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(54) **Title:** TRANSGENIC PLANTS WITH INCREASED STRESS TOLERANCE AND YIELD

(57) **Abstract:** Polynucleotides are disclosed which are capable of enhancing a growth, yield under water-limited conditions, and/or increased tolerance to an environmental stress of a plant transformed to contain such polynucleotides. Also provided are methods of using such polynucleotides and transgenic plants and agricultural products, including seeds, containing such polynucleotides as transgenes.

TRANSGENIC PLANTS WITH INCREASED STRESS TOLERANCE AND YIELD

This application claims priority benefit of U.S. provisional patent application Serial Number 60/959346, filed July 13, 2007, the contents of which are hereby incorporated by reference.

FIELD OF THE INVENTION

[0001] This invention relates generally to transgenic plants which overexpress nucleic acid sequences encoding polypeptides capable of conferring increased stress tolerance and consequently, increased plant growth and crop yield, under normal or abiotic stress conditions. Additionally, the invention relates to novel isolated nucleic acid sequences encoding polypeptides that confer upon a plant increased tolerance under abiotic stress conditions, and/or increased plant growth and/or increased yield under normal or abiotic stress conditions.

BACKGROUND OF THE INVENTION

[0002] Abiotic environmental stresses, such as drought, salinity, heat, and cold, are major limiting factors of plant growth and crop yield. Crop yield is defined herein as the number of bushels of relevant agricultural product (such as grain, forage, or seed) harvested per acre. Crop losses and crop yield losses of major crops such as soybean, rice, maize (corn), cotton, and wheat caused by these stresses represent a significant economic and political factor and contribute to food shortages in many underdeveloped countries.

[0003] Water availability is an important aspect of the abiotic stresses and their effects on plant growth. Continuous exposure to drought conditions causes major alterations in the plant metabolism which ultimately lead to cell death and consequently to yield losses. Because high salt content in some soils results in less water being available for cell intake, high salt concentration has an effect on plants similar to the effect of drought on plants. Additionally, under freezing temperatures, plant cells lose water as a result of ice formation within the plant. Accordingly, crop damage from drought, heat, salinity, and cold stress, is predominantly due to dehydration.

[0004] Because plants are typically exposed to conditions of reduced water availability during their life cycle, most plants have evolved protective mechanisms against desiccation caused by abiotic stresses. However, if the severity and duration of desiccation conditions are too great, the effects on development, growth, plant size, and yield of most crop plants are profound. Developing plants efficient in water use is therefore a strategy that has the potential to significantly improve human life on a worldwide scale.

[0005] Traditional plant breeding strategies are relatively slow and require abiotic stress-tolerant founder lines for crossing with other germplasm to develop new abiotic stress-resistant lines. Limited germplasm resources for such founder lines and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Breeding for tolerance has been largely unsuccessful.

[0006] Many agricultural biotechnology companies have attempted to identify genes that could confer tolerance to abiotic stress responses, in an effort to develop transgenic abiotic stress-tolerant crop plants. Although some genes that are involved in stress responses or water use efficiency in plants have been characterized, the characterization and cloning of plant genes that confer stress tolerance and/or water use efficiency remains largely incomplete and fragmented. To date, success at developing transgenic abiotic stress-tolerant crop plants has been limited, and no such plants have been commercialized.

[0007] In order to develop transgenic abiotic stress-tolerant crop plants, it is necessary to assay a number of parameters in model plant systems, greenhouse studies of crop plants, and in field trials. For example, water use efficiency (WUE), is a parameter often correlated with drought tolerance. Studies of a plant's response to desiccation, osmotic shock, and temperature extremes are also employed to determine the plant's tolerance or resistance to abiotic stresses. When testing for the impact of the presence of a transgene on a plant's stress tolerance, the ability to standardize soil properties, temperature, water and nutrient availability and light intensity is an intrinsic advantage of greenhouse or plant growth chamber environments compared to the field.

[0008] WUE has been defined and measured in multiple ways. One approach is to calculate the ratio of whole plant dry weight, to the weight of water consumed by the plant throughout its life. Another variation is to use a shorter time interval when biomass accumulation and water use are measured. Yet another approach is to use measurements from restricted parts of the plant, for example, measuring only aerial growth and water use. WUE also has been defined as the ratio of CO_2 uptake to water vapor loss from a leaf or portion of a leaf, often measured over a very short time period (e.g. seconds/minutes). The ratio of $^{13}C/^{12}C$ fixed in plant tissue, and measured with an isotope ratio mass-spectrometer, also has been used to estimate WUE in plants using C_3 photosynthesis.

[0009] An increase in WUE is informative about the relatively improved efficiency of growth and water consumption, but this information taken alone does not indicate whether one of these two processes has changed or both have changed. In selecting traits for improving crops, an increase in WUE due to a decrease in water use, without a change in growth would have particular merit in an irrigated agricultural system where the water input costs were high. An increase in WUE driven mainly by an increase in growth without a corresponding jump in water use would have applicability to all agricultural systems. In many agricultural systems where water supply is not limiting, an increase in growth, even if it came at the expense of an increase in water use (i.e. no change in WUE), could also increase yield. Therefore, new methods to increase both WUE and biomass accumulation are required to improve agricultural productivity.

[0010] Concomitant with measurements of parameters that correlate with abiotic stress tolerance are measurements of parameters that indicate the potential impact of a transgene on crop yield. For forage crops like alfalfa, silage corn, and hay, the plant biomass correlates with the total yield. For grain crops, however, other parameters have been used to estimate yield, such as plant size, as measured by total plant dry weight, above-ground dry weight, above-ground fresh weight, leaf area, stem volume, plant height, rosette diameter, leaf length, root length, root mass, tiller number, and leaf number. Plant size at an early developmental stage will typically correlate with plant size later in development. A larger plant with a greater leaf area can typically absorb more light and carbon dioxide than a smaller plant and therefore will likely gain a greater weight during the same period. This is in addition to the potential continuation of the micro-environmental or genetic advantage that the plant had to achieve the larger size initially. There is a strong genetic component to plant size and growth rate, and so for a range of diverse genotypes plant size under one environmental condition is likely to correlate with size under another. In this way a standard environment is used to approximate the diverse and dynamic environments encountered at different locations and times by crops in the field.

[0011] Harvest index, the ratio of seed yield to above-ground dry weight, is relatively stable under many environmental conditions and so a robust correlation between plant size and grain yield is possible. Plant size and grain yield are intrinsically linked, because the majority of grain biomass is dependent on current or stored photosynthetic productivity by the leaves and stem of the plant. Therefore, selecting for plant size, even at early stages of development, has been used as to screen for for plants that may demonstrate increased yield when exposed to field testing. As with abiotic stress tolerance, measurements of plant size in early development, under standardized conditions in a growth chamber or greenhouse, are standard practices to measure potential yield advantages conferred by the presence of a transgene.

[0012] There is a need, therefore, to identify additional genes expressed in stress tolerant plants and/or plants that are efficient in water use that have the capacity to confer stress tolerance and/or increased water use efficiency to the host plant and to other plant species. Newly generated stress tolerant plants and/or plants with increased water use efficiency will have many advantages, such as an increased range in which the crop plants can be cultivated, by for example, decreasing the water requirements of a plant species. Other desirable advantages include increased resistance to lodging, the bending of shoots or stems in response to wind, rain, pests, or disease.

SUMMARY OF THE INVENTION

[0013] The present inventors have discovered that transforming a plant with certain polynucleotides results in enhancement of the plant's growth and response to environmental stress, and accordingly the yield of the agricultural products of the plant is increased, when the polynucleotides are present in the plant as transgenes. The polynucleotides capable of mediating such enhancements have been isolated from Arabidopsis thaliana, Capsicum annuum, Escherichia coli, Physcomitrella patens, Saccharomyces cerevisiae, Triticum aestivum, Zea mays, Glycine max, Linum usitatissimum, Triticum aestivum, Oryza sativa, Helianthus annuus, and Brassica napus and the sequences thereof are set forth in the Sequence Listing as indicated in Table 1.

Table 1

Gene Name	Organism	Polynucleotide SEQ ID NO	Amino acid SEQ ID NO
At2g20725	A. thaliana	1	2
At3g26085	A. thaliana	3	4
AtFACE-2	A. thaliana	5	6
ZM57353913	Z. mays	7	8
ZM59252659	Z. mays	9	10
CASAR82A	C. annuum	11	12
b3358	E. coli	13	14
EST564	P. patens	15	16
BN49502266	B. napus	17	18
GM49788080	G. max	19	20
GM53049821	G. max	21	22
ZM58462719	Z. mays	23	24
ZM61092633	Z. mays	25	26
ZM62016485	Z. mays	27	28
ZM62051019	Z. mays	29	30
ZM65086957	Z. mays	31	32
ZM68587657	Z. mays	33	34
EST390	P. patens	35	36
BN51363030	B. napus	37	38
BN42986056	B. napus	39	40
BN49389066	B. napus	41	42
BN51339479	B. napus	43	44
ZM57651070	Z. mays	45	46
ZM62073276	Z. mays	47	48
EST257	P. patens	49	50
LU61665952	L. usitatissimum	51	52
TA56863186	T. aestivum	53	54
ZM62026837	Z. mays	55	56
ZM65457595	Z. mays	57	58
ZM67230154	Z. mays	59	60
EST465	P. patens	61	62
YBL109w	S. cerevisiae	63	64
YBL100c	S. cerevisiae	65	66
YKL184w	S. cerevisiae	67	68
YPL091w	S. cerevisiae	69	70
TA54587433	T. aestivum	71	72

Gene Name	Organism	Polynucleotide SEQ ID NO	Amino acid SEQ ID NO
ZM68532504	Z. mays	73	74
BN42856089	B. napus	75	76
BN43206527	B. napus	77	78
HA66872964	H. annuus	79	80
LU61662612	L. usitatissimum	81	82
OS32806943	O. sativa	83	84
OS34738749	O. sativa	85	86
ZM59400933	Z. mays	87	88
ZM62132060	Z. mays	89	90
ZM59202533	Z. mays	91	92
BN41901422	B. napus	93	94
BN47868329	B. napus	95	96
BN42671700	B. napus	97	98
ZM68416988	Z. mays	99	100

[0014] In one embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a CAAX amino terminal protease family protein.

[0015] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a prenyl-dependent CAAX protease.

[0016] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a SAR8.2 protein precursor.

[0017] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a putative membrane protein.

[0018] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a protein phosphatase 2C protein.

[0019] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a mitochondrial carrier protein.

[0020] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a protein kinase.

[0021] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a peptidyl prolyl isomerase.

[0022] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a unknown protein 1.

[0023] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a unknown protein 2.

[0024] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a ornithine decarboxylase.

[0025] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a glutathione reductase.

[0026] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a unknown protein 3.

[0027] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a protein phosphatase 2A protein.

[0028] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a MEK1 protein kinase.

[0029] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a AP2 domain containing transcription factor.

[0030] In a further embodiment, the invention concerns a seed produced by the transgenic plant of the invention, wherein the seed is true breeding for a transgene comprising the polynucleotide described above. Plants derived from the seed of the invention demonstrate increased tolerance to an environmental stress, and/or increased plant growth, and/or increased yield, under normal or stress conditions as compared to a wild type variety of the plant.

[0031] In a still another aspect, the invention concerns products produced by or from the transgenic plants of the invention, their plant parts, or their seeds, such as a foodstuff, feedstuff, food supplement, feed supplement, cosmetic or pharmaceutical.

[0032] The invention further provides certain isolated polynucleotides identified in Table 1, and certain isolated polypeptides identified in Table 1. The invention is also embodied in recombinant vector comprising an isolated polynucleotide of the invention.

[0033] In yet another embodiment, the invention concerns a method of producing the aforesaid transgenic plant, wherein the method comprises transforming a plant cell with an expression vector comprising an isolated polynucleotide of the invention, and generating from the plant cell a transgenic plant that expresses the polypeptide encoded by the polynucleotide. Expression of the polypeptide in the plant results in increased tolerance to an environmental stress, and/or growth, and/or yield under normal and/or stress conditions as compared to a wild type variety of the plant.

[0034] In still another embodiment, the invention provides a method of increasing a plant's tolerance to an environmental stress, and/or growth, and/or yield. The method comprises the steps of transforming a plant cell with an expression cassette comprising an isolated polynucleotide of the invention, and generating a transgenic plant from the plant cell, wherein the transgenic plant comprises the polynucleotide.

BRIEF DESCRIPTION OF THE DRAWINGS

[0035] Figure 1 shows an alignment of the disclosed amino acid sequences At-FACE-2 (SEQ ID NO:6), ZM57353913 (SEQ ID NO:8), and ZM59252659 (SEQ ID NO:10). The alignment was generated using Align X of Vector NTI .

[0036] Figure 2 shows an alignment of the disclosed amino acid sequences EST564 (SEQ ID NO:16), BN49502266 (SEQ ID NO:18), GM49788080 (SEQ ID NO:20), GM53049821 (SEQ ID NO:22), ZM58462719 (SEQ ID NO:24), ZM61092633 (SEQ ID NO:26), ZM62016485 (SEQ ID NO:28), ZM62051019 (SEQ ID NO:30), ZM65086957 (SEQ ID NO:32), and ZM68587657 (SEQ ID NO:34). The alignment was generated using Align X of Vector NTI.

[0037] Figure 3 shows an alignment of the disclosed amino acid sequences EST390 (SEQ ID NO:36), BN51363030 (SEQ ID NO:38), BN42986056 (SEQ ID NO:40), BN49389066 (SEQ ID NO:42), BN51339479 (SEQ ID NO:44), ZM57651070 (SEQ ID NO:46), and ZM62073276 (SEQ ID NO:48). The alignment was generated using Align X of Vector NTI .

[0038] Figure 4 shows an alignment of the disclosed amino acid sequences EST257 (SEQ ID NO:50), LU61665952 (SEQ ID NO:52), TA56863186 (SEQ ID NO:54), ZM62026837 (SEQ ID NO:56), ZM65457595 (SEQ ID NO:58), ZM67230154 (SEQ ID NO:60). The alignment was generated using Align X of Vector NTI .

[0039] Figure 5 shows an alignment of the disclosed amino acid sequences ZM68532504 (SEQ ID NO:74), BN42856089 (SEQ ID NO:76), BN43206527 (SEQ ID NO:78), HA66872964 (SEQ ID NO:80), LU61662612 (SEQ ID NO:82), OS32806943 (SEQ ID NO:84), OS34738749 (SEQ ID NO:86), ZM59400933 (SEQ ID NO:88), and ZM62132060 (SEQ ID NO:90). The alignment was generated using Align X of Vector NTI .

[0040] Figure 6 shows an alignment of the disclosed amino acid sequences ZM59202533 (SEQ ID NO:92), BN41901422 (SEQ ID NO:94), BN47868329 (SEQ ID NO:96), and ZM68416988 (SEQ ID NO:100). The alignment was generated using Align X of Vector NTI .

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0041] Throughout this application, various publications are referenced. The disclosures of all of these publications and those references cited within those publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains. The terminology used herein is for the purpose of describing specific embodiments only and is not intended to be limiting. As used herein, “a” or “an” can mean one or more, depending upon the context in which it is used. Thus, for example, reference to “a cell” can mean that at least one cell can be used.

[0042] In one embodiment, the invention provides a transgenic plant that overexpresses an isolated polynucleotide identified in Table 1, or a homolog thereof. The transgenic plant of the invention demonstrates an increased tolerance to an environmental stress as compared to a wild type variety of the plant. The overexpression of such isolated nucleic acids in the plant may optionally result in an increase in plant growth or in yield of associated agricultural products, under normal or stress conditions, as compared to a wild type variety of the plant.

[0043] As defined herein, a “transgenic plant” is a plant that has been altered using recombinant DNA technology to contain an isolated nucleic acid which would otherwise not be present in the plant. As used herein, the term “plant” includes a whole plant, plant cells, and plant parts. Plant parts include, but are not limited to, stems, roots, ovules, stamens, leaves, embryos, meristematic regions, callus tissue, gametophytes, sporophytes, pollen, microspores, and the like. The transgenic plant of the invention may be male sterile or male fertile, and may further include transgenes other than those that comprise the isolated polynucleotides described herein.

[0044] As used herein, the term “variety” refers to a group of plants within a species that share constant characteristics that separate them from the typical form and from other possible varieties within that species. While possessing at least one distinctive trait, a variety is also characterized by some variation between individuals within the variety, based primarily on the Mendelian segregation of traits among the progeny of succeeding generations. A variety is considered “true breeding” for a particular trait if it is genetically homozygous for that trait to the extent that, when the true-breeding variety is self-pollinated, a significant amount of independent segregation of the trait among the progeny is not observed. In the present invention, the trait arises from the transgenic expression of one or more isolated polynucleotides introduced into a plant variety. As also used herein, the term “wild type variety” refers to a group of plants that are analyzed for comparative purposes as a control plant, wherein the wild type variety plant is identical to the transgenic plant (plant transformed with an isolated polynucleotide in accordance with the invention) with the exception that the wild type variety plant has not been transformed with an isolated polynucleotide of the invention.

[0045] As defined herein, the term “nucleic acid” and “polynucleotide” are interchangeable and refer to RNA or DNA that is linear or branched, single or double stranded, or a hybrid thereof. The term also encompasses RNA/DNA hybrids. An “isolated” nucleic acid molecule is one that is substantially separated from other nucleic acid molecules which are present in the natural source of the nucleic acid (i.e., sequences encoding other polypeptides). For example, a cloned nucleic acid is considered isolated. A nucleic acid is also considered isolated if it has been altered by human intervention, or placed in a locus or location that is not its natural site, or if it is introduced into a cell by transformation. Moreover, an isolated nucleic acid molecule, such as a cDNA molecule, can be free from some of the other cellular material with which it is naturally associated, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. While it may optionally encompass untranslated sequence located at both the 3' and 5' ends of the coding region of a gene, it may be preferable to remove the sequences which naturally flank the coding region in its naturally occurring replicon.

[0046] As used herein, the term "environmental stress" refers to a sub-optimal condition associated with salinity, drought, nitrogen, temperature, metal, chemical, pathogenic, or oxidative stresses, or any combination thereof. The terms "water use efficiency" and "WUE" refer to the amount of organic matter produced by a plant divided by the amount of water used by the plant in producing it, i.e., the dry weight of a plant in relation to the plant's water use. As used herein, the term "dry weight" refers to everything in the plant other than water, and includes, for example, carbohydrates, proteins, oils, and mineral nutrients.

[0047] Any plant species may be transformed to create a transgenic plant in accordance with the invention. The transgenic plant of the invention may be a dicotyledonous plant or a monocotyledonous plant. For example and without limitation, transgenic plants of the invention may be derived from any of the following diclotyledonous plant families: Leguminosae, including plants such as pea, alfalfa and soybean; Umbelliferae, including plants such as carrot and celery; Solanaceae, including the plants such as tomato, potato, aubergine, tobacco, and pepper; Cruciferae, particularly the genus Brassica, which includes plant such as oilseed rape, beet, cabbage, cauliflower and broccoli); and A. thaliana; Compositae, which includes plants such as lettuce; Malvaceae, which includes cotton; Fabaceae, which includes plants such as peanut, and the like. Transgenic plants of the invention may be derived from monocotyledonous plants, such as, for example, wheat, barley, sorghum, millet, rye, triticale, maize, rice, oats and sugarcane. Transgenic plants of the invention are also embodied as trees such as apple, pear, quince, plum, cherry, peach, nectarine, apricot, papaya, mango, and other woody species including coniferous and deciduous trees such as poplar, pine, sequoia, cedar, oak, and the like. Especially preferred are Arabidopsis thaliana, Nicotiana tabacum, oilseed rape, soybean, corn (maize), wheat, linseed, potato and tagetes.

[0048] As shown in Table 1, one embodiment of the invention is a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a CAAX amino terminal protease family protein. The transgenic plant of this embodiment may comprise any polynucleotide encoding a CAAX amino terminal protease family protein. The transgenic plant of this embodiment comprises a polynucleotide encoding a CAAX amino terminal protease family protein having a sequence comprising amino acids 1 to 301 of SEQ ID NO:2; and a protein having a sequence comprising amino acids 1 to 293 of SEQ ID NO:4.

[0049] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a prenyl-dependent CAAX protease. The transgenic plant of this embodiment may comprise any polynucleotide encoding a prenyl-dependent CAAX protease. The transgenic plant of this embodiment comprises a polynucleotide encoding a prenyl-dependent CAAX protease having a sequence comprising amino acids 1 to 311 of SEQ ID NO:6; a protein having a sequence comprising amino acids 1 to 313 of SEQ ID NO:8; a protein having a sequence comprising amino acids 1 to 269 of SEQ ID NO:10.

[0050] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a SAR8.2 protein precursor. The transgenic plant of this embodiment may comprise any polynucleotide encoding a SAR8.2 protein precursor. The transgenic plant of this embodiment comprises a polynucleotide encoding a SAR8.2 protein precursor having a sequence comprising amino acids 1 to 86 of SEQ ID NO:12.

[0051] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a putative membrane protein. The transgenic plant of this embodiment may comprise any polynucleotide encoding a putative membrane protein. The transgenic plant of this embodiment comprises a polynucleotide encoding a putative membrane protein having a sequence comprising amino acids 1 to 696 of SEQ ID NO:14.

[0052] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a protein phosphatase 2C protein. The transgenic plant of this embodiment may comprise any polynucleotide encoding a protein phosphatase 2C protein. The transgenic plant of this embodiment comprises a polynucleotide encoding a protein phosphatase 2C protein having a sequence comprising amino acids 1 to 284 of SEQ ID NO:16; a protein having a sequence comprising amino acids 1 to 384 of SEQ ID NO:18; a protein having a sequence comprising amino acids 1 to 346 of SEQ ID NO:20; a protein having a sequence comprising amino acids 1 to 375 of SEQ ID NO:22; a protein having a sequence comprising amino acids 1 to 390 of SEQ ID NO:24; a protein having a sequence comprising amino acids 1 to 398 of SEQ ID NO:26; a protein having a sequence comprising amino acids 1 to 399 of SEQ ID NO:28; a protein having a sequence comprising amino acids 1 to 399 of SEQ ID NO:30; a protein having a sequence comprising amino acids 1 to 399 of SEQ ID NO:32; a protein having a sequence comprising amino acids 1 to 276 of SEQ ID NO:34.

[0053] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a mitochondrial carrier protein. The transgenic plant of this embodiment may comprise any polynucleotide encoding a mitochondrial carrier protein. The transgenic plant of this embodiment comprises a polynucleotide encoding a mitochondrial carrier protein having a sequence comprising amino acids 1 to 303 of SEQ ID NO:36; a protein having a sequence comprising amino acids 1 to 315 of SEQ ID NO:38; a protein having a sequence comprising amino acids 1 to 289 of SEQ ID NO:40; a protein having a sequence comprising amino acids 1 to 303 of SEQ ID NO:42; a protein having a sequence comprising amino acids 1 to 299 of SEQ ID NO:44; a protein having a sequence comprising amino acids 1 to 299 of SEQ ID NO:46; a protein having a sequence comprising amino acids 1 to 311 of SEQ ID NO:48.

[0054] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a protein kinase. The transgenic plant of this embodiment may comprise any polynucleotide encoding a protein kinase. The transgenic plant of this embodiment comprises a polynucleotide encoding a protein kinase having a sequence comprising amino acids 1 to 356 of SEQ ID NO:50; a protein having a sequence comprising amino acids 1 to 364 of SEQ ID NO:52; a protein having a sequence comprising amino acids 1 to 361 of SEQ ID NO:54; a protein having a sequence comprising amino acids 1 to 370 of SEQ ID NO:56; a protein having a sequence comprising amino acids 1 to 377 of SEQ ID NO:58; a protein having a sequence comprising amino acids 1 to 382 of SEQ ID NO:60.

[0055] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a peptidyl prolyl isomerase. The transgenic plant of this embodiment may comprise any polynucleotide encoding a peptidyl prolyl isomerase. The transgenic plant of this embodiment comprises a polynucleotide encoding a peptidyl prolyl isomerase having a sequence comprising amino acids 1 to 523 of SEQ ID NO:62.

[0056] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding an unknown protein 1. The transgenic plant of this embodiment may comprise any polynucleotide encoding an unknown protein 1. The transgenic plant of this embodiment comprises a polynucleotide encoding a unknown protein 1 having a sequence comprising amino acids 1 to 111 of SEQ ID NO:64.

[0057] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding an unknown protein 2. The transgenic plant of this embodiment may comprise any polynucleotide encoding an unknown protein 2. The transgenic plant of this embodiment comprises a polynucleotide encoding a unknown protein 2 having a sequence comprising amino acids 1 to 104 of SEQ ID NO:66.

[0058] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a ornithine decarboxylase. The transgenic plant of this embodiment may comprise any polynucleotide encoding a ornithine decarboxylase. The transgenic plant of this embodiment comprises a polynucleotide encoding a ornithine decarboxylase having a sequence comprising amino acids 1 to 466 of SEQ ID NO:68.

[0059] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a glutathione reductase. The transgenic plant of this embodiment may comprise any polynucleotide encoding a glutathione reductase. The transgenic plant of this embodiment comprises a polynucleotide encoding a glutathione reductase having a sequence comprising amino acids 1 to 483 of SEQ ID NO:70.

[0060] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding an unknown protein 3. The transgenic plant of this embodiment may comprise any polynucleotide encoding a unknown protein 3. The transgenic plant of this embodiment comprises a polynucleotide encoding a unknown protein 3 having a sequence comprising amino acids 1 to 129 of SEQ ID NO:72.

[0061] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a protein phosphatase 2A protein. The transgenic plant of this embodiment may comprise any polynucleotide encoding a protein phosphatase 2A protein. The transgenic plant of this embodiment comprises a polynucleotide encoding a protein phosphatase 2A protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:74; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:76; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:78; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:80; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:82; a protein having a sequence comprising amino acids 1 to 307 of SEQ ID NO:84; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:86; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:88; a protein having a sequence comprising amino acids 1 to 306 of SEQ ID NO:90.

[0062] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a MEK1 protein kinase. The transgenic plant of this embodiment may comprise any polynucleotide encoding a MEK1 protein kinase. The transgenic plant of this embodiment comprises a polynucleotide encoding a MEK1 protein kinase having a sequence comprising amino acids 1 to 355 of SEQ ID NO:92; a protein having a sequence comprising amino acids 1 to 355 of SEQ ID NO:94; a protein having a sequence comprising amino acids 1 to 338 of SEQ ID NO:96; a protein having a sequence comprising amino acids 1 to 350 of SEQ ID NO:100.

[0063] In another embodiment, the invention provides a transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding an AP2 domain containing transcription factor. The transgenic plant of this embodiment may comprise any polynucleotide encoding a AP2 domain containing transcription factor. The transgenic plant of this embodiment comprises a polynucleotide encoding a AP2 domain containing transcription factor having a sequence comprising amino acids 1 to 197 of SEQ ID NO:98.

[0064] The invention further provides a seed produced by a transgenic plant expressing polynucleotide listed in Table 1, wherein the seed contains the polynucleotide, and wherein the plant is true breeding for increased growth and/or yield under normal or stress conditions and/or increased tolerance to an environmental stress as compared to a wild type variety of the plant. The invention also provides a product produced by or from the transgenic plants expressing the polynucleotide, their plant parts, or their seeds. The product can be obtained using various methods well known in the art. As used herein, the word “product” includes, but not limited to, a foodstuff, feedstuff, a food supplement, feed supplement, cosmetic or pharmaceutical. Foodstuffs are regarded as compositions used for nutrition or for supplementing nutrition. Animal feedstuffs and animal feed supplements, in particular, are regarded as foodstuffs. The invention further provides an agricultural product produced by any of the transgenic plants, plant parts, and plant seeds. Agricultural products include, but are not limited to, plant extracts, proteins, amino acids, carbohydrates, fats, oils, polymers, vitamins, and the like.

[0065] In a preferred embodiment, an isolated polynucleotide of the invention comprises a polynucleotide having a sequence selected from the group consisting of the polynucleotide sequences listed in Table 1. These polynucleotides may comprise sequences of the coding region, as well as 5' untranslated sequences and 3' untranslated sequences.

[0066] A polynucleotide of the invention can be isolated using standard molecular biology techniques and the sequence information provided herein, for example, using an automated DNA synthesizer.

[0067] "Homologs" are defined herein as two nucleic acids or polypeptides that have similar, or substantially identical, nucleotide or amino acid sequences, respectively. Homologs include allelic variants, analogs, and orthologs, as defined below. As used herein, the term "analogs" refers to two nucleic acids that have the same or similar function, but that have evolved separately in unrelated organisms. As used herein, the term "orthologs" refers to two nucleic acids from different species, but that have evolved from a common ancestral gene by speciation. The term homolog further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Table 1 due to degeneracy of the genetic code and thus encode the same polypeptide. As used herein, a "naturally occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural polypeptide).

[0068] To determine the percent sequence identity of two amino acid sequences (e.g., one of the polypeptide sequences of Table 1 and a homolog thereof), the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one polypeptide for optimal alignment with the other polypeptide or nucleic acid). The amino acid residues at corresponding amino acid positions are then compared. When a position in one sequence is occupied by the same amino acid residue as the corresponding position in the other sequence then the molecules are identical at that position. The same type of comparison can be made between two nucleic acid sequences.

[0069] Preferably, the isolated amino acid homologs, analogs, and orthologs of the polypeptides of the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99%, or more identical to an entire amino acid sequence identified in Table 1. In another preferred embodiment, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which is at least about 40-60%, preferably at least about 60-70%, more preferably at least about 70-75%, 75-80%, 80-85%, 85-90%, or 90-95%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, or more identical to a nucleotide sequence shown in Table 1.

[0070] For the purposes of the invention, the percent sequence identity between two nucleic acid or polypeptide sequences is determined using the Vector NTI 9.0 (PC) software package (Invitrogen, 1600 Faraday Ave., Carlsbad, CA92008). A gap opening penalty of 15 and a gap extension penalty of 6.66 are used for determining the percent identity of two nucleic acids. A gap opening penalty of 10 and a gap extension penalty of 0.1 are used for determining the percent identity of two polypeptides. All other parameters are set at the default settings. For purposes of a multiple alignment (Clustal W algorithm), the gap opening penalty is 10, and the gap extension penalty is 0.05 with blosum62 matrix. It is to be understood that for the purposes of determining sequence identity when comparing a DNA sequence to an RNA sequence, a thymidine nucleotide is equivalent to a uracil nucleotide.

[0071] Nucleic acid molecules corresponding to homologs, analogs, and orthologs of the polypeptides listed in Table 1 can be isolated based on their identity to said polypeptides, using the polynucleotides encoding the respective polypeptides or primers based thereon, as hybridization probes according to standard hybridization techniques under stringent hybridization conditions. As used herein with regard to hybridization for DNA to a DNA blot, the term “stringent conditions” refers to hybridization overnight at 60°C in 10X Denhart’s solution, 6X SSC, 0.5% SDS, and 100 µg/ml denatured salmon sperm DNA. Blots are washed sequentially at 62°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS, and finally 0.1X SSC/0.1% SDS. As also used herein, in a preferred embodiment, the phrase “stringent conditions” refers to hybridization in a 6X SSC solution at 65°C. In another embodiment, “highly stringent conditions” refers to hybridization overnight at 65°C in 10X Denhart’s solution, 6X SSC, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA. Blots are washed sequentially at 65°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS, and finally 0.1X SSC/0.1% SDS. Methods for performing nucleic acid hybridizations are well known in the art. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent or highly stringent conditions to a nucleotide sequence listed in Table 1 corresponds to a naturally occurring nucleic acid molecule.

[0072] There are a variety of methods that can be used to produce libraries of potential homologs from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene is then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential sequences. Methods for synthesizing degenerate oligonucleotides are known in the art.

[0073] Additionally, optimized nucleic acids can be created. Preferably, an optimized nucleic acid encodes a polypeptide that has a function similar to those of the polypeptides listed in Table 1 and/or modulates a plant’s growth and/or yield under normal and/or water-limited conditions and/or tolerance to an environmental stress, and more preferably increases a plant’s growth and/or yield under normal and/or water-limited conditions and/or tolerance to an environmental stress upon its overexpression in the plant. As used herein, “optimized” refers to a nucleic acid that is genetically engineered to increase its expression in a given plant or animal. To provide plant optimized nucleic acids, the DNA sequence of the gene can be modified to: 1) comprise codons preferred by highly expressed plant genes; 2) comprise an A+T content in nucleotide base composition to that substantially found in plants; 3) form a plant initiation sequence; 4) to eliminate sequences that cause destabilization, inappropriate polyadenylation, degradation and termination of RNA, or that form secondary structure hairpins or RNA splice sites; or 5) elimination of antisense open reading frames. Increased expression of nucleic acids in plants can be achieved by utilizing the distribution frequency of codon usage in plants in general or in a particular plant. Methods for optimizing nucleic acid expression in plants can be found in EPA 0359472; EPA 0385962; PCT Application No. WO 91/16432; U.S. Patent No. 5,380,831; U.S. Patent No. 5,436,391; Perlack et al., 1991, Proc. Natl. Acad. Sci. USA 88:3324-3328; and Murray et al., 1989, Nucleic Acids Res. 17:477-498.

[0074] An isolated polynucleotide of the invention can be optimized such that its distribution frequency of codon usage deviates, preferably, no more than 25% from that of highly expressed plant genes and, more preferably, no more than about 10%. In addition, consideration is given to the percentage G+C content of the degenerate third base (monocotyledons appear to favor G+C in this position, whereas dicotyledons do not). It is also recognized that the XCG (where X is A, T, C, or G) nucleotide is the least preferred codon in dicots, whereas the XTA codon is avoided in both monocots and dicots. Optimized nucleic acids of this invention also preferably have CG and TA doublet avoidance indices closely approximating those of the chosen host plant. More preferably, these indices deviate from that of the host by no more than about 10-15%.

[0075] The invention further provides an isolated recombinant expression vector comprising a polynucleotide as described above, wherein expression of the vector in a host cell results in the plant's increased growth and/or yield under normal or water-limited conditions and/or increased tolerance to environmental stress as compared to a wild type variety of the host cell. The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. As used herein with respect to a recombinant expression vector, “operatively linked” is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in a bacterial or plant host cell when the vector is introduced into the host cell). The term “regulatory sequence” is intended to include promoters, enhancers, and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are well known in the art. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides encoded by nucleic acids as described herein.

[0076] Plant gene expression should be operatively linked to an appropriate promoter conferring gene expression in a timely, cell specific, or tissue specific manner. Promoters useful in the expression cassettes of the invention include any promoter that is capable of initiating transcription in a plant cell. Such promoters include, but are not limited to, those that can be obtained from plants, plant viruses, and bacteria that contain genes that are expressed in plants, such as Agrobacterium and Rhizobium.

[0077] The promoter may be constitutive, inducible, developmental stage-preferred, cell type-preferred, tissue-preferred, or organ-preferred. Constitutive promoters are active under most conditions. Examples of constitutive promoters include the CaMV 19S and 35S promoters, the sX CaMV 35S promoter, the Sep1 promoter, the rice actin promoter, the Arabidopsis actin promoter, the ubiquitan promoter, pEmu, the figwort mosaic virus 35S promoter, the Smas promoter, the super promoter (U.S. Patent No. 5, 955,646), the GRP1-8 promoter, the cinnamyl alcohol dehydrogenase promoter (U.S. Patent No. 5,683,439), promoters from the T-DNA of Agrobacterium, such as mannopine synthase, nopaline synthase, and octopine synthase, the small subunit of ribulose biphosphate carboxylase (ssu-RUBISCO) promoter, and the like.

[0078] Inducible promoters are preferentially active under certain environmental conditions, such as the presence or absence of a nutrient or metabolite, heat or cold, light, pathogen attack, anaerobic conditions, and the like. For example, the hsp80 promoter from Brassica is induced by heat shock; the PPDK promoter is induced by light; the PR-1 promoters from tobacco, Arabidopsis, and maize are inducible by infection with a pathogen; and the Adh1 promoter is induced by hypoxia and cold stress. Plant gene expression can also be facilitated via an inducible promoter (For a review, see Gatz, 1997, Annu. Rev. Plant Physiol. Plant Mol. Biol. 48:89-108). Chemically inducible promoters are especially suitable if gene expression is wanted to occur in a time specific manner. Examples of such promoters are a salicylic acid inducible promoter (PCT Application No. WO 95/19443), a tetracycline inducible promoter (Gatz et al., 1992, Plant J. 2: 397-404), and an ethanol inducible promoter (PCT Application No. WO 93/21334).

[0079] In one preferred embodiment of the present invention, the inducible promoter is a stress-inducible promoter. For the purposes of the invention, stress-inducible promoters are preferentially active under one or more of the following stresses: sub-optimal conditions associated with salinity, drought, nitrogen, temperature, metal, chemical, pathogenic, and oxidative stresses. Stress inducible promoters include, but are not limited to, Cor78 (Chak et al., 2000, Planta 210:875-883; Hovath et al., 1993, Plant Physiol. 103:1047-1053), Cor15a (Artus et al., 1996, PNAS 93(23):13404-09), Rci2A (Medina et al., 2001, Plant Physiol. 125:1655-66; Nylander et al., 2001, Plant Mol. Biol. 45:341-52; Navarre and Goffeau, 2000, EMBO J. 19:2515-24; Capel et al., 1997, Plant Physiol. 115:569-76), Rd22 (Xiong et al., 2001, Plant Cell 13:2063-83; Abe et al., 1997, Plant Cell 9:1859-68; Iwasaki et al., 1995, Mol. Gen. Genet. 247:391-8), cDet6 (Lang and Palve, 1992, Plant Mol. Biol. 20:951-62), ADH1 (Hoeren et al., 1998, Genetics 149:479-90), KAT1 (Nakamura et al., 1995, Plant Physiol. 109:371-4), KST1 (Müller-Röber et al., 1995, EMBO 14:2409-16), Rha1 (Terryn et al., 1993, Plant Cell 5:1761-9; Terryn et al., 1992, FEBS Lett. 299(3):287-90), ARSK1 (Atkinson et al., 1997, GenBank Accession # L22302, and PCT Application No. WO 97/20057), PtxA (Plesch et al., GenBank Accession # X67427), SbHRGP3 (Ahn et al., 1996, Plant Cell 8:1477-90), GH3 (Liu et al., 1994, Plant Cell 6:645-57), the pathogen inducible PRP1-gene promoter (Ward et al., 1993, Plant. Mol. Biol. 22:361-366), the heat inducible hsp80-promoter from tomato (U.S. Patent No. 5187267), cold inducible alpha-amylase promoter from potato (PCT Application No. WO 96/12814), or the wound-inducible pinII-promoter (European Patent No. 375091). For other examples of drought, cold, and salt-inducible promoters, such as the RD29A promoter, see Yamaguchi-Shinozalei et al., 1993, Mol. Gen. Genet. 236:331-340.

[0080] Developmental stage-preferred promoters are preferentially expressed at certain stages of development. Tissue and organ preferred promoters include those that are preferentially expressed in certain tissues or organs, such as leaves, roots, seeds, or xylem. Examples of tissue-preferred and organ-preferred promoters include, but are not limited to fruit-preferred, ovule-preferred, male tissue-preferred, seed-preferred, integument-preferred, tuber-preferred, stalk-preferred, pericarp-preferred, leaf-preferred, stigma-preferred, pollen-preferred, anther-preferred, petal-preferred, sepal-preferred, pedicel-preferred, silique-preferred, stem-preferred, root-preferred promoters, and the like. Seed-preferred promoters are preferentially expressed during seed development and/or germination. For example, seed-preferred promoters can be embryo-preferred, endosperm-preferred, and seed coat-preferred (See Thompson et al., 1989, BioEssays 10:108). Examples of seed-preferred promoters include, but are not limited to, cellulose synthase (celA), Cim1, gamma-zein, globulin-1, maize 19 kD zein (cZ19B1), and the like.

[0081] Other suitable tissue-preferred or organ-preferred promoters include the napin-gene promoter from rapeseed (U.S. Patent No. 5,608,152), the USP-promoter from Vicia faba (Baeumlein et al., 1991, Mol. Gen. Genet. 225(3): 459-67), the oleosin-promoter from Arabidopsis (PCT Application No. WO 98/45461), the phaseolin-promoter from Phaseolus vulgaris (U.S. Patent No. 5,504,200), the Bce4-promoter from Brassica (PCT Application No. WO 91/13980), or the legumin B4 promoter (LeB4; Baeumlein et al., 1992, Plant Journal, 2(2): 233-9), as well as promoters conferring seed specific expression in monocot plants like maize, barley, wheat, rye, rice, etc. Suitable promoters to note are the lpt2 or lpt1-gene promoter from barley (PCT Application No. WO 95/15389 and PCT Application No. WO 95/23230) or those described in PCT Application No. WO 99/16890 (promoters from the barley hordein-gene, rice glutelin gene, rice oryzin gene, rice prolamin gene, wheat gliadin gene, wheat glutelin gene, oat glutelin gene, Sorghum kasirin-gene, and rye secalin gene).

[0082] Other promoters useful in the expression cassettes of the invention include, but are not limited to, the major chlorophyll a/b binding protein promoter, histone promoters, the Ap3 promoter, the β-conglycin promoter, the napin promoter, the soybean lectin promoter, the maize 15kD zein promoter, the 22kD zein promoter, the 27kD zein promoter, the g-zein promoter, the waxy, shrunken 1, shrunken 2, and bronze promoters, the Zm13 promoter (U.S. Patent No. 5,086,169), the maize polygalacturonase promoters (PG) (U.S. Patent Nos. 5,412,085 and 5,545,546), and the SGB6 promoter (U.S. Patent No. 5,470,359), as well as synthetic or other natural promoters.

[0083] Additional flexibility in controlling heterologous gene expression in plants may be obtained by using DNA binding domains and response elements from heterologous sources (i.e., DNA binding domains from non-plant sources). An example of such a heterologous DNA binding domain is the LexA DNA binding domain (Brent and Ptashne, 1985, Cell 43:729-736).

[0084] In a preferred embodiment of the present invention, the polynucleotides listed in Table 1 are expressed in plant cells from higher plants (e.g., the spermatophytes, such as crop plants). A polynucleotide may be "introduced" into a plant cell by any means, including transfection, transformation or transduction, electroporation, particle bombardment, agroinfection, and the like. Suitable methods for transforming or transfecting plant cells are disclosed, for example, using particle bombardment as set forth in U.S. Pat. Nos. 4,945,050; 5,036,006; 5,100,792; 5,302,523; 5,464,765; 5,120,657; 6,084,154; and the like. More preferably, the transgenic corn seed of the invention may be made using Agrobacterium transformation, as described in U.S. Pat. Nos. 5,591,616; 5,731,179; 5,981,840; 5,990,387; 6,162,965; 6,420,630, U.S. patent application publication number 2002/0104132, and the like. Transformation of soybean can be performed using for example a technique described in European Patent No. EP 0424047, U.S. Patent No. 5,322,783, European Patent No.EP 0397 687, U.S. Patent No. 5,376,543, or U.S. Patent No. 5,169,770. A specific example of wheat transformation can be found in PCT Application No. WO 93/07256. Cotton may be transformed using methods disclosed in U.S. Pat. Nos. 5,004,863; 5,159,135; 5,846,797, and the like. Rice may be transformed using methods disclosed in U.S. Pat. Nos. 4,666,844; 5,350,688; 6,153,813; 6,333,449; 6,288,312; 6,365,807; 6,329,571, and the like. Other plant transformation methods are disclosed, for example, in U.S. Pat. Nos. 5,932,782; 6,153,811; 6,140,553; 5,969,213; 6,020,539, and the like. Any plant transformation method suitable for inserting a transgene into a particular plant may be used in accordance with the invention.

[0085] According to the present invention, the introduced polynucleotide may be maintained in the plant cell stably if it is incorporated into a non-chromosomal autonomous replicon or integrated into the plant chromosomes. Alternatively, the introduced polynucleotide may be present on an extra-chromosomal non-replicating vector and may be transiently expressed or transiently active.

[0086] Another aspect of the invention pertains to an isolated polypeptide having a sequence selected from the group consisting of the polypeptide sequences listed in Table 1. An "isolated" or "purified" polypeptide is free of some of the cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of a polypeptide in which the polypeptide is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of a polypeptide of the invention having less than about 30% (by dry weight) of contaminating polypeptides, more preferably less than about 20% of contaminating polypeptides, still more preferably less than about 10% of contaminating polypeptides, and most preferably less than about 5% contaminating polypeptides.

[0087] The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one skilled in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities are abundant and well known to one skilled in the art.

[0088] The invention is also embodied in a method of producing a transgenic plant comprising at least one polynucleotide listed in Table 1, wherein expression of the polynucleotide in the plant results in the plant's increased growth and/or yield under normal or water-limited conditions and/or increased tolerance to an environmental stress as compared to a wild type variety of the plant comprising the steps of: (a) introducing into a plant cell an expression vector comprising at least one polynucleotide listed in Table 1, and (b) generating from the plant cell a transgenic plant that expresses the polynucleotide, wherein expression of the polynucleotide in the transgenic plant results in the plant's increased growth and/or yield under normal or water-limited conditions and/or increased tolerance to environmental stress as compared to a wild type variety of the plant. The plant cell may be, but is not limited to, a protoplast, gamete producing cell, and a cell that regenerates into a whole plant. As used herein, the term “transgenic” refers to any plant, plant cell, callus, plant tissue, or plant part, that contains at least one recombinant polynucleotide listed in Table 1. In many cases, the recombinant polynucleotide is stably integrated into a chromosome or stable extra-chromosomal element, so that it is passed on to successive generations.

[0089] The present invention also provides a method of increasing a plant's growth and/or yield under normal or water-limited conditions and/or increasing a plant's tolerance to an environmental stress comprising the steps of increasing the expression of at least one polynucleotide listed in Table 1 in the plant. Expression of a protein can be increased by any method known to those of skill in the art.

[0090] The effect of the genetic modification on plant growth and/or yield and/or stress tolerance can be assessed by growing the modified plant under normal and.or less than suitable conditions and then analyzing the growth characteristics and/or metabolism of the plant. Such analysis techniques are well known to one skilled in the art, and include dry weight, wet weight, polypeptide synthesis, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, metabolite composition, etc., using methods known to those of skill in biotechnology.

[0091] The invention is further illustrated by the following examples, which are not to be construed in any way as imposing limitations upon the scope thereof.

EXAMPLE 1

Cloning of cDNAs

[0092] cDNAs were isolated from proprietary libraries of the respective plant species using known methods. Sequences were processed and annotated using bioinformatics analyses. The degrees of amino acid identity and similarity of the isolated sequences to the respective closest known public sequences are indicated in Tables 2 through 18 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 2
Comparison of At2g20725 (SEQ ID NO: 2) to known CAAX amino terminal protease proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_565483	A. thaliana	99.70%
ABE87113	Medicago truncatula	27.00%
NP_563943	A. thaliana	25.60%
AAU90306	Solanum tuberosum	25.20%
AAM65055	A. thaliana	25.00%

Table 3
Comparison of At3g26085 (SEQ ID NO: 4) to known CAAX amino terminal protease proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_566788	A. thaliana	100.00%
BAC43478	A. thaliana	99.70%
AAM63917	A. thaliana	99.30%
NP_001078210	A. thaliana	91.00%
BAB01072	A. thaliana	65.30%

Table 4
Comparison of AtFACE-2 (SEQ ID NO: 6) to known prenyl-dependent CAAX proteases

Public Database Accession #	Species	Sequence Identity (%)
NP_850262	A. thaliana	100.00%
BAC43705	A. thaliana	99.70%
CAN61196	Vitis vinifera	36.70%
XP_695285	Danio rerio	32.70%
XP_001342272	D. rerio	32.70%

Table 5
Comparison of CASAR82A (SEQ ID NO: 12) to known SAR8.2 protein precursors

Public Database Accession #	Species	Sequence Identity (%)
AAF18935	C. annuum	100.00%
AAL56986	C. annuum	97.70%
AAL16783	C. annuum	93.00%
AAL16782	C. annuum	91.90%
AAR97871	C. annuum	52.30%

Table 6
Comparison of b3358 (SEQ ID NO: 14) to known putative membrane proteins

Public Database Accession #	Species	Sequence Identity (%)
YP_312284	Shigella sonnei	99.90%
ZP_00715046	E. coli	99.90%
ZP_00725390	E. coli	99.60%
AP_004431	E. coli	99.40%
YP_858957	E. coli	99.40%

Table 7

Comparison of EST564 (SEQ ID NO: 16) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
ABF93864	O. sativa	56.40%
NP_974411	A. thaliana	51.60%
AAC35951	Mesembryanthemum crystallinum	51.10%
EAZ25504	O. sativa	45.70%
EAZ02383	O. sativa	43.40%

Table 8

Comparison of EST390 (SEQ ID NO:36) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_172866	A. thaliana	63.50%
AAT66766	Solanum demissum	60.80%
CAH67091	O. sativa	60.00%
CAE01569	O. sativa	59.70%
CAN75338	V. vinifera	59.50%

Table 9

Comparison of EST257 (SEQ ID NO: 50) to known protein kinases

Public Database Accession #	Species	Sequence Identity (%)
NP_001043682	O. sativa	62.20%
CAN82019	V. vinifera	62.10%
AAR01726	O. sativa	61.10%
NP_001056408	O. sativa	61.10%
CAN64754	V. vinifera	60.90%

Table 10

Comparison of EST465 (SEQ ID NO: 62) to known peptidyl prolyl isomerases

Public Database Accession #	Species	Sequence Identity (%)
AAC39445	A. thaliana	54.30%
ABE85899	M. truncatula	54.20%
CAB88363	A. thaliana	54.10%
NP_566993	A. thaliana	53.80%
NP_001050182	O. sativa	53.00%

Table 11

Comparison of YBL109w (SEQ ID NO: 64) to unknown protein 1

Public Database Accession #	Species	Sequence Identity (%)
CAA84936	S. cerevisiae	49.50%
P38898	S. cerevisiae	43.10%

Table 12

Comparison of YBL100c (SEQ ID NO: 66) to unknown protein 2

Public Database Accession #	Species	Sequence Identity (%)
P38168	S. cerevisiae	100.00%

Table 13

Comparison of YKL184w (SEQ ID NO: 68) to known ornithine decarboxylases

Public Database Accession #	Species	Sequence Identity (%)
NP_012737	S. cerevisiae	100.00%
XP_445434	Candida glabrata	70.90%
XP_451651	Kluyveromyces lactis	60.30%
NP_984947	Ashbya gossypii	57.40%
XP_001385782	P. stipitis	49.80%

Table 14

Comparison of YPL091w (SEQ ID NO: 70) to known glutathione reductases

Public Database Accession #	Species	Sequence Identity (%)
NP_015234	S. cerevisiae	100.00%
AAA92575	S. cerevisiae	96.70%
BAA07109	S. cerevisiae	95.70%
XP_447042	C. glabrata	79.90%
XP_455036	K. lactis	73.30%

Table 15

Comparison of TA54587433 (SEQ ID NO: 72) to unknown protein 3

Public Database Accession #	Species	Sequence Identity (%)
EAY88696	O. sativa	22.80%
EAZ25723	O. sativa	21.90%
NP_001049087	O. sativa	21.20%

Table 16

Comparison of ZM68532504 (SEQ ID NO: 74) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
AAC72838	O. sativa	95.40%
AAA91806	O. sativa	94.10%
BAA92697	Vicia faba	93.10%
AAQ67226	Lycopersicon esculentum	92.80%
BAD17175	O. sativa	92.80%

Table 17

Comparison of ZM59202533 (SEQ ID NO: 92) to known MEK1 protein kinases

Public Database Accession #	Species	Sequence Identity (%)
AAC83393	Z. mays	100.00%
ABG45894	O. sativa	92.70%
NP_001043164	O. sativa	85.90%
BAB32405	Nicotiana tabacum	77.80%
CAC24705	N. tabacum	77.20%

Table 18

Comparison of BN42671700 (SEQ ID NO: 98) to known AP2 domain containing transcription factors

Public Database Accession #	Species	Sequence Identity (%)
NP_177631	A. thaliana	58.60%
NP_173355	A. thaliana	56.70%
AAF82238	A. thaliana	54.80%

[0093] The full-length DNA sequence of the AtFACE-2 (SEQ ID NO: 5) was blasted against proprietary databases of canola, soybean, rice, maize, linseed, sunflower, and wheat cDNAs at an e value of e^{-10} (Altschul et al., 1997, Nucleic Acids Res. 25: 3389-3402). All the contig hits were analyzed for the putative full length sequences, and the longest clones representing the putative full length contigs were fully sequenced. Two homologs from maize were identified. The degree of amino acid identity of these sequences to the closest known public sequences is indicated in Tables 19 and 20 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 19

Comparison of ZM57353913 (SEQ ID NO: 8) to known prenyl-dependent CAAX proteases

Public Database Accession #	Species	Sequence Identity (%)
NP_850262	A. thaliana	52.20%
BAC43705	A. thaliana	52.20%
NP_001055298	O. sativa	42.10%
EAZ33973	O. sativa	36.60%
XP_001353747	Drosophila pseudoobscura	33.50%

Table 20

Comparison of ZM59252659 (SEQ ID NO: 10) to known prenyl-dependent CAAX proteases

Public Database Accession #	Species	Sequence Identity (%)
NP_850262	A. thaliana	47.00%
BAC43705	A. thaliana	47.00%
EAZ33973	O. sativa	41.10%
NP_001055298	O. sativa	38.30%
CAN61196	V. vinifera	31.90%

[0094] The full-length DNA sequence of EST564 (SEQ ID NO: 15) was blasted against proprietary databases of canola, soybean, rice, maize, linseed, sunflower, and wheat cDNAs at an e value of e^{-10} (Altschul et al., 1997, Nucleic Acids Res. 25: 3389-3402). All the contig hits were analyzed for the putative full length sequences, and the longest clones representing the putative full length contigs were fully sequenced. Six homologs from maize, two homologs from soybean, and one homolog from canola were identified. The degree of amino acid identity of these sequences to the closest known public sequences is indicated in Tables 21-29 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 21
Comparison of BN49502266 (SEQ ID NO: 18) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_195118	A. thaliana	91.10%
NP_001067133	O. sativa	63.20%
EAY83661	O. sativa	60.80%
EAZ21008	O. sativa	60.50%
CAN76780	V. vinifera	57.60%

Table 22
Comparison of GM49788080 (SEQ ID NO: 20) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
EAZ02383	O. sativa	75.60%
EAZ38299	O. sativa	75.30%
CAB90634	Fagus sylvatica	73.80%
EAZ25504	O. sativa	73.00%
AAC35951	M. crystallinum	72.80%

Table 23
Comparison of GM53049821 (SEQ ID NO: 22) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
CAN72598	V. vinifera	82.40%
NP_566566	A. thaliana	73.50%
AAM61747	A. thaliana	73.50%
BAA94987	A. thaliana	73.00%
NP_001051801	O. sativa	60.20%

Table 24

Comparison of ZM58462719 (SEQ ID NO: 24) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_001058597	O. sativa	91.10%
EAZ02383	O. sativa	81.20%
EAZ38299	O. sativa	81.00%
AAD11430	M. crystallinum	75.70%
CAB90634	F. sylvatica	74.20%

Table 25

Comparison of ZM61092633 (SEQ ID NO: 26) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_001065203	O. sativa	87.00%
AAK20060	O. sativa	86.00%
NP_001048899	O. sativa	80.70%
EAY88457	O. sativa	79.90%
ABE77197	Sorghum bicolor	77.20%

Table 26

Comparison of ZM62016485 (SEQ ID NO: 28) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
ABE77197	S. bicolor	90.70%
NP_001048899	O. sativa	86.20%
EAY88457	O. sativa	85.20%
NP_001065203	O. sativa	78.50%
AAK20060	O. sativa	77.80%

Table 27

Comparison of ZM62051019 (SEQ ID NO: 30) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
ABE77197	S. bicolor	92.50%
NP_001048899	O. sativa	88.00%
EAY88457	O. sativa	87.00%
NP_001065203	O. sativa	79.50%
AAK20060	O. sativa	78.80%

Table 28
Comparison of ZM65086957 (SEQ ID NO: 32) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
ABE77197	S. bicolor	91.00%
NP_001048899	O. sativa	86.50%
EAY88457	O. sativa	85.50%
NP_001065203	O. sativa	78.80%
AAK20060	O. sativa	78.00%

Table 29
Comparison of ZM68587657 (SEQ ID NO: 34) to known protein phosphatase 2C proteins

Public Database Accession #	Species	Sequence Identity (%)
EAZ02383	O. sativa	70.60%
EAZ38299	O. sativa	70.60%
AAC35951	M. crystallinum	69.80%
ABF93864	O. sativa	68.50%
NP_974411	A. thaliana	65.00%

[0095] The full-length DNA sequence of the EST390 (SEQ ID NO: 35) was blasted against proprietary databases of canola, soybean, rice, maize, linseed, sunflower, and wheat cDNAs at an e value of e^{-10} (Altschul et al., 1997, Nucleic Acids Res. 25: 3389-3402). All the contig hits were analyzed for the putative full length sequences, and the longest clones representing the putative full length contigs were fully sequenced. Four homologs from canola and two homologs from maize were identified. The degree of amino acid identity of these sequences to the closest known public sequences is indicated in Tables 30-35 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 30
Comparison of BN51363030 (SEQ ID NO: 38) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
CAN77545	V. vinifera	71.90%
BAE71294	Trifolium pratense	71.90%
NP_194188	A. thaliana	70.70%
AAU11466	Saccharum officinarum	70.60%
AAU11465	S. officinarum	69.90%

Table 31

Comparison of BN42986056 (SEQ ID NO: 40) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_179836	A. thaliana	74.80%
AAK44155	A. thaliana	74.50%
AAM63236	A. thaliana	74.20%
CAN77545	V. vinifera	67.70%
BAE71294	Trifolium pratense	65.50%

Table 32

Comparison of BN49389066 (SEQ ID NO: 42) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
AAY97866	L. esculentum	73.50%
CAA68164	Solanum tuberosum	73.50%
CAC84547	N. tabacum	73.30%
AAR06239	Citrus junos	73.00%
CAC84545	N. tabacum	73.00%

Table 33

Comparison of BN51339479 (SEQ ID NO: 44) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
CAC84545	N. tabacum	85.60%
CAC84547	N. tabacum	85.30%
AAR06239	C. junos	85.30%
CAA68164	S. tuberosum	85.30%
CAC12820	N. tabacum	85.30%

Table 34

Comparison of ZM57651070 (SEQ ID NO: 46) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_001066927	O. sativa	57.00%
NP_680566	A. thaliana	53.80%
BAF00711	A. thaliana	51.70%
CAN71674	V. vinifera	43.20%
CAN71674	V. vinifera	43.20%

Table 35
Comparison of ZM62073276 (SEQ ID NO: 48) to known mitochondrial carrier proteins

Public Database Accession #	Species	Sequence Identity (%)
AAU11471	S.officinarum	94.90%
NP_001054904	O. sativa	92.30%
BAA08105	Panicum miliaceum	86.20%
BAA08103	P. miliaceum	85.50%
EAY80779	O. sativa	82.90%

[0096] The full-length DNA sequence of the EST257 (SEQ ID NO: 49) was blasted against proprietary databases of canola, soybean, rice, maize, linseed, sunflower, and wheat cDNAs at an e value of e^{-10} (Altschul et al., 1997, Nucleic Acids Res. 25: 3389-3402). All the contig hits were analyzed for the putative full length sequences, and the longest clones representing the putative full length contigs were fully sequenced. Three homologs from maize, one homolog from linseed, and one sequence from wheat were identified. The degree of amino acid identity of these sequences to the closest known public sequences is indicated in Tables 36-40 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 36
Comparison of LU61665952 (SEQ ID NO: 52) to known protein kinases

Public Database Accession #	Species	Sequence Identity (%)
NP_566716	A. thaliana	75.10%
CAN82019	V. vinifera	74.50%
NP_193214	A. thaliana	74.50%
ABK06452	synthetic construct	73.00%
ABK06453	synthetic construct	72.30%

Table 37
Comparison of TA56863186 (SEQ ID NO: 54) to known protein kinases

Public Database Accession #	Species	Sequence Identity (%)
AAO72550	O. sativa	87.30%
NP_001046047	O. sativa	79.80%
EAZ01979	O. sativa	73.80%
NP_001058291	O. sativa	73.60%
AAO48744	O. sativa	73.40%

Table 38
Comparison of ZM62026837 (SEQ ID NO:56) to known protein kinases

Public Database Accession #	Species	Sequence Identity (%)
AAR01726	O. sativa	83.40%
NP_001050732	O. sativa	77.00%
EAY91142	O. sativa	76.30%
EAZ27891	O. sativa	76.00%
CAN82019	V. vinifera	73.30%

Table 39
Comparison of ZM65457595 (SEQ ID NO: 58) to known protein kinases

Public Database Accession #	Species	Sequence Identity (%)
NP_001056408	O. sativa	89.60%
AAO72572	O. sativa	87.20%
NP_001043682	O. sativa	81.50%
CAN64754	V. vinifera	79.80%
NP_199811	A. thaliana	77.20%

Table 40
Comparison of ZM67230154 (SEQ ID NO: 60) to known protein kinases

Public Database Accession #	Species	Sequence Identity (%)
NP_001043682	O. sativa	87.10%
NP_001056408	O. sativa	82.80%
AAO72572	O. sativa	80.80%
EAZ12861	O. sativa	79.20%
CAN64754	V. vinifera	77.50%

[0097] The full-length DNA sequence of the ZM68532504 (SEQ ID NO: 73) was blasted against proprietary databases of canola, soybean, rice, maize, linseed, sunflower, and wheat cDNAs at an e value of e^{-10} (Altschul et al., 1997, Nucleic Acids Res. 25: 3389-3402). All the contig hits were analyzed for the putative full length sequences, and the longest clones representing the putative full length contigs were fully sequenced. Two homologs from canola, two homologs from maize, one homolog from linseed, two sequences from rice and one sequence from sunflower were identified. The degree of amino acid identity of these sequences to the closest known public sequences is indicated in Tables 41-48 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 41
Comparison of BN42856089 (SEQ ID NO: 76) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_172514	A. thaliana	97.10%
AAM65099	A. thaliana	95.80%
AAQ67226	L. esculentum	95.40%
BAA92697	Vicia faba	95.10%
CAC11129	Fagus sylvatica	94.40%

Table 42
Comparison of BN43206527 (SEQ ID NO: 78) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
NP_172514	A. thaliana	97.40%
AAM65099	A. thaliana	96.10%
AAQ67226	L. esculentum	95.10%
BAA92697	V. faba	94.10%
AAQ67225	L. esculentum	94.10%

Table 43
Comparison of HA66872964 (SEQ ID NO: 80) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
P48579	H. annuus	99.30%
BAA92697	V. faba	93.50%
CAC11129	F. sylvatica	93.10%
BAA92698	V. faba	92.80%
Q9ZSE4	Hevea brasiliensis	92.80%

Table 44
Comparison of LU61662612 (SEQ ID NO: 82) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
AAQ67226	L. esculentum	94.10%
BAA92697	V. faba	94.10%
BAA92698	V. faba	94.10%
CAN74947	V. vinifera	93.50%
CAC11129	F. sylvatica	93.10%

Table 45
Comparison of OS32806943 (SEQ ID NO: 84) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
AAC72838	O. sativa	96.10%
BAD17175	O. sativa	95.80%
AAA91806	O. sativa	94.80%
AAQ67226	L. esculentum	93.20%
BAA92697	V. faba	93.20%

Table 46
Comparison of OS34738749 (SEQ ID NO: 86) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
AAQ67226	L. esculentum	97.70%
BAA92697	V. faba	97.10%
CAC11129	F. sylvatica	96.70%
BAA92698	V. faba	96.10%
AAQ67225	L. esculentum	96.10%

Table 47
Comparison of ZM59400933 (SEQ ID NO: 88) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
AAC72838	O. sativa	95.80%
AAA91806	O. sativa	94.40%
BAA92697	V. faba	92.80%
AAQ67226	L. esculentum	92.80%
AAQ67225	L. esculentum	92.80%

Table 48
Comparison of ZM62132060 (SEQ ID NO: 90) to known protein phosphatase 2A proteins

Public Database Accession #	Species	Sequence Identity (%)
AAC72838	O. sativa	95.10%
AAA91806	O. sativa	93.80%
BAA92697	V. faba	92.80%
AAQ67226	L. esculentum	92.50%
BAD17175	O. sativa	92.50%

[0098] The full-length DNA sequence of the ZM59202533 (SEQ ID NO: 91) was blasted against proprietary databases of canola, soybean, rice, maize, linseed, sunflower, and wheat cDNAs at an e value of e^{-10} (Altschul et al., 1997, Nucleic Acids Res. 25: 3389-3402). All the contig hits were analyzed for the putative full length sequences, and the longest clones representing the putative full length contigs were fully sequenced. Two homologs from canola and one homolog from maize were identified. The degree of amino acid identity of these sequences to the closest known public sequences is indicated in Tables 49-51 (Pairwise Comparison was used: gap penalty: 10; gap extension penalty: 0.1; score matrix: blosum62).

Table 49
Comparison of BN41901422 (SEQ ID NO: 94) to known MEK1 protein kinases

Public Database Accession #	Species	Sequence Identity (%)
ABF55661	synthetic construct	79.80%
NP_849446	A. thaliana	76.30%
AAQ96337	Vitis aestivalis	66.00%
AAL62336	G. max	64.10%
AAS21304	Petroselinum crispum	63.60%

Table 50
Comparison of BN47868329 (SEQ ID NO: 96) to known MEK1 protein kinases

Public Database Accession #	Species	Sequence Identity (%)
NP_188759	A. thaliana	72.30%
CAA68958	A. thaliana	72.00%
ABF55664	synthetic construct	70.90%
AAL91161	A. thaliana	70.10%
AAU04434	L. esculentum	66.40%

Table 51
Comparison of ZM68416988 (SEQ ID NO: 100) to known MEK1 protein kinases

Public Database Accession #	Species	Sequence Identity (%)
ABI93775	Oryza minuta	80.00%
NP_001056806	O. sativa	79.70%
ABP88102	O. sativa	78.90%
CAD45180	O. sativa	75.20%
ABI93776	O. minuta	72.40%

EXAMPLE 2

Well-watered Arabidopsis plants

The polynucleotides of Table 1 are ligated into a binary vector containing a selectable marker. The resulting recombinant vector contains the corresponding gene in the sense orientation under a constitutive promoter. The recombinant vectors are transformed into an Agrobacterium tumefaciens strain according to standard conditions. A. thaliana ecotype Col-0 or C24 are grown and transformed according to standard conditions. T1 and T2 plants are screened for resistance to the selection agent conferred by the selectable marker gene. T3 seeds are used in greenhouse or growth chamber experiments.

Approximately 3-5 days prior to planting, seeds are refrigerated for stratification. Seeds are then planted, fertilizer is applied and humidity is maintained using transparent domes. Plants are grown in a greenhouse at 22°C with photoperiod of 16 hours light/8 hours dark. Plants are watered twice a week.

At 19 and 22 days, plant area, leaf area, biomass, color distribution, color intensity, and growth rate for each plant are measured using using a commercially available imaging system. Biomass is calculated as the total plant leaf area at the last measuring time point. Growth rate is calculated as the plant leaf area at the last measuring time point minus the plant leaf area at the first measuring time point divided by the plant leaf area at the first measuring time point. Health index is calculated as the dark green leaf area divided by the total plant leaf area.

EXAMPLE 3

Nitrogen stress tolerant Arabidopsis plants

The polynucleotides of Table 1 are ligated into a binary vector containing a selectable marker. The resulting recombinant vector contains the corresponding gene in the sense orientation under a constitutive promoter. The recombinant vectors are transformed into an A. tumefaciens strain according to standard conditions. A. thaliana ecotype Col-0 or C24 are grown and transformed according to standard conditions. T1 and T2 plants are screened for resistance to the selection agent conferred by the selectable marker gene.

Plants are grown in flats using a substrate that contains no organic components. Each flat is wet with water before seedlings resistant to the selection agent are transplanted onto substrate. Plants are grown in a growth chamber set to 22°C with a 55% relative humidity with photoperiod set at 16h light/ 8h dark. A controlled low or high nitrogen nutrient solution is added to waterings on Days 12, 15, 22 and 29. Watering without nutrient solution occurs on Days 18, 25, and 32. Images of all plants in a tray are taken on days 26, 30, and 33 using a commercially available imaging system. At each imaging time point, biomass and plant phenotypes for each plant are measured including plant area, leaf area, biomass, color distribution, color intensity, and growth rate.

EXAMPLE 4

Stress-tolerant Rapeseed/Canola plants

[0099] Canola cotyledonary petioles of 4 day-old young seedlings are used as explants for tissue culture and transformed according to EP1566443. The commercial cultivar Westar (Agriculture Canada) is the standard variety used for transformation, but other varieties can be used. A. tumefaciens GV3101:pMP90RK containing a binary vector is used for canola transformation. The standard binary vector used for transformation is pSUN (WO02/00900), but many different binary vector systems have been described for plant transformation (e.g. An, G. in Agrobacterium Protocols, Methods in Molecular Biology vol 44, pp 47-62, Gartland KMA and MR Davey eds. Humana Press, Totowa, New Jersey). A plant gene expression cassette comprising a selection marker gene, a plant promoter, and a polynucleotide of Table 1 is employed. Various selection marker genes can be used including the mutated acetohydroxy acid synthase (AHAS) gene disclosed in US Pat. Nos. 5,767,366 and 6,225,105. A suitable promoter is used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription.

[00100] Canola seeds are surface-sterilized in 70% ethanol for 2 min, incubated for 15 min in 55°C warm tap water and then in 1.5% sodium hypochlorite for 10 minutes, followed by three rinses with sterilized distilled water. Seeds are then placed on MS medium without hormones, containing Gamborg B5 vitamins, 3% sucrose, and 0.8% Oxoidagar.

Seeds are germinated at 24°C for 4 days in low light (< 50 µMol/m^{2}s, 16 hours light). The cotyledon petiole explants with the cotyledon attached are excised from the in vitro seedlings, and inoculated with Agrobacterium by dipping the cut end of the petiole explant into the bacterial suspension. The explants are then cultured for 3 days on MS medium including vitamins containing 3.75 mg/l BAP, 3% sucrose, 0.5 g/l MES, pH 5.2, 0.5 mg/l GA3, 0.8% Oxoidagar at 24°C, 16 hours of light. After three days of co-cultivation with Agrobacterium, the petiole explants are transferred to regeneration medium containing 3.75 mg/l BAP, 0.5 mg/l GA3, 0.5 g/l MES, pH 5.2, 300 mg/l timentin and selection agent until shoot regeneration. As soon as explants start to develop shoots, they are transferred to shoot elongation medium (A6, containing full strength MS medium including vitamins, 2% sucrose, 0.5% Oxoidagar, 100 mg/l myo-inositol, 40 mg/l adenine sulfate, 0.5 g/l MES, pH 5.8, 0.0025 mg/l BAP, 0.1 mg/l IBA, 300 mg/l timentin and selection agent).

[00101] Samples from both in vitro and greenhouse material of the primary transgenic plants (T0) are analyzed by qPCR using TaqMan probes to confirm the presence of T-DNA and to determine the number of T-DNA integrations.

[00102] Seed is produced from the primary transgenic plants by self-pollination. The second-generation plants are grown in greenhouse conditions and self-pollinated. The plants are analyzed by qPCR using TaqMan probes to confirm the presence of T-DNA and to determine the number of T-DNA integrations. Homozygous transgenic, heterozygous transgenic and azygous (null transgenic) plants are compared for their stress tolerance, for example, in the assays described in Examples 2 and 3, and for yield, both in the greenhouse and in field studies.

EXAMPLE 5

Screening for stress-tolerant rice plants

[00103] Transgenic rice plants comprising a polynucleotide of Table 1 are generated using known methods. Approximately 15 to 20 independent transformants (T0) are generated. The primary transformants are transferred from tissue culture chambers to a greenhouse for growing and harvest of T1 seeds. Five events of the T1 progeny segregated 3:1 for presence/absence of the transgene are retained. For each of these events, 10 T1 seedlings containing the transgene (hetero- and homozygotes), and 10 T1 seedlings lacking the transgene (nullizygotes) are selected by visual marker screening. The selected T1 plants are transferred to a greenhouse. Each plant receives a unique barcode label to link unambiguously the phenotyping data to the corresponding plant. The selected T1 plants are grown on soil in 10 cm diameter pots 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%. Transgenic plants and the corresponding nullizygotes are grown side-by-side at random positions. From the stage of sowing until the stage of maturity, the plants are passed several times through a digital imaging cabinet. At each time point digital, images (2048x1536 pixels, 16 million colours) of each plant are taken from at least 6 different angles.

[00104] The data obtained in the first experiment with T1 plants are confirmed in a

second experiment with T2 plants. Lines that have the correct expression pattern are selected for further analysis. Seed batches from the positive plants (both hetero- and homozygotes) in T1 are screened by monitoring marker expression. For each chosen event, the heterozygote seed batches are then retained for T2 evaluation. Within each seed batch, an equal number of positive and negative plants are grown in the greenhouse for evaluation.

[00105] Transgenic plants are screened for their improved growth and/or yield and/or stress tolerance, for example, using the assays described in Examples 2 and 3, and for yield, both in the greenhouse and in field studies.

EXAMPLE 6

Stress-tolerant soybean plants

[00106] The polynucleotides of Table 1 are transformed into soybean using the methods described in commonly owned copending international application number WO 2005/121345, the contents of which are incorporated herein by reference.

[00107] The transgenic plants generated are then screened for their improved growth under water-limited conditions and/or drought, salt, and/or cold tolerance, for example, using the assays described in Examples 2 and 3, and for yield, both in the greenhouse and in field studies.

EXAMPLE 7

Stress-tolerant wheat plants

[00108] The polynucleotides of Table 1 are transformed into wheat using the method described by Ishida et al., 1996, Nature Biotech. 14745-50. Immature embryos are co-cultivated with Agrobacterium tumefaciens that carry “super binary” vectors, and transgenic plants are recovered through organogenesis. This procedure provides a transformation efficiency between 2.5% and 20%. The transgenic plants are then screened for their improved growth and/or yield under water-limited conditions and/or stress tolerance, for example, is the assays described in Examples 2 and 3, and for yield, both in the greenhouse and in field studies.

EXAMPLE 8

Stress-tolerant corn plants

[00109] The polynucleotides of Table 1 are transformed into immature embryos of corn using Agrobacterium. After imbibition, embryos are transferred to medium without selection agent. Seven to ten days later, embryos are transferred to medium containing selection agent and grown for 4 weeks (two 2-week transfers) to obtain transformed callus cells. Plant regeneration is initiated by transferring resistant calli to medium supplemented with selection agent and grown under light at 25-27°C for two to three weeks. Regenerated shoots are then transferred to rooting box with medium containing selection agent. Plantlets with roots are transferred to potting mixture in small pots in the greenhouse and after acclimatization are then transplanted to larger pots and maintained in greenhouse till maturity.

[00110] Using assays such as the assay described in Examples 2 and 3, each of these plants is uniquely labeled, sampled and analyzed for transgene copy number. Transgene positive and negative plants are marked and paired with similar sizes for transplanting together to large pots. This provides a uniform and competitive environment for the transgene positive and negative plants. The large pots are watered to a certain percentage of the field water capacity of the soil depending the severity of water-stress desired. The soil water level is maintained by watering every other day. Plant growth and physiology traits such as height, stem diameter, leaf rolling, plant wilting, leaf extension rate, leaf water status, chlorophyll content and photosynthesis rate are measured during the growth period. After a period of growth, the above ground portion of the plants is harvested, and the fresh weight and dry weight of each plant are taken. A comparison of the drought tolerance phenotype between the transgene positive and negative plants is then made.

[00111] Using assays such as the assay described in Example 2 and 3, the pots are covered with caps that permit the seedlings to grow through but minimize water loss. Each pot is weighed periodically and water added to maintain the initial water content. At the end of the experiment, the fresh and dry weight of each plant is measured, the water consumed by each plant is calculated and WUE of each plant is computed. Plant growth and physiology traits such as WUE, height, stem diameter, leaf rolling, plant wilting, leaf extension rate, leaf water status, chlorophyll content and photosynthesis rate are measured during the experiment. A comparison of WUE phenotype between the transgene positive and negative plants is then made.

[00112] Using assays such as the assay described in Example 2 and 3, these pots are kept in an area in the greenhouse that has uniform environmental conditions, and cultivated optimally. Each of these plants is uniquely labeled, sampled and analyzed for transgene copy number. The plants are allowed to grow under theses conditions until they reach a predefined growth stage. Water is then withheld. Plant growth and physiology traits such as height, stem diameter, leaf rolling, plant wilting, leaf extension rate, leaf water status, chlorophyll content and photosynthesis rate are measured as stress intensity increases. A comparison of the dessication tolerance phenotype between transgene positive and negative plants is then made.

[00113] Segregating transgenic corn seeds for a transformation event are planted in small pots for testing in a cycling drought assay. These pots are kept in an area in the greenhouse that has uniform environmental conditions, and cultivated optimally. Each of these plants is uniquely labeled, sampled and analyzed for transgene copy number. The plants are allowed to grow under theses conditions until they reach a predefined growth stage. Plants are then repeatedly watered to saturation at a fixed interval of time. This water/drought cycle is repeated for the duration of the experiment. Plant growth and physiology traits such as height, stem diameter, leaf rolling, leaf extension rate, leaf water status, chlorophyll content and photosynthesis rate are measured during the growth period. At the end of the experiment, the plants are harvested for above-ground fresh and dry weight. A comparison of the cycling drought tolerance phenotype between transgene positive and negative plants is then made.

[00114] In order to test segregating transgenic corn for drought tolerance under rain-free conditions, managed-drought stress at a single location or multiple locations is used. Crop water availability is controlled by drip tape or overhead irrigation at a location which has less than 10cm rainfall and minimum temperatures greater than 5°C expected during an average 5 month season, or a location with expected in-season precipitation intercepted by an automated “rain-out shelter” which retracts to provide open field conditions when not required. Standard agronomic practices in the area are followed for soil preparation, planting, fertilization and pest control. Each plot is sown with seed segregating for the presence of a single transgenic insertion event. A Taqman transgene copy number assay is used on leaf samples to differentiate the transgenics from null-segregant control plants. Plants that have been genotyped in this manner are also scored for a range of phenotypes related to drought-tolerance, growth and yield. These phenotypes include plant height, grain weight per plant, grain number per plant, ear number per plant, above ground dry-weight, leaf conductance to water vapor, leaf CO_2 uptake, leaf chlorophyll content, photosynthesis-related chlorophyll fluorescence parameters, water use efficiency, leaf water potential, leaf relative water content, stem sap flow rate, stem hydraulic conductivity, leaf temperature, leaf reflectance, leaf light absorptance, leaf area, days to flowering, anthesis-silking interval, duration of grain fill, osmotic potential, osmotic adjustment, root size, leaf extension rate, leaf angle, leaf rolling and survival. All measurements are made with commercially available instrumentation for field physiology, using the standard protocols provided by the manufacturers. Individual plants are used as the replicate unit per event.

[00115] In order to test non-segregating transgenic corn for drought tolerance under rain-free conditions, managed-drought stress at a single location or multiple locations is used. Crop water availability is controlled by drip tape or overhead irrigation at a location which has less than 10cm rainfall and minimum temperatures greater than 5°C expected during an average 5 month season, or a location with expected in-season precipitation intercepted by an automated “rain-out shelter” which retracts to provide open field conditions when not required. Standard agronomic practices in the area are followed for soil preparation, planting, fertilization and pest control. Trial layout is designed to pair a plot containing a non-segregating transgenic event with an adjacent plot of null-segregant controls. A null segregant is progeny (or lines derived from the progeny) of a transgenic plant that does not contain the transgene due to Mendelian segregation. Additional replicated paired plots for a particular event are distributed around the trial. A range of phenotypes related to drought-tolerance, growth and yield are scored in the paired plots and estimated at the plot level. When the measurement technique could only be applied to individual plants, these are selected at random each time from within the plot. These phenotypes include plant height, grain weight per plant, grain number per plant, ear number per plant, above ground dry-weight, leaf conductance to water vapor, leaf CO_2 uptake, leaf chlorophyll content, photosynthesis-related chlorophyll fluorescence parameters, water use efficiency, leaf water potential, leaf relative water content, stem sap flow rate, stem hydraulic conductivity, leaf temperature, leaf reflectance, leaf light absorptance, leaf area, days to flowering, anthesis-silking interval, duration of grain fill, osmotic potential, osmotic adjustment, root size, leaf

extension rate, leaf angle, leaf rolling and survival. All measurements are made with commercially available instrumentation for field physiology, using the standard protocols provided by the manufacturers. Individual plots are used as the replicate unit per event.

[00116] To perform multi-location testing of transgenic corn for drought tolerance and yield, five to twenty locations encompassing major corn growing regions are selected. These are widely distributed to provide a range of expected crop water availabilities based on average temperature, humidity, precipitation and soil type. Crop water availability is not modified beyond standard agronomic practices. Trial layout is designed to pair a plot containing a non-segregating transgenic event with an adjacent plot of null-segregant controls. A range of phenotypes related to drought-tolerance, growth and yield are scored in the paired plots and estimated at the plot level. When the measurement technique could only be applied to individual plants, these are selected at random each time from within the plot. These phenotypes included plant height, grain weight per plant, grain number per plant, ear number per plant, above ground dry-weight, leaf conductance to water vapor, leaf CO_2 uptake, leaf chlorophyll content, photosynthesis-related chlorophyll fluorescence parameters, water use efficiency, leaf water potential, leaf relative water content, stem sap flow rate, stem hydraulic conductivity, leaf temperature, leaf reflectance, leaf light absorptance, leaf area, days to flowering, anthesis-silking interval, duration of grain fill, osmotic potential, osmotic adjustment, root size, leaf extension rate, leaf angle, leaf rolling and survival. All measurements are made with commercially available instrumentation for field physiology, using the standard protocols provided by the manufacturers. Individual plots are used as the replicate unit per event.

APPENDIX

cDNA sequence of At2g20725 from Arabidopsis (SEQ ID NO:1):

ATGATTCTAGGCCGATGGGTTTCCTTCAGTTGCGGAAACACGCCGGTGACTAATTGTT
CCGAACGACGACGACATACGGAGTTTCGTCGTCTCTCCTCTGCTAGTACTTGTCGACC
TTCTCTCATATGCTCTTGTCTCAAAAGCAAATCCTCCCAAGAAACTACTCAGATTGAACA
GTTGGGGAATGGAGAAGGGTTCTCAGTTTTGGCATCAGAGATTCCATGGGAGGATGAT
AACATATGGAGCACATTTGCTCTTTACATGTTCTCTCTGCATATTCCTCTCAGTTTTGGG
GGTTTATCCATTGTTGCCAACATACTCCACCGGCAGGTTCTTGATCCTCAGACCCAAGT
GCTATCACTTGTGGTTCTCCAAATGGTAGAACTTGCAGGGACAGTCTTGCTGCTGAGG
ACCACAGCGAAGCCTCAGTGCAAATCAATCAACTTTCTAAAGGGTAATAACGAAACAA
GGGAAGGAAGAAACTGTGTGGTTGGCTCAGCATTGGGTTTGGGATGTCTTGTGGGCTT
TATCTTCGTCACGTCGCTTGTAGCTGATCAACTCTTTGGCCCTAAGGCTGTACATGAAT
CAGAATTGGAGAAGATAATGGTGAGCGGGGAAGTGGCGAGAAGCGGATGTTTTGCTC
TCTACTGCGTAGTAGCTCCCATCCTTGAGGAGATAGTGTACAGACGCTTTCTCCTGAC
CTCCTTAGCGTCGAGAATGGAATGGTGGAAGGCACTAGTGATCAGCTCAGGAGTATTT
GCTGCAGGTCACTTCTCAGGTGAGGATTTTGTGCAGCTGTTTGGGATAGGTTGCGGTC
TCGGGTTATGTTACAGCTGGTCAGGGAACTTAGCCTCATCAGTGCTCGTCCACTCCTT
GTACAATGCATTGACACTTCTCTTCTCTTAG

The At2g20725 cDNA is translated into the following amino acid sequence (SEQ ID NO:2):

MILGRWVSFSCGNTPVTNCSERRRHTEFRRLSSASTCRPSLICSCLKSKSSQETTQIEQLG
NGEGFSVLASEIPWEDDNIWSTFALYMFSLHIPLSFGGLSIVANILHRQVLDPQTQVLSLVVL
QMVELAGTVLLLRTTAKPQCKSINFLKGNNETREGRNCVVGSALGLGCLVGFIFVTSLVAD
QLFGPKAVHESELEKIMVSGEVARSGCFALYCVVAPILEEIVYRRFLLTSLASRMEWWKAL
VISSGVFAAGHFSGEDFVQLFGIGCGLGLCYSWSGNLASSVLVHSLYNALTLLFS

cDNA sequence of At3g26085 from Arabidopsis (SEQ ID NO:3):

ATGGGTTCCATCGCTCTGCAATCTTGGAGCAGAGGAGCTTCAACTTCTCTTCATCTCCT
TTTTCGTCCAGTTGGCTCGAACCCTAAGCTATATGATGCTCGAAGAGTACAATTTGATG
TAAGAGCCTCTTCAAGTCGTAAATCACTTAAGAAACTCAAAAGAGAGTCACAACAAGGT
AAAGACATAGGCTTAAGAAATGTTACAGATGAAGAAGTTTCTTCTCCAAGATTTGAGGA
AGCTCAAGTTGATTCTTCAACTTCAAAGGACTCCATTGATGTTTTTGTTGCTGCTCCTC
GAGACAAAGTGCTTCAGGCTTGCACTGTAACTTCCGGTTTGATGGCTGCACTAGGTCT
GATCATCAGAAAGGCGTCTCATGTTGCTTCGACTGAAGGATTACTGGTTCCAGACTGC
TCTATAGATGTACCATTTGGGTTTGAAACTTGGCATCTCGGTTTAATTGCTGGAATCGT
TGTGTTTATATCGTCAAGTAGGTTCTTGCTACTTAAATCTTGGCCAGATTTTGCTGATTC
TAGTGAAGCAGCAAACCGACAGATTCTCACTTCCCTCGAACCTCTAGATTACCTTGTTG
TTGCAATGTTACCGGGAATAAGTGAGGAGCTGCTGTTTAGAGGTGCATTAATGCCTTT

GTTCGGAACTAATTGGAATGGTATTGTAGCGGTTGGCCTCATTTTCGGTTTACTTCATC
TCGGGAGCGGAAGAAAGTATTCTTTTGCAGTTTGGGCTTCGATTGTCGGTATAGTCTA
CGGTTATGCAGCTGTTTTGTCGTCGAGTCTTATCGTTCCAATGGCCTCGCACGCACTC
AACAATTTGGTGGGAGGTCTGTTGTGGCGATATAGTTCCAAGATCAAGTCATTGGAGTAA

The At3g26085 cDNA is translated into the following amino acid sequence (SEQ ID NO:4):

MGSIALQSWSRGASTSLHLLFRPVGSNPKLYDARRVQFDVRASSSRKSLKKLKRESQQGK
DIGLRNVTDEEVSSPRFEEAQVDSSTSKDSIDVFVAAPRDKVLQACTVTSGLMAALGLIIRK
ASHVASTEGLLVPDCSIDVPFGFETWHLGLIAGIVVFISSSRFLLLKSWPDFADSSEAANRQI
LTSLEPLDYLVVAMLPGISEELLFRGALMPLFGTNWNGIVAVGLIFGLLHLGSGRKYSFAVW
ASIVGIVYGYAAVLSSSLIVPMASHALNNLVGGLLWRYSSKIKSLE

cDNA sequence of AtFACE-2 from Arabidopsis (SEQ ID NO:5):

ATGGCCACCGATGGCGAGAGTATCTCGATGTCGTTGGCGGTGGCTACCTGCGTCGCG
ATGGCACTATTCTACGTTTTGATCCTTTACGTTCCCACCGTGATACTCCGTCTCCCGTC
GGCTTCTTCTTACACCGAATTCATGATTCGGCGATTCATCTGCGCGGCCATTTGTACTG
TAGCATCTCTCGTCTTCACAGCTTTTATACTTCCGATAAAAAGCTGGGAGGCCTCTTAT
ATACTTGGAGTTTATGGCATAAGGAAAGATCATCTGTGGCAAGGAGTGGTGTATCCTCT
TCTATTGACCTCGCTCGTTTATGCTGGGTCTTTGGTGTTGAAGTTGTTTACTCTCCTGG
AATCATGGAAGGAAAATGGCGGAGGATGTAGTTCCTTTAATTACATCAGAAGCTTTTTC
CAAACAATCCCTGCTTCGGTATTGACAAGTGCTTCTAATGTTTCCGTTTGGCGCAATTT
TATCGTGGCACCAGTAACTGAGGAGCTGGTTTTCCGATCATGTATGATACCTTTGCTTC
TGTGTGCTGGGTTTAGGATTAACACTGCCATCTTTCTGTGCCCAGTTCTCTTTAGCTTG
GCTCACTTAAACCATTTTAGAGAGATGTACATCAGGCATAACCGCAGCTATCTCCGGG
CTTCACTTATTGTTGGTCTTCAGCTTGGCTACACAGTCATTTTTGGTGCATATGCATCGT
TTCTCTTCATCAGAACCGGACATCTTGCTGCTCCTTTGTTTGCTCATATATTTTGCAACT
ACATGGGATTGCCTGTGCTATACGCAAATGGAAAAGGTTTGGTGAGTGCAGCGTTCTT
AGGCGGTGTGGTTGGGTTCGTCTTACTTCTCTTTCCTTTAACAAAGCCTCTCATGTACA
ACGATAGTACCAACGATTGTCCGTGTTGGCTTGGCTATTGTTTGTGGAATTGA

The AtFACE-2 cDNA is translated into the following amino acid sequence (SEQ ID NO:6):

MATDGESISMSLAVATCVAMALFYVLILYVPTVILRLPSASSYTEFMIRRFICAAICTVASLVF
TAFILPIKSWEASYILGVYGIRKDHLWQGVVYPLLLTSLVYAGSLVLKLFTLLESWKENGGG
CSSFNYIRSFFQTIPASVLTSASNVSVWRNFIVAPVTEELVFRSCMIPLLLCAGFRINTAIFLC
PVLFSLAHLNHFREMYIRHNRSYLRASLIVGLQLGYTVIFGAYASFLFIRTGHLAAPLFAHIFC
NYMGLPVLYANGKGLVSAAFLGGVVGFVLLLFPLTKPLMYNDSTNDCPCWLGYCLWN

cDNA sequence of ZM57353913 from corn (SEQ ID NO:7):

CGAAGCCACGCGACCGACTGTGTTACGATCCCAAATCTTCACTCCCGACGAAATCTAG
AATCCAATGAGCAATCTCGACTGACGCCTGCTTCACCAGATTATGGCGACGCCGGCG
GGCCTCCTTCTCGCCTCGCCGCCGGTGATATCAGGTGTCGCGGCGATGGCGGCGTG
CGCCGCAATGGCAGTATTCTACGTCGCTGTCCTCTATGC
CCCGACGGTCATCCTCCGGTTCCCACCCCCAACCTCACTCCGCACCTTCCTCCACCGT
CGCTTCGCCTGTGCCGCCGTCGCATCCGCCGCCTCCGTCCTTGCCACTGCGTCCCTC
CTCCGAGTCTGGAGCCTCAGCGACTTCGCTGATATGTTTGCTGTGTTCGGCATTAGGA
AGGATCACTTGATTCAGGCCGTGGCTATTCCACTTCTCCTGACATCCCTAGTGTATGCT
GGGTCATTCGTCGCTAGAGTGTGGCTCCTAGTGAGCTCGTGGGGCGGTGGCGATGAG
GTGGAGATAGGCTGCGCACAGAGGCTTGCACAATGGATCCAAGCTGCTGTTGCGGAT
GTTATGGTTTGGCGGAACTATGTAGTGGCACCATTTACTGAGGAGCTGGTTTTCAGGG
CATGCATGATACCTCTTCTGCTCTGTGGGGGATTCAAAATGTCTACAATTATATTTCTGA
GTCCAATCTTCTTCAGTCTAGCGCACTTGAACCATTTTTTCGAACTACACCAGCAGGGA
TGTAACTTTATGAGAGCGCTATTGATTGTAGGTGTCCAGTTAGGCTACACTGTCATTTT
TGGGTGGTATGCAACATTCTTGTTAATCCGAACAGGGAATCTGTTATGTCCAATTATTG
CTCACGTCTTCTGTAATATGATGGGTTTACCTGTTTTCTCGTCACCACGAACAAAAGGA
GCGGCATTGGTAGCGTTTCTGGCTGGTTCAATAGCCTTCTTTTGGCTGCTTTTCCCTGC
AACAAGTCCTGAACTGTACAACAGCAGTTTTGATCGCTGCAGTTGCTGGCATGGCTTTT
GCAATTGGAAATAACATAGAACTAGATTGGAAAGCAATGGGTCCTAACTTGAAGCTACT
AACAATTGAAACCTCCAGGCCCTAGCTGACACTTCTGACGGATTTTCTATTTGCAGAAA
CTCCATATGAATGTCTTAAAACGTTTTGTAGAAATGTGTCCCTTGTTTTAGCTTAAGACT
CAAGAGCTTAAACTAGCAAAAGATTGTATTTTGCCACTTGTTAAATACGTGCTGATCAT
GAAATCGCTGTCAATCCCTTCTCAAAGTGGAATTTGACTTTGTTGAGCTGCTTTTATTTA
TATTGTGCTTGCTACTGCAGCGCCTAGAGTTTGTAGATTACACATCATGGACCCGTCTG
ATATTGTAAACGAGAGACATGTTTCTAAGTTAATATGCTCCCTCCATTTATTTAAAAAAA
AAAAAAA

The ZM57353913 cDNA is translated into the following amino acid sequence (SEQ ID NO:8):

MATPAGLLLASPPVISGVAAMAACAAMAVFYVAVLYAPTVILRFPPPTSLRTFLHRRFACAA
VASAASVLATASLLRVWSLSDFADMFAVFGIRKDHLIQAVAIPLLLTSLVYAGSFVARVWLL
VSSWGGGDEVEIGCAQRLAQWIQAAVADVMVWRNYVVAPFTEELVFRACMIPLLLCGGF
KMSTIIFLSPIFFSLAHLNHFFELHQQGCNFMRALLIVGVQLGYTVIFGWYATFLLIRTGNLLC
PIIAHVFCNMMGLPVFSSPRTKGAALVAFLAGSIAFFWLLFPATSPELYNSSFDRCSCWHG
FCNWK

cDNA sequence of ZM59252659 from corn (SEQ ID NO:9):

CCCAAATCTTCATTTCCGACGAAATCGAGAATCCAATGTGCAATCTCGACTGACGCCTG
CTTCAACAGATTATGGCGACGCGGTGGGTCTCCTTCTCGCCTCGCCGCCGGAATATCA

GGGTCGCGCGATGGGTCGTGCGCCAACGGAAGGATTCTACGTCGCTGTCCTCTATGC
CCCGACGGTCATCCTCCGGGTCCCACCCCCAAGCTCACTCCGCACCTTCCTCCACCG
TCGCTTCGCCTGTGCCGCCGTCGCATCCGCCGCCTCCGTCCTTGCCACTGCGTCCCT
CCTCCGAATCTGGAGCCTCAGCGACTTCGCTGATATGTTTGCTGTGTTCGGCATTAGG
AAGGATCACTTGATTCAGGCCGTGGCTATTCCACTTCTCCTGACATCCCTAGTGTATGC
TGGGTCATTCGTCGCTAGAGTGTGGCTCCTAGTGAGCTCGTGGGGCGGTGGCGATGA
GGTGGAGATAGGCTGCGCACAGAGGCTTGCACAATGGATCCAAGCTGCTGTTGCGGA
TGTTATGGTTTGGCGGAACTATGTAGTGGCACCATTTACTGAGGAGCTGGTTTTCAGG
GCATGCATGATACCTCTTCTGCTCTGTGGGGGATTCAAAATGTCTACAATTATATTTCT
GAGTCCAATCTTCTTCAGTCTAGGTGTCCAGTTAGGCTACACTGTCATTTTTGGGTGGT
ATGCAACATTCTTGTTAATCCGAACAGGGAATCTGTTATGTCCAATTACTGCTCACGTC
TTCTGTAATATGATGGGTTTACCTGTTTTCTCGTCACCACGAACAAAAGGAGCGGCATT
GGTAGCGTTTCTGGCTGGTTCAATAGCCTTCTTTTGGCTGCTTTTCCCTGCAACAAGTC
CTGAACTGTACAACAGCAGTTTTGATCGCTGCAGTTGCTGGCATGGCTTTTGCAATTG
GAAATAACATAGAACTAGATTGGAAAGCAATGGGTCCTAACTTGAAGCTACTAACAATT
GAAACCTCCAGGCCCTAGCTGACACTGCTGACGGATTTTCTATTTGCAGAAACTCCATA
TGAATGTCTTAAAACGTTTTGTAGAAATGTGTCCCTTGTTTTAGCTTAAGACTCGAGCTT
AAACTAGCAAAAGATTGTATTTTGCCACTTGTTAAATACGTGCTGATCATGAAATCGCT
GTCAATCCCTTCTCAAAGTGGAATTTGACTTTGTTGTAAAAAAAAAAA

The ZM59252659 cDNA is translated into the following amino acid sequence (SEQ ID NO:10):

MGRAPTEGFYVAVLYAPTVILRVPPPSSLRTFLHRRFACAAVASAASVLATASLLRIWSLSD
FADMFAVFGIRKDHLIQAVAIPLLLTSLVYAGSFVARVWLLVSSWGGGDEVEIGCAQRLAQ
WIQAAVADVMVWRNYVVAPFTEELVFRACMIPLLLCGGFKMSTIIFLSPIFFSLGVQLGYTVI
FGWYATFLLIRTGNLLCPITAHVFCNMMGLPVFSSPRTKGAALVAFLAGSIAFFWLLFPATS
PELYNSSFDRCSCWHGFCNWK

cDNA sequence of CASAR82A from pepper (SEQ ID NO:11):

ATGGTGTCTAAGTCCTCAATCTTCATTTGCCTGAGCCTTATCATCCTCGTGATCATGTC
TACCCAGATCGTGGCTAGAGAGATGACCAGTGAAGCTTCTGCTTCACTCACACAGGCA
ATGAACGGGAACAATATCTCTGAGACCAAGAAAGTGGGTCGTCACTTGGTGAAGGGCT
TGGATAAGATCTTCAAGGCTGGAAAGGTGATCTACTGCAAGACCTGCAAAACCTGCCA
CGGTCGCTGCGATTACTGTTGCGCC

The CASAR82A cDNA is translated into the following amino acid sequence (SEQ ID NO:12):

MVSKSSIFICLSLIILVIMSTQIVAREMTSEASASLTQAMNGNNISETKKVGRHLVKGLDKIFK
AGKVIYCKTCKTCHGRCDYCCA

cDNA sequence of b3358 from E.coli (SEQ ID NO:13):

ATGTGGCGCAGACTGATTTATCACCCCGATATCAACTATGCACTTCGACAAACGCTGG
TGCTATGTTTGCCCGTGGCCGTTGGGTTAATGCTTGGCGAATTACGATTCGGTCTGCT
CTTCTCCCTCGTTCCTGCCTGTTGCAATATTGCGGGCCTTGATA
CGCCTCATAAACGTTTTTTCAAACGCTTAATCATTGGTGCGTCGCTGTTTGCCACCTGT
AGCTTGCTGACACAGCTACTACTGGCAAAAGATGTTCCCCTGCCCTTTTTGCTGACCG
GATTAACGCTGGTACTTGGCGTCACTGCTGAGCTGGGGCCATTGCACGCAAAATTGCT
TCCTGCATCGCTGCTCGCCGCCATTTTTACCCTCAGTTTGGCGGGATACATGCCGGTC
TGGGAACCGTTGCTCATCTATGCGTTGGGCACTCTCTGGTACGGATTGTTTAACTGGT
TTTGGTTCTGGATCTGGCGCGAACAACCGCTGCGCGAGTCACTAAGTCTGCTGTACCG
TGAACTGGCAGATTATTGTGAAGCCAAATACAGCCTGCTTACCCAGCACACCGACCCT
GAAAAAGCGCTGCCGCCGCTGCTGGTGCGCCAGCAAAAAGCGGTCGATCTAATTACC
CAGTGCTATCAGCAAATGCATATGCTTTCCGCGCAAAATAATACTGACTACAAGCGGAT
GCTGCGTATTTTCCAGGAGGCGCTGGATTTACAGGAACATATTTCGGTCAGTTTGCAT
CAGCCGGAAGAGGTGCAAAAGCTGGTCGAGCGTAGCCATGCGGAAGAAGTTATCCGC
TGGAATGCGCAAACCGTCGCCGCTCGCCTGCGCGTGCTGGCTGATGACATTCTTTAC
CATCGCCTGCCAACGCGTTTTACGATGGAAAAGCAAATTGGCGCACTGGAAAAAATCG
CCCGCCAGCATCCGGATAATCCGGTTGGGCAATTCTGCTACTGGCATTTCAGCCGCAT
CGCCCGCGTGCTGCGCACCCAAAAACCGCTCTATGCCCGTGACTTACTGGCCGATAA
ACAGCGGCGAATGCCATTACTTCCGGCGCTGAAAAGTTATCTGTCACTAAAGTCTCCG
GCGCTACGCAATGCCGGACGACTCAGTGTGATGTTAAGCGTTGCCAGCCTGATGGGC
ACCGCGCTGCATCTGCCGAAGTCGTACTGGATCCTGATGACGGTATTGCTGGTGACAC
AAAATGGCTATGGCGCAACCCGTCTGAGGATTGTGAATCGCTCCGTGGGAACCGTGG
TCGGGTTAATCATTGCGGGCGTGGCGCTGCACTTTAAAATTCCCGAAGGTTACACCCT
GACGTTGATGCTGATTACCACCCTCGCCAGCTACCTGATATTGCGCAAAAACTACGGC
TGGGCGACGGTCGGTTTTACTATTACCGCAGTGTATACCCTGCAACTATTGTGGTTGA
ACGGCGAGCAATACATCCTTCCGCGTCTTATCGATACCATTATTGGTTGTTTAATTGCT
TTCGGCGGTACTGTCTGGCTGTGGCCGCAGTGGCAGAGCGGGTTATTGCGTAAAAAC
GCCCATGATGCTTTAGAAGCCTATCAGGAAGCGATTCGCTTGATTCTTAGCGAGGATC
CGCAACCTACGCCACTGGCCTGGCAGCGAATGCGGGTAAATCAGGCACATAACACTC
TGTATAACTCATTGAATCAGGCGATGCAGGAACCGGCGTTTAACAGCCATTATCTGGC
AGATATGAAACTGTGGGTAACGCACAGCCAGTTTATTGTTGAGCATATTAATGCCATGA
CCACGCTGGCGCGGGAACACCGGGCATTGCCACCTGAACTGGCACAAGAGTATTTAC
AGTCTTGTGAAATCGCCATTCAGCGTTGTCAGCAGCGACTGGAGTATGACGAACCGGG
TAGTTCTGGCGATGCCAATATCATGGATGCGCCGGAGATGCAGCCGCACGAAGGCGC
GGCAGGTACGCTGGAGCAGCATTTACAGCGGGTTATTGGTCATCTGAACACCATGCAC
ACCATTTCGTCGATGGCATGGCGTCAGCGACCGCATCACGGGATTTGGCTGAGTCGC
AAGTTGCGGGATTCGAAGGCGTAA

The b3358 cDNA is translated into the following amino acid sequence (SEQ ID NO:14):

MWRRLIYHPDINYALRQTLVLCLPVAVGLMLGELRFGLLFSLVPACCNIAGLDTPHKRFFKR
LIIGASLFATCSLLTQLLLAKDVPLPFLLTGLTLVLGVTAELGPLHAKLLPASLLAAIFTLSLAG
YMPVWEPLLIYALGTLWYGLFNWFWFWIWREQPLRESLSLLYRELADYCEAKYSLLTQHT
DPEKALPPLLVRQQKAVDLITQCYQQMHMLSAQNNTDYKRMLRIFQEALDLQEHISVSLHQ
PEEVQKLVERSHAEEVIRWNAQTVAARLRVLADDILYHRLPTRFTMEKQIGALEKIARQHP
DNPVGQFCYWHFSRIARVLRTQKPLYARDLLADKQRRMPLLPALKSYLSLKSPALRNAGR
LSVMLSVASLMGTALHLPKSYWILMTVLLVTQNGYGATRLRIVNRSVGTVVGLIIAGVALHF
KIPEGYTLTLMLITTLASYLILRKNYGWATVGFTITAVYTLQLLWLNGEQYILPRLIDTIIGCLIA
FGGTVWLWPQWQSGLLRKNAHDALEAYQEAIRLILSEDPQPTPLAWQRMRVNQAHNTLY
NSLNQAMQEPAFNSHYLADMKLWVTHSQFIVEHINAMTTLAREHRALPPELAQEYLQSCEI
AIQRCQQRLEYDEPGSSGDANIMDAPEMQPHEGAAGTLEQHLQRVIGHLNTMHTISSMA
WRQRPHHGIWLSRKLRDSKA

cDNA sequence of EST564 from moss (SEQ ID NO:15):

ATGTCATGCGACGTTCTCTGCCAATCTTTCAAGGAGGTAGAGGGCAAGTTCTTGGAAA
TCGTCGAAAGGGCTTGGGCCGTCAAGCCGCAAATTGCCGCTGTTGGATCTTGTTGTTT
GGTGGGAGCCGTATGGGATTCCAAACTGTACATCGCTAGTCTTGGAGATTCTCGAGCT
GTTTTAGGTAGTTGCTCTCGTGACACTGGCCTTCCAGTTGCTAAGCAAATTTCAACAGA
GCACAACGCAAGCATCGAGTCTATCCGGAATGAGTTGTTCGCAAAGCATAGTGATGAT
CCGCAGATCGTGGTTTTGAAGCATGGAGTGTGGCGTGTGAAGGGTATTATTCAGATTT
CACGCTCAATTGGTGATTTTTACTTGAAGAAAGCCGAATTTAATCAGCCGCCTCTTATA
GCCAGGTTCCGG
CTTCCAGATCCCCTCAAGAGACCTGTCATAAGCTCAGAGCCGGAGTGCAACGTCATTA
CACTCGGCCCGGATGACGAATTCGTCATTTTTGCATCTGATGGCCTTTGGGAGCACTT
GAGCAGCAAAGAGGCCGTAGACATTGTGTATAGTCATCCCCGGGCTGGGATTGCCAG
GCGTCTGATCAAAGCTGCTCTTCAAAAAGCTGCTACTAAACGTGAAATGCGGTACTCT
GATTTGAAAGGGATTGAGCGCGGGATACGACGGCATTTTCATGATGACATAACTGTTG
TGGTTCTTTATTTGGACACTAAACTGCTCAACAGAGGTGGTAGTATTTCTAATCATATTT
CTTCGAAATGTCCAATTGACATGCCAAAAGGCGATAACCCTCCGTCGTTAGTTAGCTCT
AACATGAACTTAGCTTTTAACAAATAA

The EST564 cDNA is translated into the following amino acid sequence (SEQ ID NO:16):

MSCDVLCQSFKEVEGKFLEIVERAWAVKPQIAAVGSCCLVGAVWDSKLYIASLGDSRAVL
GSCSRDTGLPVAKQISTEHNASIESIRNELFAKHSDDPQIVVLKHGVWRVKGIIQISRSIGDF
YLKKAEFNQPPLIARFRLPDPLKRPVISSEPECNVITLGPDDEFVIFASDGLWEHLSSKEAV
DIVYSHPRAGIARRLIKAALQKAATKREMRYSDLKGIERGIRRHFHDDITVVVLYLDTKLLNR
GGSISNHISSKCPIDMPKGDNPPSLVSSNMNLAFNK

cDNA sequence of BN49502266 from canola (SEQ ID NO:17):

CCAATAATCAAATCAAAACCCTTTCGATCAGTTGTTNCAGGAAAAAAAAAAACCCTTTC
GATCTCATTCCATTTCGAATCAGAAAACCCTAGCAATTGACGATGTTGCGAGCTTTAGC
GCGGCCTCTCGAACGGTGTTTAGGAAGCAGAGCGAGCGGCGACGGTTTGCTCTGGCA
ATCGGAGTTGAAACCACACGCCGGCGGAGATTACTCGATCGCGGTGGTTCAAGCCAA
TTCTAGCCTAGAGGATCAGAGTCAGGTGTTCACGTCTTCCTCCGCTACTTACGTCGGC
GTCTACGACGGCCATGGCGGACCCGAAGCTTCTAGATTCGTTAACAGACATCTCTTTC
CTTATATTCAGAAGTTCGCAAAAGAACATGGAGGACTGTCTGCAGACGTTATTAAAAAA
GCATTCAAAGAAACTGAAGAGGATTTTTGCGGTATGGTTAAACGCTCACTTCCCATGAA
GCCACAGATGGCTACTGTAGGATCTTGCTGTCTCTTTGGTGCCATCTCTAACGGCACG
CTCTATGTCGCGAATCTTGGAGACTCGAGAGCCGTTCTTGGGAGCGTTGTTGCAGGG
GATGATAGTAATAGTAGTAACAAGGGTGCTGCAGCTGAACGGTTGTCCACTGATCATA
ACGTTGCTGTTGAAGAAGTGAGGAAGGAGGTTAAGGAACTTAACCCGGATGATTCGCA
GATCGTCATGTACATTCGTGGAGTTTGGAGGATTAAAGGCATTATTCAGGTATCTAGAT
CAATTGGGGATGTTTACTTGAAGAAACCGGAGTTTTACAGGGATCCGATATTCCAGCAA
CATGGAAATCACATTCCTTTGAGGAGACCCGCGATGACAGCTGAACCGTCCATTATAG
TAAGGAAGCTTAAGCCGCAAGACTTGTTTCTGATATTTGCATCAGATGGTCTCTGGGAG
CATCTTAGTGATGAAGCAGCAGTAGAAATTGTACTCAAACACCCAAGAACTGGGATTG
CAAGAAAACTTGTAAGAGCAGCTCTTGAAGAAGCAGCAAGGAAGAGAGAAATGAGATA
TGGAGATATAAAGAAAATAGCCAAAGGGGTTAGAAGACATTTCCATGACGACATAAGC
GTCGTTGTAGTTTATCTTGATCAACAAAAAACCACTTCTTCATCGAATGATAGATTGATC
CAGAAAGGAGGAATCACTGCTCCACCGGATATCTACTCGTTACGTTCAGATGAAGCTG
AGCAACGACGGCTACTCAATGTGTTATATTGATACTCTCTGGTTAGAGGGATACAACTT
GTTTACATATTTGTTTAATCTTTTACAAAGAATGTTTGTTCTTTTTTCTTTCTTTTTTTAAT
ATTTGGAGTTGGATTTGTATATTCTTTTTACCAGCAAGGAACGAAAACCCTTCTCTTTTG
GGGGCAAAACAGTTTTGGTTTTGACAAACAATATAAAGTGAAACCGTTTGCAAAAAAAA
AAAAAAAAA

The BN49502266 cDNA is translated into the following amino acid sequence (SEQ ID NO:18):

MLRALARPLERCLGSRASGDGLLWQSELKPHAGGDYSIAVVQANSSLEDQSQVFTSSSAT
YVGVYDGHGGPEASRFVNRHLFPYIQKFAKEHGGLSADVIKKAFKETEEDFCGMVKRSLP
MKPQMATVGSCCLFGAISNGTLYVANLGDSRAVLGSVVAGDDSNSSNKGAAAERLSTDH
NVAVEEVRKEVKELNPDDSQIVMYIRGVWRIKGIIQVSRSIGDVYLKKPEFYRDPIFQQHGN
HIPLRRPAMTAEPSIIVRKLKPQDLFLIFASDGLWEHLSDEAAVEIVLKHPRTGIARKLVRAAL
EEAARKREMRYGDIKKIAKGVRRHFHDDISVVVVYLDQQKTTSSSNDRLIQKGGITAPPDIY
SLRSDEAEQRRLLNVLY

cDNA sequence of GM49788080 from soybean (SEQ ID NO:19):

TCCCGGGTCGACGATTTCGTGGTTACGGGGCGGAAGGAAGGGCTGCTGTGGTACAAG
GATGCGGGGCAGCACTTGTTTGGTGAATACTCAATGGCTGTTGTCCAGGCCAACAACC
TGCTCGAGGACCAGAGCCAGATTGAGTCTGGTCCTCTCAGCCTGCTTGACACTGGCC
CTTATGGGACCTTTGTTGGTGTATATGATGGACACGGTGGGCCCGAGACGTCGCGCTA
CGTCTGTGATCATCTCTTCCAACATCTAAAACGATTTGCATCTGAGCAGAAGTCCATGT
CTATGGAGGTTATTCGGAAGGCATACCAAGCCACAGAAGAAGGTTTTTTGTCAGTGGT
TACCAAACAGTGGCCCATGAATCCCCAAATTGCTGCTGTGGGATCTTGTTGTTTGGTTG
GTGTGATTTGTGGTGGTATCCTCTATATTGCTAACCTTGGTGATTCCCGTGCTGTGCTT
GGCCGGGTGGTCAGAGCAACTGGGGAGGTTTTGGCGATCCAGCTTTCGTCAGAGCAT
AATGTGGCCATAGAATCTGTGAGACAAGAGATGCATTCTTTGCATCCGGATGACTCAAA
AATTGTGGTTCTAAAGCACAATGTATGGCGGGTGAAGGGTCTGATACAGATTTCTAGAT
CCATTGGCGATGTATACCTAAAAAAGGCTGAATTTAACAAGGAACCGTTGTATGCTAAG
TTTCGTGTGCGGGAAGGTTTTAAGAGGCCCATTTTGAGCTCTGACCCATCAATTTCTGT
CCATGAACTTCAACAGCATGATCAATTTCTCATATTTGCTTCTGATGGTCTTTGGGAACA
CCTTAGCAATCAGGATGCCGTTGATATAGTTCAAAACAACCCACACAATGGAATTGCTC
GGAGGCTCATCAAAGCTGCGTTGCAAGAAGCAGCAAAAAAGAGAGAGATGAGGTACT
CTGATTTGAAGAAAATTGACCGTGGTGTCCGCCGGCATTTCCATGATGACATCACAGTT
GTAGTTGTATTTCTTGACTCCAATCTTGTCAGCAGAGCCAGCTCAGTAAGAGGTCCTCC
TTTATCGGTGAGAGGAGGTGGTGTTCCCCTACCTTCTAGAACTTTGGCTCCCTGTGCT
GCACCTATGGAAACTTAGTTCAGGTTGATGAAGCTGGCTGTATGATCTGTTATGCTTCT
ATTTAGTGTTGTACCCTTAGCAGACATTGAGCTCTGGTGATCCACCAGATTGTATATCC
AATTTAACAGAGATTGAAAAAATGTTCGTTCA
ATTAGTACAATGTTACAAGTGACTTGGGGTATGTAGCTTGCGTGAGTAAAGCATCATGGAA

The GM49788080 cDNA is translated into the following amino acid sequence (SEQ ID NO:20):

MAVVQANNLLEDQSQIESGPLSLLDTGPYGTFVGVYDGHGGPETSRYVCDHLFQHLKRFA
SEQKSMSMEVIRKAYQATEEGFLSVVTKQWPMNPQIAAVGSCCLVGVICGGILYIANLGDS
RAVLGRVVRATGEVLAIQLSSEHNVAIESVRQEMHSLHPDDSKIVVLKHNVWRVKGLIQISR
SIGDVYLKKAEFNKEPLYAKFRVREGFKRPILSSDPSISVHELQQHDQFLIFASDGLWEHLS
NQDAVDIVQNNPHNGIARRLIKAALQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFL
DSNLVSRASSVRGPPLSVRGGGVPLPSRTLAPCAAPMET

cDNA sequence of GM53049821 from soybean (SEQ ID NO:21):

TGCTCCTCTACCACCGAACACANCCCCGGCCACCACCGAACGCTAACGTGCGCCCCT
TCCTTACCCTGCGCCTCGGCACTCTCCCTTATTCCCCCTCCTTCATAAGCTCCGCGTTA
ACCGTCCTCTCTCTCTCTCTCTCTCGGATCGGAGCGAGACTGGCGGCTCCGGCGTTG
GGGGCGTTAGGGTTAGGGTTAGGGTTTCCAAGAGATG

TGGTATGCTCCAGGCATTGATGAATCTGTTCTCGCTGTGTTGGAAGCCATTTGGCCGC
GATGCTGCTGATCGAATCGATTCCATCGGAGTTACCGGAAGAGAAGGCAAAGACGGC
TTGCTTTGGTTCCGCGACGGCGGAAAATATGGCTCTGGCGATTTCTCCATGGCCGTCG
TTCAGGCCAACCAGGTTCTCGAAGACCAGAGCCAGATCGAGTCTGGTCCTCTCGGCA
CCTTCGTCGGCATCTACGACGGTCACGGAGGACCCGACGCCTCAAGATACGTTTGCG
ATCACTTGTTTCGCCATTTTCAAGCAATATCAGCTGAGTCACGCGGGGTTGTGACAACT
GAGACAATCGAAAGAGCATTTCGCCAAACAGAAGAGGGGTACATGGCCCTCGTGTCA
GGCTCGTGGAATGCTCGACCTCATATTGCAAGTGCTGGGACCTGTTGTCTAGTTGGAG
TGATATTTCAGCAGACACTCTTTGTGGCAAACGCTGGAGATTCCCGTGTTGTATTGGGT
AAGAAAGTTGGCAACACTGGAGGTATGGCTGCAATTCAGCTGTCTACAGAACACAATG
CAAATCTTGAGGCTGTTAGGCAGGAACTTAAAGAATTACATCCTCATGATCCCCAAATT
GTTGTCCTCAAACATGGAGTGTGGAGAGTAAAAGGCATTATTCAGGTTTCTAGATCTAT
AGGTGATGTATATTTGAAGCATGCACAGTTTAACCGAGAACCACTTAATGCAAAATTCA
GACTTCCTGAACCGATGAACATGCCTATCTTGAGTGCTAATCCCACTATTCTTTCTCAT
GCTCTCCAACCAAATGATTCCTTCCTTATATTTGCATCTGATGGTTTATGGGAGCATTTG
AGTAACGAGAAAGCTGTGGATATTGTAAACAGCAATCCACATGCGGGTAGTGCCAAGA
GACTTATCAAGGCTGCTCTCCATGAAGCAGCAAGAAAACGAGAAATGCGATATTCAGA
CCTCCGTAAGATTGACAAGAAAGTTCGACGCCATTTTCATGATGATATATCCGTTATTG
TTTTATTCTTAAATCACGACCTTATTTCCAGAGGCACAGTGCTAGACCCGACACTTTCA
ATTCGAAGCGCTCTCGATCACTGACTTGTATCACTGTAAGCAGTCTTGTACGAGTTTTT
GGCAACTGTACCGATACCTGAAGCATTGGTAGGTACCTGGCTATAATATGTCATTTCTA
TGGCACATATGGCTTCTGGTACCGACATCATTCT
TGAGGCACGAGAATTTATTAAGTTATAACATATTATTAGAAATTTATTCATAAAGAGGAA
AAAAATAAATACAAAAATATCTTATTCCCTTTTCTAACCTTATAGTTTTACCCGAAATACT
GGATTTTATTTATTTGTTTGTTTTTTTGGCTGAACATAGCTAATCGAACAGCATGTTGAT
TGAATTCAAAGTTATTTTACAACAAATTATATGGAAAAAAAAAAAAAAA

The GM53049821 cDNA is translated into the following amino acid sequence (SEQ ID NO:22):

MLQALMNLFSLCWKPFGRDAADRIDSIGVTGREGKDGLLWFRDGGKYGSGDFSMAVVQA
NQVLEDQSQIESGPLGTFVGIYDGHGGPDASRYVCDHLFRHFQAISAESRGVVTTETIERA
FRQTEEGYMALVSGSWNARPHIASAGTCCLVGVIFQQTLFVANAGDSRVVLGKKVGNTG
GMAAIQLSTEHNANLEAVRQELKELHPHDPQIVVLKHGVWRVKGIIQVSRSIGDVYLKHAQ
FNREPLNAKFRLPEPMNMPILSANPTILSHALQPNDSFLIFASDGLWEHLSNEKAVDIVNSN
PHAGSAKRLIKAALHEAARKREMRYSDLRKIDKKVRRHFHDDISVIVLFLNHDLISRGTVLDP
TLSIRSALDH

cDNA sequence of ZM58462719 from corn (SEQ ID NO:23):

CGTGGCGACGCCCAAATCGAGCGACCTGATCGAGGCCCCTCGCCCCTACTCGCTGAA
TCCCAATCCGAGCCCGCCAATTGGGCGCCCCCCCCCGCCCACGCAAAGGACAGATAG

AAGAAAATTATTGGCGCTCTGACAAATCCAACTGAGGTTTTCTTGGACTACAGATGAAG
CGGGCTCGAAGGGCGTATGTGCAAGAGATGACTGATGAGGGATGCTAGTGAAATTGA
TGAACTTGTTACGGGCGTGCTGGCGACCGTCATCGAACCGGCATGCCCGAACAGGCT
CAGATGTTACCGGTAGGCAGGATGGACTTCTATGGTACAAGGACGCCGGGCAACATG
TCAATGGGGAGTTCTCCATGGCTGTTGTTCAGGCAAATAACTTACTTGAGGACCAGTG
TCAGATCGAGTCGGGCCCACTGAGTTTTCTAGATTCTGGACCATATGGCACTTTCGTT
GGTGTTTACGATGGGCATGGTGGTCCAGAGACGGCCTGCTATATCAATGATCATCTTT
TCCAGAATCTGAAAAGATTTGCATCTGAACAGAATGCAATGTCTGCTGATGTACTGAAG
AAGGCATATGAAGCTACAGAAGATGGATTCTTCTCCATTGTTACCAAACAATGGCCTGT
AAAGCCTCAGATAGCAGCTGTCGGCTCATGCTGCCTGGTCGGTGTAATTTGTGGTGGC
ATGCTTTATGTTGCCAATGTTGGGGATTCCCGTGTCGTTTTAGGAAAACATGTTAAGGC
CACTGGAGAAGTTTTGGCTGTCCAACTGTCAGCAGAACATAATGTTAGTATTGCGTCC
GTGAGAAAAGAACTGCAGTCAATGCACCCAGAAGATAGGCACATTGTTGTTCTCAAGC
ACAATGTTTGGCGTGTTAAAGGACTAATTCAGGTTTGTAGATCAATTGGTGATGCATAT
CTCAAAAAGCAAGAGTTCAACAGGGAACCCCTATATGCAAAATTTCGCCTCCGTGAAC
CTTTTCACAAGCCAATACTAAGTTCAGAACCATCAATCAGTGTGCAACCACTACAACCA
CACGACCAGTTTCTCATATTTGCATCTGATGGACTTTGGGAGCAGTTAACCAACCAAGA
GGCAGTTGATATTGTTCGAAGTAGCCCCCGCAGTGGCTGTGCTAGGAGGCTGATAAG
AGCGGCACTGCAAGAGGCAGCCAAGAAAAGAGAGATGAGGTACTCGGACCTCAAGAA
GATTGACCGCGGTGTTCGCCGCCACTTCCACGACGACATAACAGTCATAGTAGTGTTC
CTTGACTCCGGCCTCGTAAGCCAGGCGAGCACACACCGAGGTCCAACTCTTTCCTTGC
GAGGCGGTGGCGGCAGCGCTGGCCTGCGCAGCAACACACTTGCACCTACGTGACTAT
AAAGTGCCTGGTGGAGTGGAGGCTACTGACTGAAGGTGGTTTTCTTTCCTTGTGTCGA
ATGTGTTATATATGTACTTGTACCAGCCAAGATCATTCATCCCCCCCCCTAAAATGGTG
TAAAGAAGTAGGAGAGGCGCCGAAGTTCCTCACCAGCGTATCTGAATGCCCTCAATGG
TGTCAAGTTGTGGACTCAAGTGGATAGCTTCGCTGAATCTTCTGATGATGCTCTGTGGA
AAGCTCGAATCCTTTCCACCTGAAAAAGCAAGTAATATGTCTTCCAGTGCTGGAATTAA
CCCCTAGTGCATATATATATGTATGAAATAATAATAAGGCAAAAGGAGGAGTAACTTAT
TTAACTAATGCTGTGAGGTGTATTTATGTTTTGTATGTGTACTGCTTTTGACTGCTACTG
CATCTACTGTTGTTAATTGACCACTGGTGAAGTGAAATCACTGGTTTCGTAAAAAAAAA
AAAAAA

The ZM58462719 cDNA is translated into the following amino acid sequence (SEQ ID NO:24):

MLVKLMNLLRACWRPSSNRHARTGSDVTGRQDGLLWYKDAGQHVNGEFSMAVVQANNL
LEDQCQIESGPLSFLDSGPYGTFVGVYDGHGGPETACYINDHLFQNLKRFASEQNAMSAD
VLKKAYEATEDGFFSIVTKQWPVKPQIAAVGSCCLVGVICGGMLYVANVGDSRVVLGKHV
KATGEVLAVQLSAEHNVSIASVRKELQSMHPEDRHIVVLKHNVWRVKGLIQVCRSIGDAYL
KKQEFNREPLYAKFRLREPFHKPILSSEPSISVQPLQPHDQFLIFASDGLWEQLTNQEAVDI
VRSSPRSGCARRLIRAALQEAAKKREMRYSDLKKIDRGVRRHFHDDITVIVVFLDSGLVSQ
ASTHRGPTLSLRGGGGSAGLRSNTLAPT

cDNA sequence of ZM61092633 from corn (SEQ ID NO:25):

AGCTTCCTCCCTCTTCCCTGGTCTGGTCGCTTCTCCTGTAGCTGTAATTTTTGAGAGTC
CCTCTCAAACTTTGCTTGCTTGCGCTCTCCATATATCCTGTGGATCGGAGAGGATGCTC
TGATCTACCTGTCTGTTCTTCGATCGAGTCTGAGAGATTTGGGAGGAGGAGGGAAACA
AAGCGAAAGAGCCCATCTTTTTTGTCTTTTTGGTTCGGTTTCGTGGTTGCTTCTTTTGG
ACCCCGCGGAGGAGCCCACCGTTTCTACAAAAACCCAATCTTTGCTGCCTTCTCAGCG
GTCGAGATCGATAGGTTTCCAGATCTGAGGCTCCGTGTTCTGGCTGTGAGATCGGAG
GCGCAGCAATCCGAGCACGCAGCTAGTAGGGAAAGTATCCGAGAAAAGTTGCAGATT
TTGCTGGGGGCAACGGAGCGAGAACAAGTTACTGCAGAAGGAAAGGGCAAAGGTGG
GGGAGGCGCCGGAGATGAGGGATGCTATCAGCTCTGATGGATTATTTGAAATCTTGCT
GGGGTCCGGCATCACCGGCTGGGCGTCCCCGCAAAGGATCGGATGCCACCGGCCGC
CAGGACGGGCTCCTGTGGTACAAGGACGGCGGGCAGGTCGTCGATGGTGAGTTCTC
CATGGCCGTGGTCCAGGCCAATAACCTATTGGAGGACCATAGCCAGGTTGAATCCGG
GCCGCTTAGCACATCGGAGCCTGGACTGCAAGGCACCTTCGTCGGGGTCTACGATGG
GCACGGTGGCCCGGAGACAGCGCGTTACATCAATGACCATCTCTTCAACCACTTGAG
GAGATTCGCATCTGAGCACAAGTGCATGTCAGCGGATGTGATTCGGAAGGCATTCCGA
GCGACTGAGGAGGGTTTCATTTCTGTGGTTAGTAACCAATGGTCATTGAGACCTCAATT
AGCAGCTGTAGGCTCTTGCTGTCTAGTTGGTGTGGTTTGCAGCGGAACTCTATATGTT
GCAAACCTTGGGGACTCCCGTGCTGTTCTGGGGAGACTTGTCAAGGGAACTGGGGAG
GTTTTGGCAATGCAGCTCTCAGCAGAACACAATGCATCCTATGAGGAGGTTAGACGAG
AGCTGCAGGCATCACATCCTGATGATCCCCATATTGTGGTCCTAAAACACAATGTTTGG
CGTGTAAAGGGTATTATCCAGATAACAAGGTCAATTGGAGATGTGTATCTGAAGAAACC
AGAATTTAATAGAGAACCTTTGCACAGCAAGTTTCGTCTTCAGGAAACTTTTAGGAGAC
CACTTCTTAGTTCTGATCCAGCAATTACTGTCCACCAAATACAGCCAACTGATAAGTTC
ATCATTTTTGCATCTGATGGACTCTGGGAACATCTTAGTAATCAGGAAGTGGTTGACAT
GGTCCAAAGTAGCCCGCGTAATGGAATCGCACGAAAGTTAGTAAAGTCTGCAGTGCAG
GAAGCAGCGAAGAAGAGGGAGATGCGGTATTCAGACCTCAAGAAAGTTGATCGGGGG
GTGAGGCGGCACTTCCACGACGATATAACTGTCATTGTGGTATTTTTCGATTCAAACGC
CATGACAACTGCTGCCTGGAGCAGACCCTCGGTCTCTCTCCGAGGGGGTGGGTTTCC
AATCCATTCAAACACCCTTGCTCCATTCTCGGTTCCTACAGAGCTAAACAACTCCTACT
GAAACCACGCGGTATGTGAAGGAGCCAGGCAAGAGGATAAAAAAAAAGTAAAGGAAA
ACGGAGAAGGAAAAACAGCTGTTGTGATCAGTTGTAGTGTATTTCACCGTTCATGTTCA
TTTAAAACATTTTTTAGATTCTCAAGTCTCAACCTGGTGACCAGTGCACTGATAGCAAG
GTATAAGATTAGATTATTCTTAGCTTTTTTATCCTCTTTTTTTTTTCTCGTCCTTACCCTTT
AGATTCACTCATGGGATATCCGATATCAGGTGCTTGTACATTCTTTGGTTCAACTTGTG
ATAATAGTTCATCGCCCCCCTCTTTTCGCAAAAAAAAAAA

The ZM61092633 cDNA is translated into the following amino acid sequence (SEQ ID NO:26):

MLSALMDYLKSCWGPASPAGRPRKGSDATGRQDGLLWYKDGGQVVDGEFSMAVVQAN
NLLEDHSQVESGPLSTSEPGLQGTFVGVYDGHGGPETARYINDHLFNHLRRFASEHKCMS
ADVIRKAFRATEEGFISVVSNQWSLRPQLAAVGSCCLVGVVCSGTLYVANLGDSRAVLGR
LVKGTGEVLAMQLSAEHNASYEEVRRELQASHPDDPHIVVLKHNVWRVKGIIQITRSIGDV
YLKKPEFNREPLHSKFRLQETFRRPLLSSDPAITVHQIQPTDKFIIFASDGLWEHLSNQEVV
DMVQSSPRNGIARKLVKSAVQEAAKKREMRYSDLKKVDRGVRRHFHDDITVIVVFFDSNA
MTTAAWSRPSVSLRGGGFPIHSNTLAPFSVPTELNNSY

cDNA sequence of ZM62016485 from corn (SEQ ID NO:27):

TGTCTTGCTGCTGGCGCGCCGGGGCTCCGATTGCGCTCCAGATCTGAGGCACCTGCT
CGGTGGATTCCAGGAATCCGAGCACCAACTCGACAGGGGAGTTCTCAGGGTAAAGAG
GCTGAGAGCGCGTTGGAGATTTGGACTATAAGAGCGAGCGAGCGAGCTGGGTGCCTT
GCTGCCTTGAGGACGCCGTCAAGAAACCGCGTGGAGGGGAGGGCGATGAGATGAGG
GATGCTGGCCGCGGTGATGGACTACTTCAGCACCTGCTGGGGCCCGCGGTCTCGTGC
GGGGCACCGGGGCAAGGGCTCCGACGCCGCCGGCCGGCAGGACGGCCTCCTCTGG
TACAAGGACGCCGGGCAGCTCGTCACCGGGGGGTTCTCCATGGCCGTGGTGCAGGC
CAACCAGCTGCTTGAGGACCAGAGCCAGGTGGAGTCCGGATCGCTCTCCCTGGCTGA
CTACGGCCCGCAGGGCACCTTCGTCGGCGTCTATGATGGCCATGGCGGCCCGGAGA
CGTCCCGGTTCATCAATGACCACCTCTTCAACCATCTCAGGAGATTCGCAACTGAGCA
CAAGTCCATGTCAGCAGACGTGATCCGGAAAGCTTTCCAAGAAACTGAGGAGGGCTTT
CTTTCTCTAGTCATCAAGGAATGGTCTTTCAAGCCTCAGATTGCATCAGTTGGCTCCTG
TTGCCTTGTTGGTGTAATCTGTGCTGGGACTCTCTATGTTGCAAACCTGGGCGACTCG
CGTGCAGTTCTTGGAAGGCTTGTGAAAGCAACTGGAGAGGTTCTGGCCACTCAGTTGT
CAGCGGAGCACAATGCATGCTATGAAGAAGTTAGACAAGAGCTGCAGTCATCACATCC
TGATGATCCACGTATTGTGGTTCTCAAACATAACGTTTGGCGAGTGAAGGGTCTCATCC
AGATCTCAAGATCTATCGGAGATGTATATCTAAAGAAACCGGAGTATAACAGAGAACCT
CTTCACAGCAAGTTTCGGCTTCGAGAAACCTTCCAGAAGCCGATTCTTAGTTCTGAACC
TCAAATTACTGAACACCGAATACAGCCAAACGATCAGTTTGTTATATTTGCTTCCGATG
GTCTATGGGAGCACCTCAGCAATCAGGAAGCTGTTGACCTTGTCCAAAGTAGTCCCCG
TAATGGAATCGCTCGGAGACTAGTGAAAGCCGCGATGCAAGAAGCTGCCAAGAAGAG
GGAGATGAGATACTCAGACCTCAAGAAGATCGACCGTGGCGTGAGGAGGCATTTCCA
CGACGATATAACCGTCGTCGTGGTGTTCCTCGACTCGGATGCCATGAGCAAAGCTAGC
TGGAGCAAGAGCCCCTCGTTTTCTCTCCGAGGGGGCGGCGTCACCCTTCCCGCCAAG
TCCCTCGCACCCTTCTCGGCTCCGGCACAGTTGAACGGCACCCACTGAAGCTGCTACT
GCTCTTGAAAAGAAGGGCACAGTGCAGATCTGCTAGAGATGATGAGAGAAGCAGCAAT
CAAGTGTAGCTGTTGCTCGTACACCTGCTGTGCTGTTGCTGTTTGCAAAGCTGCCGTC
TTGACTCCGCCTGGTAATTAGTGTACTGATAGCGAGGTATAGAAATTAGGTTATTTGTT
AGCGACGCAAATCCTTTCTTTTTTTTTCTTCTCCCTCTGTTCTTATCTCTTTTCTCTTCAT
CATGGAGGAAACAGGTGGCTGTAAATTTGTCCAGAACATGTTTTCCCTAATAGCCCAAC
AAAAAAAAAAA

The ZM62016485 cDNA is translated into the following amino acid sequence (SEQ ID NO:28):

MLAAVMDYFSTCWGPRSRAGHRGKGSDAAGRQDGLLWYKDAGQLVTGGFSMAVVQAN
QLLEDQSQVESGSLSLADYGPQGTFVGVYDGHGGPETSRFINDHLFNHLRRFATEHKSM
SADVIRKAFQETEEGFLSLVIKEWSFKPQIASVGSCCLVGVICAGTLYVANLGDSRAVLGRL
VKATGEVLATQLSAEHNACYEEVRQELQSSHPDDPRIVVLKHNVWRVKGLIQISRSIGDVY
LKKPEYNREPLHSKFRLRETFQKPILSSEPQITEHRIQPNDQFVIFASDGLWEHLSNQEAVD
LVQSSPRNGIARRLVKAAMQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSDAM
SKASWSKSPSFSLRGGGVTLPAKSLAPFSAPAQLNGTH

cDNA sequence of ZM62051019 from corn (SEQ ID NO:29):

TTTTCTCTTATCCAGCTTCTTAGCATGATTCTCTTTGATCCCGGAGAGCAGCCACCGGT
CCAACTAGTCCTTGCTGTTGGTCTGCCGGAACTTTTGATTGCTCTCCAGATCTGAGGC
ACCTGCTGGGTGGATTCCAGGAACCCGAGCACGAAGTTGACAGGTGAGTTCTCAGGG
AAAAAGGGGAGGAAGGAAGAGGCTGAAAGGGCGGTG
GAGAGAGAAAGACTATAAGGGCGAGCTGAGTCCCTTGAGGATGCCGTCAAGAAACCG
CGTGGAGAGGAGGGCGATGAGATGAGGGATGCTGGCCGCGGTGATGGACTACTTCA
GCTCCTGCTGGGGCCCGCGATCGGGCGCCGGGCACCGGGGCAAGGGCTCCGACGC
CGCCGGCCGGCAGGACGGTCTCCTCTGGTACAAGGACGCCGGCCAGCTCGTCACTG
GGGAGTTCTCCATGGCCGTGGTGCAGGCCAACCAGCTCCTCGAGGACCAGAGCCAAG
TAGAGTCCGGATCGCTCTCCCTGGCTGACCCGGGCCCACAGGGCACCTTCGTCGGCG
TCTATGATGGCCATGGCGGCCCGGAGACGTCCCGGTTCATCAATGACCACCTCTTCAA
CCATCTCAGAAGGTTTGCAACTGAGCACAAGTTTATGTCAGCGGACGTGATCCGGAAA
GCTTTCCAAGCAACTGAGGAGGGCTTTCTTTCTCTAGTCAGCAAGGAATGGTCTTTGAA
GCCTCAGATTGCTTCAGTGGGCTCCTGCTGCCTTGTTGGTGTAATCTGTGCTGGGACT
CTCTATGTTGCAAACGTGGGCGACTCACGTGCAGTTCTTGGAAGGCTTGTTAAGGCAA
CTGGAGAGGTTGTGGCCATGCAGTTGTCATCGGAGCACAATGCGTGCTATGAGGAAG
TTAGACAAGAACTGCAGTCATCACATCCTGACGATCCACATATTGTGGTTCTCAAACAC
AATGTTTGGCGAGTGAAGGGTCTCATCCAGATCTCAAGATCTATTGGAGATGTATATCT
AAAGAAACCAGAGTACAACAGAGAACCACTTCACAGCAAGTTTCGGCTTCGAGAAACC
TTCCAGAGGCCGACCCTTAGTTCTGAACCTCAAATTACTGAACATCGAATACAGCCGAA
CGATCAATTTGTTATATTTGCTTCTGATGGTCTATGGGAGCACCTCAGCAATAAGGAAG
CAGTTGACCTTGTCCAAAGTAGTCCCCGAAATGGAATCGCTCGGAGGCTAGTGAAAGC
CGCGATGCAAGAAGCTGCCAAGAAGAGGGAGATGAGATACTCAGACCTCAAGAAGAT
CGACCGTGGTGTGAGAAGGCATTTCCACGACGATATAACTGTCGTCGTGGTATTCCTC
GATTCGGATGCCATGAGCAAAGCTAGCTGGAGCAAAAGCCCCTCGGTTTCTCTCCGAG
GGGGCGGTGTCGCCCTCCCTGCGAAGTCCCTCGCACCTTTCTCAGCTCCGGCACGGC
TGAACAGCACCTACTGAAGTTGCTACCACTCTTGAAAGGAAGAACACAGTGCAGATCT
GCAGTGGTGAGAGAGAGAGAGAAAACAGCAACCAAGTGTAGCGTTACAGTTACACCT
GCTGTGTTGTTGCTCTTTGCAAAACTACTGTCTAGACTCCGCCTGGTAATTAGTGTACT

GATAGCGAGGTAAAAAAAGTTAGATTATTTGTTAGCGACACACATCCTTTCACCTTCTC
TTCTCTCCCTCGATTCCTATCCCTTTTCTCTTCATCCTTGAGAGAACAGGTGGATGTAA
ATTGTTCAGAACATGTTTTCCCTTATAGTCCATCATATCCCGCTTTTTTCGTGTTGAAAA
AAAAAAAAAA

The ZM62051019 cDNA is translated into the following amino acid sequence (SEQ ID NO:30):

MLAAVMDYFSSCWGPRSGAGHRGKGSDAAGRQDGLLWYKDAGQLVTGEFSMAVVQAN
QLLEDQSQVESGSLSLADPGPQGTFVGVYDGHGGPETSRFINDHLFNHLRRFATEHKFMS
ADVIRKAFQATEEGFLSLVSKEWSLKPQIASVGSCCLVGVICAGTLYVANVGDSRAVLGRL
VKATGEVVAMQLSSEHNACYEEVRQELQSSHPDDPHIVVLKHNVWRVKGLIQISRSIGDVY
LKKPEYNREPLHSKFRLRETFQRPTLSSEPQITEHRIQPNDQFVIFASDGLWEHLSNKEAV
DLVQSSPRNGIARRLVKAAMQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSDA
MSKASWSKSPSVSLRGGGVALPAKSLAPFSAPARLNSTY

cDNA sequence of ZM65086957 from corn (SEQ ID NO:31):

CTCTGTCTCCTTGGATTTGCGCTTGTGCTCGTCTGGCCGCATACTAGTATCCGCACCA
GAGAGGAGACACCTCCGACTCCGACCTGCTCTTGCATATAGATTGGACAGAGAGTGA
GGGAGAGAGAGAGCGCGCGCTGAAGGGGTGCCAAAGGGAGATTTTTTTTTTTTAAT
CCAGCTTCTTAGCCTGACTGACTCTCTTTGATCCCGG
AGAGCAGCCGCCAGCCCAACTAATCCTTGCTGCTGGCGCGCCGGGGCTCTGATTGCG
CTCCAGATCTGAGGCACCTGCTCGGTGGATTCCAGGAATCCGAGCACCAACTCGACA
GGGAGAGTTCTCAGGGTAAAGGACGACGCTTGATGCACACGGGACGGGACAACGAGT
TGGCCGCAAGTTTTGTTTGCACACGCACACGACCCACCAGCTCACGCGTTTTTTTTTT
TTTTTTGCTTCTTAACTCGCTTTGATTGCATCTGTTGTTTCGGAAGGAAGAGGCTGAGA
GCGCGTTGGAGATTTGGACTATAAGAGCGAGCGAGCGAGCGAGCTGGGTGCCTTGAG
GACGCCGTCAAGAAACCGCGTGGAGGGGAGGGCGATGAGATGAGGGATGCTGGCCG
CGGTGATGGACTACTTCAGCACCTGCTGGGGCCCGCGGTCTCGTGCGGGGCACAGG
GGCAAGGGCTCCGACGCCGCCGGCCGGCAGGACGGCCTCCTCTGGTACAAGGACGC
CGGGCAGCTCGTCACCGGGGGGTTCTCCATGGCCGTGGTGCAGGCCAACCAGCTGC
TTGAGGACCAGAGCCAGGTGGAGTCCGGATCGCTCTCCCTGGCTGACTACGGCCCGC
AGGGCACCTTCGTCGGCGTCTATGATGGCCATGGCGGCCCGGAGACGTCCCGGTTCA
TCAATGACCACCTCTTCAACCATCTCAGGAGATTTGCAACTGAGCACAAGTCCATGTCA
GCAGACGTGATCCGGAAAGCTTTCCAAGAAACTGAGGAGGGCTTTCTTTCTCTAGTCA
TCAAGGAATGGTCTTTCAAGCCTCAGATTGCATCAGTTGGCTCCTGTTGCCTTGTTGGT
GTAATCTGTGCTGGGACTCTCTATGTTGCAAACCTGGGCGACTCCCGTGCAGTTCTTG
GAAGGCTTGTTAAGGCAACTGGAGAGGTTCTGGCCACGCAGTTGTCAGCGGAGCACA
ATGCATGCTATGAAGAAGTTAGACAAGAGCTGCAGTCATCACATCCTGATGATCCACG
TATTGTGGTTCTAAAACATAACGTTTGGCGAGTGAAGGGTCTCATCCAGATCTCAAGAT
CTATCGGAGATGTATATCTAAAGAAACCGGAGTATAACAGAGAACCTCTTCACAGCAA

GTTTCGGCTTCGAGAAACCTTCCAGAAGCCGATTCTTAGTTCTGAACCTCAAATTACTG
AACACCGAATACAGCCAAACGATCAGTTTGTTATATTTGCTTCTGATGGTCTATGGGAG
CACCTCAGCAATCAGGAAGCTGTTGACCTTGTCCAAAGTAGTCCCCGTAATGGAATCG
CTCGGAGACTAGTGAAAGCCGCGATGCAAGAAGCTGCCAAGAAGAGGGAGATGAGAT
ACTCAGACCTCAAGAAGATCGACCGTGGCGTGAGGAGGCATTTCCACGACGATATAAC
CGTCGTCGTGGTGTTCCTCGACTCGGATGCCATGAGCAAAGCTAGCTGGAGCAAGAG
CCCCTCGGTTTCTCTCCGAGGGGGCGGCGTCACCCTTCCCGCCAAGTCCCTCGCACC
CTTCTCGGCTCCGGCACAGTTGAACGGCACCCACTGAAGCTGCTACTGCTCTTGAAAA
GGGGCACAGTGCAGATCTGCTAGAGATGATGAGAGAAGCAGCAATCAAGTCAAGTGT
AGCTGTTGCTCGTACACCTGCTGTGCTGTTGCTGTTTGCAAAGCTGCCGTCTTGACTC
CGCCTGGTAATTAGTGTACTGATAGCGAGGTATAGAAATTAGGTTATTTGTTAGCGACG
CAAATCCTTTCTTTTTTTTCTTCTTCTCTCTCTGTTCTTATCCCTTTTCTCTTCATCATGG
AGGAAACAGGTGGCTGTAAATTTGTCCAGAACGTGTTTTCCCTAATAGCCCATCATATC
CCGCTATTTTTCTTGTTAAAAAAAAAA

The ZM65086957 cDNA is translated into the following amino acid sequence (SEQ ID NO:32):

MLAAVMDYFSTCWGPRSRAGHRGKGSDAAGRQDGLLWYKDAGQLVTGGFSMAVVQAN
QLLEDQSQVESGSLSLADYGPQGTFVGVYDGHGGPETSRFINDHLFNHLRRFATEHKSM
SADVIRKAFQETEEGFLSLVIKEWSFKPQIASVGSCCLVGVICAGTLYVANLGDSRAVLGRL
VKATGEVLATQLSAEHNACYEEVRQELQSSHPDDPRIVVLKHNVWRVKGLIQISRSIGDVY
LKKPEYNREPLHSKFRLRETFQKPILSSEPQITEHRIQPNDQFVIFASDGLWEHLSNQEAVD
LVQSSPRNGIARRLVKAAMQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSDAM
SKASWSKSPSVSLRGGGVTLPAKSLAPFSAPAQLNGTH

cDNA sequence of ZM68587657 from corn (SEQ ID NO:33):

GGACGCCGGGCAACATGTCAATGGGGAGTTCTCCATGGCTGTTGTTCAGGCAAATAAC
TTACTTGAGGACCAGTGTCAGATCGAGTCGGGCCCACTGAGTTTTCTAGATTCTGGAC
CATATGGCACTTTCGTTGGTGTTTACGATGGGCATGGTGGTCCAGAGACGGCCTGCTA
TATCAATGATCATCTTTTCCAGAATCTGAAAAGTAA
CTTGCTAACCTTTAAATCTGTGCAGTAGCACTATTCCCGTTTCTTAGCACTATATCTGCA
TTTGGCTTTCAGTTTGCACATAAAGGAGATCATCCATTTTTTCATGGCTTGTATTTAGGA
TTTGCATCTGAGCAGAATGCAATGTCTGCTGATGTACTGAAGAAGGCATATGAAGCTAC
AGAAGATGGATTCTTCTCCATTGTTACCAAA
CAATGGCCTGTAAAGCCTCAGATAGCAGCTGTCGGCTCATGCTGCCTGGTCGGTGTAA
TTTGTGGTGGCATGCTTTATGTTGCCAATGTTGGGGATTCCCGTGTCGTTTTAGGAAAA
CATGTTAAGGCCACTGGAGAAGTTTTGGCTGTCCAACTGTCAGCAGAACATAATGTTA
GTATTGCGTCCGTGAGAAAAGAACTGCAGTCAATG
CACCCAGAAGATAGGCACATTGTTGTTCTCAAGCACAATGTTTGGCGTGTTAAAGGACT
AATTCAGGTTTGTAGATCAATTGGTGATGCATATCTCAAAAAGCAAGAGTTCAACAGGG

AACCCCTATATGCAAAATTTCGCCTCCGTGAACCTTTTCACAAGCCAATACTAAGTTCA
GAACCATCAATCAGTGTGCAACCACTACAACCA
CACGACCAGTTTCTCATATTTGCATCTGATGGACTTTGGGAGCAGTTAACCAACCAAGA
GGCAGTTGATATTGTTCGAAGTAGCCCCCGCAGTGGCTGTGCTAGGAGGCTGATAAG
AGCGGCACTGCAAGAGGCAGCCAAGAAAAGAGAGATGAGGTACTCGGACCTCAAGAA
GATTGACCGCGGTGTTCGCCGCCACTTCCACGACGACATAACAGTCATAGTAGTGTTC
CTTGACTCCGGCCTCGTAAGCCAGGCGAGCACACACCGAGGTCCAACTCTTTCCTTGC
GAGGCGGTGGCGGCAGCGCTGGCCTGCGCAGCAACACACTTGCACCTACGTGACTAT
AAAGTGCCTGGTGGAGTGGAGGCTACTGACTGAAGGTGGTTTTCTTTCCTTGTGTCGA
ATGTGTTATATATGTACTTGTACCAGCCAAGATCATTCATCCCCCCCCCTAAAATGGTG
TAAAGAAGTAGGAGAGGCGCCGAAGTTCCTCACCAGCGTATCTGAATGCCCTCAATGG
TGTCAAGTTGTGGACTCAAGTGGATAGCTTCGCTGAATCTTCTGATGATGCTCTGTGGA
AAGCTCGAATCCTTTCCACCTGAAAAAGCAAGTAATATGTCTTCCAGTGCTGGAATTAA
CCCCTAGTGCATATATATATGTATGAAATAATAATAAGGCAAAAGGAGGAGTAACTTAT
TTAACTAATGCTGTGAGGTGTATTTATGTTTTGTATGTGTACTGCTTTTGACTGCTACTG
CATCTACTGTTGTTAATTGAAAAAAAAAAAAAAA

The ZM68587657 cDNA is translated into the following amino acid sequence (SEQ ID NO:34):

MSADVLKKAYEATEDGFFSIVTKQWPVKPQIAAVGSCCLVGVICGGMLYVANVGDSRVVL
GKHVKATGEVLAVQLSAEHNVSIASVRKELQSMHPEDRHIVVLKHNVWRVKGLIQVCRSIG
DAYLKKQEFNREPLYAKFRLREPFHKPILSSEPSISVQPLQPHDQFLIFASDGLWEQLTNQE
AVDIVRSSPRSGCARRLIRAALQEAAKKREMRYSDLKKIDRGVRRHFHDDITVIVVFLDSGL
VSQASTHRGPTLSLRGGGGSAGLRSNTLAPT

cDNA sequence of EST390 from moss (SEQ ID NO:35):

ATCCCGGGTGGAGCCCTTTCAAGCCTCACGCATTCTGGATTCGCTCCCGGCTTCGAAT
GCTTGAGTGGTTCTAAGTGATGAGATAGCGCCGTCTAGGGAGAATTTCGAATTTGCGC
TAGAACATGGGTGGTTATTCCATCAGTGTGGCAGCGCCCACAGATATTGCAGTGAAAG
GTTGAACACAACGACCCAAGGACAACCTGCACCTTCCAACAGTCAGCGTGAGGTGAAA
AGATAGGCCAGTTTTCAGCTGCACATAACCTTCACTTCTGCAGGCGCAGAACACGTGC
GGTACTGAGCAATGGGGTCCTCTAAGGCAGAAGAGAATTTGGCCTTACGGCTGGGCC
TCACTGCAGCGTCAGCCATGGCGTCGGAGTCTGTGACCTTCCCAATCGATATCACGAA
AACCCGCCTGCAGCTCCAAGGCGAAATGGGTGCCACAGCTGGCGCACCCAAGCGAG
GAGCGATCAGCATGGCGATCTCTATAGGCAAGGAGGAGGGCATTGCCGGTCTTTATA
GGGGCCTTTCTCCGGCACTTTTGCGTCATGTATTTTACACAAGCATTCGTATTGTTGCG
TATGAAAATCTACGTACCGCCCTCAGTCATGGCGAACACCCGGAAAATCTGTCCGTTG
CAAAAAAGGCTTTCATCGGTGGCACTTCCGGTATTATTGGGCAGGTGATAGCGAGTCC
AGCGGATTTGGTGAAGGTGCGCATGCAAGCGGATGGGAGGCTGGTGAAGCTTGGGC

AGCAGCCACGCTACACCGGAGTAGCTGACGCATTCACCAAGATTGCCCGAGCCGAGG
GTGTGACAGGGCTGTGGCGTGGAGTGGGACCCAATGCTCAACGTGCCTTCCTCGTCA
ACATGGGGGAGCTTGCATGCTACGACCAGTCGAAGCAATGGATCATAGGACGCGGCA
TTGCTGCCGACAACATCGGAGCTCACACGCTTGCATCAGTGATGTCTGGGTTATCAGC
TACTATTCTGAGCTGCCCTGCCGATGTGGTGAAGACCCGGATGATGAACCAAGGCGCT
GCAGGTGCCGTGTACCGCAACTCTCTGGATTGTCTCACCAAAACCGTGAAGGCTGAAG
GCGTGATGGCGCTGTGGAAGGGCTTCTTCCCGACGTGGACAAGGCTGGGCCCTTGG
CAATTCGTGTTTTGGGTCTCATATGAGCAGCTCCGCCGCATCAGCGGTCT
ATCATCCTTCTAATAAGTAAAGCCTCGCAGTTGTTTTGGGTGTGAAACTTACATGGCAT
TCAGCTCTTACAAAGATTTCACATGCTTGAAGATTTTGAGGTGCTGTTTTTTTATCATT
TTTGTTCCTTCTCTTTTCTGCCTCAATTGGATGTCATAGCT
GAGGCTATGAAGCTTAGTTTCATTGACAAATGTTTACATTTGTTAGCAATGTGTAGTAGT
GCACTTGCGTTAACCG

The EST390 cDNA is translated into the following amino acid sequence (SEQ ID NO:36):

MGSSKAEENLALRLGLTAASAMASESVTFPIDITKTRLQLQGEMGATAGAPKRGAISMAISI
GKEEGIAGLYRGLSPALLRHVFYTSIRIVAYENLRTALSHGEHPENLSVAKKAFIGGTSGIIG
QVIASPADLVKVRMQADGRLVKLGQQPRYTGVADAFTKIARAEGVTGLWRGVGPNAQRA
FLVNMGELACYDQSKQWIIGRGIAADNIGAHTLASVMSGLSATILSCPADVVKTRMMNQGA
AGAVYRNSLDCLTKTVKAEGVMALWKGFFPTWTRLGPWQFVFWVSYEQLRRISGLSSF

cDNA sequence of BN51363030 from canola (SEQ ID NO:37):

AGAAAACAAATAAAAATCAAATCGTTACAGCAATGGGCGTCAAAAGTTTCGTGGAAGGT
GGGATTGCCCCTGTAGTCGCCGGCTGCTCCACTCACCCTCTCGATCTCATCAAGGTTC
GCCTTCAGCTCCACGGCGAAGCTTCCGCCGTCACTCTCCTCCGCCCAGCTCTCGCTTT
CCACAATTCTCCCCCAGCTTTTCTGGAGACGACTC
ATTCGGTCCCTAAAGTAGGACCCATCTCCCTCGGAATCAACCTCGTCAAAACCGAAGG
CGCCGCCGCGCTTTTCTCCGGCGTCTCCGCCACACTCCTCCGTCAGACTCTCTACTCC
ACCACCAGGATGGGTCTCTACGAGGTGTTGAAAAACAAATGGACTGATCCCGAGTCCG
GTAAGCTGAGTCTCACTCGTAAAATCGCCGCGGGGCTAGTCGGTGGCGGGATCGGAG
CCGCCGTCGGGAACCCAGCCGACGTGGCGATGGTAAGGATGCAAGCCGACGGGAGG
CTTCCCGTGGCAGAGCGTCGTAACTACGCGGGCGTAGGAGACGCGATCAAGAGGATG
GCGAAGCAAGAAGGCGTGGTGAGCCTGTGGCGCGGCTCGGCTCTGACGATCAACAG
GGCGATGATAGTGACGGCGGCGCAGCTCGCGTCGTACGATCAGTTCAAGGAAGGGAT
GGTGGAGAGCGGGGGGATGAAAGATGGGCTCGGGACTCACGTGGTGGCGAGCTTCG
CGGCGGGGATCGTGGCGGCTGTTGCGTCGAATCCGGTGGATGTGATAAAGACGAGG
GTGATGAATATGAAGGTGGATGCGCGTGGTGGGGAGGCTCAGTACAAAGGCGCGTGG
GATTGTGCGGTGAAGACGGTTAGAGCTGAAGGACCGATGGCTCTTTATAAAGGGTTTG
TTCCTACGGTTTGCAGGCAAGGACCTTTCACTGTTGTGCTCTTTGTTACGTTGGAGCAA
GTCAAGAAGCTGCTTCGTGATTTTTGATTATCATTTGAAGGTTATGATGATGAGGACGA

CTAAGAATAAGAATGCTAGTAGTATTGATTTGATAGGGATTTTTCGTATTGGGTTATTCA
TTTTCG

The BN51363030 cDNA is translated into the following amino acid sequence (SEQ ID NO:38):

MGVKSFVEGGIAPVVAGCSTHPLDLIKVRLQLHGEASAVTLLRPALAFHNSPPAFLETTHSV
PKVGPISLGINLVKTEGAAALFSGVSATLLRQTLYSTTRMGLYEVLKNKWTDPESGKLSLTR
KIAAGLVGGGIGAAVGNPADVAMVRMQADGRLPVAERRNYAGVGDAIKRMAKQEGVVSL
WRGSALTINRAMIVTAAQLASYDQFKEGMVESGGMKDGLGTHVVASFAAGIVAAVASNPV
DVIKTRVMNMKVDARGGEAQYKGAWDCAVKTVRAEGPMALYKGFVPTVCRQGPFTVVLF
VTLEQVKKLLRDF

cDNA sequence of BN42986056 from canola (SEQ ID NO:39):

TCTAAAAAAACTTTTTGTCTGAACGGCATATGTCTCAGAGACCTCAAGTTCCTCATTCTT
CTTCTATAGCTTTCGGTCTCCATTCTCATCTCCTAATCTCCAGTGAGATCAGCTCCAATT
CCAACTGGTCTCTCTAAGAAAAAAATAATCAAACCTTTTCAAAATTTTCTCTCGGATTTT
CTCGGAATAAAAATCTAACCTTTCTGACTTTTTTGATTTTCGATTTGATAAAAACAAGAA
ATGGGTCTTAAGGGTTTCGCTGAAGGAGGCATCGCATCGATCGTAGCGGGATGTTCG
ACCCACCCGCTTGATCTAATCAAGGTCTGAATGCAGCTCCAAGGGGAATCAGCCTCGA
TTCAGACAAATCTCCGACCAGCTCTTGCTTTCCAGACTTCCTCCGCCGTTCACGCGCC
TTCGCCTCCTCCGCGCGTGGGTATAATCACCATCGGATCTCGCATCATCAGACAAGAA
GGCACGTGCACTCTCTTCTCCGGCATCTCCGCCACCTCCGCCACCGTTCTCCGCCAG
ACTCTCTACTCGACGACTCGCATGGGTCTATACGACATCCTGAAAACCAAATGGACCG
ACCCGGAAACCAAAACCATACCTTTGACCCGCAAACTCGCCGCCGGGTTCATCGCCG
GAGGTATCGGCGCCGCCGTCGGGAACCCGGCGGATGTCGCCATGGTGCGCATGCAA
GCCGACGGGAGGCTCCCGGTGGTCGACCGGAGGAACTACAAGAGCGTTTTGGACGC
GATCGCGCAGATGGTTCGCGGCGAAGGCGTCACGTCGCTGTGGAGAGGTTCGTCGAT
GACGATCAACAGAGCGATGCTCGTGACG
GCGTCGCAGCTGGCTACGTACGACTCGGTGAAAGAGACGATTTTGGAGAAAGGGTTG
ATGAGGGACGGGCTCGGGACTCACGTGACGTCGAGCTTCGCGGCGGGGTTTGTGGC
TTCGGTCGCGTCGAACCCCGTGGATGTGATCAAGACGAGAGTGATGAATATGAAAGTG
GAGGCGGGGAAAACGGCGCCGTATAAGGGAGCGGTTGATTGCGCGTTGAAGACGGT
GAGAGCGGAAGGGATCATGGCTTTATACAAAGGGTTTCTGCCGACGGTGTCGAGACA
AGCACCGTTCACGGTGATTATGTTTGTGACACTTGAACAAGTTAAGAAGGTGTTCAAGG
ACTTTGACTTTTGAGACAAGAGTTAAAGATGATGGTGGCGATAATTTGCTTTAAACTAAA
TAAATTTTGTTTTTTTTTATTGTATTTTCTTT

The BN42986056 cDNA is translated into the following amino acid sequence (SEQ ID NO:40):

MQLQGESASIQTNLRPALAFQTSSAVHAPSPPPRVGIITIGSRIIRQEGTCTLFSGISATSAT
VLRQTLYSTTRMGLYDILKTKWTDPETKTIPLTRKLAAGFIAGGIGAAVGNPADVAMVRMQ
ADGRLPVVDRRNYKSVLDAIAQMVRGEGVTSLWRGSSMTINRAMLVTASQLATYDSVKET
ILEKGLMRDGLGTHVTSSFAAGFVASVASNPVDVIKTRVMNMKVEAGKTAPYKGAVDCAL
KTVRAEGIMALYKGFLPTVSRQAPFTVIMFVTLEQVKKVFKDFDF

cDNA sequence of BN49389066 from canola (SEQ ID NO:41):

CGACGATTTCGTTTAATATAAACATCACCAAGTGAATCTCTCCGCCTCTCTCTCTCTTTC
TCTGCGGAATCTCTTCGTCTCGTTGCGTTCGAGAGTTCCGTACGATTCCCAACAAGAA
AGGGAAGAGATGGCGGAGGAGAAGAAAGTAGCTCCGATTGGTATCTGGACTGCCGTG
AAGCCTTTCGTCAATGGCGGTGCCTCTGGTATGCT
CGCCACTTGCGTTATCCAGCCTATTGACATGATCAAGGTGAGGATTCAACTAGGTCAG
GGATCTGCAGCTAGTGTGACCACCACCATGTTGAAGAATGAAGGTATCGGTGCCTTCT
ACAAGGGATTATCAGCTGGTTTGCTGAGGCAAGCAACTTACACCACAGCTCGTCTTGG
ATCATTCAAGATGCTGACTGCGAAAGCAAGCGAGGCTAACGATGGGAAGCCACTACC
GCTGTATCAAAAAGCTCTATGTGGTCTGACAGCTGGTGCTATCGGTGCCTGCGTTGGT
AGTCCAGCCGATTTAGCGCTTATCAGAATGCAAGCTGATAACACTTTGCCGTTAGCTCA
GCGCAGGAACTATACCAACGCCTTCCATGCGCTTTACCGTATTAGCGCTGATGAAGGA
GTTTTGGCGCTTTGGAAAGGTTGTGGGCCAACTGTGGTCAGAGCAATGGCTTTGAACA
TGGGGATGCTTGCGTCTTATGATCAAAGTGCTGAGTATATGAGAGATAATCTTGGTCTT
GGGGAGACATCCACAGTCGTAGGAGCAAGTGCTGTTTTGGGATTCTGCGCTGCGGCT
TGCAGTCTTCCATTTGACTTTGTCAAAACACAGATCCAAAAAATGCAACCCGACGCTCA
GGGTAAATATCCATACACTGGTTCGCAGGACTGTGCGATGCAAAACAGGAGGACCTTT
GAAATTCTACACAGGCTTTCCGGTATACTGCGTCAGGATCGCCCCTCACGTCATGGTG
ACATGGATCTTCCTGAACCAGATTACAAAGTTCCAAAAGAACATTGGGATGTGATCTTC
AAGCAAACCTTATGAAGTGCGCGGTG
AAAATATGATGAGAAGAATTCATTTGCTTTTTAATCATATACATGATTAG

The BN49389066 cDNA is translated into the following amino acid sequence (SEQ ID NO:42):

MAEEKKVAPIGIWTAVKPFVNGGASGMLATCVIQPIDMIKVRIQLGQGSAASVTTTMLKNE
GIGAFYKGLSAGLLRQATYTTARLGSFKMLTAKASEANDGKPLPLYQKALCGLTAGAIGAC
VGSPADLALIRMQADNTLPLAQRRNYTNAFHALYRISADEGVLALWKGCGPTVVRAMALN
MGMLASYDQSAEYMRDNLGLGETSTVVGASAVLGFCAAACSLPFDFVKTQIQKMQPDAQ
GKYPYTGSQDCAMQNRRTFEILHRLSGILRQDRPSRHGDMDLPEPDYKVPKEHWD-
VIFKQTL

cDNA sequence of BN51339479 from canola (SEQ ID NO:43):

CTTTCTCCGCCTATCTCTTTCTCTCCGCGGATTCTCTTCTTCTCGTTTCGACTCCGTAC
GATCCCCAAAGAAAAAAAGAGATGGCGGAAGAGAAAAAAGTAGCTCCGATTGGTGTCT
GGAATACCGTGAAGCCCTTCGTCAATGGCGGTGCCTCCGGTATGCTCGCCACTTGCG
TTATCCAGCCGATCGACATGATCAAGGTGAGGATTC
AACTAGGTCAGGGATCTGCAGTCAGTGTGACCAAGAACATGTTGAAGAATGATGGTAT
TGGTGCTTTCTACAAGGGATTGTCTGCTGGTTTGCTAAGGCAAGCAACTTACACCACA
GCCCGTCTTGGATCCTTCAAGATGCTGACTGCAAAAGCAATTGAGGCTAACGATGGGA
AGCCGCTACCTCTGTACCAGAAGGCTCTATGTGGTC
TGACAGCTGGTGCAATCGGTGCTTGCGTTGGTAGTCCAGCTGACTTGGCGCTTATCAG
AATGCAAGCTGATAACACCTTGCCGTTAGCTCAGCGCAGGAACTATACCAATGCCTTC
CATGCGCTTTACCGTATTAGCGCTGATGAAGGAGTTTTGGCACTTTGGAAAGGTTGTG
GTCCTACTGTGGTCAGAGCTATGGCTTTGAACATGG
GAATGCTTGCTTCTTATGATCAAAGTGCTGAGTACATGAGAGATAATCTCGGTCTTGGG
GAGACTTCTACGGTCGTAGGAGCAAGTGCTGTTTCTGGATTCTGCGCTGCGGCTTGCA
GTCTTCCATTTGACTTTGTCAAAACTCAGATCCAGAAGATGCAACCTGACGCTCAGGG
GAAGTATCCATACACGGGTTCGCTTGACTGTGCCA
TGCAAACCTTGAAGTCAGGAGGACCTCTTAAATTCTACACAGGTTTCCCTGTTTACTGC
GTCAGGATCGCCCCTCACGTCATGATGACATGGATCTTCCTGAACCAGATTACAAAGT
TTCAAAAGACCATTGGTCTGTGAGCTTCAAGCATTGTGAAGTGCGCGCTGAGAATAAG
TTGAAAACGAAAACGCAATTGGAATTGTGTTAGAT
TTGCTTTTTATTCAATATACATGATCGCATGCCTTAACGCATTATTTGAAGTGTTGGAGA
CTTTA

The BN51339479 cDNA is translated into the following amino acid sequence (SEQ ID NO:44):

MAEEKKVAPIGVWNTVKPFVNGGASGMLATCVIQPIDMIKVRIQLGQGSAVSVTKNMLKND
GIGAFYKGLSAGLLRQATYTTARLGSFKMLTAKAIEANDGKPLPLYQKALCGLTAGAIGACV
GSPADLALIRMQADNTLPLAQRRNYTNAFHALYRISADEGVLALWKGCGPTVVRAMALNM
GMLASYDQSAEYMRDNLGLGETSTVVGASAVSGFCAAACSLPFDFVKTQIQKMQPDAQG
KYPYTGSLDCAMQTLKSGGPLKFYTGFPVYCVRIAPHVMMTWIFLNQITKFQKTIGL

cDNA sequence of ZM57651070 from corn (SEQ ID NO:45):

CTAGCACGTGAAAATTCCTTCGGCTCCAGTTATTACGGAGGATTAGGTTGGTGAACTG
GTGACTGGAGCTGGAATCGCATTTCTTGCTCTTTGGTCTCTCCAGAATCATCCTCCGG
CCAGCCGTTCTTGGAATCCTCCCGAGATTCGCTTGCCCGCCCTTTTCTTTTCAAGTGG
ATCTGAACTTGGGAGGGAACCCCGATGCAGCCGCGG
TACGGAGAAGCACGACAACCGCTGCCGGGGCGGTACGCGCTGTACCACTTCGGCAC
CAGCGGCGCCGCCGTCGCCGCCGCCACCGCCGTGACCCATCCGTTCGATGTTATCAA
AGTCAGGCTTCAAATGCAGCTTGCTGGGCAAAGAGGAAACTTAGTTGGAATGGGAACA

ATATTTACACAAATGGTTGAAAGGGAAGGGACTCGGTCACTCTACCTGGGACTTGCAC
CAGCGTTGGCGAGAGCTGTTGTCTATGGTGGCCTTCGGTTTGGACTGTATGAGCCCTG
CAAGCATGTCTGCAGTTATGCATTTGGTTCAACAAACTTTGCTTTTAAATTTGCATCTGG
AGTCATTGCTGGGGGCCTTGCAACTGCTTTAACAAATCCCATGGAAGTTTTGAAGGTG
AGGCTGCAGATGAGTAAAAGCAGTACCAGTACAATAAGAGAGATGAGAAAAGTTATAG
CGCACGAAGGGTTTAAAGCACTTTGGAAAGGAGTCGGCCCAGCAATGACAAGAGCAG
GTTGCCTTACTGCATCACAAATGGCGACTTACGATGAGGCCAAACAGGCCTTAATGAA
GTGGACACCACTTGAAGAAGGTTTTCAGTTACATCTCATCTCGAGTTTCATAGCTGGAA
CAGCTGGTACTCTTGTGACCTCACCTGTAGACATGATCAAAACACGGTTAATGCTGCAA
CAGGAGTCCAAAGGCGCCAGAGTATACAGGAACGGATTCCATTGTGCTTCCCAGGTTG
TGGTGACAGAGGGTGTGAAATCACTTTATAAAGGTGGATTTGCCACATTCGCGAGAGT
AGGCCCTCAGACAACGATTACCTTTATCGTGTGCGAGAAACTGCGCGAACTTGCAGGA
ATGACTGCCATCTAGTGCCACCCCAAATTGCATAATGTGTGGGGTCCAACGGTTGAAC
AGCATACTCTACCCGAGTTTTCACACCATTCTTTATTCACTATTCATGATGAGAAGGGA
GAAGATAAGCACCCACTGGGATGTCTAAGGATTGGGAAGCCCAGAGCTCCTTCAGATT
TATCATACCTCATTTGAAATTTCGAAATAGCGTGATTGTTCTTATGTTTGCTCTAAGACT
TACTCATCATATCTCCAATCTCATCTTGTATTTCAAACTACACTCTACAAACAATACAGT
CTGTAGTGTAAAAACATTATTTTGGGTGACCATATGGGTAACCTGCTGTACAAAAAAAAAA

The ZM57651070 cDNA is translated into the following amino acid sequence (SEQ ID NO:46):

MQPRYGEARQPLPGRYALYHFGTSGAAVAAATAVTHPFDVIKVRLQMQLAGQRGNLVGM
GTIFTQMVEREGTRSLYLGLAPALARAVVYGGLRFGLYEPCKHVCSYAFGSTNFAFKFAS
GVIAGGLATALTNPMEVLKVRLQMSKSSTSTIREMRKVIAHEGFKALWKGVGPAMTRAGC
LTASQMATYDEAKQALMKWTPLEEGFQLHLISSFIAGTAGTLVTSPVDMIKTRLMLQQESK
GARVYRNGFHCASQVVVTEGVKSLYKGGFATFARVGPQTTITFIVCEKLRELAGMTAI

cDNA sequence of ZM62073276 from corn (SEQ ID NO:47):

GCCGCCTCTCCTACTGCATCTCCCTCGCTCTCGTCGCCTCGTTCGCTTCGCCTCCGCC
CCGCCCCGCCCCGAGCAGAGCGCAGCCCTATCCGGAGCTGGGATGGCGGACGCGAA
GCAGCAGCAGCAGCAGCAGCAGCAGCCACAGCAGGCGGCAGCGGCAGCCACCGGC
GTGTGGAAGACGGTCAAGCCCTTCGTTAACGGCGAGGCCTCTGGGATGCTCGCGACC
TGCGTCATCCAGCCTATCGACATGGTCAAGGTGAGGATCCAGTTGGGTGAGGGCTCT
GCTGGTCAGGTCACAAGGAACATGCTTGCAAATGAGGGTGTCCGTTCTTTCTACAAGG
GTTTGTCCGCCGGATTGCTGAGGCAAGCGACGTACACGACTGCTCGTCTTGGATCCTT
TAGGGTTCTAACTAACAAAGCAGTTGAAAAGAATGAAGGGAAGCCATTGCCTCTATTTC
AGAAAGCTTTTATTGGTCTGACTGCTGGTGCAATTGGTGCTTGTGTTGGTAGTCCTGCT
GATCTGGCACTCATTAGAATGCAAGCCGATTCGACCCTGCCAGTTGCACAACGACGCA
ACTATAAGAATGCTTTCCATGCACTCTACCGTATCAGTGGTGATGAGGGAGTCCTTGC

GCTTTGGAAGGGTGCAGGTCCAACTGTGGTGAGAGCTATGGCACTCAATATGGGTATG
CTTGCTTCCTATGACCAGAGTGTCGAGCTATTTAGGGACAAATTTGGCGCAGGAGAAA
TTTCTACTGTTGTTGGAGCCAGCGCTGTTTCTGGATTCTTTGCCTCAGCATGCAGTTTG
CCCTTTGACTATGTGAAGACACAGATTCAGAA
GATGCAACCTGATGCGAATGGCAAGTACCCATACACAGGGTCTTTGGACTGTGCTGTG
AAGACCTTCAAGAGCGGTGGCCCATTCAAGTTCTACACTGGTTTCCCGGTGTACTGCG
TCAGGATTGCACCCCATGTCATGATGACCTGGATATTCTTGAATCAGATCCAGAAGTTT
GAGAAGAAGATCGGCATATAGGATTCCCATCGGAC
GGATACAGGGTTGACAGTTCTATGCTATTACTGCTTGACTCTGTAATAACATTCCAGCT
GCTTTCGCACCATGGTAGTTGGTTTTGGTAGAGACAAGTCTGTTACAATTTTTTACCTTA
GCTTTCCAATTATTGTGTTGCAATAATCGAATTAATTGTTGCTGGGGGATTTTTTTGGGG
GGTTGGGAGGGTGGCATGCTTTTGTTGGCTG
GGATGTAGCCATAAGGAGAGGGGGATACTGCCTAGTTATGTCATTGAATGGAATTGGA
CCATATTTTATACAGATTTTTACCTTCAAAAAAAAAAAAAA

The ZM62073276 cDNA is translated into the following amino acid sequence (SEQ ID NO:48):

MADAKQQQQQQQPQQAAAAATGVWKTVKPFVNGEASGMLATCVIQPIDMVKVRIQLGE
GSAGQVTRNMLANEGVRSFYKGLSAGLLRQATYTTARLGSFRVLTNKAVEKNEGKPLPLF
QKAFIGLTAGAIGACVGSPADLALIRMQADSTLPVAQRRNYKNAFHALYRISGDEGVLALW
KGAGPTVVRAMALNMGMLASYDQSVELFRDKFGAGEISTVVGASAVSGFFASACSLPFDY
VKTQIQKMQPDANGKYPYTGSLDCAVKTFKSGGPFKFYTGFPVYCVRIAPHVMMTWIFLN
QIQKFEKKIGI

cDNA sequence of EST257 from moss (SEQ ID NO:49):

CCCGGGGATTCAGCAGTACTTCACAAGAAGAATAGCATGGTGCGTGCAGATCTTGTCA
ACCTTGCGGACTTAGATACTGCTCTAAACAGAGTTCATAATAAGCTACCTAATTCCATA
GAAACAGCTAGTGCAGAGCCTCCTGCTCCTCCAGAAGAATGGGAAATAAATCCTCGAG
AGATCACTTTGAAGCATATGATTGCGCGTGGCACCTTTGGGACTGTCCACAAAGGAGT
GTACAAAGGTCAGGATGTCGCAGTTAAGCTACTTGAGTGGGGCGAGGAGAATACCAT
GAAGAAAACAGAGGTTCAATACTACAGAAACCAATTCAGACAAGAGGTTGCTGTGTGG
CATAAACTCGACCACCCTAATGTCACGAAGTTCATCGGAGCCTCGATGGGGAACTCAG
ATTTGCGGATTCCCTCAGCCGTGGATGGTGATGATGGATTCCATCATGTGCCGAACAA
TGCTTGTTGTGTTGTCGTTGAGTACCTTGCAGGCGGGACTCTTAAAGATCATCTCATTC
GCAGCCGGCGGAAAAAACTCTCGTACAAGGTGGTCGTGCAATTAGCCTTGGATGTTTC
TAGAGGGCTTGCATACCTCCATTCTCAGAAGATCGCTCATCGTGACGTGAAGACAGAG
AACATGTTGCTCGATAAACAGATGAGGGTCAAAATTGCAGATTTCGGAGTTGCACGAG
TGGAGGCATCCAATCCCAAGGACATGACTGGTGATACTGGTACCCCAGGATACATGGC
TCCGGAGATTCTCGACGGCAAGCCCTACAACAAGAAGTGCGATGTGTACAGCTTCGG
GATCTGTTTGTGGGAAGTTTATTGCTGCGACATGCCGTACTTGGACCTCTCCTTTGCG

GACATGACATCGGCAGTTGTGCATCAGAATTTGAGACCCGAGGTGCCCAAGTGCTGC
CCTCAGGGACTCGCGGATATCATGAGGCAGTGTTGGGATGCAAATCCTGAGAAACGG
CCTGCCATGGCTGATGTGGTGCAGATGCTGGAGGCTCTAGACACCTCCAAAGGTGGA
GGTATGATACCAACAGACGCCCAGCCGCATGGGTGTCTCTGTTTTGGGAGATTCAAGG
GCCCATAGCACGTTTTTGGTTTTTTTTTCCTTAATTGTGGTTTTACATTTTATTTATATTT
TTCCCTTTTTTAATGTAGGGATGACATGATAATAAGTGTGCAAACATTTTGTTGTCTCCC
CTGGTTTCGTTTCAAGCGTAGCTGCTTGACTTGCAATTTCAGTAACCTGGTGCAGGAC
CCGTTAAC

The EST257 cDNA is translated into the following amino acid sequence (SEQ ID NO:50):

MVRADLVNLADLDTALNRVHNKLPNSIETASAEPPAPPEEWEINPREITLKHMIARGTFGTV
HKGVYKGQDVAVKLLEWGEENTMKKTEVQYYRNQFRQEVAVWHKLDHPNVTKFIGASM
GNSDLRIPSAVDGDDGFHHVPNNACCVVVEYLAGGTLKDHLIRSRRKKLSYKVVVQLALD
VSRGLAYLHSQKIAHRDVKTENMLLDKQMRVKIADFGVARVEASNPKDMTGDTGTPGYM
APEILDGKPYNKKCDVYSFGICLWEVYCCDMPYLDLSFADMTSAVVHQNLRPEVPKCCPQ
GLADIMRQCWDANPEKRPAMADVVQMLEALDTSKGGGMIPTDAQPHGCLCFGRFKGP

cDNA sequence of LU61665952 from linseed (SEQ ID NO:51):

AGGGTGATCACGAGGGAGGTATGAATTCTAAGGTGAAGGGAAATGGAAGTGTTAGTA
GAAAAGATATGATTTTTCGAGCGGATCGAATCGATTTGAAGATCCTGGATGTACAGCTA
GAGAAGCACCTGAGTAGGGTGTGGTCGAGGAACACCACAGACAACGCTAAGCCTAAA
GAAGAGTGGGAGATTGATTTGTCTAAGTTGGACATCAAAACCCAGATAGCTCGTGGTA
CTTATGGCACTGTTTATAAAGGCACTTATGATAATCAAGATGTTGCAGTGAAAGTGTTG
GATTGGGGGGAAGATGGTATGACTACAGTATCTGAAGCTGCTTCTCTTCGAGCATCAT
TTCGTCAAGAGGTTGCTGTTTGGCATAAGCTTGACCATCCTAATGTTACCAAATTCGTT
GGAGCATCGATGGGAACTTCAAATCTCAAGGTTTCAAATAATAAATCTGATGGTCAGCA
TACTGCTAGAGCATGTTGTGTTGTGGTTGAGTATCAACCTGGTGGAACACTAAAGCAG
TACTTGATAAGAAATAGGCGAAAGAAACTTCCTTATAAAGTTGTAATACAACTTGCTTTG
GATCTCTCTAGGGGTTTGAGTTACCTACATTCGAAGAAAATTGTGCACCGTGATGTGAA
GTCGGAAAACATGTTGCTTGATAATCATAGAAATCTTAGGATTGCGGATTTTGGTGTTG
CTCGAGTCGAAGCTCAAAATCCAAGTGATATGACTGGTGAAACTGGTACCCTTGGATA
CATGGCACCTGAGGTCCTTGATGGCAAGCCATATAACAGAAGGTGTGATGTTTATAGC
TTCGGCATATGTTTATGGGAAATCTATTGTTGTGATATGCCATATCCAGATCTTAGCTTT
GCTGATGTGACGTCCGCGGTTGTTCGACAAAACTTGAGGCCGGAGATTCCGAGATGTT
GTCCAAGTTCACTAGGAAGCATCATGAAGAAATGTTGGGATGCACAATCAGAGAACCG
TCCAGAAATGGCTGAAGTGGTGAAGATGTTGGAAGCCATTGATACAAGTAAAGGAGGA
GGAATGATCCCTGAAGACCAGAACCCTGGTTGTTTCTGCTTCGCCCCAACCCGTGGCC
CTTAAACCCCCTTATTAATTTACTCCCCAAACAGTCCTCATCCATCTATGTGTGCACAAA
TTTCAATTTCTTTATATTTGAGTTGTTTCTTTGTTTATCATTTTCTTGTGTTCTTCACTTC

TGCACATATTTTGATTTTGAACTACCTAAAGGGAGTGAAAGGATTAATGTTATAAGTAAA
AAAAAAAAAAAA

The LU61665952 cDNA is translated into the following amino acid sequence (SEQ ID NO:52):

MNSKVKGNGSVSRKDMIFRADRIDLKILDVQLEKHLSRVWSRNTTDNAKPKEEWEIDLSKL
DIKTQIARGTYGTVYKGTYDNQDVAVKVLDWGEDGMTTVSEAASLRASFRQEVAVWHKL
DHPNVTKFVGASMGTSNLKVSNNKSDGQHTARACCVVVEYQPGGTLKQYLIRNRRKKLP
YKVVIQLALDLSRGLSYLHSKKIVHRDVKSENMLLDNHRNLRIADFGVARVEAQNPSDMTG
ETGTLGYMAPEVLDGKPYNRRCDVYSFGICLWEIYCCDMPYPDLSFADVTSAVVRQNLRP
EIPRCCPSSLGSIMKKCWDAQSENRPEMAEVVKMLEAIDTSKGGGMIPEDQNPGCFCFAP
TRGP

cDNA sequence of TA56863186 from wheat (SEQ ID NO:53):

AGCACTGACAACTACAACCTCGCTGGTGGCTCCGTTACCATGTCAGTGGACAACAGCA
GCGTGGGCTCGAACGAGTCCCGCACCGTCATACTTAAGCACCCGGGCCTCCGTGATG
CTCCAACCGCAAGCTACTCGGTTGGCAACAGTGTCTTTCGTCCCAACCGTGTGGCTGC
GCACACCCTAAATGAAGATGCATTGGCCAGGGTTCTGATGGACCCAAATCATCCAACA
GAGATACTTAGCAAGTACCAGCAGTGGGCCATTGATCTGGGGAGGTTGGATATGGGG
GTTCCCTTTGCACAGGGAGCCTTTGGGAAGCTGTACCGGGGAACATATATTGGAGAAG
ATGTTGCCATTAAGCTGCTGGAGAAGCCTGACAATGATATCGAGAGAGCACAATCGTT
GGAACAGCAGTTTGTGCAAGAAGTTATGATGTTATCTACCCTAAGGCACCCAAATATAG
TAAGATTTATAGGGGCTTGCAGGAAGTCAATTGTGTGGTGCATTATTACTGAGTATGCA
AAAGGTGGCTCAGTCAGGCAGTTCCTGGCAAAAAGGCAGAACAAGTCGGTACCTTTGA
GGCTGGCTGTCAAACAAGCATTGGATGTAGCGAGGGGAATGGCGTATGTGCATGCTC
TGGGATTTATCCATAGGGACCTGAAGTCGGATAATCTTCTAATTGCAGCAGACAGATCC
ATTAAGATTGCTGACTTTGGAGTTGCTCGAATTGAAGTGAAAACAGAGGGGATGACAC
CAGAGACAGGAACCTACCGCTGGATGGCACCGGAAATGATCCAGCACAGGCCTTATG
ATCATAAGGTTGATGTCTACAGCTTTGGGATTGTCTTGTGGGAGCTTATAACTGGCATG
CTTCCTTTCACAAACATGACAGCTGTTCAGGCGGCTTTTGCTGTTGTAAATAAGGGTGC
TCGTCCAGCGATCCCACATGACTGCCTGCCTTCCCTAACCCACATCATGACGCGCTGT
TGGGATGCAAACCCTGAAGTTCGCCCACCATTCACCGAGATCGTCTGCATGCTTGAGA
ACGCCGAGATGGAGGTCGTGAGCCATGTCCGTAAAGCGCGCTTCCGCTGCTGCGTTG
CTGAACCCATGACCACCGACTGAAACTAAAGCAGGTTAGACTATCGCAGCGGGCATTA
GGGAAGAAAACAGGTAAGGATGAAGAAAAGAGGCAATGCCAATGTGTTCATCGTTGTC
AGTGCGTGGGGTCTGTGTGCCTTTACCAGTGCGCATTCTGTCTTGTGTAAGTTGCACA
CCTCAAGTAAAAGTAATTTCGTATAGATGTTGCCTTGTATGCTAACAAAGACCTAATGG
AGCTTTTCCGTGTTAATAATATCCGCTTGCTCTTGTACTCGTGCAAGTTTGTGCCAAAA
AAAAAAAAAAA

The TA56863186 cDNA is translated into the following amino acid sequence (SEQ ID NO:54):

MSVDNSSVGSNESRTVILKHPGLRDAPTASYSVGNSVFRPNRVAAHTLNEDALARVLMDP
NHPTEILSKYQQWAIDLGRLDMGVPFAQGAFGKLYRGTYIGEDVAIKLLEKPDNDIERAQSL
EQQFVQEVMMLSTLRHPNIVRFIGACRKSIVWCIITEYAKGGSVRQFLAKRQNKSVPLRLA
VKQALDVARGMAYVHALGFIHRDLKSDNLLIAADRSIKIADFGVARIEVKTEGMTPETGTYR
WMAPEMIQHRPYDHKVDVYSFGIVLWELITGMLPFTNMTAVQAAFAVVNKGARPAIPHDC
LPSLTHIMTRCWDANPEVRPPFTEIVCMLENAEMEVVSHVRKARFRCCVAEPMTTD

cDNA sequence of ZM62026837 from corn (SEQ ID NO:55):

CGCGCGGCCAAACTCCTGTTCTTCCACCTGCTGGCTGCTCCTGCCTCCCCTGCGCCC
CAAACCCACCCGCCTCGCCGTCCCCGCAGGCCGCAGCCTGCTCTCGGCTCCCGCCG
CCGTCTACCGCGTCCTGCGGCTGCGGTGTTGCGTCACCTCGGGTTCGCCTTAACTTC
CACAATCCTCGCCGTCCTGGTGCTCCGCCGCCCCTCCCTT
TGTACTCGCGCTGGAGCTGCAGATCCACCGCGACCTGGCGACCAATTCCTCCTCCCG
CTGAAGAATTGGCGACCTTGGCCTCCGCCCCCGCGGCGCGGAGGAGTCAACTGTGGT
AGCAACCACCGCGGAGGCTGCAAGCCTTCGGTAAGGGAGGAAAGTTGACTTGTTGGA
AGCCGGTCCAGGGCCGCGATGACGTCGACCGCCGCCGGCGCGTCGTCGTCGGCGG
CGAAGAGCGAGTCCTACCTGCGGGCCGACAAGATCGACCTCGAGAGCCTGGACATCC
AGCTGGAGAAGCAGCTGGCCAAGACCTGGGAGAAGCACAAGGGGTCGTACAACCAG
GGGCCCAGGGAGGACTGGGAGATCGACCTCGCCAAGCTCGAGATTCGCTACGTCATA
GCGCAGGGCACCTACGGCACGGTGTATCGCGGCACGTATGATGGGCAGGACGTCGC
AGTAAAACTATTGGATTGGGGTGAAGATGGCTTTGCGTCAGAAACTGAAACTGCCACA
CTGCGAGCATCATTTAAGCAGGAGGTTGCTGTCTGGCATGAGCTCAACCATCCGAATG
TTACAAAGTTTGTTGGTGCATCAATGGGTACTACAGACCTTAAGATTCCAGCCAATAGT
TCTAACAGTGGTGGGCGCACTGAGCTGCCGCCAAAAGCATGTTGTGTTGTGGTCGAAT
ATCTCGCTGGAGGATCACTGAAGCAGTATTTAATAAAGAACAGGCGAAGGAAGCTTGC
ATACAAGGTTGTTGTTCAGATAGCACTGGATCTTGCCAGAGGATTGAACTATCTACATT
CAAGAAAGATAGTACATCGGGATGTAAAAACTGAAAATATGCTGCTCGATACACAGCG
AAACCTTAAGATTGCTGATTTTGGTGTTGCTCGTGTTGAGGCTCAGAATCCAAAGGACA
TGACAGGCGCGACTGGGACACTTGGCTACATGGCCCCAGAGGTGCTTGAAGGCAAGC
CATACAACAGAAAGTGTGATGTCTACAGTTTTGGCATATGCTTATGGGAAATATACTGC
TGTGACATGCCATATCCAGACCTCAGTTTTGCAGACGTCTCGTCCGCCGTCGTTCACC
AGAACCTGCGGCCTGACATCCCTCGCTGCTGCCCAAGCCCAATGGCGAACATCATGC
GGAAGTGCTGGGACGCAAACCCGGATAAGCGCCCTGACATGGACGACGTGGTGCGG
TTCCTGGAGGCCCTCGACACGAGCAAGGGCGGTGGCATGATACCAGAAGGCCAGGC
AGGCGGGTGCTTGTGTTTCTTCAGAGCCCGTGGTCCTTAGAACCAACCAACCCTTTCC
AGCCATCCTCTACTTGTCTCTGCCATACTACAGTATTGGAGCCAGATGTAGGCCTTTGT
TGTTCATCGGATAGGGGATTGCAGATAACTTGATGACAATCTTTGTGATTGGTTGACAC

TTGTTATACGTTCTATAGTGATGTGAATACCAGTGAGGAGTCCATAATACAGAGTGAAA
AAAAAAA

The ZM62026837 cDNA is translated into the following amino acid sequence (SEQ ID NO:56):

MTSTAAGASSSAAKSESYLRADKIDLESLDIQLEKQLAKTWEKHKGSYNQGPREDWEIDLA
KLEIRYVIAQGTYGTVYRGTYDGQDVAVKLLDWGEDGFASETETATLRASFKQEVAVWHE
LNHPNVTKFVGASMGTTDLKIPANSSNSGGRTELPPKACCVVVEYLAGGSLKQYLIKNRRR
KLAYKVVVQIALDLARGLNYLHSRKIVHRDVKTENMLLDTQRNLKIADFGVARVEAQNPKD
MTGATGTLGYMAPEVLEGKPYNRKCDVYSFGICLWEIYCCDMPYPDLSFADVSSAVVHQN
LRPDIPRCCPSPMANIMRKCWDANPDKRPDMDDVVRFLEALDTSKGGGMIPEGQAGGCL
CFFRARGP

cDNA sequence of ZM65457595 from corn (SEQ ID NO:57):

ACCTCGCCACCCTCCTGCCTCCTCCGCATCCGCGCCCCCTCGCTTAGCCTAAACCGC
GGGGCAGCTAGTCTCGCCACCGCAGGCCGCACCGGTCATCACACCGAAGCGCACGC
GGGGAGCCCCCGTAGAGTTCCGGGGCGACCAGGCCAACTAACGCCATGAAGGAGGA
AGGCGGCGGCGGGGACGCGGGGTTCGTGCGGGCGGACCAGATCGACCTCAAGAGC
CTGGACGAGCAGCTGGAGCGCCATCTCACCCGCGCCTGGACCATGGAGAAGCGCAA
GGAGGAGGCCTCCGCCGGCGCTGGCGCCGGCGCCAGGCAGCACCAGCAGTCCCGG
CGCCCGCGGAGGGAGGACTGGGAGATCGACCCCGCCAAGCTTGTCGTCAAGGGCGT
CATCGCCCGCGGCACCTTTGGCACCGTCCACCGCGGCATCTACGACGCTCACGACGT
CGCAGTGAAACTACTTGATTGGGGAGAGGATGGGCATAGATCAGAACAAGACATTGCA
GCACTAAGAGCAGCTTTTTCACAAGAGGTCTCTGTTTGGCATAAGCTTGACCATCCAAA
TGTAACCAAGTTTATTGGAGCTATAATGGGTGCAAGGGATCTGAATATTCAAACGGAAA
ACGGCCACATTGGCATGCCAACTAATATCTGCTGTGTCGTTGTGGAGTACCTTCCTGG
TGGTGCACTAAAATCATTTCTGATAAAGAACAGGAGAAAGAAGCTAGCTTTTAAGGTCG
TTGTTCAAATCGCTCTTGACCTTGCCAGGGGATTAAGCTATCTCCATTCCAAGAAGATT
GTGCACCGTGATGTGAAGACTGAAAATATGCTTCTTGACAAAACGAGAACCGTGAAGA
TCGCTGATTTTGGTGTTGCTCGCCTTGAAGCTTCAAATCCCAGTGACATGACGGGCGA
AACTGGAACGCTTGGTTACATGACACCTGAGGTTCTCAATGGAAATCCCTACAACAGG
AAATGCGATGTTTACAGCTTCGGGATCTGTTTGTGGGAGATATACTGCTGTGATATGCC
ATATCCTGACTTGAGCTTTTCTGAGGTCACGTCTGCGGTTGTCCGTCAGAACCTGAGG
CCGGAGATACCACGCTGCTGCCCGAGCTCTCTATCGAACGTGATGAAGCGCTGCTGG
GACGCCAACCCCGACAAGCGACCTGAGATGGCCGAGGCGGTGTCCATGCTGGAGGC
GATCGACACGTCGAAGGGTGGAGGCATGATCCCTGTGGACCAGCGGCCAGGATGCCT
TGCGTGCTTCCGGCAGTACAGAGGTCCATGACAGATAGGTGGAAACCTGTTGGAGCT
GCGGCCTCTAGATCTCGTGGATGCCGATCGATCGCGTGTTGTTTTCTGGGGAAGCAAA

CTGGTTAATGGAGCTAGCCCGCCTTACCGGCTCGTGTAAATCCTCTGTCCATCAATTCT
GTAACTCTGTTTTATCGATTAATGAAAAGAACCGGGCTTGCTCGAAAAAAAAAAAAAAA

The ZM65457595 cDNA is translated into the following amino acid sequence (SEQ ID NO:58):

MKEEGGGGDAGFVRADQIDLKSLDEQLERHLTRAWTMEKRKEEASAGAGAGARQHQQS
RRPRREDWEIDPAKLVVKGVIARGTFGTVHRGIYDAHDVAVKLLDWGEDGHRSEQDIAAL
RAAFSQEVSVWHKLDHPNVTKFIGAIMGARDLNIQTENGHIGMPTNICCVVVEYLPGGALK
SFLIKNRRKKLAFKVVVQIALDLARGLSYLHSKKIVHRDVKTENMLLDKTRTVKIADFGVARL
EASNPSDMTGETGTLGYMTPEVLNGNPYNRKCDVYSFGICLWEIYCCDMPYPDLSFSEVT
SAVVRQNLRPEIPRCCPSSLSNVMKRCWDANPDKRPEMAEAVSMLEAIDTSKGGGMIPV
DQRPGCLACFRQYRGP

cDNA sequence of ZM67230154 from corn (SEQ ID NO:59):

CGGCAACCCACTATCTCATGCGCTCACATGGAGACTCCCGCACGAACTGGAATCATCT
CCGCCTCGCCACCTCTTCATCTTCTTCCCCAGTAGCCGCCGCCACCACCACTGCAGCA
GCCAAACCACGTGACACCTCCCGCGCCGCTCAACCCCACAGCATCCGTTGCCACCGC
CGCTCACCTCCCCGGCGCTCCCGGCTACAACCACTGC
AAGCATGAGGCAGCCAACCAGCGCGGGCGGCGACGCTGGGTTCTTGCGCGCGGACC
AGATCGACCTCAAGAGCCTGGACGAGCAGCTCGAGCGCCACCTCGGACATCCCGCG
GAGCGGGTAGTTGGCCCAGTCTCTGGGACAGGGAGCCGCCGCGGCGAAACGGCCAA
GCTGGGTCCGGAGGAGCTGACGCCACTGCAGCGGTGCCGTGAGGACTGGGAGATCG
ACCCTACCAAGCTCATCATCAAGGGCGTCATCGCGCGCGGCACCTTTGGCACCGTCC
ACCGCGGCGTCTACGACGGCCAGGACGTCGCTGTAAAATTGCTTGACTGGGGCGAAG
ATGGCCATAGATCAGAACAAGAAATTGGTGCACTAAGAGCAGCGTTTGCACAAGAGGT
CGCTGTCTGGCATAAGCTTGAGCATCCAAACGTTACTAAGTTTATTGGGGCTATAATGG
GCGCAAGAGATTTAAATATACAAACGGAACATGGACAGCTTGGCATGCCAAGCAATAT
TTGCTGTGTTGTTGTTGAGTACCTTGCTGGAGGTGCGCTGAAAAATTTTCTGATAAAGA
ACAGGAGAAGGAAACTTGCCTTTAAAGTTGTGGTCCAAATAGCTCTTGACCTTGCCAG
GGGATTATGCTACCTCCACTCAAAGAAAATAGTGCACCGTGATGTCAAGACTGAAAAC
ATGCTTCTGGACAAGACGAGAACGGTAAAGATCGCTGATTTTGGTGTTGCTCGAGTCG
AGGCTTCAAATCCTAGCGATATGACGGGAGAAACAGGGACGCTTGGTTACATGGCTCC
TGAGGTTCTCAATGGCCATGCTTACAACAGGAAGTGTGACGTGTACAGCTTTGGGATC
TGCCTGTGGGAGATATACTGCTGTGACATGCCGTACCCTGATCTCAGTTTTTCTGAGG
TCACCTCTGCCGTCGTTCGCCAGAATCTGAGGCCTGAGATACCGCGCTGCTGCCCGA
GCTCGCTAGCGAATGTGATGAAGCGATGCTGGGACGCGAACCCGGACAAGCGTCCCG
AGATGGCGGAGGTGGTGTCCATGCTGGAGGCGATCGACACGTCCAAGGGTGGCGGC
ATGATCCCTAAGGACCAGACGCAGGGCTGCCTCTCGTGCTTCCGCCAGTACCGAGGT
CCCTAACGCAGGGTTGTTTATTTATACCCGGTGAAATGATGATATTGGTCTCTACACTA
CAACTCAGTGTAATCTAATCGCAGAAGTGGCTATATAATGGAGAAGCTTATCATTGCTT

GCCATGGGTGTAAATGGATGGGGCGGGGTGGTTGACGATTGGTGTGCTTGTATGCTC
GCTTCGAGTTATAATGCTTGCTGTAAGTTAAGGTGTGGAAAAAAAAAAAAAA

The ZM67230154 cDNA is translated into the following amino acid sequence (SEQ ID NO:60):

MRQPTSAGGDAGFLRADQIDLKSLDEQLERHLGHPAERVVGPVSGTGSRRGETAKLGPE
ELTPLQRCREDWEIDPTKLIIKGVIARGTFGTVHRGVYDGQDVAVKLLDWGEDGHRSEQEI
GALRAAFAQEVAVWHKLEHPNVTKFIGAIMGARDLNIQTEHGQLGMPSNICCVVVEYLAG
GALKNFLIKNRRRKLAFKVVVQIALDLARGLCYLHSKKIVHRDVKTENMLLDKTRTVKIADFG
VARVEASNPSDMTGETGTLGYMAPEVLNGHAYNRKCDVYSFGICLWEIYCCDMPYPDLSF
SEVTSAVVRQNLRPEIPRCCPSSLANVMKRCWDANPDKRPEMAEVVSMLEAIDTSKGGG
MIPKDQTQGCLSCFRQYRGP

cDNA sequence of EST465 from moss (SEQ ID NO:61):

GGGCCTCCTTCCTAGCCTTCATCTGCTGCGACGATGGAGGAGCTCGCCTCATCTGATG
TTCCGAACAAGTTGAAGAAGAAGGAATCTAAGATGAAGAAGAGGGTTATAACTCCAGG
GGCCTTGCTGAAGGCAGTAGTAAGGTCTGGAGAGGGGACTAAACGTCCTGTAGAAGG
TGATCAGATTATCTTCCATTATGTCACACGAACAAATCAGGGAGTGGTGGTTGAGACAT
CGCGATCTGACTTTGGAGGAAAGGGAGTTCCTCTTAGACTTGTTCTGGGAAAAAGCAA
AATGATTGCTGGATGGGAGGAAGGCATCACCACCATGGCCAAAGGTGAAATAGCTATG
CTGAAAGTGCAACCTGAATTACATTATGGTGACCCGGAGTGTCCTGTACCAGTGCCCG
AGAACTTTCCAGTTTCTGATGAGCTCCTTTACGAAGTGGAGTTGTTCAACTTCTGTAAG
GCGAAGATTATCACAGAGGATCTTGGTGTGACAAAAGTGGTCTTAGAAGAGGGTGAGG
GCTGGGAAACTGCAAGGCCTCCGTACGAGGTGAAGCTTTGGATTACAGGCCGGATCT
TAGGTGGGTCCACATTTTTTACTCATAAAGAGTGCGATCCCATTCATGTTGAATTCGGC
AAGGAACAGTTGCCAGAAGGACTTGAGAAGGCAGTCGGCACTATGACGAGGAAAGAA
AAGTCAATTATCTACATTTCAAGTTCATACTGTACGAATTCTTCAAATGCATACAAATTG
AATATATCTCCTCAAGCGCAAGAACTAGAATTTGAAGTGCAGTTGGTGCAGCTCATTCA
GGTAAGAGACATGTTTGGAGATGGAGGATTGATTAAGAGACGCCTGCGAGACGGACT
AGGTGAATTTCCTGTGGACTGTCCTCTGCAAGATAGTGTGCTTAGAGTCCACTATAAG
GCTATGCTACCTGATGATGGCGGCAGAATATTTATTGACACCAGAAGTAATGGAGGGG
AGCCTGTTGAGTTTGCTTCTGGTGAGGGTGTGGTACCAGAGGGACTTGAGGCAAGTTT
GAGGTTGATGCTTCCGGGGGAGCTCGCACTGATCAACAGCGTCTCTAAGTACGCATAT
GACAAATTTCAAAGGCCAGAGAGTGTTCCAGAGGGAGCTTCAGTCCAATGGGAAGTG
GAATTACTGGAATTTGAGAGTGCAAAGGATTGGACGGGCCTTAATTTTCAAGAGATCAT
GGCTGAAGCTGATTCCATAAAGACCACAGGTAACCGGTTATTTAAGGAGGGCAAGCAC
GAGCTGGCTAAAGCTAAGTACGAAAAGGTGTTGAGGGATTTCAGACATGTAAACCCTG
GCAGTGATGAAGAAGCAAAGGAACTACAAGACACCAATAACGCACTGCGGCTTAATGT
AGCAGCTTGTTATCATAAACTCCATGAGTACATCAAATGCATAGAAACATGCAACAAGG
TGCTAGAAGGTAACCCGCATCATGTCAAAGGGTTATTTCGCCGAGGAACTGCTTACAT

GGAAACGGGGGACTTTGATGAAGCTAGAGCTGATTTCAAGCAGATGATAACAGTTGAC
AAGGCTGTCACAGTTGATGCAACTGCTGCTTTACAGAAGCTCAAGCAAAAAGAACGGG
AAGCTGAGCTGAAAGCTAAGAAACAGTTCAAAGGGCTATTTGACTTAAAACCTGGAGA
ACTCTCTGAGGGGCTAGAAGAGGTAAAGCCCGTAAGCGAAATCCATGAGAAGACTGTT
GTCAACGAGGAACTTCCGATAGCATCTATGGATCAACATCAACACTCAAAGCACGAAA
CAGAGGAAGGGAGCCATGAATCGCCCAGGGCAAGCAGCCGATTGTTAAGACTTCTGA
AAGGTGGAGAGCACCTGATAAGGACAGTCACTTTTGGGAAGTGTACGATTCTTTAATTT
TTCATATTGCTACTGCTAGGATCTCCCCTTTTTACTGTACTGGTGACTACCTTATGCTCA
TTTACATTTCTAAGCCGTTATAGCTGTTATTAACCATTCGATAATGTACTATGAACAATAT
TCCACTAGCGTTTTATGGCTATTTTTCATTAAGTCCTCGTGCCGTTA

The EST465 cDNA is translated into the following amino acid sequence (SEQ ID NO:62):

MEELASSDVPNKLKKKESKMKKRVITPGALLKAVVRSGEGTKRPVEGDQIIFHYVTRTNQG
VVVETSRSDFGGKGVPLRLVLGKSKMIAGWEEGITTMAKGEIAMLKVQPELHYGDPECPV
PVPENFPVSDELLYEVELFNFCKAKIITEDLGVTKVVLEEGEGWETARPPYEVKLWITGRIL
GGSTFFTHKECDPIHVEFGKEQLPEGLEKAVGTMTRKEKSIIYISSSYCTNSSNAYKLNISP
QAQELEFEVQLVQLIQVRDMFGDGGLIKRRLRDGLGEFPVDCPLQDSVLRVHYKAMLPDD
GGRIFIDTRSNGGEPVEFASGEGVVPEGLEASLRLMLPGELALINSVSKYAYDKFQRPESV
PEGASVQWEVELLEFESAKDWTGLNFQEIMAEADSIKTTGNRLFKEGKHELAKAKYEKVL
RDFRHVNPGSDEEAKELQDTNNALRLNVAACYHKLHEYIKCIETCNKVLEGNPHHVKGLFR
RGTAYMETGDFDEARADFKQMITVDKAVTVDATAALQKLKQKEREAELKAKKQFKGLFDL
KPGELSEGLEEVKPVSEIHEKTVVNEELPIASMDQHQHSKHETEEGSHESPRASSRLLRLL
KGGEHLIRTVTFGKCTIL

cDNA sequence of YBL109w from yeast (SEQ ID NO:63):

ATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACATATATATATA
CCCTAACACTACCCTAACCCTACCCTATTTCAACCCTTCCAACCTGTCTCTCAACTTAC
CCTCACATTACCCTACCTCTCCACTTGTTACCCTGTCCCATTCAACCATACCACTCCCA
ACCACCATCCATCCCTCTACTTACTACCACCAATCAACCGTCCACCATAACCGTTACCC
TCCAATTAGCCATATTCAACTTCACTACCACTTACCCTGCCATTACTCTACCATCCACCA
TCTGCTACTCACCATACTGTTGTTCTACCCTCCATATTAA

The YBL109w cDNA is translated into the following amino acid sequence (SEQ ID NO:64):

MSLRPCLTPSSMQYSDIYIYPNTTLTLPYFNPSNLSLNLPSHYPTSPLVTLSHSTIPLPTTIHP
STYYHQSTVHHNRYPPISHIQLHYHLPCHYSTIHHLLLTILLFYPPY

cDNA sequence of YBL100c from yeast (SEQ ID NO:65):

ATGTTGTTCAAACCAAAAACACGAGCAATACCATCACCGACTGCAAGAACTCTACCAGT
TTCGTTCAAATTGGCCTCGTCGGACACACCCTTAATTCTTTCCTCTAAGATGGAGGAAA
CTTCTGTGGGTTGTGCCTTGGTGGAAGCCAATCTTCTGGTGGAAGCCAAAGCAGCAGC
GGCAGGTCTTGCGGCCTTGGTAGAGTTAATTAGAGTTCTCGATAGAGAACGAATAGCA
GCAGTACGAGCCAACATTATTATATGTGCGTGTTTTTTTATTTATTTTGTTACTGTTCTT
GCGATAGTTATGAGAGCTAA

The YBL100c cDNA is translated into the following amino acid sequence (SEQ ID NO:66):

MLFKPKTRAIPSPTARTLPVSFKLASSDTPLILSSKMEETSVGCALVEANLLVEAKAAAAGL
AALVELIRVLDRERIAAVRANIIICACFFYLFCYCSCDSYES

cDNA sequence of YKL184w from yeast (SEQ ID NO:67):

ATGTCTAGTACTCAAGTAGGAAATGCTCTATCTAGTTCCACTACTACTTTAGTGGACTT
GTCTAATTCTACGGTTACCCAAAAGAAGCAATATTATAAAGATGGCGAGACGCTGCACA
ATCTTTTGCTTGAACTAAAGAATAACCAAGATTTGGAACTTTTACCGCATGAACAAGCG
CATCCTAAAATATTTCAAGCGCTCAAGGCTCGTATTGGTAGAATTAATAATGAAACGTG
CGACCCCGGTGAGGAGAACTCGTTTTTCATATGCGATTTGGGAGAAGTCAAGAGATTA
TTCAACAACTGGGTGAAGGAGCTTCCTAGAATTAAGCCATTTTATGCCGTCAAATGTAA
TCCTGATACCAAGGTTTTGTCATTATTAGCAGAGTTGGGCGTTAATTTCGATTGCGCTT
CCAAAGTGGAAATTGACAGAGTATTATCGATGAACATCTCGCCGGATAGAATTGTTTAC
GCTAATCCTTGTAAAGTAGCATCTTTCATTAGATATGCAGCTTCAAAAAATGTAATGAAG
TCTACTTTTGACAATGTAGAAGAATTGCATAAAATCAAAAAGTTTCATCCTGAGTCTCAG
TTGTTATTAAGAATCGCTACCGATGACTCTACCGCTCAATGTCGACTTTCCACCAAATA
TGGCTGTGAAATGGAAAACGTAGACGTTTTATTAAAGGCTATAAAGGAACTAGGTTTAA
ACCTGGCTGGTGTTTCTTTCCACGTCGGTTCAGGCGCTTCTGATTTTACAAGCTTATAC
AAAGCCGTTAGAGATGCAAGAACGGTATTTGACAAAGCTGCTAACGAATACGGGTTGC
CCCCTTTGAAGATTTTGGATGTAGGTGGTGGATTTCAATTTGAATCCTTCAAAGAATCA
ACTGCTGTTTTGCGTCTAGCGCTAGAGGAATTTTTCCCTGTAGGTTGTGGTGTTGATAT
AATTGCAGAGCCTGGCAGATACTTTGTAGCTACAGCGTTCACTTTGGCATCTCATGTGA
TTGCGAAGAGAAAACTGTCTGAGAATGAAGCAATGATTTACACTAACGATGGTGTATAC
GGGAACATGAATTGTATTTTATTCGATCATCAAGAGCCCCATCCAAGAACCCTTTATCA
TAATTTGGAATTTCATTACGACGATTTTGAATCCACTACTGCGGTCCTCGACTCTATCAA
CAAAACAAGATCTGAGTATCCATATAAAGTTTCCATCTGGGGACCCACATGTGATGGTT
TGGATTGTATTGCCAAAGAGTATTACATGAAGCATGATGTTATAGTCGGTGATTGGTTT
TATTTTCCTGCCCTGGGTGCCTACACATCATCGGCGGCTACTCAATTCAACGGCTTTGA
GCAGACTGCGGATATAGTATACATAGACTCTGAACTCGATTAA

The YKL184w cDNA is translated into the following amino acid sequence (SEQ ID NO:68):

MSSTQVGNALSSSTTTLVDLSNSTVTQKKQYYKDGETLHNLLLELKNNQDLELLPHEQAHP
KIFQALKARIGRINNETCDPGEENSFFICDLGEVKRLFNNWVKELPRIKPFYAVKCNPDTKV
LSLLAELGVNFDCASKVEIDRVLSMNISPDRIVYANPCKVASFIRYAASKNVMKSTFDNVEE
LHKIKKFHPESQLLLRIATDDSTAQCRLSTKYGCEMENVDVLLKAIKELGLNLAGVSFHVGS
GASDFTSLYKAVRDARTVFDKAANEYGLPPLKILDVGGGFQFESFKESTAVLRLALEEFFP
VGCGVDIIAEPGRYFVATAFTLASHVIAKRKLSENEAMIYTNDGVYGNMNCILFDHQEPHPR
TLYHNLEFHYDDFESTTAVLDSINKTRSEYPYKVSIWGPTCDGLDCIAKEYYMKHDVIVGD
WFYFPALGAYTSSAATQFNGFEQTADIVYIDSELD

cDNA sequence of YPL091w from yeast (SEQ ID NO:69):

ATGCTTTCTGCAACCAAACAAACATTTAGAAGTCTACAGATAAGAACTATGTCCACGAA
CACCAAGCATTACGATTACCTCGTCATCGGGGGTGGCTCAGGGGGTGTTGCTTCCGC
AAGAAGAGCTGCATCTTATGGTGCGAAGACATTACTAGTTGAAGCTAAGGCTCTTGGT
GGTACCTGTGTTAACGTGGGTTGTGTTCCGAAGAAAGTCATGTGGTATGCTTCTGACC
TCGCTACTAGAGTATCCCATGCAAATGAATATGGATTATATCAGAATCTTCCATTAGATA
AAGAGCATTTGACTTTTAATTGGCCAGAATTTAAGCAGAAAAGGGATGCTTATGTCCAT
AGGTTGAACGGTATATACCAGAAGAATTTAGAAAAAGAAAAAGTGGATGTTGTATTTGG
ATGGGCTAGATTCAATAAGGACGGTAATGTTGAAGTTCAGAAAAGGGATAATACTACTG
AAGTTTACTCCGCTAACCATATTTTAGTTGCGACCGGTGGAAAGGCTATTTTCCCCGAA
AACATTCCAGGTTTCGAATTAGGTACTGATTCTGATGGGTTCTTTAGATTGGAAGAACA
ACCTAAGAAAGTTGTTGTTGTTGGCGCTGGTTATATTGGTATTGAGCTAGCAGGTGTGT
TCCATGGGCTGGGATCCGAAACGCACTTGGTAATTAGAGGTGAAACTGTCTTGAGAAA
ATTTGATGAATGCATCCAGAACACTATTACTGACCATTACGTAAAGGAAGGCATCAACG
TTCATAAACTATCCAAAATTGTTAAGGTGGAGAAAAATGTAGAAACTGACAAACTGAAA
ATACATATGAATGACTCAAAGTCCATCGATGACGTTGACGAATTAATTTGGACAATTGG
ACGTAAATCCCATCTAGGTATGGGTTCAGAAAATGTAGGTATAAAGCTGAACTCTCATG
ACCAAATAATTGCTGATGAATATCAGAACACCAATGTTCCAAACATTTATTCTCTAGGTG
ACGTTGTTGGAAAAGTTGAATTGACACCTGTCGCTATTGCAGCGGGCAGAAAGCTGTC
TAATAGACTTTTTGGTCCAGAGAAATTCCGTAATGACAAACTAGATTACGAGAACGTCC
CCAGCGTAATTTTCTCACATCCTGAAGCCGGTTCCATTGGTATTTCTGAGAAGGAAGCC
ATTGAAAAGTACGGTAAGGAGAATATAAAGGTCTACAATTCCAAATTTACCGCCATGTA
CTATGCTATGTTGAGTGAGAAATCACCCACAAGATATAAAATTGTTTGTGCGGGACCAA
ATGAAAAGGTTGTCGGTCTGCACATTGTTGGTGATTCCTCTGCAGAAATCTTGCAAGG
GTTCGGTGTTGCTATAAAGATGGGTGCCACTAAGGCTGATTTCGATAATTGTGTTGCTA
TTCATCCGACTAGCGCAGAAGAATTGGTTACTATGAGATAA

The YPL091w cDNA is translated into the following amino acid sequence (SEQ ID NO:70):

MLSATKQTFRSLQIRTMSTNTKHYDYLVIGGGSGGVASARRAASYGAKTLLVEAKALGGT
CVNVGCVPKKVMWYASDLATRVSHANEYGLYQNLPLDKEHLTFNWPEFKQKRDAYVHRL

NGIYQKNLEKEKVDVVFGWARFNKDGNVEVQKRDNTTEVYSANHILVATGGKAIFPENIPG
FELGTDSDGFFRLEEQPKKVVVVGAGYIGIELAGVFHGLGSETHLVIRGETVLRKFDECIQN
TITDHYVKEGINVHKLSKIVKVEKNVETDKLKIHMNDSKSIDDVDELIWTIGRKSHLGMGSEN
VGIKLNSHDQIIADEYQNTNVPNIYSLGDVVGKVELTPVAIAAGRKLSNRLFGPEKFRNDKL
DYENVPSVIFSHPEAGSIGISEKEAIEKYGKENIKVYNSKFTAMYYAMLSEKSPTRYKIVCAG
PNEKVVGLHIVGDSSAEILQGFGVAIKMGATKADFDNCVAIHPTSAEELVTMR

cDNA sequence of TA54587433 from wheat (SEQ ID NO:71):

ATGGCGGTCATGTCACGGTTGAAGAGGCTGGCGGCGCCCGCGCTGCTGGTGCTGCTT
GCGCTGGCGGCGTCCGCGGCCGTGGCGGCGAAGACGACCCAGGACGGCGCGGAGG
CGGCGCCGGGCAAGGATGAAGAGTCGTGGACGGGGTGGGCCAAGGACAAGATCTCC
GAGGGGCTGGGGCTCAAGCACGACGCTGACGAGGAGGCCGCGCGCGAGACCGTCC
AGCACACCGCCTCCGAGACGGGGAGTCAGGTGAGCGGCAAGGCAGCGGACGCCAAG
GAGGCGGCCAAGGGAACGGTCGGGGAGAAGCTCGGGGAGGTGAAGGACAAGGTCA
CCGGCGCAGCAGCCGACGGCAAGGACAAGACGCACCGCAAGGATGACTTGCTGTGA

The TA54587433 cDNA is translated into the following amino acid sequence (SEQ ID NO:72):

MAVMSRLKRLAAPALLVLLALAASAAVAAKTTQDGAEAAPGKDEESWTGWAKDKISEGLG
LKHDADEEAARETVQHTASETGSQVSGKAADAKEAAKGTVGEKLGEVKDKVTGAAADGK
DKTHRKDDLL

cDNA sequence of ZM68532504 from corn (SEQ ID NO:73):

ATGCCGTCGCACGGGGATCTGGACCGGCAGATCGCGCAGCTGCGCGACTGCAAGTA
CCTGCCCGAGGCGGAGGTCAAGGCGCTCTGCGAGCAGGCCAAGGCCATCCTTATGG
AGGAGTGGAACGTGCAGCCCGTGCGCTGTCCTGTCACCGTCTGTGGCGACATCCACG
GCCAGTTCTATGACCTCATCGAGCTCTTCCGCATCGGCGGCGACGCTCCCGACACCA
ACTACCTCTTCATGGGCGACTACGTCGATCGTGGGTACTATTCAGTTGAAACAGTTTCT
CTGTTAGTGGCTTTGAAAGTCCGTTACAGAGATAGAATTACAATACTTAGAGGAAATCA
TGAGAGCAGACAAATCACTCAAGTATATGGCTTCTATGATGAATGCTTAAGAAAGTATG
GAAATGCAAATGTCTGGAAGTATTTTACAGACTTGTTTGATTTTTTGCCTCTCACAGCTC
TTATAGAAAATCAGGTCTTCTGTCTTCACGGTGGCCTCTCTCCGTCATTGGACACGTTG
GATAATATTCGTTCTCTTGATCGCGTACAGGAGGTTCCTCATGAAGGACCCATGTGTGA
TCTTTTGTGGTCTGACCCAGATGACCGATGTGGATGGGGAATTTCACCAAGAGGAGCA
GGTTACACATTTGGGCAAGACATTGCGCAGCAGTTCAACCATACAAATGGTCTTTCTCT
CATTTCAAGGGCCCATCAACTTGTAATGGAAGGATTTAATTGGTGCCAGGATAAGAATG
TAGTCACAGTCTTCAGCGCGCCTAATTATTGTTACCGCTGTGGTAACATGGCTGCTATT

CTTGAAATCGGGGAAAACATGGACCAGAACTTCCTTCAATTCGACCCGGCACCTCGGC
AAATTGAGCCAGACACAACTCGGAAAACCCCAGACTACTTTTTGTAA

The ZM68532504 cDNA is translated into the following amino acid sequence (SEQ ID NO:74):

MPSHGDLDRQIAQLRDCKYLPEAEVKALCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFY
DLIELFRIGGDAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKYFTDLFDFLPLTALIENQVFCLHGGLSPSLDTLDNIRSLDRV
QEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVM
EGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRKTP
DYFL

cDNA sequence of BN42856089 from canola (SEQ ID NO:75):

AAAACTCCAAAAACAAACCATTTTCCATCTCTCAGGCCAAAAAAACCAGAGATTTGATC
TCTCTGGCGATTCATCATCCTCTTCATCCACCACACGCCGTATAAGTTAAAGGATCGGT
GGTGGTCTCTCGATGCCGCCGAACGGAGATCTAGACCGTCAGATCTCCCAGCTGATG
GAGTGTAAACCGCTATCTGAGGCCGATGTGAAGACGCTCTGCGATCAAGCGAGGGCC
ATCCTCGTCGAGGAGTGGAACGTTCAGCCCGTGAAGTGTCCTGTCACCGTCTGCGGC
GATATCCACGGACAGTTCTATGACCTTATCGAGCTCTTTCGAATCGGTGGGAATCCTC
CGGATACTAACTACCTCTTCATGGGAGACTATGTAGACCGTGGCTACTATTCAGTAGAA
ACAGTTTCTCTATTGGTGGCACTGAAAGTGCGATACAGGGATAGGATTACAATCTTGC
GAGGGAATCACGAGAGTCGGCAGATTACTCAAGTCTATGGGTTTTATGATGAATGTTT
GAGGAAGTATGGAAATGCAAATGTCTGGAAGTTTTTCACGGACCTTTTCGATTATCTTC
CTCTTACTGCTCTCATAGAGAGTCAGGTTTTCTGCTTGCATGGAGGGCTTTCACCTTCT
CTGGACACCCTTGATAATATCCGAAGCTTGGATCGTATACAAGAGGTTCCACATGAAG
GACCAATGTGTGATTTATTATGGTCTGATCCCGATGATCGATGTGGGTGGGGAATATCT
CCACGAGGTGCTGGTTATACATTTGGACAAGACATCGCAACTCAGTTTAATCACAACAA
TGGACTCAGTCTCATATCAAGAGCACATCAACTTGTCATGGAAGGCTTTAACTGGTGTC
AGGACAAAAATGTTGTGACGGTGTTTAGTGCACCAAACTATTGCTACCGGTGTGGAAA
CATGGCAGCTATTCTAGAGATAGGAGAGAACATGGACCAGAACTTCCTCCAGTTCGAT
CCAGCTCCTCGTCAAGTCGAACCAGATACTACCCGCAAGACCCCTGATTATTTTTTGTG
ATTTATTTGCATTTTTTTTTCTTTTGTTCCCAACCATTTATAATTTTTAAAAAATCTGTTTT
ATCTTGCTTATGAATAATCATTCTAGTGTCTCTTCAAAAAAAAAAAAAAA

The BN42856089 cDNA is translated into the following amino acid sequence (SEQ ID NO:76):

MPPNGDLDRQISQLMECKPLSEADVKTLCDQARAILVEEWNVQPVKCPVTVCGDIHGQFY
DLIELFRIGGNPPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKFFTDLFDYLPLTALIESQVFCLHGGLSPSLDTLDNIRSLDRIQ

EVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIATQFNHNNGLSLISRAHQLVME
GFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQVEPDTTRKT-
PDYFL

cDNA sequence of BN43206527 from canola (SEQ ID NO:77):

CCAAAGACCATTTGATCTCTGGCGATTTCATCTTCCGATATGCCGCCGAACGGAGATC
TAGACCGTCAGATCGAGCATCTGATGGAGTGCAAACCTTTATCGGAGGAGGATGTGAG
GACGCTCTGCGATCAAGCTAAGGCCATCCTCGTCGAGGAATGGAACGTCCAGCCCGT
GAAATGCCCCGTCACCGTCTGCGGCGATATCCACGGCCAGTTCTATGACCTTATCGAG
CTTTTCCGAATCGGTGGTAACGCCCCCGATACGAATTACCTCTTCATGGGTGACTATGT
AGACCGTGGCTACTATTCAGTGGAAACGGTTTCTTTATTGGTGGCATTGAAAGTCAGAT
ACAGGGATAGGATTACAATCTTGCGAGGGAACCACGAGAGTCGTCAGATCACCCAAGT
ATATGGTTTTTATGACGAGTGCTTGAGGAAGTACGGAAACGCAAATGTGTGGAAGTATT
TCACAGACCTTTTCGATTATCTTCCTCTTACTGCTCTTATCGAGAGTCAGGTTTTCTGTT
TGCATGGAGGGCTATCACCTTCTCTGGATACACTTGATAATATCCGAAGCTTGGATCGT
ATACAAGAGGTTCCACACGAAGGACCAATGTGTGATTTACTATGGTCTGATCCAGATGA
TCGATGCGGGTGGGGAATATCTCCAAGAGGTGCTGGTTATACATTTGGACAGGATATA
GCAACTCAGTTTAATCACAACAATGGACTCAGTCTCATATCAAGAGCGCATCAGCTTGT
CATGGAAGGTTTTAACTGGTGTCAGGATAAGAATGTGGTGACGGTGTTTAGTGCACCA
AACTATTGCTACCGGTGTGGAAACATGGCAGCGATTCTAGAGATAAGTGAGAACATGG
AGCAGAACTTCCTTCAGTTTGATCCAGCTCCAAGACAAGTCGAACCTGATACTACCCGT
AAGACCCCTGATTATTTTTTGTGATTTTATTTGTATTTTTTTTTCTTCTAAGCGGAGTTCG
AGTTTCCCTCAAAACGAAAGAAAGAAACAAACATCATTTTGTTGTTGTTGATGTGATTGC
TGAGAACAAAGTTTGTAGTAGAAGCGTCTATATATAGAATAGTGTCTTCTCATTGTCATT
TCACTTGTTACTGCATAGAGGAATGAGGTTTCGAACCCTGCCCGCCACTTTCATTTCAG
TTTCATTTATAAAATATGAGTTTGATACCGAAAAAAAAAAAAAAA

The BN43206527 cDNA is translated into the following amino acid sequence (SEQ ID NO:78):

MPPNGDLDRQIEHLMECKPLSEEDVRTLCDQAKAILVEEWNVQPVKCPVTVCGDIHGQFY
DLIELFRIGGNAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQVFCLHGGLSPSLDTLDNIRSLDRIQ
EVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIATQFNHNNGLSLISRAHQLVME
GFNWCQDKNVVTVFSAPNYCYRCGNMAAILEISENMEQNFLQFDPAPRQVEPDTTRKT-
PDYFL

cDNA sequence of HA66872964 from sunflower (SEQ ID NO:79):

CTAAAAATATCTTTAACCGCCGGCTGCCATGACGGAACCCTAAGCAACTTCTCCGGCG
ACTCCGGCGGAGCTCCGTTCAACCTAAATGCGAATCATTCTTCCAGATCTTCAAATCCG

AACACACAAATCACGTAACAATGCCGTCGCAATCGGATCTGGACCGTCAGATCGAGCA
CTTGATGGACTGTAAACCGCTGCCGGAGGCGGAGGTGCGGACGTTGTGTGATCAGGC
GAGGACGATTTTGGTCGAGGAGTGGAATGTGCAGCCGGTGAAGTGTCCGGTGACTGT
TTGCGGTGATATTCATGGGCAGTTTCATGATTTGCTTGAGCTGTTTCGGATCGGAGGA
AGTGCTCCGGACACGAATTACTTGTTTATGGGAGATTATGTTGATCGAGGCTATTACTC
GGTGGAGACTGTTACGCTTCTTGTGGCATTGAAAGTTCGTTACAGAGATAGGATTACTA
TTCTCAGAGGAAACCATGAGAGCAGGCAGATAACTCAAGTGTATGGATTTTACGATGA
ATGCTTGAGGAAGTACGGAAACGCAAATGTATGGAAACATTTCACTGACCTTTTTGATT
ATCTACCTCTCACTGCCCTTATCGAGAGTCAGATATTCTGTCTCCATGGTGGCTTGTCT
CCATCTTTGGATACACTAGATAACATACGTGCTTTAGATCGCATACAAGAGGTTCCTCA
TGAGGGGCCAATGTGTGACCTTTTGTGGTCTGATCCTGATGACCGGTGTGGTTGGGG
AATATCTCCTCGTGGAGCCGGTTACACTTTCGGGCAGGATATAGCCGCACAGTTTAAC
CATACAAACGGGCTCTCGCTTATTTCTCGGGCTCACCAGCTTGTCATGGAAGGTTACA
ATTGGTCTCAGGAGAACAACGTTGTAACCATATTTAGTGCACCAAACTACTGCTATAGA
TGCGGGAATATGGCTGCGATACTTGAGGTTGGAGAGAATATGGACCAGAATTTCTTAC
AATTTGACCCAGCCCCTCGTCAGGTTGAGCCCGATGTTGCACGAAGAACTCCGGATTA
CTTCCTGTAAATTTGTGTTGGATAATATGACCTTTGCATGCATCCTATTTATGTTGTTAT
AGTTTTCGCTTTCCCCTGCTAGAGAGTCCCCCTATTCTTGAGAATTAAAGACAATATGT
ATGATTGTTTGTCCCTTGTTCTATTTGAGATTATTTGTTTAAAAAAAAAAAAAAA

The HA66872964 cDNA is translated into the following amino acid sequence (SEQ ID NO:80):

MPSQSDLDRQIEHLMDCKPLPEAEVRTLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFH
DLLELFRIGGSAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKHFTDLFDYLPLTALIESQIFCLHGGLSPSLDTLDNIRALDRIQ
EVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQLVME
GYNWSQENNVVTIFSAPNYCYRCGNMAAILEVGENMDQNFLQFDPAPRQVEPDVARRTPDYFL

cDNA sequence of LU61662612 from linseed (SEQ ID NO:81):

CATCTCTCTTTCTCTCTCTTCCATTTTCGTTCTTTTGAATCTCCGTTAGCCCTACAAATC
CATGGTCATGGCCTGAGAGAGATAGAGGGATAGAGCTCTCAGTTCCTAATCACCTTAC
CTGACCTAACCCCACGGACATATTATCGAAGGTCTGCGAGCAGGAGAGCGCAGGAGG
AAGAGTGGGGCCAGGGTACGATGCCGTCCCACGCCGATCTGGACCGTCAGATCGAG
CACTTGATGCAGTGCAAGCCACTTTCTGAGGCCGAAGTGAAGGCTCTCTGCGAGCAG
GCCAGGGCCGTCCTCGTCGAGGAATGGAACGTCCAGCCGGTCAAGTGTCCGGTGACT
GTCTGCGGCGACATCCACGGCCAGTTTCACGATCTTGTCGAGCTCTTTCGAATCGGAG
GAAACGCCCCTGACACGAACTACCTCTTCATGGGCGACTATGTAGATCGAGGGTATTA
TTCGGTGGAGACTGTCACCCTTCTAGTCGCCTTGAAAGTAAGATATAGAGATAGGATC
ACAATTCTGAGAGGAAATCATGAAAGTCGTCAAATAACTCAAGTGTATGGATTCTATGA

TGAGTGCTTGAGAAAATATGGAAATGCCAATGTGTGGAAACATTTTACCGATCTCTTTG
ATTATCTACCACTTACAGCTCTGATTGAGAGTCAGGTCTTCTGCTTACATGGTGGACTT
TCCCCTTCACTAGACACGCTAGACAACATTCGCTCCCTTGATCGTATCCAAGAGGTTCC
GCACGAGGGTCCTATGTGCGACCTCCTATGGTCGGACCCGGATGACCGTTGCGGGTG
GGGGATCTCTCCTCGTGGAGCTGGCTACACCTTTGGACAGGACATATCTCAACAGTTC
AACCACACGAACGGCCTTTCTCTCATATCCAGAGCTCACCAGCTGGTCATGGAAGGTT
ACAATTGGGCCCAGGACAAGAATGTGGTGACGGTGTTCAGCGCCCCGAACTACTGCT
ACCGGTGTGGGAACATGGCGGCCATTCTCGAGATCGGAGAGAACATGGAGCAGAACT
TCCTGCAGTTCGACCCAGCTCCTCGACAGATCGAACCGGAGACGACTCGCAGAACAC
CCGATTATTTTTGTGAAATGCATAGCTTCTTCTTCCTCCCTCCTTCTTGCTTGGAAATG
GGATCCGTGTCCATTTTTTCTAATCGCCTGCCCTGCTATGTGCTTATGTTTTTTGTAGAT
GCATTCATCATCATCATATCCAGAATAGAGAAGAAATTTTGGTGTTTGCTTTGATTGAGA
AAAGGCGGGGAGGGAAAAATCGGCCTCTAGAGATGCTGGGTGTTGTCATTTTTCTTCT
TCTTCTTCCTCCTTTTGGGATGGTTTCGTTTTTACTTTTTCTTTTGGGTTTCTATTGTTTA
TCCTGCATTCATTTGAGTTTAACAAAGTTTATTATTTACAGTCTGGGTGTGTTATTAATAT
TATTCACTGTGGTCTTGTACCAAAAAAAAAAAAAAA

The LU61662612 cDNA is translated into the following amino acid sequence (SEQ ID NO:82):

MPSHADLDRQIEHLMQCKPLSEAEVKALCEQARAVLVEEWNVQPVKCPVTVCGDIHGQF
HDLVELFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQIT
QVYGFYDECLRKYGNANVWKHFTDLFDYLPLTALIESQVFCLHGGLSPSLDTLDNIRSLDRI
QEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDISQQFNHTNGLSLISRAHQLVM
EGYNWAQDKNVVTVFSAPNYCYRCGNMAAILEIGENMEQNFLQFDPAPRQIEPETTRRTP
DYFL

cDNA sequence of OS32806943 from rice (SEQ ID NO:83):

GAGGCTTGAGCTCCACCTCCACCTCCTCCACCTCCAACCCCCGATCCCCCGCAAACC
CTAGCCCTCTCCCCCACCCTCCTCGCCGGCGGCGAGCGGCGGCGGCGCGCGGCGG
GACCCGGAGCCCCCAGTAGCGCCTCCTCCGTCCTCCCCTCCCTGAGGTGCGGGGGA
GAGGATGCCGTCGTCGCACGGGGATCTGGACCGGCAGATCGCGCAGCTGCGGGAGT
GCAAGCACCTGGCGGAGGGGGAGGTGAGGGCGCTGTGCGAGCAGGCGAAGGCCAT
CCTCATGGAGGAGTGGAACGTGCAGCCGGTGCGGTGCCCCGTCACGGTCTGCGGCG
ACATCCACGGCCAGTTCTACGACCTCATCGAGCTCTTCCGCATCGGCGGCGAGGCGC
CCGACACCAACTACCTCTTCATGGGCGACTACGTCGACCGTGGCTACTACTCAGTGGA
GACTGTTTCGTTGTTGGTGGCTTTGAAAGTACGCTACAGAGATCGAATTACAATATTGA
GAGGAAATCATGAGAGCAGACAAATCACTCAAGTGTACGGCTTCTACGATGAATGCTT
GAGAAAGTATGGAAATGCAAATGTATGGAAATACTTTACAGACTTGTTTGATTATTTGCC
TCTCACAGCTCTTATAGAAAACCAGGTGTTCTGCCTTCACGGTGGTCTCTCTCCATCAT
TGGATACTTTAGATAACATCCGTGCTCTTGATCGTATACAAGAGGTTCCTCATGAAGGA

CCCATGTGTGATCTTTTGTGGTCTGACCCAGATGACAGATGCGGGTGGGGAATTTCAC
CGAGAGGAGCAGGTTATACATTTGGGCAAGATATCGCTCAACAGTTTAACCATACAAAT
GGTCTATCTCTCATCTCAAGGGCACATCAACTTGTAATGGAAGGATTTAATTGGTGTCA
GGACAAGAATGTTGTGACGGTCTTCAGTGCACCAAACTACTGTTATCGCTGTGGTAAC
ATGGCTGCAATTCTTGAGATTGGCGAAAACATGGATCAGAACTTCCTCCAATTTGATCC
AGCTCCTCGGCAAATTGAACCAGACACAACACGCAAGACTCCCGACTACTTTTTGTAAT
TTGTGGTGTTGACAATTTTAACTCACCTGTGTTGATGCTCCTCTCCTCCGCGGTGTCGG
GGTCTGTAGATCTTCTGTCCTTAGATACGGGTTCCACGAGCCCGGCTGTATGTCTCTC
AATTCTTTTGTTTGGAGATTTTGTTGCTGCTTCTCAACCTTTATACAAGACGTTAAAAGT
TACATGCACTGGATTTTTTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAA
AAAAAAAAAAA

The OS32806943 cDNA is translated into the following amino acid sequence (SEQ ID NO:84):

MPSSHGDLDRQIAQLRECKHLAEGEVRALCEQAKAILMEEWNVQPVRCPVTVCGDIHGQF
YDLIELFRIGGEAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQIT
QVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIENQVFCLHGGLSPSLDTLDNIRALDRI
QEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVM
EGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRKTP
DYFL

cDNA sequence of OS34738749 from rice (SEQ ID NO:85):

GGTCGACGCCGTCACCGTCGCGCCAACTGCCGCAAACCGAATAAACCGAATCGATCT
GAGAGAAGAAGAAGAAGAAGACGCGATCTCGGAGGTGGGAGCGAAACGAAACGATG
CCGTCTCACGCGGATCTGGAACGACAGATCGAGCAGCTGATGGAGTGCAAGCCTCTG
TCGGAGTCGGAGGTGAAGGCGCTGTGTGATCAAGCGAGGGCGATTCTCGTGGAGGAA
TGGAACGTGCAACCGGTGAAGTGCCCCGTCACCGTCTGCGGCGATATTCACGGCCAG
TTTTACGATCTCATCGAGCTGTTTCGGATTGGAGGGAACGCACCCGATACCAATTATCT
CTTCATGGGTGATTATGTAGATCGTGGATACTATTCAGTGGAGACTGTTACACTTTTGG
TGGCTTTGAAAGTCCGTTACAGAGATAGAATCACAATTCTCAGGGGAAATCATGAAAGT
CGTCAAATTACTCAAGTGTATGGCTTCTATGATGAATGCTTGAGAAAATATGGAAATGC
CAATGTCTGGAAATACTTTACAGACTTGTTTGATTATTTACCTCTGACTGCCCTCATTGA
GAGTCAGATTTTCTGCTTGCATGGAGGTCTCTCACCTTCTTTGGATACACTGGATAACA
TCAGAGCATTGGATCGTATACAAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTT
GTGGTCTGACCCTGATGATCGCTGTGGATGGGGAATATCTCCACGTGGTGCAGGATA
CACATTTGGACAGGATATAGCTGCTCAGTTTAATCATACCAATGGTCTCTCCCTGATAT
CGAGAGCTCATCAGCTTGTTATGGAAGGATTCAATTGGTGCCAGGACAAAAATGTGGT
GACTGTATTTAGTGCACCAAATTACTGTTACCGATGTGGGAATATGGCTGCTATACTAG
AAATAGGAGAGAATATGGATCAGAATTTCCTTCAGTTTGATCCAGCGCCCAGGCAAATT
GAGCCTGACACCACACGCAAGACTCCAGATTATTTTTATAATTTCATTTATCTGCCTGT

TTGTAGTTACTGCTCTCTGCCATTACTGTAGATGTGTCTTTAAGGAAAGGAGTTTTGCT
GTTTAAGTGGAGGGTGGTCATCAACATAATTCTTTCTTTTGGAGTTTACCTCCTGCTGC
TGCCGCTGCCGCTGCCTTATTTGTACAAGAAACCAATAGAACTGACACAAGCCACCAA
TTGGGGTTGTATATTTTTGGGAGGAAGCGGTAATAACATGGTATATCTTGTTCTGTAAT
CCTTTTTCTTTAAATTGAATCTCAAGTTAGAGAGCAAAAAAAAAAAAA

The OS34738749 cDNA is translated into the following amino acid sequence (SEQ ID NO:86):

MPSHADLERQIEQLMECKPLSESEVKALCDQARAILVEEWNVQPVKCPVTVCGDIHGQFY
DLIELFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQIFCLHGGLSPSLDTLDNIRALDRIQ
EVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQLVME
GFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRKTPDYFL

cDNA sequence of ZM59400933 from corn (SEQ ID NO:87):

CTGACCGCCAGCGGGCCCGCAGGCCGGAGAAGGAGTCGGAGTCGCCCCCACCCACC
CACCCTCTGCCGCGGGCGGGGAGCGGGCGGCGGACGAGATGCCGTCGCACGGGGA
TCTGGACCGGCAGATCGCGCAGCTGCGCGACTGCAAGTACCTGCCCGAGGCGGAGG
TCAAGGTGCTCTGCGAGCAGGCCAAGGCCATCCTCATGGAGGAATGGAACGTGCAGC
CCGTGCGCTGCCCCGTCACCGTCTGCGGCGACATCCACGGCCAGTTCTATGACCTCA
TCGAGCTCTTCCGCATCGGCGGCGACTCTCCCGACACCAACTACCTCTTCATGGGCG
ACTACGTCGATCGTGGCTATTATTCAGTTGAAACGGTTTCTCTGTTAGTGGCTTTGAAA
GTCCGTTACAGAGATAGAATTACAATACTTCGAGGAAATCATGAGAGCAGACAAATCAC
TCAAGTGTACGGCTTCTATGATGAATGCTTAAGAAAATATGGAAATGCAAATGTATGGA
AGTATTTTACAGACTTGTTTGATTATTTGCCTCTCACAGCTCTTATAGAAAATCAGGTCT
TCTGTCTTCATGGAGGCCTCTCTCCGTCATTGGACACATTGGATAACATTCGTTCTCTT
GATCGCATACAGGAGGTACCTCATGAAGGACCCATGTGTGATCTTTTGTGGTCTGACC
CAGATGACCGATGTGGGTGGGGAATTTCACCCAGAGGAGCAGGTTACACATTTGGGC
AAGACATTGCACAGCAGTTCAACCATACAAATGGTCTCTCTCTCATTTCAAGGGCCCAT
CAACTTGTAATGGAAGGATTTAATTGGTGCCAGGATAAGAATGTAGTCACAGTCTTCAG
TGCGCCTAATTACTGTTACCGCTGTGGTAACATGGCTGCTATTCTTGAAATCGGGGAAA
ACATGGACCAGAACTTCCTTCAATTCAACCCCGCACCTCGGCAAATTGAGCCAGACAC
AACTCGCAAAACCCCAGACTACTTTCTGTAATTGTGGTGGTGACCTTAACTTTCTGGTG
TTTGATGCTCCTCTCTTCCGCAGCATCAGGGTATGTAGATCTTGTCCTTAGATATGGGT
CCCATGTGCCCGGCCTTAACGTCTCCCTATTCTTTTGTTTGGAGATTTTGTTTCTGCTT
CTCGATCTTGATACAAGATGTTAGAAGTTGAATGCCAGTGTATTTTTTTCAAAAAAAAAAA

The ZM59400933 cDNA is translated into the following amino acid sequence (SEQ ID NO:88):

MPSHGDLDRQIAQLRDCKYLPEAEVKVLCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFY
DLIELFRIGGDSPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIENQVFCLHGGLSPSLDTLDNIRSLDRIQ
EVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVME
GFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFNPAPRQIEPDTTRKTP-
DYFL

cDNA sequence of ZM62132060 from corn (SEQ ID NO:89):

AATCGTCGCTCCACCTCCTCCTCGTCTATCGCCGATCTCCCCCAAACCCTAGCCCCGA
CCTGACCGCCGGCGGGCCCGCCGGCCGGAGAAGGAGTCGCTCCCACCCATCCAACT
TCTGCGGCGGAAGGGGAGCGGGCGGCGGACGAGATGCCGTCGCACGGGGATCTGG
ACCGGCAGATCGCGCAGCTGCGCGACTGCAAGTACCTGCCCGAGGCGGAGGTCAAG
GCGCTCTGCGAGCAGGCCAAGGCCATCCTTATGGAGGAGTGGAACGTGCAGCCCGT
GCGCTGTCCTGTCACCGTCTGTGGCGACATCCACGGCCAGTTCTATGACCTCATCGAG
CTCTTCCGCATCGGCGGCGACGCTCCCGACACCAACTACCTCTTCATGGGCGACTAC
GTCGATCGTGGGTACTATTCAGTTGAAACAGTTTCTCTGTTAGTGGCTTTGAAAGTCCG
TTACAGAGATAGAATTACAATACTTAGAGGAAATCATGAGAGCAGACAAATCACTCAAG
TATATGGCTTCTATGATGAATGCTTAAGAAAGTATGGAAATGCAAATGTCTGGAAGTAT
TTTACAGACTTGTTTGATTTTTTGCCTCTCACAGCTCTTATAGAAAATCAGGTCTTCTGT
CTTCACGGTGGCCTCTCTCCGTCATTGGACACGTTGGATAATATTCGTTCTCTTGATCG
CGTACAGGAGGTTCCTCATGAAGGACCCATGTGTGATCTTTTGTGGTCTGACCCAGAT
GACCGATGTGGATGGGGAATTTCACCAAGAGGAGCAGGTTACACATTTGGGCAAGAC
ATTGCGCAGCAGTTCAACCATACAAATGGTCTTTCTCTCATTTCAAGGGCCCATCAACT
TGTAATGGAAGGATTTAATTGGTGCCAGGATAAGAATGTAGTCACAGTCTTCAGCGCG
CCTAATTATTGTTACCGCTGTGGTAACATGGCTGCTATTCTTGAAATCGGGAAAAACAT
GGACCAGAACTTCCTTCAATTCGACCCGGCACCTCGGCAAATTGAGCCAGACACAACT
CGGAAAACCCCAGACTACTTTTTGTAATTGTGGTGGTGACATTAACTTACTGGTGTTGA
TGCTCCTCTTTTCCGCAGCATCAGGGTCTGTAGATCATCTGTCCTTAGATATGGGTTCC
ATGAGCCCGACCTGTACGTCTCCCAATTCTTTTGTTTGGAGATTTTGTTGCCGCTTAAC
GATCTTTATACAATATGTTAAAAAGTTAAATGCCATTGGATTTTTCTCCAAAAAAAAAAA

The ZM62132060 cDNA is translated into the following amino acid sequence (SEQ ID NO:90):

MPSHGDLDRQIAQLRDCKYLPEAEVKALCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFY
DLIELFRIGGDAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQ
VYGFYDECLRKYGNANVWKYFTDLFDFLPLTALIENQVFCLHGGLSPSLDTLDNIRSLDRV
QEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVM

EGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGKNMDQNFLQFDPAPRQIEPDTTRKTP
DYFL

cDNA sequence of ZM59202533 from corn (SEQ ID NO:91):

ATGAAGGGGAAGAAGCCGGTCAAGGAGCTCAAGCTCACCGTGCCGGCGCAGGAGAC
CCCGGTAGACAAGTTCCTGACGGCAAGTGGCACGTTCAAGGATGGTGAGCTGAGGCT
CAATCAGAGCGGCTTGCGGCTTATCTCTGAGGAAAACGGGGATGAAGATGAATCTACA
AAGCTGAAGGTGGAAGATGTGCAGTTATCAATGGATGATCTTGAGATGATTCAAGTCAT
TGGCAAAGGAAGCGGTGGTGTTGTCCAGCTAGTGAGGCACAAATGGGTGGGCACATT
GTTTGCCTTAAAGGGTATTCAAATGAACATTCAGGAGTCAGTTCGTAAACAAATAGTAC
AGGAGCTCAAAATAAACCAAGCAACACAGAGCCCTCATATAGTTATGTGCCATCAATCT
TTTTACCACAATGGTGTAATATATCTTGTTCTTGAGTACATGGACCGTGGATCGCTTGC
AGACATTGTTAAGCAAGTGAAGACTATTCTGGAGCCATACCTTGCAGTACTTTGTAAGC
AGGTCTTGGAGGGTTTATTGTATCTTCATCATCAAAGGCACGTGATTCACAGGGACATA
AAACCATCTAACTTGTTGGTCAACCGTAAAGGTGAAGTCAAGATTACCGACTTCGGAGT
GAGTGCTGTGCTAGCAAGCTCAATAGGTCAGCGAGATACATTTGTTGGAACCTACAAC
TATATGGCGCCTGAGCGGATTAGTGGTAGCACTTATGACTACAAAAGTGACATATGGA
GTTTGGGCTTAGTTATACTTGAGTGTGCCATTGGCCGGTTCCCTTATATACCTTCGGAA
GGTGAAGGTTGGTTAAGCTTTTATGAACTTCTGGAGGCCATTGTCGATCAGCCACCAC
CTTCTGCACCTGCAGATCAGTTCTCTCCAGAATTCTGCTCATTTATCTCCTCTTGCATAC
AGAAAGATCCGGCTCAGAGGATGTCTGCTTCAGAACTCTTGAATCACCCTTTTTTGAAG
AAGTTCGAGGATAAGGACTTAAACCTGGGGATTCTTGTGGAGAACCTGGAACCTCCAA
TGAATATACCCGAATAG

The ZM59202533 cDNA is translated into the following amino acid sequence (SEQ ID NO:92):

MKGKKPVKELKLTVPAQETPVDKFLTASGTFKDGELRLNQSGLRLISEENGDEDESTKLKV
EDVQLSMDDLEMIQVIGKGSGGVVQLVRHKWVGTLFALKGIQMNIQESVRKQIVQELKINQ
ATQSPHIVMCHQSFYHNGVIYLVLEYMDRGSLADIVKQVKTILEPYLAVLCKQVLEGLLYLH
HQRHVIHRDIKPSNLLVNRKGEVKITDFGVSAVLASSIGQRDTFVGTYNYMAPERISGSTYD
YKSDIWSLGLVILECAIGRFPYIPSEGEGWLSFYELLEAIVDQPPPSAPADQFSPEFCSFISS
CIQKDPAQRMSASELLNHPFLKKFEDKDLNLGILVENLEPPMNIPE

cDNA sequence of BN41901422 from canola (SEQ ID NO:93):

GTCATTCTTCTAATTTCTCTGACCTCTGCTACTGTCTATCCGTTCGTGTTGCTTTGATCT
CTCTAATCAGACATGAAGAGAGGCAGCTTGAGTCTTAATCCCATCTCTCTCCCTCCTCC
TGAGCAATCCATCTCCAAATTCTTAACACAGAGCGGAACGTTCAAGGATGGAGACCTT
CAAGTGAACAAAGATGGAATCCAGACAGTATCTCATTCTGAGCCTGGAGCTCCACCAC
CTATTGATCCATTGGACAACCAGTTGAGTTTGGCTGACCTTGAAGTGATCAAAGTCATT

GGCAAAGGAAGCAGTGGTAGTGTTCAGCTGGTTAAACACAAACTAACTCAACAGTTTTT
CGCTACTAAGGTTATTCAGTTAAACACAGAAGAGTCCACATGTCGAGCCATTTCTCAGG
AGCTGAGGATAAACTTGGCATCTCAATGTCCATATCTCGTCTCATGTTATCAGTCTTTCT
ACCATAACGGTCTCGTCTCAATCGTAATGGAGTTCATGGACGGTGGATCTCTTTTGGAT
TTGTTGAAGAAAGTCCAGAGAGTTCCTGAAAACATGCTCGCTGCCATCTCCAAGCGAG
TGCTCCGAGGCTTGTGCTATATTCACGATGAGAGGCGAATCATTCACCGGGACTTGAA
GCCTTCCAACTTGCTAATCAATCACAGAGGTGAAGTCAAGATCGCAGACTTTGGTGTC
AGCAAGATCTTGTCTAGCACAAGCAGTCTAGCGCATACCTTCGTGGGCACAGACTTCT
ATATGTCGCCAGAGAGAATCAGTGGGAAAGCGTATGGGAACAAGTGTGATATTTGGAG
TTTGGGAGTGGTTCTGCTCGAATGTGCAACGGGTAAGTTTCCGTATACTCCTCCTGAA
AACATGAAGGGATGGACTAGCATGTATGAGCTAGTTGACGCCATTGTTGAAAACCCGC
CTCCTCGTGCACCTTCCCACCTGTTCTCTCCAGAGTTTTGCTCCTTCATCTCGCAATGT
GTACAAAAAGATCCAAGGGACCGGAAATCAGCAATGGAGCTTCTGGACCATAGGTTCG
TAAACATGTTTGAAGATGTGGATGTGGATCTCTCGTCTTACTTCACCGCCGCAGGATCT
TTGATTCCCCCACTAGCCAACAGCTAGAACCGAGTTTGAACAATCCTTTTAACACCAAG
TTATATATATGTATTTTATATCCACTGGAAGAGACGATATTTACGAGATGTTGCGACTTA
TGAGAGAATTCTCTTGATAGACATTTATATTTTCAAGTATTGAAATTTATTTGGGTAAAAA
AAAAAAAAAA

The BN41901422 cDNA is translated into the following amino acid sequence (SEQ ID NO:94):

MKRGSLSLNPISLPPPEQSISKFLTQSGTFKDGDLQVNKDGIQTVSHSEPGAPPPIDPLDN
QLSLADLEVIKVIGKGSSGSVQLVKHKLTQQFFATKVIQLNTEESTCRAISQELRINLASQCP
YLVSCYQSFYHNGLVSIVMEFMDGGSLLDLLKKVQRVPENMLAAISKRVLRGLCYIHDERRI
IHRDLKPSNLLINHRGEVKIADFGVSKILSSTSSLAHTFVGTDFYMSPERISGKAYGNKCDIW
SLGVVLLECATGKFPYTPPENMKGWTSMYELVDAIVENPPPRAPSHLFSPEFCSFISQCVQ
KDPRDRKSAMELLDHRFVNMFEDVDVDLSSYFTAAGSLIPPLANS

cDNA sequence of BN47868329 from canola (SEQ ID NO:95):

CCAGATCGTTAAACCATAATCCAAACCAAGCTTGCAAAAACTTTTGATCCTAAACCGAG
ATGAAACCAATCCAACCGCCACCAGGAGTAATCGGTCCGGTTAAGAACCGCCCTCGC
CGCCGTCCAGACCTCTCCTTACCACTTCCTCACCGCGACGTTTCCCTCGCCGTACCTC
TCCCCCTCCCACCAACTTCCGGCGGCGGTTCCACCACCTCAGAGCCTAAAAGCTACTC
AGACTTAGTACGTGGCAACCGGATCGGAAGCGGAGCCGGTGGAACGGTTTACAGAGT
AGTCCACCGTCCAACCTCCCGCGTATACGCACTCAAGATAATCAACGGTAACCACGAT
GACACTGTTCGTGGCCAGATCTGCAGAGAGATCAAGATTCTCCGAGACGTGAATCACC
CCAACGTGGTGAAATGCCACGAGATGTTCGATCAAAACGGAGAGATCCAGGTCTTGCT
CGAGCTCATGGACCAAGGATCTTTAGAAGGTGCTCATATCTCGAACGAGCAACAGTTA
TCTGACCTATCTCGTCAGATACTAAACGGTTTGGCTTATCTTCACGGCCGTCATATAGT
CCATAGAGACATAAAGCCATCGAATCTACTTATAAACTCGGACAATAACGTCAAGATTG

CTGATTTTGGAGTGAGCAGGGTCTTGGCTCAGACCCTGTCTCCGTGTAAGTCCTCTGT
TGGGACTATTGCTTACATGAGTCCTGAGAGGATCAACACGGATTTGAATCAGGGGATG
TATGATGGTTGCGCTGGGGATATTTGGAGCTTCGGTGTTAGTGTTCTTGAGTTTTTCTT
GGGGAGGTTTCCTTTTAATGTGAATAGGCTAGGTGATTGGGCTAGTCTTATGTGTGCTA
TTTGTATGTCTAAGCCGCCTGAAGCTCCTGCCACGGCGTCTCCGGAGTTTAGACACTT
TGTTTCGTGTTGTTTGCAGAGAGAACCGGGGAGGAGGCAAACTGCTGTTCAGCTTTTG
CAACATCCTTTTGTGCGTAGAGGGGCGATTCAGAGTCAGAATAGGTCTCCTCAGAATC
TACATCAACTCTTGCCTCCTCCACACTAAAGGTTTAGTTTTGTCTGATAATGTTTCTACA
CTAAAGGTTGATCATGTCTTGCTGTTTAGACAAACTATATCATTGTCTTGTACTTAGCTG
AAAGCAAAGCGTATATAGTTTGAATCACTTTGCACCTCATGATGGTTAATTTCACTAAGT
AATTCAGTAGTAGAGTCATTAAATGTAAAAAAAAAAAAAAA

The BN47868329 cDNA is translated into the following amino acid sequence (SEQ ID NO:96):

MKPIQPPPGVIGPVKNRPRRRPDLSLPLPHRDVSLAVPLPLPPTSGGGSTTSEPKSYSDLV
RGNRIGSGAGGTVYRVVHRPTSRVYALKIINGNHDDTVRGQICREIKILRDVNHPNVVKCH
EMFDQNGEIQVLLELMDQGSLEGAHISNEQQLSDLSRQILNGLAYLHGRHIVHRDIKPSNLL
INSDNNVKIADFGVSRVLAQTLSPCKSSVGTIAYMSPERINTDLNQGMYDGCAGDIWSFGV
SVLEFFLGRFPFNVNRLGDWASLMCAICMSKPPEAPATASPEFRHFVSCCLQREPGRRQT
AVQLLQHPFVRRGAIQSQNRSPQNLHQLLPPPH

cDNA sequence of BN42671700 from canola (SEQ ID NO:97):

CTGCAAACTAAAATCTAGAACCGGAACAGATCTAAACCAAACCAAACCGAACCGGGTG
TCTTTGTTTGTAACTCTCCAAATGGTGAAGAAAGCGATGAAGGAGGAAGAAGAAGCAG
AGATGAGAAACTCGTCGATGCAGTCAAAGTACAAAGGCGTGAGGAAGAGGAAGTGGG
GCAAATGGGTTTCGGAGATCAGACTTCCCAACAGCAGAGAGCGAATCTGGCTAGGCT
CTTTCGACACTCCCGAGAAGGCGGCGCGTGCCTTCGACGCCGCCCAGTTTTGTCTCC
GCGGCTGCCAATCCGGTTTCAATTTCCCCGATAATCCGCCGTCGATCTCCGGCGGAA
GGTCGCTGACGCCTCCGGAGATCCGGGAAGCGGCTGCTCGATACGCAAACGCTCAG
GACGACGATATTATCATCACCACCGGAGAAGAAGAATCGGTTTTGTCCGAAACCCGAC
CGGAGTCTCCTTCAACAACCTCCGTGTCTGAAGCAGATACGTCGCTGGATTGCGATCT
ATCGTTCTTAGACACGCTTCCTAATGATTTCGGGATGTTTTCTGTGTTTGATGACTTCTC
CGACGGCTTCTCCGGCGATCAGTTTACAGAGGTTTTACCCGTTGAAGATTACGGAGAT
GTGATTTTTGATGAGTCTCTGTTTCTTTGGGATTTTTAAATGTGTAAAGAGTTTTGAATT
GTTGTTTATTCGGGTCATGGAGAGTAATCTGGATATTTTTGTAAGTCGGAGCTCCAGCG
ACCCGGGAACTTGATCATTCTTGCTTTGGTTGATGATATCTATCATTCCTTCATTTTTTG
TTGTTATTAATGAAAATATTTGGATAAAATAGCAATTACAGAAAAAAAAAAAAAAAAAA

The BN42671700 cDNA is translated into the following amino acid sequence (SEQ ID NO:98):

MVKKAMKEEEEAEMRNSSMQSKYKGVRKRKWGKWVSEIRLPNSRERIWLGSFDTPEKA
ARAFDAAQFCLRGCQSGFNFPDNPPSISGGRSLTPPEIREAAARYANAQDDDIIITTGEEES
VLSETRPESPSTTSVSEADTSLDCDLSFLDTLPNDFGMFSVFDDFSDGFSGDQFTEVLPVE
DYGDVIFDESLFLWDF

cDNA sequence of ZM68416988 from corn (SEQ ID NO:99):

CTCGCCTCGCCTTCCTCCGAGCCCCGGCGAGGAAGAGGAACCCGCCGCCGCCGCCG
CCGGACGCACTTCCGATGGCGACGCCACGGAAGCCGATCAAGCTCACGCTGCCGTCC
CACGAGACCACCATCGGCAAGTTCCTGACGCACAGCGGGACGTTCACGGACGGGGAT
CTGCGCGTGAACAAGGACGGCCTCCGCATCGTCTCGCGGAGGGAGGGAGGCGAGGC
TCCTCCTATAGAGCCGTTGGATAGTCAACTGAGCTTAGATGATCTAGACGTTATAAAAG
TGATCGGGAAAGGTAGCAGCGGAAATGTGCAATTGGTCCGCCACAAATTTACTGGCCA
GTTTTTTGCTCTGAAGGTTATTCAACTAAATATTGATGAGAGTATACGCAAACAGATTGC
CAAGGAGTTGAAGATAAACTTATCAACACAGTGCCAATATGTTGTTGTGTTCTATCAGT
GTTTCTATTTCAATGGTGCCATTTCTATTGTTTTGGAATACATGGATGGTGGCTCCCTTG
CAGATTTCCTGAAGACTGTTAAAACCATTCCAGAGGCCTACCTCGCTGCTATCTGTACG
CAGATGCTAAAAGGACTGATCTATTTGCATAACGAGAAGCGCGTTATACACCGAGATCT
GAAACCATCAAATATATTGATAAATCATAGGGGTGAAGTAAAAATATCAGATTTTGGTGT
GAGTGCCATTATATCTAGTTCCTCTTCGCAACGAGATACATTTATTGGCACACGCAACT
ACATGGCGCCAGAAAGAATCGATGGAAAGAAACATGGTTCTATGAGTGATATCTGGAG
TTTGGGACTAGTGATACTGGAATGTGCAACCGGCATCTTTCCATTTCCTCCTTGTGAAA
GCTTCTACGAACTTCTCGTGGCTGTTGTTGATCAACCGCCACCTTCTGCGCCGCCGGA
TCAGTTTTCACCAGAATTCTGTGGGTTCATTTCTGCATGTCTCCAGAAGGATGCTAATG
ACAGGTCATCAGCCCAAGCCTTATTGGACCATCCGTTCCTGAGCATGTATGATGACCT
GCATGTAGATCTTGCTTCGTACTTCACGACAGCAGGATCTCCTCTCGCCACCTTCAATT
CCAGGCAACTCTAATTTTTTTGTCCTCCTTATTACGCGAACGGTGTGGCGACAAATTTC
TCTTTTTGGACAAGGCTTGGATTGTGTACTGAGCTGTAATGATCTTGTGTGTGTCAGGT
CGGTGATTGGCTCCATCACTTTACATATATGACATACATGTACAGCCTTTTAGGATAAA
AATGAGCACTGAAGTTTTGCCTATCTGTATATCGGCAGCAAACGTTTGGTCATGTTTGT
TTCACCTTGTAATGTATTGACTCAGATATGGGATTGGTCATTGTCTCTAAAAAAAAAAA

The ZM68416988 cDNA is translated into the following amino acid sequence (SEQ ID NO:100):

MATPRKPIKLTLPSHETTIGKFLTHSGTFTDGDLRVNKDGLRIVSRREGGEAPPIEPLDSQL
SLDDLDVIKVIGKGSSGNVQLVRHKFTGQFFALKVIQLNIDESIRKQIAKELKINLSTQCQYVV
VFYQCFYFNGAISIVLEYMDGGSLADFLKTVKTIPEAYLAAICTQMLKGLIYLHNEKRVIHRD

LKPSNILINHRGEVKISDFGVSAIISSSSSQRDTFIGTRNYMAPERIDGKKHGSMSDIWSLGL
VILECATGIFPFPPCESFYELLVAVVDQPPPSAPPDQFSPEFCGFISACLQKDANDRSSAQA
LLDHPFLSMYDDLHVDLASYFTTAGSPLATFNSRQL

CLAIMS

1. A transgenic plant transformed with an expression cassette comprising an isolated polynucleotide encoding a full-length polypeptide having a sequence as set forth in any one of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, and 100.

2. An isolated polynucleotide having a sequence selected from the group consisting of the polynucleotide sequences set forth in Table 1.

3. An isolated polypeptide having a sequence selected from the group consisting of the polypeptide sequences set forth in Table 1.

4. A method of producing a transgenic plant comprising at least one polynucleotide listed in Table 1, wherein expression of the polynucleotide in the plant results in the plant's increased growth and/or yield under normal or water-limited conditions and/or increased tolerance to an environmental stress as compared to a wild type variety of the plant comprising the steps of:
   (a) introducing into a plant cell an expression vector comprising at least one polynucleotide listed in Table 1, and
   (b) generating from the plant cell a transgenic plant that expresses the polynucleotide,

   wherein expression of the polynucleotide in the transgenic plant results in the plant's increased growth and/or yield under normal or water-limited conditions and/or increased tolerance to environmental stress as compared to a wild type variety of the plant.

5. A method of increasing a plant's growth and/or yield under normal or water-limited conditions and/or increasing a plant's tolerance to an environmental stress comprising the steps of increasing the expression of at least one polynucleotide listed in Table 1 in the plant.

Figure 1

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SEQ ID NO:6     (1) -------MATDGESISMSLAVATCVAMALFYVLILYVPTVILRLPSASSYTEFMIRRFICAAICT
SEQ ID NO:10    (1) ---------------------MGRAPTEGFYVAVLYAPTVILRVPPPSSLRTFLHRRFACAAVAS
SEQ ID NO:8     (1) MATPAGLLLASPPVISGVAAMAACAAMAVFYVAVLYAPTVILRFPPPTSLRTFLHRRFACAAVAS

SEQ ID NO:6    (59) VASLVFTAFILPIKSW-EASYILGVYGIRKDHLWQGVVYPLLLTSLVYAGSLVLKLFTLLESWKE
SEQ ID NO:10   (45) AASVLATASLLRIWSLSDFADMFAVFGIRKDHLIQAVAIPLLLTSLVYAGSFVARVWLLVSSWG-
SEQ ID NO:8    (66) AASVLATASLLRVWSLSDFADMFAVFGIRKDHLIQAVAIPLLLTSLVYAGSFVARVWLLVSSWG-

SEQ ID NO:6   (123) NGGGCSSFNYIRSFFQTIPASVLTSASNVSVWRNFIVAPVTEELVFRSCMIPLLLCAGFRINTAI
SEQ ID NO:10  (109) -----GGDEVEIGCAQRLAQWIQAAVADVMVWRNYVVAPFTEELVFRACMIPLLLCGGFKMSTII
SEQ ID NO:8   (130) -----GGDEVEIGCAQRLAQWIQAAVADVMVWRNYVVAPFTEELVFRACMIPLLLCGGFKMSTII

SEQ ID NO:6   (188) FLCPVLFSLAHLNHFREMYIRHNRSYLRASLIVGLQLGYTVIFGAYASFLFIRTGHLAAPLFAHI
SEQ ID NO:10  (169) FLSPIFFS------------------------LGVQLGYTVIFGWYATFLLIRTGNLLCPITAHV
SEQ ID NO:8   (190) FLSPIFFSLAHLNHFFELHQQG-CNFMRALLIVGVQLGYTVIFGWYATFLLIRTGNLLCPIIAHV

SEQ ID NO:6   (253) FCNYMGLPVLYA-NGKGLVSAAFLGGVVGFVLLLFPLTKPLMYNDSTNDCPCWLGYCLWN-
SEQ ID NO:10  (210) FCNMMGLPVFSSPRTKGAALVAFLAGSIAFFWLLFPATSPELYNSSFDRCSCWHGFCNWK-
SEQ ID NO:8   (254) FCNMMGLPVFSSPRTKGAALVAFLAGSIAFFWLLFPATSPELYNSSFDRCSCWHGFCNWK-
```

Figure 2

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SEQ ID NO:16    (1) -----------------------------------------------------------------
SEQ ID NO:18    (1) ----------------MLRALARPLERCLGSRASGDGLLWQSELKPHAGGDYSIAVVQANSSLED
SEQ ID NO:20    (1) -----------------------------------------------------MAVVQANNLLED
SEQ ID NO:24    (1) -MLVKLMNLLRACWRPSSNRHARTGSDVTGRQ---DGLLWYKDAGQHVNGEFSMAVVQANNLLED
SEQ ID NO:34    (1) -----------------------------------------------------------------
SEQ ID NO:26    (1) MLSALMDYLKSCWGPASPAGRPRKGSDATGRQ---DGLLWYKDGGQVVDGEFSMAVVQANNLLED
SEQ ID NO:28    (1) MLAAVMDYFSTCWGPRSRAGHRGKGSDAAGRQ---DGLLWYKDAGQLVTGGFSMAVVQANQLLED
SEQ ID NO:32    (1) MLAAVMDYFSTCWGPRSRAGHRGKGSDAAGRQ---DGLLWYKDAGQLVTGGFSMAVVQANQLLED
SEQ ID NO:30    (1) MLAAVMDYFSSCWGPRSGAGHRGKGSDAAGRQ---DGLLWYKDAGQLVTGEFSMAVVQANQLLED
SEQ ID NO:22    (1) MLQALMNLFSLCWKPFGRDAADRIDSIGVTGREGKDGLLWFRDGGKYGSGDFSMAVVQANQVLED

SEQ ID NO:16    (1) ------------------------------------------------------MSCDVLCQSFK
SEQ ID NO:18   (50) QSQVFTS--------SSATYVGVYDGHGGPEASRFVNRHLFPYIQKFAKEHG-GLSADVIKKAFK
SEQ ID NO:20   (13) QSQIESGPLSLLDTGPYGTFVGVYDGHGGPETSRYVCDHLFQHLKRFASEQK-SMSMEVIRKAYQ
SEQ ID NO:24   (62) QCQIESGPLSFLDSGPYGTFVGVYDGHGGPETACYINDHLFQNLKRFASEQN-AMSADVLKKAYE
SEQ ID NO:34    (1) ------------------------------------------------------MSADVLKKAYE
SEQ ID NO:26   (63) HSQVESGPLSTSEPGLQGTFVGVYDGHGGPETARYINDHLFNHLRRFASEHK-CMSADVIRKAFR
SEQ ID NO:28   (63) QSQVESGSLSLADYGPQGTFVGVYDGHGGPETSRFINDHLFNHLRRFATEHK-SMSADVIRKAFQ
SEQ ID NO:32   (63) QSQVESGSLSLADYGPQGTFVGVYDGHGGPETSRFINDHLFNHLRRFATEHK-SMSADVIRKAFQ
SEQ ID NO:30   (63) QSQVESGSLSLADPGPQGTFVGVYDGHGGPETSRFINDHLFNHLRRFATEHK-FMSADVIRKAFQ
SEQ ID NO:22   (66) QSQIESG--------PLGTFVGIYDGHGGPDASRYVCDHLFRHFQAISAESRGVVTTETIERAFR

SEQ ID NO:16   (12) EVEGKFLEIVERAWAVKPQIAAVGSCCLVGAVWDSKLYIASLGDSRAVLGSCSRDTGL------P
SEQ ID NO:18  (106) ETEEDFCGMVKRSLPMKPQMATVGSCCLFGAISNGTLYVANLGDSRAVLGSVVAGDDSNSSNKGA
SEQ ID NO:20   (77) ATEEGFLSVVTKQWPMNPQIAAVGSCCLVGVICGGILYIANLGDSRAVLGRVVRATGE------V
SEQ ID NO:24  (126) ATEDGFFSIVTKQWPVKPQIAAVGSCCLVGVICGGMLYVANVGDSRVVLGKHVKATGE------V
SEQ ID NO:34   (12) ATEDGFFSIVTKQWPVKPQIAAVGSCCLVGVICGGMLYVANVGDSRVVLGKHVKATGE------V
SEQ ID NO:26  (127) ATEEGFISVVSNQWSLRPQLAAVGSCCLVGVVCSGTLYVANLGDSRAVLGRLVKGTGE------V
SEQ ID NO:28  (127) ETEEGFLSLVIKEWSFKPQIASVGSCCLVGVICAGTLYVANLGDSRAVLGRLVKATGE------V
SEQ ID NO:32  (127) ETEEGFLSLVIKEWSFKPQIASVGSCCLVGVICAGTLYVANLGDSRAVLGRLVKATGE------V
SEQ ID NO:30  (127) ATEEGFLSLVSKEWSLKPQIASVGSCCLVGVICAGTLYVANVGDSRAVLGRLVKATGE------V
SEQ ID NO:22  (123) QTEEGYMALVSGSWNARPHIASAGTCCLVGVIFQQTLFVANAGDSRVVLGKKVGNTGG------M


SEQ ID NO:16   (71) VAKQISTEHNASIESIRNELFAKHSDDPQIVVLKHGVWRVKGIIQISRSIGDFYLKKAEFNQPPL
SEQ ID NO:18  (171) AAERLSTDHNVAVEEVRKEVKELNPDDSQIVMYIRGVWRIKGIIQVSRSIGDVYLKKPEFYRDPI
SEQ ID NO:20  (136) LAIQLSSEHNVAIESVRQEMHSLHPDDSKIVVLKHNVWRVKGLIQISRSIGDVYLKKAEFNKEPL
SEQ ID NO:24  (185) LAVQLSAEHNVSIASVRKELQSMHPEDRHIVVLKHNVWRVKGLIQVCRSIGDAYLKKQEFNREPL
SEQ ID NO:34   (71) LAVQLSAEHNVSIASVRKELQSMHPEDRHIVVLKHNVWRVKGLIQVCRSIGDAYLKKQEFNREPL
SEQ ID NO:26  (186) LAMQLSAEHNASYEEVRRELQASHPDDPHIVVLKHNVWRVKGIIQITRSIGDVYLKKPEFNREPL
SEQ ID NO:28  (186) LATQLSAEHNACYEEVRQELQSSHPDDPRIVVLKHNVWRVKGLIQISRSIGDVYLKKPEYNREPL
SEQ ID NO:32  (186) LATQLSAEHNACYEEVRQELQSSHPDDPRIVVLKHNVWRVKGLIQISRSIGDVYLKKPEYNREPL
SEQ ID NO:30  (186) VAMQLSSEHNACYEEVRQELQSSHPDDPHIVVLKHNVWRVKGLIQISRSIGDVYLKKPEYNREPL
SEQ ID NO:22  (182) AAIQLSTEHNANLEAVRQELKELHPHDPQIVVLKHGVWRVKGIIQVSRSIGDVYLKHAQFNREPL

SEQ ID NO:16  (136) IARFRLPDPLKRPVISSEPECNVITLGPDDEFVIFASDGLWEHLSSKEAVDIVYSHPRAGIARRL
SEQ ID NO:18  (236) FQQHGNHIPLRRPAMTAEPSIIVRKLKPQDLFLIFASDGLWEHLSDEAAVEIVLKHPRTGIARKL
SEQ ID NO:20  (201) YAKFRVREGFKRPILSSDPSISVHELQQHDQFLIFASDGLWEHLSNQDAVDIVQNNPHNGIARRL
SEQ ID NO:24  (250) YAKFRLREPFHKPILSSEPSISVQPLQPHDQFLIFASDGLWEQLTNQEAVDIVRSSPRSGCARRL
SEQ ID NO:34  (136) YAKFRLREPFHKPILSSEPSISVQPLQPHDQFLIFASDGLWEQLTNQEAVDIVRSSPRSGCARRL
SEQ ID NO:26  (251) HSKFRLQETFRRPLLSSDPAITVHQIQPTDKFIIFASDGLWEHLSNQEVVDMVQSSPRNGIARKL
SEQ ID NO:28  (251) HSKFRLRETFQKPILSSEPQITEHRIQPNDQFVIFASDGLWEHLSNQEAVDLVQSSPRNGIARRL
SEQ ID NO:32  (251) HSKFRLRETFQKPILSSEPQITEHRIQPNDQFVIFASDGLWEHLSNQEAVDLVQSSPRNGIARRL
SEQ ID NO:30  (251) HSKFRLRETFQRPTLSSEPQITEHRIQPNDQFVIFASDGLWEHLSNKEAVDLVQSSPRNGIARRL
SEQ ID NO:22  (247) NAKFRLPEPMNMPILSANPTILSHALQPNDSFLIFASDGLWEHLSNEKAVDIVNSNPHAGSAKRL

SEQ ID NO:16  (201) IKAALQKAATKREMRYSDLKGIERGIRRHFHDDITVVVLYLDTKLLNRGGSISNHISSKCPIDMP
SEQ ID NO:18  (301) VRAALEEAARKREMRYGDIKKIAKGVRRHFHDDISVVVVYLDQQKTTSSSNDRLIQKGGITAPPD
SEQ ID NO:20  (266) IKAALQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSNLVSRASSVRGPPLSVRGGGVP
SEQ ID NO:24  (315) IRAALQEAAKKREMRYSDLKKIDRGVRRHFHDDITVIVVFLDSGLVSQASTHRGPTLSLRGGGGS
SEQ ID NO:34  (201) IRAALQEAAKKREMRYSDLKKIDRGVRRHFHDDITVIVVFLDSGLVSQASTHRGPTLSLRGGGGS
SEQ ID NO:26  (316) VKSAVQEAAKKREMRYSDLKKVDRGVRRHFHDDITVIVVFFDSNAMTTAAWSR-PSVSLRGGGFP
SEQ ID NO:28  (316) VKAAMQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSDAMSKASWSKSPSFSLRGGGVT
SEQ ID NO:32  (316) VKAAMQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSDAMSKASWSKSPSVSLRGGGVT
SEQ ID NO:30  (316) VKAAMQEAAKKREMRYSDLKKIDRGVRRHFHDDITVVVVFLDSDAMSKASWSKSPSVSLRGGGVA
SEQ ID NO:22  (312) IKAALHEAARKREMRYSDLRKIDKKVRRHFHDDISVIVLFLNHDLISRGTVLD-PTLSIRSALDH

SEQ ID NO:16  (266) KGDNPPSLVSSNMNLAFNK-
SEQ ID NO:18  (366) IYSLRSDEAEQRRLLNVLY-
SEQ ID NO:20  (331) LPSRTLAPCAAPMET-----
SEQ ID NO:24  (380) AGLRSNTLAPT---------
SEQ ID NO:34  (266) AGLRSNTLAPT---------
SEQ ID NO:26  (380) IHSNTLAPFSVPTELNNSY-
SEQ ID NO:28  (381) LPAKSLAPFSAPAQLNGTH-
SEQ ID NO:32  (381) LPAKSLAPFSAPAQLNGTH-
SEQ ID NO:30  (381) LPAKSLAPFSAPARLNSTY-
SEQ ID NO:22  (376) --------------------
```

Figure 3

```
SEQ ID NO:36     (1) -----------------MGSSKAEENLALRLGLTAASAMASESVTFPIDITKTRLQLQGEM----
SEQ ID NO:40     (1) ---------------------MQLQG----------ESASIQTNLRPALAFQTSSAVHAPS----
SEQ ID NO:38     (1) -----------------MGVKSFVEG--------GIAPVVAGCSTHPLDLIKVRLQLHGEASAVT
SEQ ID NO:42     (1) ------------MAEEKKVAPIGIWTAVKPFVNGGASGMLATCVIQPIDMIKVRIQLGQGS----
SEQ ID NO:44     (1) ------------MAEEKKVAPIGVWNTVKPFVNGGASGMLATCVIQPIDMIKVRIQLGQGS----
SEQ ID NO:48     (1) MADAKQQQQQQQQPQQAAAAATGVWKTVKPFVNGEASGMLATCVIQPIDMVKVRIQLGEGS----
SEQ ID NO:46     (1) ----------MQPRYGEARQPLPGRYALYHFGTSGAAVAAATAVTHPFDVIKVRLQMQLAG----

SEQ ID NO:36    (45) ----------------GATAGAPKRGAISMAISIGKEEGIAGLYRGLSPA---LLRHVFYTSIRI
SEQ ID NO:40    (31) --------------------PPPRVGIITIGSRIIRQEGTCTLFSGISATSATVLRQTLYSTTRM
SEQ ID NO:38    (41) LLRPALAFHNSPPAFLETTHSVPKVGPISLGINLVKTEGAAALFSGVSAT---LLRQTLYSTTRM
SEQ ID NO:42    (50) --------------------------AASVTTTMLKNEGIGAFYKGLSAG---LLRQATYTTARL
SEQ ID NO:44    (50) --------------------------AVSVTKNMLKNDGIGAFYKGLSAG---LLRQATYTTARL
SEQ ID NO:48    (62) --------------------------AGQVTRNMLANEGVRSFYKGLSAG---LLRQATYTTARL
SEQ ID NO:46    (52) -------------------QRGNLVGMGTIFTQMVEREGTRSLYLGLAPA---LARAVVYGGLRF

SEQ ID NO:36    (91) VAYENLRTALSHGEHPENLSVAKKAFIGGTSGIIGQVIASPADLVKVRMQADGRLVKLGQQPRYT
SEQ ID NO:40    (76) GLYDILKTKWTDPETKT-IPLTRKLAAGFIAGGIGAAVGNPADVAMVRMQADGRLPVVDRR-NYK
SEQ ID NO:38   (103) GLYEVLKNKWTDPESGK-LSLTRKIAAGLVGGGIGAAVGNPADVAMVRMQADGRLPVAERR-NYA
SEQ ID NO:42    (86) GSFKMLTAKASEANDGKPLPLYQKALCGLTAGAIGACVGSPADLALIRMQADNTLPLAQRR-NYT
SEQ ID NO:44    (86) GSFKMLTAKAIEANDGKPLPLYQKALCGLTAGAIGACVGSPADLALIRMQADNTLPLAQRR-NYT
SEQ ID NO:48    (98) GSFRVLTNKAVEKNEGKPLPLFQKAFIGLTAGAIGACVGSPADLALIRMQADSTLPVAQRR-NYK
SEQ ID NO:46    (95) GLYEPCKHVCSYAFGST--NFAFKFASGVIAGGLATALTNPMEVLKVRLQMS---K------SST

SEQ ID NO:36   (156) GVADAFTKIARAEGVTGLWRGVGPNAQRAFLVNMGELACYDQSKQWIIGRGIAADNIGAHTLASV
SEQ ID NO:40   (139) SVLDAIAQMVRGEGVTSLWRGSSMTINRAMLVTASQLATYDSVKETILEKGLMRDGLGTHVTSSF
SEQ ID NO:38   (166) GVGDAIKRMAKQEGVVSLWRGSALTINRAMIVTAAQLASYDQFKEGMVESGGMKDGLGTHVVASF
SEQ ID NO:42   (150) NAFHALYRISADEGVLALWKGCGPTVVRAMALNMGMLASYDQSAEYMRDN-LGLGETSTVVGASA
SEQ ID NO:44   (150) NAFHALYRISADEGVLALWKGCGPTVVRAMALNMGMLASYDQSAEYMRDN-LGLGETSTVVGASA
SEQ ID NO:48   (162) NAFHALYRISGDEGVLALWKGAGPTVVRAMALNMGMLASYDQSVELFRDK-FGAGEISTVVGASA
SEQ ID NO:46   (149) STIREMRKVIAHEGFKALWKGVGPAMTRAGCLTASQMATYDEAKQALMKWTPLEEGFQLHLISSF

SEQ ID NO:36   (221) MSGLSATILSCPADVVKTRMMNQGAAG----AVYRNSLDCLTKTVKAEGVMALWKGFFPTWTRLG
SEQ ID NO:40   (204) AAGFVASVASNPVDVIKTRVMNMKVEAG-KTAPYKGAVDCALKTVRAEGIMALYKGFLPTVSRQA
SEQ ID NO:38   (231) AAGIVAAVASNPVDVIKTRVMNMKVDARGGEAQYKGAWDCAVKTVRAEGPMALYKGFVPTVCRQG
SEQ ID NO:42   (214) VLGFCAAACSLPFDFVKTQIQKMQPDAQG-KYPYTGSQDCAMQNRRTFEILHRLSGILRQDRPSR
SEQ ID NO:44   (214) VSGFCAAACSLPFDFVKTQIQKMQPDAQG-KYPYTGSLDCAMQTLKSGGPLKFYTGFPVYCVRIA
SEQ ID NO:48   (226) VSGFFASACSLPFDYVKTQIQKMQPDANG-KYPYTGSLDCAVKTFKSGGPFKFYTGFPVYCVRIA
SEQ ID NO:46   (214) IAGTAGTLVTSPVDMIKTRLMLQQESKG--ARVYRNGFHCASQVVVTEGVKSLYKGGFATFARVG

SEQ ID NO:36   (282) PWQFVFWVSYEQLRRISGLSSF-----
SEQ ID NO:40   (268) PFTVIMFVTLEQVKKVFKDFDF-----
SEQ ID NO:38   (296) PFTVVLFVTLEQVKKLLRDF-------
SEQ ID NO:42   (278) HGDMDLPEPDYKVPKEHWDVIFKQTL-
SEQ ID NO:44   (278) PHVMMTWIFLNQITKFQKTIGL-----
SEQ ID NO:48   (290) PHVMMTWIFLNQIQKFEKKIGI-----
SEQ ID NO:46   (277) PQTTITFIVCEKLRELAGMTAI-----
```

Figure 4

```
SEQ ID NO:50     (1) -----------------MVRADLVNLADLDTALNRVHNKLPNSIETASAEPPAPP----------
SEQ ID NO:54     (1) ---MSVDNSSVGSNESRTVILKHPGLRDAPTASYSVGNSVFRPNRVAAHTLNEDALARVLMDPNH
SEQ ID NO:52     (1) -MNSKVKGNGSVSRKDMIFRADRIDLKILDVQLEKHLSRVWSRNTTDNAKPK-------------
SEQ ID NO:58     (1) ------MKEEGGGGDAGFVRADQIDLKSLDEQLERHLTRAWTMEKRKEEASAGAGAGARQHQQSR
SEQ ID NO:60     (1) -----MRQPTSAGGDAGFLRADQIDLKSLDEQLERHLGHPAERVVGPVSGTGSRRGETAKLGPEE
SEQ ID NO:56     (1) MTSTAAGASSSAAKSESYLRADKIDLESLDIQLEKQLAKTWEKHKGSYNQGP--R----------

SEQ ID NO:50    (39) --------EEWEINPREITLKHMIARGTFGTVHKGVYKGQDVAVKLLEWGEENTMKKTEVQYYRN
SEQ ID NO:54    (63) PTEILSKYQQWAIDLGRLDMGVPFAQGAFGKLYRGTYIGEDVAIKLLEKPDN---DIERAQSLEQ
SEQ ID NO:52    (52) --------EEWEIDLSKLDIKTQIARGTYGTVYKGTYDNQDVAVKVLDWGEDGMTTVSEAASLRA
SEQ ID NO:58    (60) ----RPRREDWEIDPAKLVVKGVIARGTFGTVHRGIYDAHDVAVKLLDWGEDGHRSEQDIAALRA
SEQ ID NO:60    (61) LTPLQRCREDWEIDPTKLIIKGVIARGTFGTVHRGVYDGQDVAVKLLDWGEDGHRSEQEIGALRA
SEQ ID NO:56    (54) --------EDWEIDLAKLEIRYVIAQGTYGTVYRGTYDGQDVAVKLLDWGEDGFASETETATLRA

SEQ ID NO:50    (96) QFRQEVAVWHKLDHPNVTKFIGASMGNSDLRIPSAVDGDDGFHHVPNNACCVVVEYLAGGTLKDH
SEQ ID NO:54   (125) QFVQEVMMLSTLRHPNIVRFIGACR--------------------KSIVWCIITEYAKGGSVRQF
SEQ ID NO:52   (109) SFRQEVAVWHKLDHPNVTKFVGASMGTSNLKVS----NNKSDGQHTARACCVVVEYQPGGTLKQY
SEQ ID NO:58   (121) AFSQEVSVWHKLDHPNVTKFIGAIMGARDLN----IQTENGHIGMPTNICCVVVEYLPGGALKSF
SEQ ID NO:60   (126) AFAQEVAVWHKLEHPNVTKFIGAIMGARDLN----IQTEHGQLGMPSNICCVVVEYLAGGALKNF
SEQ ID NO:56   (111) SFKQEVAVWHELNHPNVTKFVGASMGTTDLKIPANSSNSGGRTELPPKACCVVVEYLAGGSLKQY

SEQ ID NO:50   (161) LIRSRRKKLSYKVVVQLALDVSRGLAYLHSQKIAHRDVKTENMLLDKQMRVKIADFGVARVEASN
SEQ ID NO:54   (170) LAKRQNKSVPLRLAVKQALDVARGMAYVHALGFIHRDLKSDNLLIAADRSIKIADFGVARIEVKT
SEQ ID NO:52   (170) LIRNRRKKLPYKVVIQLALDLSRGLSYLHSKKIVHRDVKSENMLLDNHRNLRIADFGVARVEAQN
SEQ ID NO:58   (182) LIKNRRKKLAFKVVVQIALDLARGLSYLHSKKIVHRDVKTENMLLDKTRTVKIADFGVARLEASN
SEQ ID NO:60   (187) LIKNRRRKLAFKVVVQIALDLARGLCYLHSKKIVHRDVKTENMLLDKTRTVKIADFGVARVEASN
SEQ ID NO:56   (176) LIKNRRRKLAYKVVVQIALDLARGLNYLHSRKIVHRDVKTENMLLDTQRNLKIADFGVARVEAQN

SEQ ID NO:50   (226) PKDMTGDTGTPGYMAPEILDGKPYNKKCDVYSFGICLWEVYCCDMPYLDLSFADMTSAVVHQNLR
SEQ ID NO:54   (235) EG-MTPETGTYRWMAPEMIQHRPYDHKVDVYSFGIVLWELITGMLPFTNMTAVQAAFAVVNKGAR
SEQ ID NO:52   (235) PSDMTGETGTLGYMAPEVLDGKPYNRRCDVYSFGICLWEIYCCDMPYPDLSFADVTSAVVRQNLR
SEQ ID NO:58   (247) PSDMTGETGTLGYMTPEVLNGNPYNRKCDVYSFGICLWEIYCCDMPYPDLSFSEVTSAVVRQNLR
SEQ ID NO:60   (252) PSDMTGETGTLGYMAPEVLNGHAYNRKCDVYSFGICLWEIYCCDMPYPDLSFSEVTSAVVRQNLR
SEQ ID NO:56   (241) PKDMTGATGTLGYMAPEVLEGKPYNRKCDVYSFGICLWEIYCCDMPYPDLSFADVSSAVVHQNLR

SEQ ID NO:50   (291) PEVPKCCPQGLADIMRQCWDANPEKRPAMADVVQMLEALDTSKGGGMIPTDAQPHGCLCFGRFKG
SEQ ID NO:54   (299) PAIPHDCLPSLTHIMTRCWDANPEVRPPFTEIVCMLENAEMEVVSHVRK--ARFRCCVAEPMTTD
SEQ ID NO:52   (300) PEIPRCCPSSLGSIMKKCWDAQSENRPEMAEVVKMLEAIDTSKGGGMIPEDQNPG-CFCFAPTRG
SEQ ID NO:58   (312) PEIPRCCPSSLSNVMKRCWDANPDKRPEMAEAVSMLEAIDTSKGGGMIPVDQRPGCLACFRQYRG
SEQ ID NO:60   (317) PEIPRCCPSSLANVMKRCWDANPDKRPEMAEVVSMLEAIDTSKGGGMIPKDQTQGCLSCFRQYRG
SEQ ID NO:56   (306) PDIPRCCPSPMANIMRKCWDANPDKRPDMDDVVRFLEALDTSKGGGMIP-EGQAGGCLCFFRARG

SEQ ID NO:50   (356) P-
SEQ ID NO:54   (362) --
SEQ ID NO:52   (364) P-
SEQ ID NO:58   (377) P-
SEQ ID NO:60   (382) P-
SEQ ID NO:56   (370) P-
```

Figure 5

```
SEQ ID NO:74     (1) -MPSHGDLDRQIAQLRDCKYLPEAEVKALCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFYDLIE
SEQ ID NO:90     (1) -MPSHGDLDRQIAQLRDCKYLPEAEVKALCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFYDLIE
SEQ ID NO:88     (1) -MPSHGDLDRQIAQLRDCKYLPEAEVKVLCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFYDLIE
SEQ ID NO:84     (1) MPSSHGDLDRQIAQLRECKHLAEGEVRALCEQAKAILMEEWNVQPVRCPVTVCGDIHGQFYDLIE
SEQ ID NO:76     (1) -MPPNGDLDRQISQLMECKPLSEADVKTLCDQARAILVEEWNVQPVKCPVTVCGDIHGQFYDLIE
SEQ ID NO:78     (1) -MPPNGDLDRQIEHLMECKPLSEEDVRTLCDQAKAILVEEWNVQPVKCPVTVCGDIHGQFYDLIE
SEQ ID NO:80     (1) -MPSQSDLDRQIEHLMDCKPLPEAEVRTLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFHDLLE
SEQ ID NO:82     (1) -MPSHADLDRQIEHLMQCKPLSEAEVKALCEQARAVLVEEWNVQPVKCPVTVCGDIHGQFHDLVE
SEQ ID NO:86     (1) -MPSHADLERQIEQLMECKPLSESEVKALCDQARAILVEEWNVQPVKCPVTVCGDIHGQFYDLIE

SEQ ID NO:74    (65) LFRIGGDAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:90    (65) LFRIGGDAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:88    (65) LFRIGGDSPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:84    (66) LFRIGGEAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:76    (65) LFRIGGNPPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:78    (65) LFRIGGNAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:80    (65) LFRIGGSAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:82    (65) LFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQITQVYGFYDE
SEQ ID NO:86    (65) LFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQITQVYGFYDE

SEQ ID NO:74   (130) CLRKYGNANVWKYFTDLFDFLPLTALIENQVFCLHGGLSPSLDTLDNIRSLDRVQEVPHEGPMCD
SEQ ID NO:90   (130) CLRKYGNANVWKYFTDLFDFLPLTALIENQVFCLHGGLSPSLDTLDNIRSLDRVQEVPHEGPMCD
SEQ ID NO:88   (130) CLRKYGNANVWKYFTDLFDYLPLTALIENQVFCLHGGLSPSLDTLDNIRSLDRIQEVPHEGPMCD
SEQ ID NO:84   (131) CLRKYGNANVWKYFTDLFDYLPLTALIENQVFCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCD
SEQ ID NO:76   (130) CLRKYGNANVWKFFTDLFDYLPLTALIESQVFCLHGGLSPSLDTLDNIRSLDRIQEVPHEGPMCD
SEQ ID NO:78   (130) CLRKYGNANVWKYFTDLFDYLPLTALIESQVFCLHGGLSPSLDTLDNIRSLDRIQEVPHEGPMCD
SEQ ID NO:80   (130) CLRKYGNANVWKHFTDLFDYLPLTALIESQIFCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCD
SEQ ID NO:82   (130) CLRKYGNANVWKHFTDLFDYLPLTALIESQVFCLHGGLSPSLDTLDNIRSLDRIQEVPHEGPMCD
SEQ ID NO:86   (130) CLRKYGNANVWKYFTDLFDYLPLTALIESQIFCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCD

SEQ ID NO:74   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA
SEQ ID NO:90   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA
SEQ ID NO:88   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA
SEQ ID NO:84   (196) LLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA
SEQ ID NO:76   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIATQFNHNNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA
SEQ ID NO:78   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIATQFNHNNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA
SEQ ID NO:80   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQLVMEGYNWSQENNVVTIFSA
SEQ ID NO:82   (195) LLWSDPDDRCGWGISPRGAGYTFGQDISQQFNHTNGLSLISRAHQLVMEGYNWAQDKNVVTVFSA
SEQ ID NO:86   (195) LLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQLVMEGFNWCQDKNVVTVFSA

SEQ ID NO:74   (260) PNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRKTPDYFL-
SEQ ID NO:90   (260) PNYCYRCGNMAAILEIGKNMDQNFLQFDPAPRQIEPDTTRKTPDYFL-
SEQ ID NO:88   (260) PNYCYRCGNMAAILEIGENMDQNFLQFNPAPRQIEPDTTRKTPDYFL-
SEQ ID NO:84   (261) PNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRKTPDYFL-
SEQ ID NO:76   (260) PNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQVEPDTTRKTPDYFL-
SEQ ID NO:78   (260) PNYCYRCGNMAAILEISENMEQNFLQFDPAPRQVEPDTTRKTPDYFL-
SEQ ID NO:80   (260) PNYCYRCGNMAAILEVGENMDQNFLQFDPAPRQVEPDVARRTPDYFL-
SEQ ID NO:82   (260) PNYCYRCGNMAAILEIGENMEQNFLQFDPAPRQIEPETTRRTPDYFL-
SEQ ID NO:86   (260) PNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRKTPDYFL-
```

Figure 6

```
SEQ ID NO:92      (1) MKGKKPVKELKLTVPAQETPVDKFLTASGTFKDGELRLNQSGLRLISEENGDEDESTKLKVEDVQ
SEQ ID NO:96      (1) ---MKPIQPPPGVIGPVKNRPRRRPDLSLPLPHRDVSLAVP-LPLPPTSGGGS-------TTSEP
SEQ ID NO:94      (1) -MKRGSLSLNPISLPPPEQSISKFLTQSGTFKDGDLQVNKDGIQTVSHSEPGAP--PPIDPLDNQ
SEQ ID NO:100     (1) --MATPRKPIKLTLPSHETTIGKFLTHSGTFTDGDLRVNKDGLRIVSRREGGE--APPIEPLDSQ

SEQ ID NO:92     (66) LSMDDLEMIQVIGKGSGGVVQLVRHKWVGTLFALKGIQMNIQESVRKQIVQELKINQATQSPHIV
SEQ ID NO:96     (55) KSYSDLVRGNRIGSGAGGTVYRVVHRPTSRVYALKIINGNHDDTVRGQICREIKILRDVNHPNVV
SEQ ID NO:94     (63) LSLADLEVIKVIGKGSSGSVQLVKHKLTQQFFATKVIQLNTEESTCRAISQELRINLASQCPYLV
SEQ ID NO:100    (62) LSLDDLDVIKVIGKGSSGNVQLVRHKFTGQFFALKVIQLNIDESIRKQIAKELKINLSTQCQYVV

SEQ ID NO:92    (131) MCHQSFYHNGVIYLVLEYMDRGSLADIVKQVKTILEPYLAVLCKQVLEGLLYLHHQRHVIHRDIK
SEQ ID NO:96    (120) KCHEMFDQNGEIQVLLELMDQGSLEGAHIS----NEQQLSDLSRQILNGLAYLHG-RHIVHRDIK
SEQ ID NO:94    (128) SCYQSFYHNGLVSIVMEFMDGGSLLDLLKKVQRVPENMLAAISKRVLRGLCYIHDERRIIHRDLK
SEQ ID NO:100   (127) VFYQCFYFNGAISIVLEYMDGGSLADFLKTVKTIPEAYLAAICTQMLKGLIYLHNEKRVIHRDLK

SEQ ID NO:92    (196) PSNLLVNRKGEVKITDFGVSAVLASSIGQRDTFVGTYNYMAPERI-----SGSTYDYKSDIWSLG
SEQ ID NO:96    (180) PSNLLINSDNNVKIADFGVSRVLAQTLSPCKSSVGTIAYMSPERINTDLNQGMYDGCAGDIWSFG
SEQ ID NO:94    (193) PSNLLINHRGEVKIADFGVSKILSSTSSLAHTFVGTDFYMSPERI-----SGKAYGNKCDIWSLG
SEQ ID NO:100   (192) PSNILINHRGEVKISDFGVSAIISSSSSQRDTFIGTRNYMAPERI-----DGKKHGSMSDIWSLG

SEQ ID NO:92    (256) LVILECAIGRFPYIPSEGEG-WLSFYELLEAIVDQPPPSAPADQFSPEFCSFISSCIQKDPAQRM
SEQ ID NO:96    (245) VSVLEFFLGRFPFNVNRLG----DWASLMCAICMSKPPEAPAT-ASPEFRHFVSCCLQREPGRRQ
SEQ ID NO:94    (253) VVLLECATGKFPYTPPENMKGWTSMYELVDAIVENPPPRAPSHLFSPEFCSFISQCVQKDPRDRK
SEQ ID NO:100   (252) LVILECATGIFPFPPCES------FYELLVAVVDQPPPSAPPDQFSPEFCGFISACLQKDANDRS

SEQ ID NO:92    (320) SASELLNHPFLKKFEDKDLNLGILVENLEPPMNIPE-----
SEQ ID NO:96    (305) TAVQLLQHPFVRRGAIQSQNRSP--QNLHQLLPPPH-----
SEQ ID NO:94    (318) SAMELLDHRFVNMFEDVDVDLSSYFTAAGSLIPPLANS---
SEQ ID NO:100   (311) SAQALLDHPFLSMYDDLHVDLASYFTTAGSPLATFNSRQL-
```