctgagc	gtattgtagg	gcaaggttca	tttgggattg	tcttccaggc	aaaatgtctg	480
gagacaggtg	agacagttgc	tatcaagaag	gttcttcagg	ataagcgcta	caagaaccgt	540
gagcttcaga	ccatgcgcct	tcttgaccac	ccaaatgttg	tagctctgaa	gcactgtttc	600
ttctctacaa	ctgagaagga	tgaactgtat	ctaaacttgg	ttcttgagta	tgtgcctgaa	660
actgttcatc	gtgttgtaaa	gcattacaac	aagatgaacc	agcgtatgcc	acttatctat	720
gtgaagctgt	atatgtacca	gatttgtagg	gcattagctt	acatccataa	tagcatcgga	780
gtttgccaca	gagatatcaa	gccacagaat	cttctggtaa	acccacatac	ccatcaactc	840
aagctatgtg	actttgggag	tgcaaaaagt	ctgggtcaagg	gagaaccgaa	catatcgta	900
atttgcctcc	gatactatag	ggctccggag	ctcatatttg	gtgccaccga	atacactaca	960
gctattgaca	tctggtctgc	tggtatgtgt	cttgctgaac	ttatgttagg	gcagcctctg	1020
tttctgtgtg	aaagtgtgtg	agaccaactt	gtggaaatca	tcaaggtcct	tggaacacct	1080
acaagggagg	aaattaaatg	catgaatcca	aactataccg	agttcaagtt	tccacagatt	1140
aaagcacacc	catggcacia	ggtattccat	aaaagggttg	ctccagaagc	tgttgatctt	1200

PF57967.ST25.txt

```

gtctctaggc  tgctccagta  ctcacccaac  ctaagatgca  ctgctgtgga  agcacttggt  1260
caccattctt  ttgatgagct  tcgagaccct  aatgctcgcc  ttccgaatgg  ccgctttttg  1320
cctcctctct  tcaacttcaa  gcctcatgaa  ctgaaaggaa  tcccatcaga  tattatggcg  1380
aaattgatcc  cagaacatgt  gaagaagcaa  tgctcctatg  caggagtatg  agacagcttc  1440
cgcacgaccc  ccctggaaat  ttccatgaca  agtgcccatt  tcctccccc  tggacgacga  1500
tggatcgcca  gcatatgcgt  gcatgatggt  tggtgaggat  gtgaagttac  gttgttggtg  1560
tgtgaccacc  tagagcttga  acagaaggaa  aa

```

<210> 147
 <211> 408
 <212> PRT
 <213> Oryza sativa

```

<400> 147
Met GIY Ser Val GIY Val Ala Pro Ser GIY Leu Lys Asn Ser Ser Ser
1      5      10      15
Thr Ser Met GIY Ala GIU Lys Leu Pro Asp GIn Met His Asp Leu Lys
20      25      30
lie Arg Asp Asp Lys GIU Val GIU Ala Thr lie H e Asn GIY Lys GIY
35      40      45
Thr GIU Thr GIY His H e H e Val Thr Thr Thr GIY GIY Arg Asn GIY
50      55      60
GIn Pro Lys GIn Thr Val Ser Tyr Met Ala GIU Arg H e Val GIY GIn
65      70      75      80
GIY Ser Phe GIY lie Val Phe GIn Ala Lys Cys Leu GIU Thr GIY GIU
85      90      95
Thr Val Ala H e Lys Lys Val Leu GIn Asp Lys Arg Tyr Lys Asn Arg
100      105      H O
GIU Leu GIn Thr Met Arg Leu Leu Asp Hxs Pro Asn Val Val Ala Leu
115      120      125
Lys His Cys Phe Phe Ser Thr Thr GIU Lys Asp GIU Leu Tyr Leu Asn
130      135      140
Leu Val Leu GIU Tyr Val Pro GIU Thr Val His Arg Val Val Lys His
145      150      155      160
Tyr Asn Lys Met Asn GIn Arg Met Pro Leu H e Tyr Val Lys Leu Tyr
165      170      175
Met Tyr GIn H e Cys Arg Ala Leu Ala Tyr H e His Asn Ser H e GIY
180      185      190
Val Cys His Arg Asp H e Lys Pro GIn Asn Leu Leu Val Asn Pro His
195      200      205
Thr His GIn Leu Lys Leu Cys Asp Phe GIY Ser Ala Lys Val Leu Val
210      215      220
Lys GIY GIU Pro Asn H e Ser Tyr H e Cys Ser Arg Tyr Tyr Arg Ala
225      230      235      240
Pro GIU Leu H e Phe GIY Ala Thr GIU Tyr Thr Thr Ala H e Asp H e
245      250      255
Trp Ser Ala GIY Cys Val Leu Ala GIU Leu Met Leu GIY GIn Pro Leu
260      265      270
Phe Pro GIY GIU Ser GIY Val Asp GIn Leu Val GIU H e H e Lys Val
275      280      285
Leu GIY Thr Pro Thr Arg GIU GIU H e Lys Cys Met Asn Pro Asn Tyr
290      295      300
Thr GIU Phe Lys Phe Pro GIn H e Lys Ala His Pro Trp His Lys Val
305      310      315      320

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<210> 149
<211> 411
<212> PRT
<213> Oryza sativa
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PF57967 .ST25 .txt

<-400> 149

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Met Ala Ser Val GIY Val Val Arg Ser Ser Leu GIY Phe GIn Asn GIU
1      5      10      15
Thr Ser Thr Ser GIY Asp Ala Asp Arg Leu Pro Asn GIU Met Ser Asn
      20      25      30
Met Ser lie Arg Asp Asp Asn Lys Asp lie Asp Asp lie Val Val Asn
      35      40      45
GIY Asn GIY Thr GIU Pro GIY His Val H e Val Thr Ser H e Asp GIY
      50      55      60
Arg Asn GIY GIn Ala Lys GIn Thr lie Ser Tyr Met Ala GIU Arg Val
65      70      75      80
Val GIY His GIY Ser Phe GIY Thr Val Phe GIn Ala Lys Cys Leu GIU
      85      90      95
Thr GIY GIU Thr Val Ala H e Lys Lys Val Leu GIn Asp Lys Arg Tyr
      100      105      H O
Lys Asn Arg GIU Leu GIn Thr Met Arg Val Leu Asp His Pro Asn Val
      115      120      125
Val Ser Leu Lys His Cys Phe Phe Ser Lys Thr GIU Lys GIU GIU Leu
      130      135      140
Tyr Leu Asn Leu Val Leu GIU Tyr Val Pro GIU Thr Ala His Arg Val
145      150      155      160
H e Lys His Tyr Asn Lys Met Asn GIn Arg Met Pro Leu H e Tyr Ala
      165      170      175
Lys Leu Tyr Met Tyr GIn H e Cys Arg Ala Leu Ala Tyr H e His Asn
      180      185      190
Thr H e GIY Val Cys His Arg Asp H e Lys Pro GIn Asn Leu Leu Val
      195      200      205
Asn Pro His Thr His GIn Leu Lys Leu Cys Asp Phe GIY Ser Ala Lys
      210      215      220
Val Leu Val Lys GIY GIU Pro Asn H e Ser Tyr H e Cys Ser Arg Tyr
225      230      235      240
Tyr Arg Ala Pro GIU Leu H e Phe GIY Ala Thr GIU Tyr Thr Thr Ala
      245      250      255
H e Asp Val Trp Ser Ala GIY Cys Val Leu Ala GIU Leu Leu Leu GIY
      260      265      270
GIn Pro Leu Phe Pro GIY Asp Ser GIY Val Asp GIn Leu Val GIU H e
      275      280      285
H e Lys Val Leu GIY Thr Pro Thr Arg GIU GIU H e Lys Cys Met Asn
      290      295      300
Pro Asn Tyr Thr GIU Phe Lys Phe Pro GIn H e Lys Ala His Pro Trp
305      310      315      320
His Lys H e Phe His Lys Arg Met Pro Ala GIU Ala Val Asp Leu Val
      325      330      335
Ser Arg Leu Leu GIn Tyr Ser Pro Tyr Leu Arg Ser Thr Ala Ser GIU
      340      345      350
Ala Leu H e His Pro Phe Phe Asp GIU Leu Arg Asp Pro Asn Thr Arg
      355      360      365
Leu Pro Asn GIY Arg Phe Leu Pro Pro Leu Phe Asn Phe Lys Pro His
      370      375      380
GIU Leu Lys GIY Met Pro Met GIU Phe Leu Val Lys Leu H e Pro GIU
385      390      395      400
His Ala Arg Lys GIn Cys Ala Phe Val GIY Trp
      405      410

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PF57967.ST25.txt

<210> 150
 <211> 2261
 <212> DNA
 <213> Oryza sativa

<400> 150
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 cctcctcctc cccccgcgcc gatcttgccc cgctccctcg ccgcagctgc gggcttgccc 180
 tagcccgccg catcgccgac gtactacgcc cgctcggctc caggctccag atccggcctc 240
 cagggcggtgc ccgctgctgg acggcgctct cccgcgtccg tggctacctc ctccctcggg 300
 tttgcgttgc cgtcgccgaa gcgatccggt ggtggattgt gtgtagctct gtaacaaagg 360
 atcttggtcc ataggagtga accagaaggt acaaaacttc ttggctatta tgacatcggg 420
 gggcttagta gattcttcat cagggtttccc ggaaacgagt actagtggag ccactgatcg 480
 tctgacagat gatatcagcg agatgagcat aagagataag gaagttgaag ctgtagtggg 540
 cagtggcaat agtatggaca taggtcacac tattgtgaca actgttgggt gaagaaatgg 600
 gcagccaaag cagacaatta gttacatcgc agagcgtgct gttgggcgtg gttcatttgg 660
 agttgtcttc caggctaagt gtctagaaac tggtgagaga gttgctgtaa agaaagtctt 720
 tcaagatgcg agatacaaga accgggagct gcaaacgatg caagttctcg atcaccctcaa 780
 tgttgcatgc ttgaagcatt acttttgctc gactactgcy aaggaggagc tatacctcaa 840
 cttggttctt gaatatgtgc cagaaactgt tcatcgtggt attagacatt acaataagat 900
 gagccaacgc atgccattga tttatgttaa actttatatg taccagattt gtagggcttt 960
 ggcatacatt cataactgtg tgggagtatg ccacagagat ataaagccac agaatatatt 1020
 ggtgaatcca cataatcatc agttgaaatt gtgtgacttt ggcagtgcaa aagtcctggg 1080
 gaaaggggaa ccaaatattt catatatctg tcttagatac tacagagccc cagcactcat 1140
 atttggggct acagagtaca cgacagctat tgatgtgtgg tctgctggct gtgttcttgc 1200
 tgaactactt ctagggcagc ctgtttttcc tggtgacagt ggcgtcgacc aactgtttga 1260
 aattatcaag gtactgggta ctccaacaag ggaagaaatc aaacatatga atccgaacta 1320
 cactgagttt aagttccccc aaatcaaagc tcacccatgg cacaagatct ttcataaaag 1380
 aatgccatct gaagctgtag atcttgtgtc tcggcttctg cagtactcac cacacctccg 1440
 gtgcagtgca ttggagggtg taattcatcc attcttcgat gaactacgag atccaaatgc 1500
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 aggagcatca atggaatttc ttgtgaagtt ggttccacag catgctaaga agcaatgtgc 1620
 cttcttagga ttatgagcag acagttcata cactaatcgg gtattacgtt ggtctacttg 1680
 gttccgtaga acagcatggc ctgcagattt attgaatggg ccctaatttt gttctacgtg 1740
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 gagtggttat tgattggggc ttgtatatgt gtctgccctt gacttgagaa ctttattcac 1860
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 cctctatcag gtttcaccga ccatcagatt taagtcttcc agtttgtagg gctaagccaa 1980
 aaaagttcta tgtgtgaaga gttggagaca tctggttggg tacaagctat ttgattgtat 2040
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 tgatatagtt gtgtgccact tttaaacacc taaacaactc tgttcaatgt tgaaatgttt 2160
 ggcattgtatc aacatatcac ctcatatttt cgaggttgat tttgtacacc tgatatctgt 2220
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<210> 151
 <211> 408
 <212> PRT
 <213> Oryza sativa

<400> 151
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 1 5 10 15

PF57967.ST25.txt

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

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<210> 152
 <211> 1634
 <212> DNA

PF57967.ST25.txt

<213> Arabidopsis thaliana

<400> 152

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aaccacaaaa	tccttactcg	tacggatctc	tctctcttta	atataccta	tcttctcttc	180
atcgatctga	gattttttacg	ttttcatcgg	cttgaaagtt	tgaagagttt	tgtagcctga	240
aaaatggcgt	cagtggtgat	agctccta	cctggagcaa	gagactctac	tggtgttgat	300
aaattgcctg	aagaaatgaa	tgacatgaaa	attcgtgacg	ataaagaaat	ggaagcgaca	360
gtggtagatg	gaaatggaac	agagactgga	catatcattg	tgactactat	tggtggtaga	420
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gttttacaag	ataggaggta	caagaaccgt	gagcttcaaa	ccatgaggct	acttgaccat	600
cctaattgtg	tgtctctgaa	acattgtttc	ttctcaacca	ctgaaaaaga	tgagctttac	660
ctcaatcttg	ttcttgagta	cgttccagaa	actgttcatc	gtgttatcaa	acactacaac	720
aaactgaatc	agagaatgcc	tcttatatac	gtcaaaacttt	acacttatca	gatttttaga	780
gccttatctt	acattcaccg	atgcattggt	gtgtgtcatc	gtgacataaa	acctcaaaac	840
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ttggtaaaag	gagaacccaa	catttcctac	atctgctcga	ggtattacag	agcacctgaa	960
cttatttttg	gagcaaccga	gtatacgaca	gccattgatg	tctggtctgc	aggatgtgtt	1020
ctagctgaac	tattgcttgg	acagcccttg	ttccctggtg	agagcgggtg	tgatcaactt	1080
gtagagatta	tcaaggctct	gggaacgcct	actagagaag	aaatcaagtg	catgaaccca	1140
aactacacgg	aattcaaatt	ccctcagatt	aaagctcatc	catggcacaa	gattttccac	1200
aaacgcagtc	ctccagaagc	tggtgatttg	gtctcaagac	ttcttcaata	ctctccta	1260
ctacgaagtg	ccgctctcga	cacattagtc	cacccattct	ttgatgagtt	aagagaccca	1320
aacgcacgtc	tacctaattg	acgtttcctt	ccaccgcttt	tcaacttcaa	gcctcacgag	1380
ctgaaaggtg	taccattgga	gatggtagct	aagttagtag	ctgagcatgc	aaggaagcag	1440
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ataaattacc	tctctatgta	tcaatatgtc	acaaactgat	atgcaccctt	tggtgtgtgt	1560
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caagattttt	tatc					1634

<210> 153

<211> 405

<212> PRT

<213> Arabidopsis thaliana

<400> 153

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GIy	VaI	Asp	Lys	Leu	Pro	GIu	GIu	Met	Asn	Asp	Met	Lys	H e	Arg	Asp
			20					25					30		
Asp	Lys	GIu	Met	GIu	Ala	Thr	VaI	VaI	Asp	GIy	Asn	GIy	Thr	GIu	Thr
			35				40					45			
GIy	His	lie	lie	VaI	Thr	Thr	H e	GIy	GIy	Arg	Asn	GIy	GIn	Pro	Lys
	50					55					60				
GIn	Thr	H e	Ser	Tyr	Met	Ala	GIu	Arg	VaI	VaI	GIy	His	GIy	Ser	Phe
65					70				75					80	
GIy	VaI	VaI	Phe	GIn	Ala	Lys	Cys	Leu	GIu	Thr	GIy	GIu	Thr	VaI	Ala
			85					90						95	
lie	Lys	Lys	VaI	Leu	GIn	Asp	Arg	Arg	Tyr	Lys	Asn	Arg	GIu	Leu	GIn
			100					105					H O		
Thr	Met	Arg	Leu	Leu	Asp	His	Pro	Asn	VaI	VaI	Ser	Leu	Lys	His	Cys
		115					120					125			

PF57967 .ST25 .txt

Phe Phe Ser Thr Thr GIu Lys Asp GIu Leu Tyr Leu Asn Leu Val Leu
 130 135 140
 GIu Tyr Val Pro GIu Thr Val His Arg Val lie Lys His Tyr Asn Lys
 145 150 155 160
 Leu Asn GIn Arg Met Pro Leu lie Tyr Val Lys Leu Tyr Thr Tyr GIn
 165 170 175
 lie Phe Arg Ala Leu Ser Tyr lie His Arg Cys lie GIy Val Cys His
 180 185 190
 Arg Asp lie Lys Pro GIn Asn Leu Leu Val Asn Pro His Thr His GIn
 195 200 205
 Val Lys Leu Cys Asp Phe GIy Ser Ala Lys Val Leu Val Lys GIy GIu
 210 215 220
 Pro Asn lie Ser Tyr lie Cys Ser Arg Tyr Tyr Arg Ala Pro GIu Leu
 225 230 235 240
 H e Phe GIy Ala Thr GIu Tyr Thr Thr Ala H e Asp Val Trp Ser Ala
 245 250 255
 GIy Cys Val Leu Ala GIu Leu Leu Leu GIy GIn Pro Leu Phe Pro GIy
 260 265 270
 GIu Ser GIy Val Asp GIn Leu Val GIu H e H e Lys Val Leu GIy Thr
 275 280 285
 Pro Thr Arg GIu GIu H e Lys Cys Met Asn Pro Asn Tyr Thr GIu Phe
 290 295 300
 Lys Phe Pro GIn H e Lys Ala His Pro Trp His Lys H e Phe His Lys
 305 310 315 320
 Arg Met Pro Pro GIu Ala Val Asp Leu Val Ser Arg Leu Leu GIn Tyr
 325 330 335
 Ser Pro Asn Leu Arg Ser Ala Ala Leu Asp Thr Leu Val His Pro Phe
 340 345 350
 Phe Asp GIu Leu Arg Asp Pro Asn Ala Arg Leu Pro Asn GIy Arg Phe
 355 360 365
 Leu Pro Pro Leu Phe Asn Phe Lys Pro His GIu Leu Lys GIy Val Pro
 370 375 380
 Leu GIu Met Val Ala Lys Leu Val Pro GIu His Ala Arg Lys GIn Cys
 385 390 395 400
 Pro Trp Leu GIy Leu
 405

<210> 154

<211> 1669

<212> DNA

<213> Arabidopsis thaliana

<400> 154

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tttttctctg	ggtttcccg	atttgaagag	cgtgacaaag	gaagaatctt	ttattaaaac	180
aaattcttct	gttttaatct	tgggatggcc	tcggtgggca	tagagcctag	tgccgcggtt	240
agagaatcta	ctggaaacgt	tactgatgct	gatagattac	ccgaggagat	gaaggacatg	300
aaaattcaag	atgataaaga	aatggaagct	acgattgtta	atggcaatgt	gactgagact	360
ggccatataa	tagtaactac	tataggagga	agaaatggcc	agccaaaaca	gacaatcagt	420
tacatggcgg	agcgagtgtg	tggacatggc	tcctttggtg	ttgtgtttca	ggccaaatgt	480
ttagaaacag	gagaaactgt	tgctataaag	aaagttctac	aagatcggag	gtacaagaat	540
cgtgagcttc	aaacaatgag	gctacttgac	catccaaatg	ttgtgtcttt	gaaacattgt	600
ttcttctcta	caaccgaaaa	agatgagcct	tatctcaact	tggttctgga	atacgttccg	660

PF57967.ST25.txt

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ggcgtatgtc atcgagacat caaacctcaa aacttggttg taaatccaca cactcatcaa 840
gtgaaactat gcgatTTTTg aagtgcgaaa gtattggtta aaggagagcc aaacatttca 900
tacatttgct cgaggatatta cagagcacct gagctcattt ttggagccac cgagtatact 960
acagccattg atgtctggtc tgcaggatgt gttctcgccg agcttcttct cgggcagcca 1020
ttgttcccg gtgagagcgg tgttgatcaa cttgtagaga ttataaaggt ttgggaaca 1080
ccaacaagg aagaaatcaa atgcatgaac ccgaattaca cagagttcaa atttcctcag 1140
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ttggtctcaa ggcttcttca atactctccc aatctccgtt gtgctgctct tgattcattg 1260
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<210> 155

<211> 409

<212> PRT

<213> Arabidopsis thaliana

<400> 155

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

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PF57967.ST25. txt

Ala Pro GIu Leu H e Phe GIy Ala Thr GIu Tyr Thr Thr Ala H e Asp
 245 250 255
 VaI Trp Ser Ala GIy Cys VaI Leu Ala GIu Leu Leu Leu GIy GIn Pro
 260 265 270
 Leu Phe Pro GIy GIu Ser GIy VaI Asp GIn Leu VaI GIu H e H e Lys
 275 280 285
 VaI Leu GIy Thr Pro Thr Arg GIu GIu H e Lys Cys Met Asn Pro Asn
 290 295 300
 Tyr Thr GIu Phe Lys Phe Pro GIn H e Lys Ala His Pro Trp His Lys
 305 310 315 320
 H e Phe His Lys Arg Met Pro Pro GIu Ala VaI Asp Leu VaI Ser Arg
 325 330 335
 Leu Leu GIn Tyr Ser Pro Asn Leu Arg Cys Ala Ala Leu Asp Ser Leu
 340 345 350
 VaI His Pro Phe Phe Asp GIu Leu Arg Asp Pro Asn Ala Arg Leu Pro
 355 360 365
 Asn GIy Arg Phe Leu Pro Pro Leu Phe Asn Phe Lys Pro His GIu Leu
 370 375 380
 Lys GIy VaI Pro VaI GIu Met VaI Ala Lys Leu VaI Pro GIu His Ala
 385 390 395 400
 Arg Lys GIn Cys Pro Trp Leu Ser Leu
 405

<210> 156

<211> 1496

<212> DNA

<213> Arabidopsis thaliana

<400> 156

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ctctactggt	gttgataaat	tgccctgaaga	aatgaatgac	atgaaaaattc	gtgacgataa	180
agaaatggaa	gcgacagtgg	tagatggaaa	tggaaacagag	actggacata	tcattgtgac	240
tactattggt	ggtagaaaatg	gccaaacaaa	acagacaatt	agctacatgg	ctgagcgtgt	300
tgttggtcac	ggatcttttg	gtgttggtgt	ccaagcgaaa	tgtcttgaga	caggagaaac	360
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gaggctactt	gaccatccta	atgttggtgtc	tctgaaacat	tgtttcttct	caaccactga	480
aaaagatgag	ctttacctca	atcttggtct	tgagtacgtt	ccagaaactg	ttcatcgtgt	540
tatcaaacac	tacaacaaac	tgaatcagag	aatgcctctt	atatacgtca	aactttacac	600
ttatcagatt	tttagagcct	tatcttacat	tcaccgatgc	attggtgtgt	gtcatcgtga	660
cataaaacct	caaaacttgt	tggtaaatcc	gcacactcat	caagtaaagc	tatgtgattt	720
tggaagtgca	aaagtattgg	taaaaggaga	accaaacatt	tcctacatct	gctcgaggta	780
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gtctgcagga	tgtgttctag	ctgaactatt	gcttgagacag	ccctgtgtcc	ctggtgagag	900
cgggtgtgat	caacttgtag	acattatcaa	ggtcttgga	acgcctacta	gagaagaaat	960
caagtgcacg	aacccaaact	acacggaatt	caaattccct	cagattaaag	ctcatccatg	1020
gcacaagatt	ttccacaaac	gcacgcctcc	agaagctgtt	gatttggtct	caagacttct	1080
tcaatactct	cctaactctac	gaagtgcgcg	tctcgacaca	ttagtccacc	cattctttga	1140
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acaacaaaca	cttcttataa	attacctctc	tatgtatcaa	tatgtcacaa	actgatatgc	1380
accctttgtt	tggtgtatga	gtagagaaaa	aaagagttat	tactatgggt	ggttggttca	1440
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PF57967.ST25.txt

<210> 157
 <211> 405
 <212> PRT
 <213> Arabidopsis thaliana

<400> 157
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 35 40 45
 Gly His H e H e Val Thr Thr H e Gly Gly Arg Asn Gly Gln Pro Lys
 50 55 60
 Gln Thr H e Ser Tyr Met Ala Glu Arg Val Val Gly Hxs Gly Ser Phe
 65 70 75 80
 Gly Val Val Phe Gln Ala Lys Cys Leu Glu Thr Gly Glu Thr Val Ala
 85 90 95
 H e Lys Lys Val Leu Gln Asp Arg Arg Tyr Lys Asn Arg Glu Leu Gln
 100 105 H O
 Thr Met Arg Leu Leu Asp His Pro Asn Val Val Ser Leu Lys His Cys
 115 120 125
 Phe Phe Ser Thr Thr Glu Lys Asp Glu Leu Tyr Leu Asn Leu Val Leu
 130 135 140
 Glu Tyr Val Pro Glu Thr Val His Arg Val H e Lys His Tyr Asn Lys
 145 150 155 160
 Leu Asn Gln Arg Met Pro Leu H e Tyr Val Lys Leu Tyr Thr Tyr Gln
 165 170 175
 H e Phe Arg Ala Leu Ser Tyr H e His Arg Cys H e Gly Val Cys His
 180 185 190
 Arg Asp H e Lys Pro Gln Asn Leu Leu Val Asn Pro His Thr His Gln
 195 200 205
 Val Lys Leu Cys Asp Phe Gly Ser Ala Lys Val Leu Val Lys Gly Glu
 210 215 220
 Pro Asn H e Ser Tyr H e Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu
 225 230 235 240
 H e Phe Gly Ala Thr Glu Tyr Thr Thr Ala H e Asp Val Trp Ser Ala
 245 250 255
 Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Leu Phe Pro Gly
 260 265 270
 Glu Ser Gly Val Asp Gln Leu Val His H e H e Lys Val Leu Gly Thr
 275 280 285
 Pro Thr Arg Glu Glu H e Lys Cys Met Asn Pro Asn Tyr Thr Glu Phe
 290 295 300
 Lys Phe Pro Gln H e Lys Ala His Pro Trp His Lys H e Phe His Lys
 305 310 315 320
 Arg Met Pro Pro Glu Ala Val Asp Leu Val Ser Arg Leu Leu Gln Tyr
 325 330 335
 Ser Pro Asn Leu Arg Ser Ala Ala Leu Asp Thr Leu Val His Pro Phe
 340 345 350
 Phe Asp Glu Leu Arg Asp Pro A&n Ala Arg Leu Pro Asn Gly Arg Phe
 355 360 365
 Leu Pro Pro Ala Phe His Phe Lys Pro His Glu Leu Lys Gly Val Pro

PF57967.ST25.txt

370 375 380
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<210> 158
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 <212> DNA
 <213> Arabidopsis thaliana

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 gcttctctag ttgctgcgta gacaagatgg tggagtgaag ttgcggcggg gacttttcag 180
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 tcttctatgg ctacaaaaca aagcaatgct tctatatgcg ctgaaaaatt acctgaaggg 300
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 ataatatgct tatcgtttct aagtaatgga gatagcttct caggattatc attagctttc 1560
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 <213> Arabidopsis thaliana

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 35 40 45

PF57967 .ST25 .txt

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Gly	GIn	Gly	Ser	Phe	Gly	H e	Val	Phe	GIn	Ala	Lys	Cys	Leu	Glu	Thr
				85					90					95	
Gly	Glu	Thr	Val	Ala	H e	Lys	Lys	Val	Leu	GIn	Asp	Lys	Arg	Tyr	Lys
				100				105					H O		
Asn	Arg	Glu	Leu	GIn	Thr	Met	Arg	Leu	Leu	Asp	Hrs	Pro	Asn	Val	Val
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Ser	Leu	Lys	His	Cys	Phe	Phe	Ser	Thr	Thr	Glu	Lys	Asp	Glu	Leu	Tyr
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145					150					155					160
Lys	Hrs	Tyr	Ser	Arg	Ala	Asn	GIn	Arg	Met	Pro	H e	H e	Tyr	Val	Lys
				165					170					175	
Leu	Tyr	Thr	Tyr	GIn	H e	Cys	Arg	Ala	Leu	Ala	Tyr	H e	His	Gly	Gly
				180				185					190		
Val	Gly	Val	Cys	His	Arg	Asp	H e	Lys	Pro	GIn	Asn	Leu	Leu	Val	Asn
		195					200				205				
Pro	His	Thr	His	GIn	Val	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Val
		210				215					220				
Leu	Val	Lys	Gly	Glu	Pro	Asn	H e	Ser	Tyr	H e	Cys	Ser	Arg	Tyr	Tyr
225					230					235					240
Arg	Ala	Pro	Glu	Leu	H e	Phe	Gly	Ala	Thr	Glu	Tyr	Thr	Thr	Thr	H e
				245					250					255	
Asp	H e	Trp	Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	GIn
			260					265					270		
Pro	Leu	Phe	Pro	Gly	Glu	Ser	Gly	Val	Asp	GIn	Leu	Val	Glu	H e	H e
		275					280					285			
Lys	Val	Leu	Gly	Thr	Pro	Thr	Arg	Glu	Glu	H e	Lys	Cys	Met	Asn	Pro
		290				295					300				
Asn	Tyr	Thr	Glu	Phe	Lys	Phe	Pro	GIn	H e	Lys	Ala	His	Pro	Trp	His
305					310					315					320
Lys	H e	Phe	His	Lys	Arg	Thr	Pro	Pro	Glu	Ala	Val	Asp	Leu	Val	Ser
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Arg	Leu	Leu	GIn	Tyr	Ser	Pro	Asn	Leu	Arg	Ser	Thr	Ala	Met	Glu	Ala
			340					345					350		
H e	Val	His	Pro	Phe	Phe	Asp	Glu	Leu	Arg	Asp	Pro	Asn	Thr	Arg	Leu
		355					360					365			
Pro	Asn	Gly	Arg	Ala	Leu	Pro	Pro	Leu	Phe	Asn	Phe	Lys	Pro	GIn	Glu
		370				375					380				
Leu	Lys	Gly	Ala	Ser	Leu	Glu	Leu	Leu	Ser	Lys	Leu	H e	Pro	Asp	His
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<211> 1230

<212> DNA

<213> Arabidopsis thaliana

<400> 160

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60

PF57 967 . ST25 . txt

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gcacctgagc	tcatttttgg	agccaccgag	tatactacag	ccattgatgt	ctggctctgca	780
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atgaacccga	attacacaga	gttcaaattt	cctcagatta	aagctcatcc	atggcataag	960
atTTTccaca	agagaatgcc	tccagaagct	gttgatttgg	tctcaaggct	tcttcaatac	1020
tctcccaatc	tccgttgtgc	tgctcttgat	tcattggtcc	accatttctt	tgacgagcta	1080
agagatccga	atgcgcgatt	acccaacgga	cgtttccttc	caccgctctt	taactttaag	1140
cctcatgaac	ttaaagggtgt	gcctgtggag	atgggtggcga	agttagttcc	agaacatgcg	1200
aggaagcaat	gtccgtggct	cagtttatga				1230

<210> 161

<211> 409

<212> PRT

<213> Arab₁dops_{1s} thal₁ana

<400> 161

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			20					25					30		
Lys	H e	GIn	Asp	Asp	Lys	GIu	Met	GIu	Ala	Thr	H e	VaI	Asn	GIy	Asn
			35				40					45			
VaI	Thr	GIu	Thr	GIy	His	H e	H e	VaI	Thr	Thr	H e	GIy	GIy	Arg	Asn
	50				55						60				
GIy	GIn	Pro	Lys	GIn	Thr	H e	Ser	Tyr	Met	Ala	GIu	Arg	VaI	VaI	GIy
65				70					75					80	
His	GIy	Ser	Phe	GIy	VaI	VaI	Phe	GIn	Ala	Lys	Cys	Leu	GIu	Thr	GIy
			85					90						95	
GIu	Thr	VaI	Ala	H e	Lys	Lys	VaI	Leu	GIn	Asp	Arg	Arg	Tyr	Lys	Asn
			100					105					H O		
Arg	GIu	Leu	GIn	Thr	Met	Arg	Leu	Leu	Asp	His	Pro	Asn	VaI	VaI	Ser
		115					120					125			
Leu	Lys	His	Cys	Phe	Phe	Ser	Thr	Thr	GIu	Lys	Asp	GIu	Leu	Tyr	Leu
		130				135					140				
Asn	Leu	VaI	Leu	GIu	Tyr	VaI	Pro	GIu	Thr	VaI	His	Arg	VaI	H e	Lys
145				150					155					160	
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			165						170					175	
Tyr	Thr	Tyr	GIn	H e	Phe	Arg	Ser	Leu	Ser	Tyr	H e	His	Arg	Cys	H e
			180					185					190		
GIy	VaI	Cys	His	Arg	Asp	H e	Lys	Pro	GIn	Asn	Leu	Leu	VaI	Asn	Pro
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PF57967.ST25. txt

210 215 220
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 225 230 235 240
 Ala Pro GIu Leu H e Phe GIy Ala Thr GIu Tyr Thr Thr Ala H e Asp
 245 250 255
 VaI Trp Ser Ala GIy Cys VaI Leu Ala GIu Leu Leu Leu GIy GIn Pro
 260 265 270
 Leu Phe Pro GIy GIu Ser GIy VaI Asp GIn Leu VaI GIu H e H e Lys
 275 280 285
 VaI Leu GIy Thr Pro Thr Arg GIu GIu H e Lys Cys Met Asn Pro Asn
 290 295 300
 Tyr Thr GIu Phe Lys Phe Pro GIn H e Lys Ala His Pro Trp His Lys
 305 310 315 320
 H e Phe His Lys Arg Met Pro Pro GIu Ala VaI Asp Leu VaI Ser Arg
 325 330 335
 Leu Leu GIn Tyr Ser Pro Asn Leu Arg Cys Ala Ala Leu Asp Ser Leu
 340 345 350
 VaI His Pro Phe Phe Asp GIu Leu Arg Asp Pro Asn Ala Arg Leu Pro
 355 360 365
 Asn GIy Arg Phe Leu Pro Pro Leu Phe Asn Phe Lys Pro His GIu Leu
 370 375 380
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 405

<210> 162
 <211> 1967
 <212> DNA
 <213> Zea mays

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PF57967.ST25.txt

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attcctagct acctgttgcc taaaaaaaaa aaaaaaaaaa ctcgtgc 1967

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<210> 163
 <211> 408
 <212> PRT
 <213> Zea mays

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

PF57967 .ST25 .txt

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 305 310 315 320
 Phe His Lys Arg Met Pro Pro GIu Ala VaI Asp Leu VaI Ser Arg Leu
 325 330 335
 Leu GIu Tyr Ser Pro Asn Leu Arg Cys Thr Ala Met GIu Ala Leu VaI
 340 345 350
 His Pro Phe Phe Asp GIu Leu Arg Asp Pro Asn Thr Arg Leu Pro Asn
 355 360 365
 GIy Arg Phe Leu Pro Pro Leu Phe Asn Phe Lys Pro His GIu Leu Lys
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 385 390 395 400
 Lys GIu Cys Ser Tyr VaI GIy Leu
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<210> 164
 <211> 1752
 <212> DNA
 <213> Zea mays

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 gttgaaatca tcaaggttct gggcacaccc acacgtgaag aaattaagt catgaatcca 1080
 aattataccg agtttaaatt cccgcaaatt aaagctcacc catggcataa gatattccat 1140
 aaaaggatgc ctgctgaagc ggtagatctc gtgtccaggc ttctgcagta ctcacaaaa 1200
 cttcggctga ctgctttgga agcattgggt catccgttct ttgatgaact tcgggatcca 1260
 aacacccgct taccgaatgg tcgttttctt ccgcctctct tcaattttta gccccatgag 1320
 ctgaagaacg tgccggcgga tttcatgggt aaattgggtc ctgagcatgc acggaagcaa 1380
 tgtgccttcg taggggtggg atctctggat aagaggatga cgactcgatg attagctgag 1440
 gaccaagtta atgtctgtta gaaactgccg gagatcgaca ttgccagatg tgggtggga 1500
 taagataggc aatatgtgtg attatttttt gtctgaggtt atcaccccc ttgccccaga 1560
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 ctgcatgccc cctgggtaca tgtatcggtt tgagcagaat tctgtttgcc tgaatcgtgc 1680
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 aaaaaaaaaa aa 1752

PF57967 .ST25 .txt

<210> 165

<-211> 410

<212> PRT

<213> Zea mays

<400> 165

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

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PF57967.ST25.txt

Leu Lys Asn Val Pro Ala Asp Phe Met Val Lys Leu Val Pro GIu His
 385 390 395 400
 Ala Arg Lys Gln Cys Ala Phe Val GIy Trp
 405 410

<210> 166
 <211> 1800
 <212> DNA
 <213> Medicago sativa

<400> 166
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 ttctctgtgt tgagttgaag agttgatttg ggggttggat gttcagtttt gaagctgtgt 180
 atgatctgaa aggaaataat taagtaaagt gttttgact ttttttaaga agatatgatg 240
 gcatcaggtg gtgttgcacc tgcttctgga ttatagata agaatgaag ttcagttggg 300
 gttgaaaagt tgcctgagga gatgaatgac atgaaaatta gggatgataa ggaaatggaa 360
 gccgctacca ttgtagatgg aaatgggacc gaaaccggac atataattgt cacaaccatt 420
 ggtggtaaaa atggccagcc aaagcagaca ataagttaca tggccgagcg tgtgttggg 480
 catggatctt ttggtgtagt ttttcaggca aagtgtttgg agactggaga aactgtggct 540
 ataaagaagg ttcttcaaga taagaggtac aagaaccggg aattgcaaac tatgcgcctt 600
 ctggaccacc ctaatgttgt atctttgaag cactgcttct tctcaacgac tgaaaaggac 660
 gagctttatc ttaacctggt gcttgaatat gttcctgaga ctgtcagccg tgtgattaga 720
 cactacaaca aaatgaatca aagaatgcct atgatatatg tcaaacttta ttcttaccag 780
 atttgcaggg cacttgctta tattcacaac agtattggag tatgtcacag ggatattaaa 840
 cctcaaaatt tactgggtcaa tcctcacacc caccaactga agatatgcga ctttgaagt 900
 gctaaagtct tggtaaaaagg tgaaccaaac atatcttaca tctgttctag gtactataga 960
 gctcctgagc ttatatcgg tgcaactgag tacaccacag ccattgacat ctggtcagct 1020
 ggttgcgtag ttggtgaact ttgtcttggc cagccactgt ttctggtga gagtggagta 1080
 gaccaacttg tggaaattat caaggtttta ggcaccccaa caaggaaga aatcaagtgc 1140
 atgaatccta attatacaga gtttaaattt cctcaaatca aagctcatcc atggcataag 1200
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 tctccaaatc ttcgaagcac agctttggag gctttggttc atccattcta tgatgacgtg 1320
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 gtcaatgagc tcaagggagt acctgcagag atgctggtga aactggttcc acctcatgca 1440
 agaaagcaat gtgccttgtt cgggtcatca tgaagcagcc ttgtgtagtt attaatgact 1500
 ttcttctacc tatgtaaaagg tgtatctagt caaatttcaa gtgggttaaat aggttatattc 1560
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 cttcctcgat gtagaagaaa gctgtgctgt ttaagaagca acttcagctt gattattact 1680
 ttgtaggatc tgatgtgttc actcacctta acatgaacca ttgtttattg aagtgataga 1740
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<210> 167
 <211> 412
 <212> PRT
 <213> Medicago sativa

<400> 167
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 1 5 10 15
 Asn Ala Ser Ser Val GIy Val GIu Lys Leu Pro GIu GIu Met Asn Asp
 20 25 30
 Met Lys lie Arg Asp Asp Lys GIu Met GIu Ala Ala Thr lie Val Asp
 35 40 45

PF57967.ST25.txt

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

<210> 168

<211> 1613

<212> DNA

<213> Medicago sativa

<400> 168

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60

PF57967.ST25.txt

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gatagagaaa tggaagccac cgttggtgac ggcaatggaa cggagacagg acatatcatt 240
gtcactacta ttggtggtag aaatggtcag ccaaagcaga ctataagcta tatggcagag 300
cgtgtttagt gacatggatc atttgaggt gtcttccagg ctaagtgtctt ggaaactggt 360
gaaaccgtgg ctatcaaaaa ggttcttcaa gacaagaggt acaagaaccg ggaattgcaa 420
acaatgcgac tgcttgatca cccgaatgtc gtctctttaa agcattgttt cttttcaacc 480
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cgcgtgatta agcattacag caagttgaac caaaggatgc caatgattta tgtgaagctc 600
tatacatacc agatcttttag agcattatct tatattcatc gttgcattgg agtctgtcat 660
cgggatatca agccccaaaa tctattggtc aatccacaca cccaccagggt taaattatgc 720
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cccaaaccct tataatgggta ttcagaatac ccttttcctg tatcacagca gattgtaaca 1500
tgcaatagaa gacaagtgtc tacaattatc taaatgttgt atcagtattt gtacttgtat 1560
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<210> 169

<211> 411

<212> PRT

<213> Medicago sativa

<400> 169

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

```

PF57967.ST25.txt

165 170 175
 Lys Leu Tyr Thr Tyr Gln lie Phe Arg Ala Leu Ser Tyr lie His Arg
 180 185 190
 Cys lie GIY VaI Cys His Arg Asp lie Lys Pro Gln Asn Leu Leu VaI
 195 200 205
 Asn Pro His Thr His Gln VaI Lys Leu Cys Asp Phe GIY Ser Ala Lys
 210 215 220
 VaI Leu VaI Lys GIY GIU Pro Asn H e Ser Tyr H e Cys Ser Arg Tyr
 225 230 235 240
 Tyr Arg Ala Pro GIU Leu H e Phe GIY Ala Thr GIU Tyr Thr Thr Ala
 245 250 255
 lie Asp VaI Trp Ser VaI GIY Cys VaI Leu Ala GIU Leu Leu GIY
 260 265 270
 Gln Pro Leu Phe Pro GIY GIU Arg GIY VaI Asp Gln Leu VaI GIU H e
 275 280 285
 H e Lys VaI Leu GIY Thr Pro Thr Arg GIU GIU H e Lys Cys Met Asn
 290 295 300
 Pro Asn Tyr Thr GIU Phe Lys Phe Pro Gln H e Lys Ala His Pro Trp
 305 310 315 320
 His Lys H e Phe His Lys Arg Met Pro Ala GIU Ala VaI Asp Leu VaI
 325 330 335
 Ser Arg Leu Leu Gln Tyr Ser Pro Asn Leu Arg Cys Gln Ala Leu Asp
 340 345 350
 Cys Leu Thr His Pro Phe Phe Asp GIU Leu Arg Asp Pro Asn Ala Arg
 355 360 365
 Leu Pro Thr GIY Arg Phe Leu Pro Pro Leu Phe Asn Phe Lys Pro His
 370 375 380
 GIU Leu Lys GIY VaI Pro VaI GIU Thr Leu Met Lys Leu VaI Pro GIU
 385 390 395 400
 His Ala Arg Lys Gln Cys Pro Phe Leu GIY Leu
 405 410

<210> 170
 <211> 1543
 <212> DNA
 <213> Medicago sativa

<400> 170
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 gttgataagt tacctgatga gattcttggc atgagaatta aggatgataa ggaaatggaa 180
 gcacatgtgg tagatggaaa tagtactgaa gcaggacatg taattgtcac taccattggt 240
 ggtaaaaaatg gccagccaaa gcagacaata agctacatgg ctgagcgtgc tgttggacag 300
 ggatcatttg gtgtagtttt ccaggctaag tgcttggaga caggtgaaac tgtggctata 360
 aaaaagggttc ttcaagacaa gaggtataag aaccgggaat tgcaaacaat gcgccttctg 420
 gaccacccca atgttgtaac tttgaagcat tgtttctttt caacaactga aaaagacgag 480
 ctctatctta acttggtact tgagtttggt cctgagactg tccatcgtgt gatcagacac 540
 tacagcaaaa tgaatcagag gatgccattg atatacgtaa aactttattc ttaccagata 600
 tgtagatcac tagcttatat tcataactgt gttggagtgt ctcataggga cataaaacct 660
 caaaattttac tgggtcaatcc tcacacccat cagctgaagc tgtgtgactt tgggagtgca 720
 aaagtcttgg tcaagggtga accaaacata tcttacatct gttcagggtta ttatagagct 780
 cctgagctta tatttgggtgc aactgaatac acctcagcca ttgacatttg gtcagctggc 840
 tgtgtgcttg gcgaactatt gcttggccag cctctctttc ccggtgcgag tggagtagac 900
 cagctcgttg aaattatcaa ggtttttaggt accccaacaa gggaagaaat aaagtgtatg 960

PF57967.ST25.txt

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aatcctaatt  acactgagtt  caaattccca  caaatcaaag  ctcattccatg  gcacaagatc  1020
tttcgcaagc  gtatgccacc  ggaagctgtg  gatctcgtct  caagactact  tcaatactct  1080
ccaaatcttc  gaagcacagc  ttggaggct  ctggttcac  ccttctttga  tgaattgcgt  1140
gatccaaata  ccgcttacc  aaatgggcga  catcttcctc  ctttatttaa  cttcaaagcc  1200
aacgagctta  agggagtgc  tgctgaaatg  ctggtgaagt  tggttccgtc  tcacgcaaga  1260
aagcagtgtt  cttgtttgc  gtcgtcatag  acttagaatg  ctgtcttgtg  taaatattat  1320
ggactccctg  ttgtagaat  tgtatgtagc  ctgtttcatg  ttgttaatag  tctctctttt  1380
gttatttggt  ccattaattt  gtttctacca  aagaaaacca  cctcagttta  ttataagttt  1440
caagttgatc  tctcttcacg  atttaattgt  tctcctgatc  ttcaattatt  aacagattgt  1500
attaactatt  aactattaac  tagaacaatt  gtttattcta  gcg  1543

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<210> 171

<211> 411

<212> PRT

<213> Medicago sativa

<400> 171

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

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PF57967.ST25. txt

290 295 300
 Asn Tyr Thr GIu Phe Lys Phe Pro GIn H e Lys Ala His Pro Trp His
 305 310 315 320
 Lys H e Phe Arg Lys Arg Met Pro Pro GIu Ala VaI Asp Leu VaI Ser
 325 330 335
 Arg Leu Leu GIn Tyr Ser Pro Asn Leu Arg Ser Thr Ala Leu GIu Ala
 340 345 350
 Leu VaI His Pro Phe Phe Asp GIu Leu Arg Asp Pro Asn Thr Arg Leu
 355 360 365
 Pro Asn GIy Arg His Leu Pro Pro Leu Phe Asn Phe Lys Ala Asn GIu
 370 375 380
 Leu Lys GIy VaI Pro Ala GIu Met Leu VaI Lys Leu VaI Pro Ser His
 385 390 395 400
 Ala Arg Lys GIn Cys Ser Leu Phe Ala Ser Ser
 405 410

<210> 172
 <211> 1724
 <212> DNA
 <213> Nicotiana tabacum

<400> 172
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 gactttttga ggtgataata gtctgcaaaa ttccaggaaa tgacttcagt aggcttagca 180
 cctgtatccg gtttgagaga atccagtagc catagtgttg gtgtagatag gctgcctgag 240
 gagatgaatg acatgagaat cagggatgat aaggaaatcg aagcagctat tgtggatggt 300
 aatgggactg agacaggcca tataatagtg acaactattg gtggtagaca tggtcagcca 360
 aaacagacta tcagttatat ggctgaacgt attgttggac aaggatcatt tggagtgggt 420
 ttccaggcaa aatgcttaga gactggtgaa actgtttgcta ttaaaaagggt tcttcaagac 480
 aagagatata agaacaggga gctgcagacc atgcgtcttc ttgatcacc aaatgttggtg 540
 tgcctgaagc actgcttctt ttcaacaact gagaaggatg aagtatatct taatttgggtt 600
 ctgaataacg tccctgaaac tgtccatcgt gttattaaac actacaataa gttgaatcaa 660
 aggatgccat tgatactagt gaagctttat acatatcaga ttttcagggc attgtcttac 720
 atccatcaca caattggagt gtgccacagg gacataaagc ctcaaatct tttggtgaat 780
 ccacatactc accaggttaa attgtgtgac ttggaagtg ctaaagttct ggttaaagga 840
 gaaccaaata tttcttacat ctgctctagg tattatagag cgctgaact tataatttggg 900
 gcaacagagt acactaccgc tattgacatc tgggtctgctg gctgtgttct agccgagcta 960
 cttcttgggc agcctttgtt tccgggtgaa agtggagtgt atcagcttgt tgagattatt 1020
 aaggctcttg gtactcttac cagggaagaa attaaatgca tgaatccaaa ttataacgag 1080
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 gcttttagagg cagtgaacca tgccttcttc gatgagcttc gtgaccta aaacgcctc 1260
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 ggtttatgag ttcccactgt acggtagata taatttaagt gtaagctatg ttatttctct 1440
 gtatccattt ttcccccttt gctccccaca tgtaccagtt gtctctttgt attattatcc 1500
 tagttttgtaa aagcagaggt aggatgtggt cttaacatt ccttacctcc aacactttcc 1560
 ttccacctg ttccctttat gtctactgt tgtaactttt atgtgggttaa ggggtggactg 1620
 ctttctatat gaactattat tttatgatga aatttcaaag tgatttttag tgaaaaaaa 1680
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1724

<210> 173
 <211> 409

PF57967.ST25.txt

<212> PRT

<213> Nicotiana tabacum

<400> 173

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Met Thr Ser Val GIY Leu Ala Pro Val Ser GIY Leu Arg GIU Ser Ser
1      5      10      15
Ser Hrs Ser Val GIY Val Asp Arg Leu Pro GIU GIU Met Asn Asp Met
      20      25      30
Arg lie Arg Asp Asp Lys GIU lie GIU Ala Ala lie Val Asp GIY Asn
      35      40      45
GIY Thr GIU Thr GIY His H e Val Thr Thr H e GIY GIY Arg His
      50      55      60
GIY GIn Pro Lys GIn Thr H e Ser Tyr Met Ala GIU Arg H e Val GIY
65      70      75      80
GIn GIY Ser Phe GIY Val Val Phe GIn Ala Lys Cys Leu GIU Thr GIY
      85      90      95
GIU Thr Val Ala H e Lys Lys Val Leu GIn Asp Lys Arg Tyr Lys Asn
      100      105      H O
Arg GIU Leu GIn Thr Met Arg Leu Leu Asp His Pro Asn Val Val Cys
      115      120      125
Leu Lys His Cys Phe Phe Ser Thr Thr GIU Lys Asp GIU Val Tyr Leu
      130      135      140
Asn Leu Val Leu GIU Tyr Val Pro GIU Thr Val His Arg Val H e Lys
145      150      155      160
His Tyr Asn Lys Leu Asn GIn Arg Met Pro Leu H e Leu Val Lys Leu
      165      170      175
Tyr Thr Tyr GIn H e Phe Arg Ala Leu Ser Tyr H e His His Thr H e
      180      185      190
GIY Val Cys His Arg Asp H e Lys Pro GIn Asn Leu Leu Val Asn Pro
      195      200      205
His Thr His GIn Val Lys Leu Cys Asp Phe GIY Ser Ala Lys Val Leu
      210      215      220
Val Lys GIY GIU Pro Asn H e Ser Tyr H e Cys Ser Arg Tyr Tyr Arg
225      230      235      240
Ala Pro GIU Leu H e Phe GIY Ala Thr GIU Tyr Thr Thr Ala H e Asp
      245      250      255
H e Trp Ser Ala GIY Cys Val Leu Ala GIU Leu Leu Leu GIY GIn Pro
      260      265      270
Leu Phe Pro GIY GIU Ser GIY Val Asp GIn Leu Val GIU H e H e Lys
      275      280      285
Val Leu GIY Thr Pro Thr Arg GIU GIU H e Lys Cys Met Asn Pro Asn
      290      295      300
Tyr Asn GIU Phe Lys Phe Pro GIn H e Lys Ala His Pro Trp His Lys
305      310      315      320
H e Phe His Lys Arg Met Pro Pro GIU Ala Val Asp Leu Val Ser Arg
      325      330      335
Leu Leu GIn Tyr Ser Pro Asn Leu Arg Cys Thr Ala Leu GIU Ala Val
      340      345      350
Thr His Ala Phe Phe Asp GIU Leu Arg Asp Pro Asn Thr Arg Leu Pro
      355      360      365
Asn GIY Arg Val Leu Pro Pro Leu Phe Asn Phe Lys Ala His GIU Leu
      370      375      380
Lys GIY Val Ser Ala GIU Asn Leu Leu Lys Leu Val Pro GIU His Ala
385      390      395      400

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PF57967.ST25.txt

Arg Lys Gln Cys Pro Ser Leu Gly Leu
405

<210> 174
<211> 1573
<212> DNA
<213> Triticum aestivum

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<400> 174
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gaccgacttc cgaacgagat gggcaatatg agcataaggg atgacaggga ccctgaggat 120
atagtagtca acggcaatgg gacggaacca ggccatatta tagtcacaag cattgaggga 180
agaaatgggc aagcaaaaaca gaccattagc tacatggctg agcgtgtggt tggtaatggg 240
tcattttgaa ctgtttttcca ggctaagtgt cttgaaactg gcgagacggt ggctataaag 300
aaggttcttc aagacaagag atataagaac cgtgagctgc aaacgatgcg agttcttgac 360
cacccaaatg ttgtggcttt aaagcattgt tttttctcaa agactgagaa agaggagctt 420
tacctcaacc tgggtgcttga gtatgtgccg gagactgctc atcgtgtcat taagcattat 480
aacaagatga accaacgcat gccattgata tatgcaaaac tgtacatgta tcagatatgt 540
agatcttttg catacattca caacagcatt ggagtatgcc acagagacat caagcctcaa 600
aatcttcttg tgaatccaca tacgcaccaa ttgaaattat gtgacttcgg aagtgcgaaa 660
gtgttggtta aaggagaacc aaatatttcc tatatctgtt caaggtacta tagagcccca 720
gagctcatat ttggtgctac tgaatacaca acggcaattg acgtttggtc tgctggctgt 780
gttcttctgt aactccttct aggacagcct atattccctg gcgacagtgg tgttgatcag 840
cttgttgtaa tcatcaaggt tttaggtacc cctacaagag aagaaattaa gtgcatgaat 900
ccaaattata cggagttaa attcccacaa atcaaagctc acccatggca caagatcttc 960
cataaaagaa tgcctgctga agcagtagat ctgtgtctca gactcttgca atattcacca 1020
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aactgtgcct ttgtaggatg gtgatccgcc agacggctgc ttgaagttta gttcagaaca 1260
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attctttccc cctactgccg atgtaacaaa ccacccatga tactgtaagt agatgagaag 1440
tgtttcgacc gttttccct gagctcatgt gctatgcaat gaaggatgca ccctatgtac 1500
cgccaatatt tgggtccagta tttgttcag gatcgaggcc cccaaaaaaa aaaaaaaaaa 1560
aaaaaaaaa aaa 1573

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<210> 175
<211> 381
<212> PRT
<213> Triticum aestivum

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<400> 175
Met Gly Asn Met Ser lie Arg Asp Asp Arg Asp Pro Glu Asp H e Val
1 5 10 15
Val Asn GIy Asn GIy Thr GIu Pro GIy His H e H e Val Thr Ser H e
20 25 30
GIu GIy Arg Asn GIy Gln Ala Lys GIu Thr H e Ser Tyr Met Ala GIu
35 40 45
Arg Val Val GIy Asn GIy Ser Phe GIy Thr Val Phe Gln Ala Lys Cys
50 55 60
Leu GIu Thr GIy GIu Thr Val Ala H e Lys Lys Val Leu Gln Asp Lys
65 70 75 80
Arg Tyr Lys Asn Arg GIu Leu Gln Thr Met Arg Val Leu Asp His Pro

```

PF57967.ST25.txt

```

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

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<210> 176

<211> 1581

<212> DNA

<213> Petunia hybπ da

<400> 176

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ctgtttttgtg tttttgtaaa atgtgagctg ttcttttagct acagggtttga agctgttaat 120
ctgtcatttg agttgtgccc attactcagt agtataagta agtttatattt tgttgctgat 180
atggcgtctg gtataatgcc ttcggctggt ggaaaacatc gaactgatgc catgcttggt 240
gacaaacttc ccgaagaaat aaatgaaatg aagatcagag atgataaagc agaaaaggaa 300
atggaagcag ctgtagtgga tggaaatgga actgaaaaag gccacatcat cgtgacaact 360
attgggggca aaaatggtga gcctaagcag accattagtt acatggccga gcgtgttggt 420
ggacagggtt cgtttggaat agtgttccag gccaaatgcc ttgaaactgg agaaactggt 480
gcaataaaaa aggtttttaca ggataagaga tacaagaatc gggaattgca aacaatacgc 540
cttctagatc atcctaattg tgttgcactg aggcactgct tcttttcaac cacagaaaag 600

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PF57_967.ST25.txt

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gatgagcttt atctgaattt ggtccttgaa tatgtaccag agactgtcta ccgtgtcttg 660
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cagattttca gagcttttggc ctacatacac ggcataggag tctgccacag ggacatcaag 780
cctcagaatc tacttggtcaa cccccacacc caccagctta agctctgcga ctttgggagt 840
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gcacccgaac ttatatctcg agcaactgaa tacacttttg caattgacat ttggtctgtg 960
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gatcagcttg ttgaaataat caagggttctt ggaacaccaa ctgaggagga aatcaagagt 1080
atgaatccaa attacactga gttcaaattc ccacaaatca aagctcacc ttggcacaaa 1140
atttttcata agcggatgcc tccagaagct gtggaccttg tgtcaaggct tctccaatat 1200
tctccaaatt tgaggtccac tgcgttggag gcttgcactc acactttctt tgatgaactc 1260
cgtgatccta agactcgctt ccctaattgt cgccatttgc cactctttt caacttcagg 1320
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aatgctatct acttgaactt g 1581

```

<210> 177

<211> 409

<212> PRT

<213> Pet un₁a hybr₁da

<400> 177

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

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PF57967.ST25.txt

Ala Pro GIu Leu lie Phe GIy Ala Thr GIu Tyr Thr Phe Ala lie Asp
 245 250 255
 lie Trp Ser VaI GIy Cys VaI Leu Ala GIu Leu Leu Leu GIy GIn Pro
 260 265 270
 Leu Phe Pro GIy GIu Ser GIy VaI Asp GIn Leu VaI GIu lie lie Lys
 275 280 285
 VaI Leu GIy Thr Pro Thr Arg GIu GIu lie Lys Ser Met Asn Pro Asn
 290 295 300
 Tyr Thr GIu Phe Lys Phe Pro GIn lie Lys Ala His Pro Trp His Lys
 305 310 315 320
 lie Phe His Lys Arg Met Pro Pro GIu Ala VaI Asp Leu VaI Ser Arg
 325 330 335
 Leu Leu GIn Tyr Ser Pro Asn Leu Arg Ser Thr Ala Leu GIu Ala Cys
 340 345 350
 Thr His Thr Phe Phe Asp GIu Leu Arg Asp Pro Lys Thr Arg Leu Pro
 355 360 365
 Asn GIy Arg Pro Leu Pro Pro Leu Phe Asn Phe Arg Pro GIn GIu Leu
 370 375 380
 Lys GIy Ala Ser Ala Asp Leu Leu Asn Lys Leu lie Pro GIu His Ala
 385 390 395 400
 Lys Lys GIn Cys Thr Phe Leu GIy VaI
 405

<210> 178
 <211> 2193
 <212> DNA
 <213> Oryza sativa

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 catccaccta ctttagtgcc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
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 gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600
 tcaactagca acacatctct aatatcactc gcctatttaa tacatttagg tagcaatata 660
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 aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa 780
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PF57967.ST25.txt

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agctgtaatc	gggatagtta	tactgcttgt	tcttatgatt	catttccttt	gtgcagttct	2160
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<210> 179

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> primer: prm5797

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<210> 180

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> primer: prm5798

<400> 180

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<210> 181

<211> 1243

<212> DNA

<213> Oryza sativa

<400> 181

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ttattccgga	gcatgattgg	gaaggaggga	cataaggccc	atgtcgcattg	tgtttgacg	180
gtccagatct	ccagatcact	cagcaggatc	ggccgcgttc	gcgtagcacc	cgcggtttga	240
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gcacgccgcc	gccgccgacc	cggctctgcg	tttgcaccgc	cttgcacgcg	atacatcggg	360
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ccattaggaa	gtaaccttgt	cattacttat	accagtacta	catactatat	agtattgatt	720
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PF57967.ST25.txt

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gcgcgcgcac	aggcacaaat	tacgtacaaa	acgcatgacc	aaatcaaaac	caccggagaa	1020
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aggaaaaaaaa	aacaaaacac	accaagcaa	ataaaagcga	caa		1243