

(12) PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 199954197 B2**
(10) Patent No. **762390**

(54) Title
Genes involved in tolerance to environmental stress

(51)⁶ International Patent Classification(s)
C12N 015/82 C12N 009/12
A01H 005/00 C12N 015/10
C12N 005/10 C12Q 001/68

(21) Application No: 199954197 (22) Application Date: 1999 . 08 . 04

(87) WIPO No: WO00/08187

(30) Priority Data

(31) Number	(32) Date	(33) Country
98202634	1998 . 08 . 04	EP

(43) Publication Date : 2000 . 02 . 28
(43) Publication Journal Date : 2000 . 05 . 04
(44) Accepted Journal Date : 2003 . 06 . 26

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(56) Related Art
WO 00/47714
PRANDL R ET AL, MOLECULAR AND GENERAL GENETICS, MAY 1998
258: 269-278

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/82, 15/10, 9/12, 5/10, C12Q 1/68, A01H 5/00		A2	(11) International Publication Number: WO 00/08187
			(43) International Publication Date: 17 February 2000 (17.02.00)
(21) International Application Number: PCT/EP99/05652		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 4 August 1999 (04.08.99)			
(30) Priority Data: 98202634.6 4 August 1998 (04.08.98) EP			
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(74) Agent: DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		Published Without international search report and to be republished upon receipt of that report.	
(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS			
(57) Abstract The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.			



Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant
5 molecular biology. In particular, the invention relates to improvements of crop
productivity of useful plants. One of the major limitations of crop productivity is the
effect of environmental stress conditions on plant growth and development. An
important goal of molecular biology is the identification and isolation of genes that can
provide resistance or tolerance to such stresses. For agriculture, the creation of
10 transgenic plants containing such genes provides the potential for improving the stress
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on
the growth of plants and the productivity of crops. The physiological response to these
stresses arises out of changes in cellular gene expression. Expression of a number of
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be
classified into two groups: those that directly protect against environmental stresses
and those that regulate gene expression and signal transduction in the stress
response. The first group includes proteins that likely function by protecting cells from
20 dehydration, such as the enzymes required for biosynthesis of various
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,
Bray et al., 1997). The second group of gene products includes transcription factors,
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the
30 hypothesis that the genetic information for tolerance to environmental stress conditions
exists in all higher plants. In glycophytes, this information would only be expressed in
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of
35 evidence also demonstrate that even mild environmental stress conditions throughout
the growth season have a negative impact on plant growth and crop productivity. It is

for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively-easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO₂ etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as herein before defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 μ plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5 The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10 The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15 The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30 Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which
 5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent
 10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1
 15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or at
 20 least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having
 25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 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 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid
 30 comprising at least part of any of SEQ ID NO 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,
 35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 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, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (a) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or

95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

5 More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- 10 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

20 The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or
 25 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88,
 30 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from Arabidopsis

thaliana, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

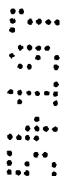
More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

5

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated
- 10 as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

15 Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at
20 least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.



25 Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.



30 Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the
35 same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms
 5 (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

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

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%,
 20 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into
 25 account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above
 30 except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of
 35 amino acids having amide-containing side chains is asparagine and glutamine; a

group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 3 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO 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, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably

includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

5 The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 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,
10 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to
15 environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant
20 expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method
25 comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a
30 plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonosoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to another preferred embodiment, the present invention relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,

- a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

5 (b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

.....

25 A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

.....

30 The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above.

35 According to this embodiment, other polynucleic acids modulating the expression or

the activity of a protein according to the present invention may be introduced transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is
 5 required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

10 Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible
 15 promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA
 20 levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress
 25 conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the
 30 activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the

inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

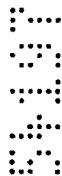
For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

5 Generally, higher homology can be used to compensate for the use of a shorter sequence.

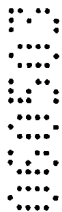
Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should
10 be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with
15 virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the
20 activity of the constructs.

A number of classes of ribozymes have been identified. One class of ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado
25 sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).



Another method of suppression of gene expression is sense suppression.
30 Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.



The suppressive effect may occur where the introduced sequence contains no
35 coding sequence per se, but only intron or untranslated sequences homologous to

sequences present in the primary transcript of the endogenous sequence. The introduced sequence generally will be substantially identical to the endogenous sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

- (a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,
- 5 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also
 10 referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as
 15 defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 3, 5, 9,
 20 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed
 25 in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant
 30 cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-, tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or*
 35 *more* polynucleic acids according to the invention into the genome of the plant. More

specifically, the constitutive promoter can be, but is not restricted to, one of the following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell (1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be

obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative
 5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a
 10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can
 15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,
 20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

25 Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress
 30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of
 35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5 The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10 The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein
15 having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 4 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

The present invention also relates to the cloning of the genomic counterpart of
20 any of the cDNA sequences as represented in SEQ ID NO 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present
25 invention also relates to the coding region as well as the promoter region of any of said genomic clones.

The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30 The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the
35 primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region
 5 under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this
 10 region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb
 15 long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic
 20 acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

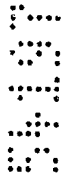
The present invention also relates to a pharmaceutical or agrochemical
 25 composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or
 30 resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for
 35 plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references
5 mentioned herein are incorporated by reference.



BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A en B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2.

Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

- + : similar growth to the DY wild type cells;
- ++ : growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
- +++ : growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
- ++++ : growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of
5 the present invention.

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EXAMPLES

Example 1. Construction of the cDNA library.

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM Tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H₂O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)₁₄-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

Example 2. Yeast transformation and selection for osmotolerance.

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the *Arabidopsis* cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected *Arabidopsis* cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected *Arabidopsis* cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD₆₀₀ at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

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Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction

BY2 cells are stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-cDNA or pBIN-35S-ASAt-cDNA recombinant binary vectors. PBIN-35S-At-cDNA is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the *Arabidopsis thaliana* cDNA from the genes according to the present invention. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-cDNA is the pBIN-35S-CaMVter vector in which the At-cDNA was cloned in the antisense orientation, between the CaMV 35S RNA promoter and terminator.

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Example 8. Overexpression of At-cDNA sense and antisense RNA in plant cells

Transgenic plant cells overexpressing *At-cDNA* are generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells are stably transformed by *A. tumefaciens* carrying the *At-cDNA* driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-RNA* also is overexpressed under the control of the same promoter. Control lines are obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-cDNA*-overexpressing tobacco transgenic cell lines are selected with a high and similar *At-cDNA* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-cDNA* are chosen that show an undetectable tobacco cDNA transcript level. Marked differences in growth are observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-cDNA* are clearly more tolerant than control lines. Inhibition of the endogenous cDNA expression is correlated with a higher sensitivity to those stresses. To understand the basis of stress

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tolerance in *At-cDNA*-overexpressing plant cells, expression of stress-induced genes is followed in control and stress conditions. Tobacco kin1 and HSP17.6A homologues already were induced in *At-cDNA*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought),
 5 suggesting that *At-cDNA* overexpression may mimic a stress signal.

Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey
 10 (1992) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strains carrying pBIN-35S-At-HSP17.6A, pBIN-35S-At-c74 recombinant binary vectors. pBIN-35S-At-HSP17.6A recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing At-HSP17.6A cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI
 15 fragment of pYES-HSP17.6A containing the At-HSP17.6A cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp receptor gene was deleted and replaced by the At-HSP17.6A cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-c74 was constructed with a similar strategy as pBIN-35S-
 20 AtHSP17.6A with an intermediary pYES-Atc74 vector. The At-c74 cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with
 25 T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-c74 was cloned in pBINm-gfp4 as explained supra.

Example 10. Tolerance to environmental stress in plant cells

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with, At-HSP17.6A and At-c74. The growth of these transgenic calli
 30 during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-CaMVter. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with
 35 At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed

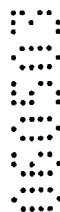
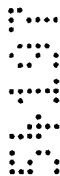
with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

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Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75
10 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60
15 % humidity, 16 hours light/8 hours dark, 70 microeinstein. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic
20 lines transformed with At-HSP17.6A or At-c74 survived very well (Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1
25 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter. After sowing, seeds were kept overnight at 4 degrees (to
30 enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinstein. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was
35 inhibited and eventually they died. On the contrary, the transgenic lines transformed



with, At-HSP17.6A or At-c74 survived very well (see Figure 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefore seeds from transgenic plants transformed with pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l⁻¹ sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast,

more than 70 % of the seeds from transgenic lines overexpressing At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

Example 12. Southern hybridisation of At-cDNA genes in other plants

- 5 To investigate whether homologues of the cDNA of the present invention exist in other plant species, a Southern hybridisation analysis was performed using the full length At-cDNAs of the present invention as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.
- 10 DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N; Amersham, Little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200
- 15 gm⁻³ denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA

- Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x
- 20 SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

- The reference to any prior art in this specification is not, and should not be
- 25 taken as, an acknowledgment or any form of suggestion that that prior art forms part of the common general knowledge in Australia.

- Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and
- 30 "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

Table 1

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++
signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++

signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to <i>Dictpyostelium mekA</i> (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and <i>Arabidopsis</i> HAT7 homeotic protein	73	++	++++
signalling	similar to <i>E. coli</i> sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, <i>Arabidopsis</i> LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, <i>Arabidopsis</i> LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent – kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	<i>Arabidopsis</i> cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 – sequence	107	+++	++++
unknown	chromosome 4 – sequence	109	+	++++
unknown	chromosome 5 – sequence	111	++++	+++
unknown	chromosome 5 – sequence	113	++++	++
unknown	chromosome 5 – sequence	115	++++	++++
unknown	chromosome 5 – sequence	117	+	++++
unknown	chromosome 5 – sequence	119	+	++++
signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++

TABLE 2
EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF
THE PRESENT INVENTION

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α -amylase (<i>Amy32b</i>)	Aleurone	Lanahan <i>et al.</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin β -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	http://salus.medium.edu/mmg/tierney/html
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	http://salus.medium.edu/mmg/tierney/html
chalcone synthase (<i>chsA</i>)	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/gwrdc/csh95-1.html
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	http://salus.medium.edu/mmg/tierney/html
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
β -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	http://salus.mediam.edu/mmg/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.mediam.edu/mmg/tierney/html
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczynski <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i> (1987)

Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
LEAFY	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

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Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wilihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

- 42A-

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or
5 group of integers or steps.

The reference to any prior art in this specification is not, and should not be taken as, an acknowledgment or any form of suggestion that such prior art forms part of the common general knowledge in Australia.

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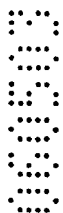
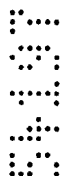
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EDITORIAL NOTE

APPLICATION NUMBER - 54197/99

The following Sequence Listing pages 1 to 234 are part of the description. The claims pages follow on pages 48 to 53.

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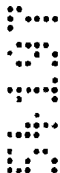
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Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
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 Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala
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 Ser Gly Leu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

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Leu Glu Asp Tyr His Leu Ile Glu Lys Val Ala Asn Phe Thr Arg Glu
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Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala
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 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
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205 210 215

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Thr Thr Glu Lys Glu Ile Ser Asp Asp Glu Asp Glu Asp Glu Pro Lys
220 225 230

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 Asp Lys Ile Arg Phe Glu Ser Leu Thr Asp Lys Ser Lys Leu Asp Gly
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 Gln Pro Glu Leu Phe Ile Arg Leu Val Pro Asp Lys Pro Asn Lys Thr
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 Asn Asn Leu Gly Thr Ile Ala Arg Ser Gly Thr Lys Glu Phe Met Glu
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 Ser Phe Thr Val Thr Arg Asp Val Asp Gly Glu Pro Leu Gly Arg Gly
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 His Phe Ser Val Glu Gly Gln Leu Glu Phe Lys Ala Ile Leu Phe Val
 305 310 315 320

Pro Lys Arg Ala Pro Phe Asp Leu Phe Asp Thr Arg Lys Lys Leu Asn
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 Asp Lys Leu Val Glu Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp
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 45 50 55
 tta tac gag ctt tct gct gag tat gaa ggg aag cgt gag cct agc aag 242
 Leu Tyr Glu Leu Ser Ala Glu Tyr Glu Gly Lys Arg Glu Pro Ser Lys
 60 65 70 75
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 Leu Glu Glu Leu Gly Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser
 80 85 90
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 Ile Val Ile Ser Lys Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu
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Glu Glu Thr Phe Lys Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu			
140	145	150	155
gag atc ttt gat gcc ttg aag aat cag act gtg gat ctg gtt ttg act			530
Glu Ile Phe Asp Ala Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr			
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gct cat cct act cag tct gtg cgt aga tca ttg ctt cag aag cat ggg			578
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agg ata agg gac tgt ctt gct caa ctc tat gca aag gac att act cct			626
Arg Ile Arg Asp Cys Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro			
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Asp Asp Lys Gln Glu Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala			
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Val Pro Lys Phe Leu Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly			
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Ile Asp Glu Arg Val Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser			
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Trp Met Gly Gly Asp Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val			
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tat aac caa atc gag aat ctg atg ttt gag tta tct atg tgg cgt tgc			1010
Tyr Asn Gln Ile Glu Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys			
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415 420 425	
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Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly	
430 435 440	
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Leu Ser Leu Val Arg Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr	
445 450 455	
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Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
460 465 470 475	
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Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
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Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp	
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Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro	
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ctt aga gtt gtt cca ctc ttt gag aag cta gct gat ctt gaa gca gct	1730
Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
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655 660 665	
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Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly	
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Glu Met Ala Val Val Ala Thr Glu Glu Tyr Arg Ser Val Val Phe Gln	
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Glu Pro Arg Phe Val Glu Tyr Phe Arg Leu Ala Thr Pro Glu Leu Glu	
735 740 745	
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Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro Ser	
750 755 760	
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Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr	
765 770 775	
caa aca aga ttc cat ctt cct gta tgg tta ggt ttc gga gca gca ttt	2402
Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe	
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Arg Tyr Ala Ile Lys Lys Asp Val Arg Asn Leu His Met Leu Gln Asp
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Met Tyr Lys Gln Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Ile Glu
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atg gtg ttc gcc aag gga gac ccc ggg atc gct gct ttg tac gac aaa 2546
Met Val Phe Ala Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys
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ctt ctt gtc tca gaa gat tta tgg gct ttt gga gag aaa ctc aga gcc 2594
Leu Leu Val Ser Glu Asp Leu Trp Ala Phe Gly Glu Lys Leu Arg Ala
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aac ttt gat gaa acc aag aac ctc gtc ctc cag act gct gga cat aaa 2642
Asn Phe Asp Glu Thr Lys Asn Leu Val Leu Gln Thr Ala Gly His Lys
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gac ctt ctt gaa gga gat cct tac ttg aaa cag aga cta agg cta cgt 2690
Asp Leu Leu Glu Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg
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gac tct tac att acg acc ctc aac gtt tgc caa gcc tac aca ttg aag 2738
Asp Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys
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agg atc cgt gat gca aac tac aat gtg act ctg cga cca cac att tct 2786
Arg Ile Arg Asp Ala Asn Tyr Asn Val Thr Leu Arg Pro His Ile Ser
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aaa gag atc atg caa tca agc aaa tca gca caa gag ctc gtc aag ctt 2834
Lys Glu Ile Met Gln Ser Ser Lys Ser Ala Gln Glu Leu Val Lys Leu
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aac ccc acg agt gaa tac gcg cct gga ctt gag gac aca ctt atc tta 2882
Asn Pro Thr Ser Glu Tyr Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu
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acc atg aag ggt att gct gca gga ttg caa aac acc ggt taa gtgagtca 2932
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Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser Ile Val Ile Ser Lys		
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Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu Glu Val Gln		
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Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys Lys Gly Asp Phe Val		
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Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu Glu Ile Phe Asp Ala		
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Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr Ala His Pro Thr Gln		
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Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly Arg Ile Arg Asp Cys		
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Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val Thr Arg Asp Val Cys		
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Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys Thr Asp Glu Phe Arg		
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Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg Lys Asp Ala Ala Lys		

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Lys Leu Phe Gly Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp
30 35 40

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Gly Ala Ala Thr Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly
45 50 55 60

cct ccc gtc gtc atg aac cct atc agt cgc cag aat ttc atc gtc aag 244
Pro Pro Val Val Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys
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Ser Arg Pro Glu
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Glu Tyr Leu Lys Glu Ile Thr Lys Ala Arg Arg Glu Leu Arg Ser Leu
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aaatgtttgt atcatctggt ttttatgaag a tgg cac gat gct gga acc tat      315
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                      40                      45

gat gct caa tcg aag acc ggt gga cct aat ggc tct atc agg aac gaa      363
Asp Ala Gln Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu
                      50                      55                      60

gaa gag cac act cat ggt gcc aac agt ggt ttg aag atc gct ctc gat      411
Glu Glu His Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp
                      65                      70                      75

ctc tgt ggtaggattt tgatttagtt tttgtagatt cactttctgg ataatttcat      467
Leu Cys

gcgatgtatc cgttttatgt tgtggtttta gaacactggt caaaataatt acattatgct 527

tttggaatg gactttgtat cgcttaatta tgagatccta tctttgatgt ttca gag      584
                      Glu
                      80

ggc gtg aaa gct aag cat ccc aaa atc aca tac gca gac ctg tat cag      632
Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
                      85                      90                      95

gtgagttaag gctgtgagag aaatcttttt gatgtccttg ttgctttttc tgcacatttg 692

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cttgtttgtt aggagactta gttgatagtt gagcagctgt gtaaatatgg ttacagtgtg 812

aatttgtttc aggagatgtt actgattgtg atttggttta caaaaatcat agattgacta 872

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gtgtaccagt ttaatggcaa ttaagttttg ggtatgaatt atttactttt aagtgttttg 1172

tttcag ctt gct ggt gtg gta gca gtt gag gtt act ggt gga cct gac      1220
Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp
                      100                      105                      110

atc gtg ttc gtt ccc ggg aga aag g tatactttct catctcttga      1265

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Ile Val Phe Val Pro Gly Arg Lys A
115

gacattataa cagcttatca gtttaacact aaagcaaaca taattactgt atgtttcttc 1325

ttgatagg at tca aat gtc tgc ccc aag gaa gga aga ctt cct gat gcc 1374
sp Ser Asn Val Cys Pro Lys Glu Gly Arg Leu Pro Asp Ala
120 125 130

aaa caa ggt acactaaatt ctgtatcaa ttataacaaa cttttcatgt 1423
Lys Gln Gly
135

tttctactga taatcttgtt ttggaattgg aagatttttt ctatgaattc acattgttta 1483

tatctctgta ggt ttc caa cat ctc aga gat gtc ttc tac cgc atg gga 1532
Phe Gln His Leu Arg Asp Val Phe Tyr Arg Met Gly
140 145

cta tct gat aag gat att gtg gca ctc tca ggg ggt cat act ctg 1577
Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His Thr Leu
150 155 160

gtaaatcat tggtcactta cttaacttcc gttgtttttg aacaaatag ctgttgtgac 1637

ttatgaccac attgggtgtt tag gga agg gct cac ccg gag agg tca ggc ttt 1690
Gly Arg Ala His Pro Glu Arg Ser Gly Phe
165 170

gat gga cca tgg acc caa gag ccg ctg aat ttt gac aac tcc tac ttc 1738
Asp Gly Pro Trp Thr Gln Glu Pro Leu Asn Phe Asp Asn Ser Tyr Phe
175 180 185

gt gtaattttca tttctttatc ctgagagatt ttctttgtgc atttttttaa 1790
Va

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ggttatccat gattatttac tgttttgta c c agg gaa ctg ctg aaa gga gaa 1903
l Arg Glu Leu Leu Lys Gly Glu
190 195

tca gag ggc ttg ttg aaa ctt cca act gac aag acc tta ttg gaa gac 1951
Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr Leu Leu Glu Asp
200 205 210

ccg gag ttc cgt cgt ctt gtt gag ctt tat gca aaggtataat atactggaga 2004
Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala
215 220

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aaaccaaatt atctagggtt ttgttctaga gaaccccacg gatccttate gcctttatag 2184

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ggcag gat gaa gat gca ttc ttc aga gac tac gcg gaa tcg cac aag aaa 2414
    Asp Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys
        225                230                235
ctc tct gag ctt ggt ttc aac cca aac tcc tca gca ggc aaa gca gtt 2462
Leu Ser Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val
    240                245                250
gca gac agc acg att ctg gca cag agt gcg ttc ggg gtt gca gtt gct 2510
Ala Asp Ser Thr Ile Leu Ala Gln Ser Ala Phe Gly Val Ala Val Ala
    255                260                265                270
gct gcg gtt gtg gca ttt ggt tac ttt tac gag atc cgg aag agg atg 2558
Ala Ala Val Val Ala Phe Gly Tyr Phe Tyr Glu Ile Arg Lys Arg Met
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Lys

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

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Arg Met Gly Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His
145                      150                      155                      160

Thr Leu Gly Arg Ala His Pro Glu Arg Ser Gly Phe Asp Gly Pro Trp
                      165                      170                      175

Thr Gln Glu Pro Leu Asn Phe Asp Asn Ser Tyr Phe Val Arg Glu Leu
                      180                      185                      190

Leu Lys Gly Glu Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr
                      195                      200                      205

Leu Leu Glu Asp Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala Asp
210                      215                      220

Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys Leu Ser
225                      230                      235                      240

Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val Ala Asp
                      245                      250                      255

Ser Thr Ile Leu Ala Gln Ser Ala Phe Gly Val Ala Val Ala Ala Ala
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Val Val Ala Phe Gly Tyr Phe Tyr Glu Ile Arg Lys Arg Met Lys
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                      1                      5

gaa cgg tgt ttg gga agc aga gct agt ggt gat ggt tta ctc tgg caa 100

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Glu Arg Cys Leu Gly Ser Arg Ala Ser Gly Asp Gly Leu Leu Trp Gln
10              15              20              25

tcg gaa ttg aga cct cac gct ggc ggt gat tat tcg atc gcg gtg gtt 148
Ser Glu Leu Arg Pro His Ala Gly Gly Asp Tyr Ser Ile Ala Val Val
              30              35              40

caa gcc aat tcc agg ctt gaa gat cag agt cag gtt ttc aca tct tct 196
Gln Ala Asn Ser Arg Leu Glu Asp Gln Ser Gln Val Phe Thr Ser Ser
              45              50              55

tct gct act tac gtc ggt gta tac gat ggt cat ggt gga cct gaa gct 244
Ser Ala Thr Tyr Val Gly Val Tyr Asp Gly His Gly Gly Pro Glu Ala
              60              65              70

tct aga ttc gtt aac aga cat ctc ttt cct tat atg cac a gtaagttata 294
Ser Arg Phe Val Asn Arg His Leu Phe Pro Tyr Met His L
              75              80              85

atcccactct tccttcccta aacttggtttt aggattcttt ctctttttga ctctttgact 354

acgtttttga tgggtcaaac ttatgagatc tctattacc tgcattttc aatattaaaa 414

gattcgaatt ttgctatgaa gttttggtct ttgtgaacat gttcaggttt gtaaattgcc 474

tcttgaattg attttgtagt catgttcttg ttagtgaaat ttacaggatt ggttttatga 534

ttgcag aa ttt gca aga gaa cat ggg gga tta tct gta gat gtt atc aaa 584
ys Phe Ala Arg Glu His Gly Gly Leu Ser Val Asp Val Ile Lys
              90              95              100

aag gca ttc aaa gaa aca gaa gaa gag ttt tgt ggt atg gtt aaa cga 632
Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys Gly Met Val Lys Arg
              105              110              115

tcc ctt ccc atg aaa ccg caa atg gct act gta gga tct tgc tgt ctt 680
Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly Ser Cys Cys Leu
              120              125              130

gtt ggt gca atc tct aat gac aca ctg tat gtt gct aat ctt ggg gac 728
Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val Ala Asn Leu Gly Asp
              135              140              145

tcg aga gcc gtt ctt gga agc gtt gtt tca ggg gtt gat agt aat aaa 776
Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly Val Asp Ser Asn Lys
              150              155              160              165

ggg gcc gta gct gaa cgg tta tct act gat cat aat gtt gct gtt gaa 824
Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His Asn Val Ala Val Glu
              170              175              180

gaa gtg aga aag gag gtt aag gca ctt aac cct gat gac tca caa atc 872
Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp Asp Ser Gln Ile
              185              190              195

gtc tta tac aca cgt gga gtt tgg cgg att aaa ggc att att cag 917
Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys Gly Ile Ile Gln

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200	205	210	
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		Val Ser Arg Ser Ile	215
ggg gat gta tac ttg aaa aaa ccg gag tat tac agg gac ccg att ttc	1319		
Gly Asp Val Tyr Leu Lys Lys Pro Glu Tyr Tyr Arg Asp Pro Ile Phe			
220 225 230			
cag cga cat gga aat ccc att cct ttg agg aga ccc gcg atg aca gcc	1367		
Gln Arg His Gly Asn Pro Ile Pro Leu Arg Arg Pro Ala Met Thr Ala			
235 240 245			
gaa ccc tcc att ata gta agg aag ctt aag cca cag gac ttg ttt ctg	1415		
Glu Pro Ser Ile Ile Val Arg Lys Leu Lys Pro Gln Asp Leu Phe Leu			
250 255 260 265			
ata ttt gca tca gat ggt ctc tgg gaa cat ctt agt gat gaa aca gcc	1463		
Ile Phe Ala Ser Asp Gly Leu Trp Glu His Leu Ser Asp Glu Thr Ala			
270 275 280			
gta gaa atc gtc ctc aaa cac cca aga act gtaagttttc cctaaactca	1513		
Val Glu Ile Val Leu Lys His Pro Arg Thr			
285 290			
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tgttctacag ggt att gcc cga aga ctt gta aga gct gct ctg gaa gaa	1622		
Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu			
295 300			
gcg gca aag aag aga gaa atg aga tat gga gat ata aag aaa ata gcc	1670		
Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala			
305 310 315 320			
aaa gga att cga cga cat ttc cat gac gac ata agc gtt att gta gtt	1718		
Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val			
325 330 335			
tat cta gat caa aac aaa acc agt tca tcg aat agt aaa ttg gtg aag	1766		
Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys			
340 345 350			
caa gga ggt atc acc gct cca ccg gat atc tac tca tta cac tct gat	1814		
Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp			
355 360 365			

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 370 375 380

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


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Pro Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg
      245                250                255
Lys Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu
      260                265                270
Trp Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His
      275                280                285
Pro Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu
      290                295                300
Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala
      305                310                315                320
Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
      325                330                335
Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
      340                345                350
Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp
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Glu Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
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Lys Glu Val Ile Asp Val Asp Cys Ser Glu Lys Lys Asp Phe Val Ile
      10              15              20

gat tgg tct tcc gct atg gat aag gaa gac gaa gtt ccc gag ctc gag 151
Asp Trp Ser Ser Ala Met Asp Lys Glu Asp Glu Val Pro Glu Leu Glu
      25              30              35

att gtt aat acc acc aaa cct act cct ccg cca ccg cca acg ttt ttc 199
Ile Val Asn Thr Thr Lys Pro Thr Pro Pro Pro Pro Pro Thr Phe Phe
      40              45              50

tcc gac gat caa acc gat tct ccg aaa ctc cta acc gat cgt gac ctc 247
Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu Thr Asp Arg Asp Leu
      55              60              65

gac gag cag cta gag cgt aaa aaa gcg atc ctg aca tta ggt ccg ggc 295
Asp Glu Gln Leu Glu Arg Lys Lys Ala Ile Leu Thr Leu Gly Pro Gly
      70              75              80              85

tta ccc gac aag ggt gag aaa att cga ctc aaa atc gct gat ctc gaa 343
Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys Ile Ala Asp Leu Glu
      90              95              100

gag gag aag cag c gtagagtttt agaaggctcg aaaatgggttc gcattctgat 396
Glu Glu Lys Gln A
      105

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Ser Asp Val Leu Pro Gln Gly Asn Ala Val Ser Lys Asp Thr Ser Arg
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125 130 135
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Lys Glu Val Ser Arg Ser Thr Phe Ser Ala Val Phe Ser Lys Pro Lys
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acg gat tct cag tca aag aaa gcc ttt ggt aaa gaa cta gaa gat ctg 1123
Thr Asp Ser Gln Ser Lys Lys Ala Phe Gly Lys Glu Leu Glu Asp Leu
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Gly Cys Glu Arg Arg Lys His Lys Ala Gly Arg Lys Pro Val Thr Arg
175 180 185
ctg agc aac ggg tgg cgg ttg ttg cca gat gta ggg aaa gct gag cac 1219
Leu Ser Asn Gly Trp Arg Leu Leu Pro Asp Val Gly Lys Ala Glu His
190 195 200
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Ser Ala Lys Gln Phe Asp Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys
205 210 215
aaa tcc aag gaa cct tat gga aag aaa agg ccc atg gaa tct tcg act 1315
Lys Ser Lys Glu Pro Tyr Gly Lys Lys Arg Pro Met Glu Ser Ser Thr
220 225 230
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Tyr Ser Leu Ile Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn
235 240 245 250
gac acc agt ggc cat gaa act cct ag gttcgtttcc aactgtttct 1409

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Asp Thr Ser Gly His Glu Thr Pro Ar
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g Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser
260 265 270

agg cgc cgt aag gtattcttgc ttactccgc tactgtatat ctgcaattg 1632
Arg Arg Arg Lys
275

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agttttcgaa cgtttgatc ctctctagat gaactgcagg atttatactt gccaggaaaa 1812

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Lys Ser

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Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu Ala Gln Pro Ser Thr
280 285 290

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Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gl
295 300

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y Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp
305 310 315

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Lys Thr Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSe
320 325 330 e

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g Phe Leu Gln Gln Gln Ile Ser S
h 335 340

tcg aat caa atc tct gct gat tgt cac ttc ttt aat acc tat ttc tac 2471
r Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe Asn Thr Tyr Phe T
345 350 355

aag aag ctc agt gac gct gtt acg tac aag gtgattagaa aaatgtgac 2521
 r Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys
 360 365

ctttaaaaat aattatctgt tggcattctt gcgattcaaa tttttatcat tggtatttat 2581

gtttaactggt ctatttatct tgccttttca atgaaatag ggg aat gac aag gat 2635
 Gly Asn Asp Lys A
 370

gcc ttc ttt gtg agg ttc agg cgg tgg tgg aag ggt att gat cta ttt 2683
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 375 380 385

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 e Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu
 390 395

ttctttttag cactctactt tgcatttttt cgcaagagtt ctcaagaatt cagattcttg 2788

taccatgttt cag t ctc cac tgg agc ctt gtg ata gtt tgc atc cct gat 2838
 r Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp
 e 400s 405 410

aag aaa gat gaa tgc ggg ttg act ata ctt cac ctt gat tct cta gga 2886
 Lys Lys Asp Glu Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly
 415 420 425

ctt cac tgc aga aaa tca att gtt gaa aat gta aaa ag gtgagatgct 2934
 Leu His Ser Arg Lys Ser Ile Val Glu Asn Val Lys Ar
 430 435

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gttcataaaa ggaaaaatta ttacactggc ttgaaaatgt acgacattta ctagtttcta 3054

tgtcaatttg ttgtag g ttt cta aaa gac gaa tgg aat tat ttg aat caa 3104
 g Phe Leu Lys Asp Glu Trp Asn Tyr Leu Asn Gln
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 Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys Val Trp Lys Asn
 455 460 465

ctc cct cgt agg atc agc gaa gct gtt gtt cag gtcagtcttt tacctttcta 3205
 Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln
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cactagaacc acaggaagtt caattcgtct tatgatatta ttctctttgt gcaaccag 3323

gtt ccg cag cag aaa aac gat ttt gat tgt ggt ccg ttt gtg ctc ttc 3371
 Val Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe
 480 485 490

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 Phe Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys
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 gac ctg gga atg gtgagtaatc tcaaaactctt ttcttgatag cgaatcacat 3471
 Asp Leu Gly Met
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 Phe Asp Lys
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 aag tgg ttt aga ccc gat gaa gcc tct gct ctg aga atc aaa atc cga 3574
 Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala Leu Arg Ile Lys Ile Arg
 520 525 530
 aac acg ctg atc gag cta ttc cgt gtc agt gac cag aca gag taa 3619
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 Pro Pro Thr Phe Phe Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu
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 Thr Asp Arg Asp Leu Asp Glu Gln Leu Glu Arg Lys Lys Ala Ile Leu
 65 70 75 80
 Thr Leu Gly Pro Gly Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys
 85 90 95
 Ile Ala Asp Leu Glu Glu Glu Lys Gln Arg Ser Asp Val Leu Pro Gln
 100 105 110
 Gly Asn Ala Val Ser Lys Asp Thr Ser Arg Gly Asn Ala Asp Ser Lys
 115 120 125
 Asp Thr Ser Arg Gln Gly Asn Ala Asp Ser Lys Glu Val Ser Arg Ser
 130 135 140
 Thr Phe Ser Ala Val Phe Ser Lys Pro Lys Thr Asp Ser Gln Ser Lys

145 150 155 160
 Lys Ala Phe Gly Lys Glu Leu Glu Asp Leu Gly Cys Glu Arg Arg Lys
 165 170 175
 His Lys Ala Gly Arg Lys Pro Val Thr Arg Leu Ser Asn Gly Trp Arg
 180 185 190
 Leu Leu Pro Asp Val Gly Lys Ala Glu His Ser Ala Lys Gln Phe Asp
 195 200 205
 Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys Lys Ser Lys Glu Pro Tyr
 210 215 220
 Gly Lys Lys Arg Pro Met Glu Ser Ser Thr Tyr Ser Leu Ile Asp Asp
 225 230 235 240
 Asp Asp Asp Asp Asp Asp Asp Asp Asn Asp Thr Ser Gly His Glu
 245 250 255
 Thr Pro Arg Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser Arg
 260 265 270
 Arg Arg Lys Lys Ser Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu
 275 280 285
 Ala Gln Pro Ser Thr Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gly
 290 295 300
 Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp Lys Thr
 305 310 315 320
 Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln
 325 330 e 335
 Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe
 340e 345 350
 Asn Thr Tyr Phe Tr Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys Gly
 355y 360 365
 Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly
 370 375 380
 Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r
 385 390 395u
 Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu
 400 405 410
 Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg
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ggc	act	cgc	ttg	aga	cca	ttg	act	ctc	agt	ttc	cca	aag	ccc	ctt	ggt	99
Gly	Thr	Arg	Leu	Arg	Pro	Leu	Thr	Leu	Ser	Phe	Pro	Lys	Pro	Leu	Val	
			15						20					25		
gat	ttt	gct	aat	aaa	ccc	atg	atc	ctt	cat	cag	ata	gag	gct	ctt	aag	147
Asp	Phe	Ala	Asn	Lys	Pro	Met	Ile	Leu	His	Gln	Ile	Glu	Ala	Leu	Lys	
			30				35						40			
gca	gtt	gga	gtt	gat	gaa	gtg	gtt	ttg	gcc	atc	aat	tat	cag	cca	gag	195
Ala	Val	Gly	Val	Asp	Glu	Val	Val	Leu	Ala	Ile	Asn	Tyr	Gln	Pro	Glu	
		45					50					55				
gtg	atg	ctg	aac	ttc	ttg	aag	gac	ttt	gag	acc	aag	ctg	gaa	atc	aaa	243
Val	Met	Leu	Asn	Phe	Leu	Lys	Asp	Phe	Glu	Thr	Lys	Leu	Glu	Ile	Lys	
	60					65					70					
atc	act	tgc	tca	caa	gag	acc	gag	cca	cta	ggt	acc	gct	ggt	cct	ctg	291
Ile	Thr	Cys	Ser	Gln	Glu	Thr	Glu	Pro	Leu	Gly	Thr	Ala	Gly	Pro	Leu	
75					80					85				90		
gct	cta	gcg	aga	gac	aaa	ttg	ctt	gat	gga	tct	gga	gag	ccc	ttc	ttt	339
Ala	Leu	Ala	Arg	Asp	Lys	Leu	Leu	Asp	Gly	Ser	Gly	Glu	Pro	Phe	Phe	

	95	100	105	
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Val Leu Asn Ser Asp Val Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu				
	110	115	120	
gag ttt cac aaa tct cac ggt ggg gaa gcc tcc ata atg gta aca aag				435
Glu Phe His Lys Ser His Gly Gly Glu Ala Ser Ile Met Val Thr Lys				
	125	130	135	
gtg gat gaa ccg tcg aaa tat gga gtg gtt gtt atg gaa gaa agc act				483
Val Asp Glu Pro Ser Lys Tyr Gly Val Val Val Met Glu Glu Ser Thr				
	140	145	150	
gga aga gtg gag aag ttt gtg gaa aag cca aaa ctg tat gta ggt aac				531
Gly Arg Val Glu Lys Phe Val Glu Lys Pro Lys Leu Tyr Val Gly Asn				
	155	160	165	170
aag atc aac gct ggg att tat ctt ctg aac cca tct gtt ctt gat aag				579
Lys Ile Asn Ala Gly Ile Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys				
	175	180	185	
att gag cta aga ccg act tca atc gaa aaa gag act ttc cct aag att				627
Ile Glu Leu Arg Pro Thr Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile				
	190	195	200	
gca gca gcg caa ggg ctc tat gct atg gtg cta cca ggg ttt tgg atg				675
Ala Ala Ala Gln Gly Leu Tyr Ala Met Val Leu Pro Gly Phe Trp Met				
	205	210	215	
gac att ggg caa ccc cgt gac tac ata acg ggt ttg aga ctc tac tta				723
Asp Ile Gly Gln Pro Arg Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu				
	220	225	230	
gac tcc ctt agg aag aaa tct cct gcc aaa tta acc agt ggg cca cac				771
Asp Ser Leu Arg Lys Lys Ser Pro Ala Lys Leu Thr Ser Gly Pro His				
	235	240	245	250
ata gtt ggg aat gtt ctt gtt gac gaa acc gct aca att ggg gaa gga				819
Ile Val Gly Asn Val Leu Val Asp Glu Thr Ala Thr Ile Gly Glu Gly				
	255	260	265	
tgt ttg att gga cca gac gtt gcc att ggt cca ggc tgc att gtt gag				867
Cys Leu Ile Gly Pro Asp Val Ala Ile Gly Pro Gly Cys Ile Val Glu				
	270	275	280	
tca gga gtc aga ctc tcc cga tgc acg gtc atg cgt gga gtc cgc atc				915
Ser Gly Val Arg Leu Ser Arg Cys Thr Val Met Arg Gly Val Arg Ile				
	285	290	295	
aag aag cat gcg tgt atc tcg agc agt atc atc ggg tgg cac tca acg				963
Lys Lys His Ala Cys Ile Ser Ser Ser Ile Ile Gly Trp His Ser Thr				
	300	305	310	
gtt ggt caa tgg gcc agg atc gag aac atg acg atc ctc ggt gag gat				1011
Val Gly Gln Trp Ala Arg Ile Glu Asn Met Thr Ile Leu Gly Glu Asp				
	315	320	325	330

gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059
 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro
 335 340 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107
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 350 355 360

aa 1109

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

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg
 210 215 220
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys
 225 230 235 240
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu
 245 250 255
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp
 260 265 270
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser
 275 280 285
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile
 290 295 300
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg
 305 310 315 320
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu
 325 330 335
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 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe
 15 20 25 30
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146
 Arg Ser Pro Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly
 35 40 45
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

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tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914
Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala
      290      295      300

tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962
Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser
      305      310      315

att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010
Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
      320      325      330

ggg gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055
Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
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Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val
      35      40      45

Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile
      50      55      60

Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly
      65      70      75      80

Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu
      85      90      95

Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser
      100      105      110

Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
      115      120      125

Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
      130      135      140

Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
      145      150      155      160

Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
      165      170      175

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Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
 180 185 190
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
 195 200 205
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
 210 215 220
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
 225 230 235 240
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
 245 250 255
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
 260 265 270
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
 275 280 285
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
 290 295 300
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
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 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg
 20 25 30
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly
 35 40 45

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tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg 191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met
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aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga 239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg
      65                      70                      75

gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga 287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg
      80                      85                      90                      95

aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg 335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu
      100                      105                      110

aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc 383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr
      115                      120                      125

gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt 431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg
      130                      135                      140

aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac 479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn
      145                      150                      155

act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa 527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys
      160                      165                      170                      175

gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag 575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys
      180                      185                      190

aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct 623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser
      195                      200                      205

gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag 671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln
      210                      215                      220

cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct 719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser
      225                      230                      235

tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca 768
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Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
 35           40           45

Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
 50           55           60

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
 65           70           75           80

Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
 85           90           95

Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
100          105          110

Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
115          120          125

His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
130          135          140

Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
145          150          155          160

Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
165          170          175

Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
180          185          190

Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
195          200          205

Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
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ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167
 Thr Glu Lys Ala Phe Leu Lys
 5 10

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 Gln Pro Lys Val Phe Leu Se
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
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aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
 35 40 45

gcc att gat g gtatgtttta gcttttaact cgttataata gataaggaac 423
 Ala Ile Asp G
 50

tcttggattg tgttgttcat atagtcgata gatttcaaat gctattttgt cttgtagaat 483

cttaagcttt ggttttagtga gttctgattc ttcagcttta tctggatcta cactactgtt 543

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gttattgtgt atttgtgtgg aacag ga gct tac gtt gac aag aaa tgc ccc 714
                               ly Ala Tyr Val Asp Lys Lys Cys Pro
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Phe Thr Gly Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys
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cac agt gcg aaa atg cag agg acc att atc gtg cga agg gat tac ctt 810
His Ser Ala Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu
                               80                               85                               90
cac ttt gtg aag aag tat cag ag gtaaattcat acattctcat acttctttcc 863
His Phe Val Lys Lys Tyr Gln Ar
                               95
atagagtctt acacattgat gtttaagaaa gtaatatcct ttttgttctt ag g tat 919
                               g Tyr
                               100
gag aag agg cat tca aac att ccg gct cat gtc tca cca tgc ttc cgt 967
Glu Lys Arg His Ser Asn Ile Pro Ala His Val Ser Pro Cys Phe Arg
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gtt aag gaa gga gac cat atc atc att ggc caa tgc ag gttatgatct 1015
Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln Cys Ar
                               120                               125
gattcaaacc tacaaattgt ctccattgat tctgattatc gtgaatttgt tttgatcttt 1075
ttgtttgtta atgattgata atttcag g cca ttg tgc aag aca gtg agg ttc 1127
                               g Pro Leu Ser Lys Thr Val Arg Phe
                               130                               135
aat gtg ttg aag gtg ata cca gct ggg tct tct tct tca ttt gga aag 1175
Asn Val Leu Lys Val Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys
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 35 40 45
 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly
 50 55 60
 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala
 65 70 75 8
 Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val
 85 90 95
 Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His
 100 105 110
 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly
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 15 20 25
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 Asp Gly Ser Val Asp Phe Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr
 30 35 40
 gga aac tgg aaa gct tgt cct ttt att ctt ggt aat gaa tgt tgt gag 196
 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu
 45 50 55

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agg cta gct tac tat ggt att gct ggg aat tta atc act tac ctc acc 244
Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr
    60                65                70

act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca 292
Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr
    75                80                85                90

tgg caa ggg act tgt tat ctc act cct ctc att gga gct gtt ctg gct 340
Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala
    95                100                105

gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att 388
Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile
    110                115                120

tat ttc atc ggg atg tct gcg tta act ctt tca gct tca gtt ccg gca 436
Tyr Phe Ile Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala
    125                130                135

ttg aag cca gcg gaa tgt att ggt gac ttt tgt cca tct gca acg cca 484
Leu Lys Pro Ala Glu Cys Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro
    140                145                150

gct cag tat gcg atg ttc ttt ggt ggg ctt tac ctg atc gct ctt gga 532
Ala Gln Tyr Ala Met Phe Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly
    155                160                165                170

act gga ggt atc aaa ccg tgt gtc tca tcc ttc ggt gcc gat cag ttt 580
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe
    175                180                185

gat gac acg gac tct cgg gaa cga gtt aga aaa gct tcg ttc ttt aac 628
Asp Asp Thr Asp Ser Arg Glu Arg Val Arg Lys Ala Ser Phe Phe Asn
    190                195                200

tgg ttt tac ttc tcc atc aat att gga gca ctt gtg tca tct agt ctt 676
Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu
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cta gtt tgg att caa gag aat cgg ggg tgg ggt tta ggg ttt ggg ata 724
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    220                225                230

cca aca gtg ttc atg gga cta gcc att gca agt ttc ttc ttt ggc aca 772
Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr
    235                240                245                250

cct ctt tat agg ttt cag aaa cct gga gga agc cct ata act cgg att 820
Pro Leu Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile
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tcc caa gtc gtg gtt gct tcg ttc cgg aaa tcg tct gtc aaa gtc cct 868
Ser Gln Val Val Val Ala Ser Phe Arg Lys Ser Ser Val Lys Val Pro
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gaa gac gcc aca ctt ctg tat gaa act caa gac aag aac tct gct att 916

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Ala Gly Ser Arg Lys Ile	Glu His Thr Asp Asp Cys Gln Tyr Leu Asp	
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aaa gcc gct gtt atc tca gaa gaa gaa tcg aaa tcc gga gat tat tcc		1012
Lys Ala Ala Val Ile	Ser Glu Glu Ser Lys Ser Gly Asp Tyr Ser	
315	320	325
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Leu Ile Arg Met Phe Pro Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala		
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gta tac gca caa atg tcc aca atg ttt gtt caa caa ggc cga gcc atg		1156
Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met		
365	370	375
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Asn Cys Lys Ile Gly Ser Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr		
380	385	390
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Phe Asp Thr Ala Ser Val Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe		
395	400	405
atc gtt ccc tta gca aga aag ttc aca gga gta gac aaa gga ttc act		1300
Ile Val Pro Leu Ala Arg Lys Phe Thr Gly Val Asp Lys Gly Phe Thr		
415	420	425
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Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met		
430	435	440
gca gct gca gct atc gtc gaa atc atc cgt ctc cat atg gcc aac gat		1396
Ala Ala Ala Ala Ile Val Glu Ile Ile Arg Leu His Met Ala Asn Asp		
445	450	455
ctt gga tta gtc gag tca gga gcc cca gtt ccc ata tcc gtc ttg tgg		1444
Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp		
460	465	470
cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc		1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe		
475	480	485
atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga		1540
Ile Gly Gln Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg		
495	500	505
agc ttg tgc agt gcc tta gct ctt ttg acc aat gca ctt ggt aac tac		1588
Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr		

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          510          515          520
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    Leu Ser Ser Leu Ile Leu Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn
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    ggg caa gaa ggt tgg att tcg gat aat ctc aat tca ggt cat ctc gat 1684
    Gly Gln Glu Gly Trp Ile Ser Asp Asn Leu Asn Ser Gly His Leu Asp
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    tac ttc ttc tgg ctc ttg gct ggt ctt agc ctt gtg aac atg gcg gtt 1732
    Tyr Phe Phe Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val
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    tac ttc ttc tct gct gct agg tat aag caa aag aaa gct tcg tcg tag 1780
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    Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr Gly Asn Trp Lys Ala Cys
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    Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly
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    Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly
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    Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg
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    Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser
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    Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro Ala Gln Tyr Ala Met Phe
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 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
 180 185 190
 Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
 195 200 205
 Asn Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp Ile Gln Glu
 210 215 220
 Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly
 225 230 235 240
 Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr Pro Leu Tyr Arg Phe Gln
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 Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala
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 Ser Phe Arg Lys Ser Ser Val Lys Val Pro Glu Asp Ala Thr Leu Leu
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 Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile Ala Gly Ser Arg Lys Ile
 290 295 300
 Glu His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser
 305 310 315 320
 Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser Asn Ser Trp Arg Leu Cys
 325 330 335
 Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
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 Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser
 355 360 365
 Thr Met Phe Val Gln Gln Gly Arg Ala Met Asn Cys Lys Ile Gly Ser
 370 375 380
 Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val
 385 390 395 400
 Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe Ile Val Pro Leu Ala Arg
 405 410 415
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 Glu Ile Ile Arg Leu His Met Ala Asn Asp Leu Gly Leu Val Glu Ser
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 ggt ctt agc gga ttc gtc ggg aag att aac tct agt atc cgt agc tct 148
 Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser
 30 35 40
 cga att ggg ctc ttt tct aag ccg cct cca ggg ctt cct gct cct aga 196
 Arg Ile Gly Leu Phe Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg
 45 50 55
 aaa gaa gaa gcg ccg tcg att cgg tgg agg aaa ggg gaa tta atc ggt 244
 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly
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Glu	Leu	Leu	Ala	Ile	Lys	Gln	Val	Leu	Ile	Ala	Pro	Ser	Ser	Ala	Ser	
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Lys	Glu	Lys	Thr	Gln	Gly	His	Ile	Arg	Glu	Leu	Glu	Glu	Glu	Val	Gln	
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Leu	Leu	Lys	Asn	Leu	Ser	His	Pro	Asn	Ile	Val	Arg	Tyr	Leu	Gly	Thr	
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Val	Arg	Glu	Ser	Asp	Ser	Leu	Asn	Ile	Leu	Met	Glu	Phe	Val	Pro	Gly	
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Gly	Ser	Ile	Ser	Ser	Leu	Leu	Glu	Lys	Phe	Gly	Ser	Phe	Pro	Glu	Pro	
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Val	Ile	Ile	Met	Tyr	Thr	Lys	Gln	Leu	Leu	Leu	Gly	Leu	Glu	Tyr	Leu	
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His	Asn	Asn	Gly	Ile	Met	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu	
		190					195					200				
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Val	Asp	Asn	Lys	Gly	Cys	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Ser	Lys	
	205				210						215					
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Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly	
	220				225				230					235		
acg	cct	tat	tgg	atg	gct	cct	gaa	gtc	att	ctc	cag	act	ggc	cat	agc	772
Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Gln	Thr	Gly	His	Ser	
			240					245					250			
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Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala	
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Thr	Gly	Lys	Pro	Pro	Trp	Ser	Glu	Gln	Tyr	Gln	Gln	Phe	Ala	Ala	Val	
		270					275					280				
ctt	cat	att	ggc	aga	aca	aaa	gct	cat	cct	cca	att	cca	gaa	gac	ctc	916
Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu	
		285				290					295					
tca	cca	gag	gct	aaa	gac	ttt	cta	atg	aaa	tgc	tta	cac	aaa	gaa	cca	964
Ser	Pro	Glu	Ala	Lys	Asp	Phe	Leu	Met	Lys	Cys	Leu	His	Lys	Glu	Pro	

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Ser Leu Arg Leu Ser Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr	320	325	330	
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Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu	335	340	345	
tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata				1108
Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile	350	355	360	
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Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys	365	370	375	
gaa ctg gga agc ttg agg agt tcc att ata tac cca cag aag tca aat				1204
Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn	380	385	390	395
aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag				1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln	400	405	410	
acc gat atg gat gat ctc tgc aac att gaa tca gtc aga aac aat gtt				1300
Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val	415	420	425	
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Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp	430	435	440	
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Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met	445	450	455	
aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act				1444
Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr	460	465	470	475
gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct				1492
Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser	480	485	490	
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Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser	495	500	505	
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Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu	510	515	520	
ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca				1636
Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala	525	530	535	

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aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732
Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp
560          565          570

gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
575          580          585

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Arg Val Met Gln Ser Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr
590          595          600

aag aag gga gta aat aat agc cgt tgt ttc tca gag ata cgt cgg aag 1876
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605          610          615

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620          625          630          635

cga cac gct ggt gca gga ggg aag act cca tta tca ggc cac aaa gga 1972
Arg His Ala Gly Ala Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
640          645          650

tag tgaacggct 1984

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<210> 34
 <211> 651
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 34
Met Gln Asp Ile Leu Gly Ser Val Arg Arg Ser Leu Val Phe Arg Ser
 1          5          10          15

Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly Gly Leu Ser Gly Phe
20          25          30

Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser Arg Ile Gly Leu Phe
35          40          45

Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg Lys Glu Glu Ala Pro
50          55          60

Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly
65          70          75          80

Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile
85          90          95

```

Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser Lys Glu Lys Thr Gln
 100 105 110
 Gly His Ile Arg Glu Leu Glu Glu Val Gln Leu Leu Lys Asn Leu
 115 120 125
 Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Ser Asp
 130 135 140
 Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser
 145 150 155 160
 Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro Val Ile Ile Met Tyr
 165 170 175
 Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn Asn Gly Ile
 180 185 190
 Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly
 195 200 205
 Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys Lys Val Val Glu Leu
 210 215 220
 Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met
 225 230 235 240
 Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile
 245 250 255
 Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala Thr Gly Lys Pro Pro
 260 265 270
 Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg
 275 280 285
 Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys
 290 295 300
 Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser
 305 310 315 320
 Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu
 325 330 335
 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile
 340 345 350
 Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile Asn Ser Leu Ile Arg
 355 360 365
 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu
 370 375 380
 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly
 385 390 395 400

Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp
 405 410 415
 Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr
 420 425 430
 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp
 435 440 445
 Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met Lys Ser Lys Ser Asn
 450 455 460
 Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr Gly Val Pro Cys Asp
 465 470 475 480
 Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp
 485 490 495
 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys
 500 505 510
 Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu Leu Glu Glu Phe His
 515 520 525
 Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala Leu Gly Asp Thr Asn
 530 535 540
 Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser Lys Thr Pro Lys Arg
 545 550 555 560
 Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp Ala Met Pro Ser Pro
 565 570 575
 Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser Arg Val Met Gln Ser
 580 585 590
 Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn
 595 600 605
 Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu
 610 615 620
 Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala
 625 630 635 640
 Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
 645 650

<210> 35

<211> 1736

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1605)

<400> 35

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atg ccc cct cct aag atg ctt cca cca acg gca agg gat tca gta gca 48
Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala
  1             5             10             15

ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg 96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp
             20             25             30

agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct 144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro
             35             40             45

cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg 192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
             50             55             60

ccc cct cct cgt cag cct cca cgt cct cca aca gca cgg tgg tca gcg 240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
             65             70             75             80

atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg ccg agt aga 288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
             85             90             95

cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg 336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
             100             105             110

cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa 384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
             115             120             125

ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg 432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
             130             135             140

gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc 480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
             145             150             155             160

gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg 528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
             165             170             175

aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg 576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
             180             185             190

ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac 624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
             195             200             205

ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc 672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly

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210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser 225 230 235 240			720
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile 245 250 255			768
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr 260 265 270			816
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val 275 280 285			864
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu 290 295 300			912
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly 305 310 315 320			960
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggg Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly 325 330 335			1008
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggc gca Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala 340 345 350			1056
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile 355 360 365			1104
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala 370 375 380			1152
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn 385 390 395 400			1200
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg 405 410 415			1248
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr 420 425 430			1296
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr 435 440 445			1344

```

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
450 455 460

gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465 470 475 480

agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
485 490 495

gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Pro
500 505 510

ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
515 520 525

gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
Gly Arg Arg Trp Arg Glu
530 535

tggaccgggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695

taaaaaaaaaac caacaaaaaaaa aaaaaaaaaaac aaaaaaaaaa a 1736

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<210> 36
 <211> 534
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 36
Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala
1 5 10 15

Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Ala Arg Trp
20 25 30

Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro
35 40 45

Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
50 55 60

Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
65 70 75 80

Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
85 90 95

Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
100 105 110

```


Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
 115 120 125
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
 130 135 140
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
 145 150 155 160
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
 165 170 175
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
 180 185 190
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
 195 200 205
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly
 210 215 220
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
 225 230 235 240
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
 245 250 255
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
 260 265 270
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
 275 280 285
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
 290 295 300
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
 305 310 315 320
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
 325 330 335
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
 340 345 350
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
 355 360 365
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
 370 375 380
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
 385 390 395 400
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
 405 410 415

```

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
      420                      425                      430
Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
      435                      440                      445
Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
      450                      455                      460
Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
      465                      470                      475                      480
Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
      485                      490                      495
Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
      500                      505                      510
Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
      515                      520                      525
Gly Arg Arg Trp Arg Glu
      530

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<210> 37
<211> 508
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (18)..(77)

<220>
<221> CDS
<222> (156)..(314)

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<220>
<221> CDS
<222> (374)..(493)

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<400> 37
gaagaaaatc tatcatc atg caa gtg gct gac ata tcc tta cag ggc gat   50
              Met Gln Val Ala Asp Ile Ser Leu Gln Gly Asp
              1                      5                      10

gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg   97
Ala Lys Lys Gly Ala Asn Leu Phe Lys
              15                      20

ccgctgaaaa ttctcaggc gcattctatc ccgcagaact ttctgacca ctttgtag   155

acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag   203
Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys
              25                      30                      35

```

```

att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
      40              45              50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
      55              60              65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
Lys Asp Asp Thr Leu
      70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
      Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
              75              80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
      85              90              95              100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503
Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
      105              110

acccc 508

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<210> 38
 <211> 112
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 38
Met Gln Val Ala Asp Ile Ser Leu Gln Gly Asp Ala Lys Lys Gly Ala
  1              5              10              15

Asn Leu Phe Lys Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly
      20              25              30

Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
      35              40              45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
      50              55              60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
      65              70              75              80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
      85              90              95

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

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<210> 39
 <211> 5156
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(609)

<220>
 <221> CDS
 <222> (686)..(841)

<220>
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 <222> (933)..(1040)

<220>
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 <222> (1130)..(1240)

<220>
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 <222> (1341)..(2729)

<220>
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 <222> (2772)..(2984)

<220>
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 <222> (4112)..(4200)

<220>
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 <222> (4241)..(4332)

<220>
 <221> CDS
 <222> (4478)..(4521)

<220>
 <221> CDS
 <222> (5088)..(5156)

<400> 39
 atg gca ccg aca cca tct tct tca aga tca aat caa act caa tac acc 48
 Met Ala Pro Thr Pro Ser Ser Ser Arg Ser Asn Gln Thr Gln Tyr Thr
 1 5 10 15
 tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
 20 25 30
 acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
 35 40 45

```

gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192
Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
50 55 60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240
Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
65 70 75 80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288
Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
85 90 95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336
Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
100 105 110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384
Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
115 120 125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
130 135 140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
145 150 155 160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
165 170 175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
180 185 190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtttc ttgattgata 629
Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys
195 200

actttagtat acattgaatt ggcttttaag gtgtgtactt tgttgttttg ttacag gtg 688
Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736
Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser
205 210 215 220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784
Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
225 230 235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832
Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
240 245 250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt 881

```

His Cys Ile
255

atgcagctta tctctgtttt aacttactag tgtggttgtt tctttttgta g atc ata 938
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala
260 265 270

ggc tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys
275 280 285

atg caa gtaaatgttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090
Met Gln
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144
Thr Ala Lys Ile Asn
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtgtt gcttgggttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355
Asp Ser Phe Glu Asp
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
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aggaggttaaa tacattatac tgcag gtt atc cac gct gcc cgg gca aat gct 4056
Val Ile His Ala Ala Arg Ala Asn Ala
305 310
act cat aac cat gga cta gat cct gac cgt ctc ctt gtt g gtatgtaaaa 4106
Thr His Asn His Gly Leu Asp Pro Asp Arg Leu Leu Val A
315 320 325
ctgattctgg atccctgatt tccttgtttt acatttaaaa agagaacgtg atattttaga 4166
gagttcgccg attggtactt taaggaagca aacatgatat gccagaacga tgtatttcat 4226
ctaagcttgt gatatgtgat tgcag cg gaa gca ttt gtt ggg aag gga ctg 4277
la Glu Ala Phe Val Gly Lys Gly Leu
330 335
ttt ggg aag aag gta gct tac cat gca aaa gga aga agc ggg att ata 4325
Phe Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile
340 345 350
tca ata ccc cgg tgt cgc cta aca gtc ata gtt aga gag acg act cca 4373
Ser Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro
355 360 365
gag gaa gaa gct gag att gca agg ctc aaa gtt cac aat ttt aag aag 4421
Glu Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys
370 375 380
aaa agc aaa cgg gag aga cag ctt gta cca cac aag ctc atc gag aca 4469
Lys Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr
385 390 395
agt cca ata tgg aac cgc aga ggt acc aaa gcc aat cat cgg tcc tca 4517
Ser Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser
400 405 410 415
gag ttg gtacggctgt ctactagta tctttgttcc cgcaattgca acaagagctt 4573
Glu Leu
ctctgttatg gtaaattgct tttttttttg gttttggttt gatattgtat tggaactcta 4633
taggacctgt ttgcttcttg tattcaataa acatgttccc agagaggaaa cttcacttaa 4693
caaaagcgtc tctgtttttc tccattctgt ttctggag gtg tta aca atc att ttg 4749
Val Leu Thr Ile Ile Leu
420
gat gta act tgt gtt gga aac atg gaa aaa aat cgt ctg gat aat ttg 4797
Asp Val Thr Cys Val Gly Asn Met Glu Lys Asn Arg Leu Asp Asn Leu
425 430 435
acg aat caa aac aac att tat cat cat aat ccc gaa g gtccataatt 4844
Thr Asn Gln Asn Asn Ile Tyr His His Asn Pro Glu G
440 445 450

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tttatcagtt tgttccactt cttaatgcaa tttttggata ttaaaagaat aaatgaatga 4904
atatacatat gcattttggtt tgttgagaat atttatttag tcattttattt aagaaattta 4964
tattttaatt ttttattatt aatatgatat ttgtttgtc actatgttac aacataattc 5024
aattttaata tcattataat tgatagtaat aataataaat aacagtcaca ggccccctacc 5084
atcatcccaa aatgattcat gcaatttagt catcaaatac atacaatctt atatacaaaa 5144
gaatcacaca gcatgtataa actaatagta tagaaattcg attaaaaaat actcccaggc 5204
tagtttttcc accttccatg aagaatagaa tcataagttt ggaaggaatt agaataagaa 5264
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acagagacta acaacacaac accactagag accccagcaa tgaagccttt agacttcaaa 6404
acagagtcac ctgacaattt aaacgaaggt agattcctag tgatcaaagc atcaccaatg 6464
gagaaattgg agttactaaa actccatgag agaatcctat ggctctgcac tagttgtcct 6524

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gtggaggcag tgaatccaac gaacatatca tcaagtaaga ctccagttag atttaatgga 6584
atgcttatga gtggtcttat gggctttcta gagctagctc tagccatcgt gacattgac 6644
gctgacccat taaactcgat ccacgcctga taattctcgc cactgttaag cttcagctcc 6704
gtgaatctct ggccgtctct gcctccatag aa acc tgc agt ttc aga tgc aac 6757
                               lu Thr Cys Ser Phe Arg Cys Asn
                               455
gga agt gag aga att gac gtc gac gcc gac gtg gtt gtc gtt gat gtc 6805
Gly Ser Glu Arg Ile Asp Val Asp Ala Asp Val Val Val Val Asp Val
460                               465                               470                               475
gtt gaa ctc ttg gtt agc gaa aac atc gaa ttc aac ggc gaa gat tcg 6853
Val Glu Leu Leu Val Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser
                               480                               485                               490
gct att ggg gtc acc gtt att ggt gaa gtt gaa gag gcc gag atg ctg 6901
Ala Ile Gly Val Thr Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu
                               495                               500                               505
aga tga gcttgcggcg gaggtttcgg agaaaggaag gaagacgaag gcgaagccgt 6957
Arg
ggc 6960

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<210> 42
 <211> 508
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 42
Met Gly Leu Val Met Arg Phe Asp Leu Tyr Leu Met Phe Val Met Leu
  1                               5                               10                               15
Met Gly Leu Gly Phe Thr Ile Ser Asn Gly Tyr Lys Phe Tyr Val Gly
                               20                               25                               30
Gly Lys Asp Gly Trp Val Pro Thr Pro Ser Glu Asp Tyr Ser His Trp
                               35                               40                               45
Ser His Arg Asn Arg Phe Gln Val Asn Asp Thr Leu His Phe Lys Tyr
                               50                               55                               60
Ala Lys Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn
  65                               70                               75                               80
Thr Cys Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser
                               85                               90                               95
Leu Phe Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn
                               100                              105                              110
Ser Gln Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser
                               115                              120                              125

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Thr Val His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser
 130 135 140
 Pro Val His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu
 145 150 155 160
 Pro Ser Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr
 165 170 175
 Ala Pro Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu Val
 180 185 190
 Val Asn Ser Ile Ile Lys Pro Ile Asp Ser Phe Leu Leu Lys Ser Leu
 195 200 205
 Pro Leu Val Val Asp Val Ala Val Gly Ile Ser Thr Ser Arg Gln Leu
 210 215 220
 Gln Ala Ser Glu Glu Pro Val Ser Ser Pro Leu Ser Ser Pro Ala Leu
 225 230 235 240
 Leu Gly Ser Gly Lys Glu Glu Glu Gln Lys Ile Ile Pro Lys Arg Gln
 245 250 255
 Lys Val Gln Ala Val Leu Lys Ser Ile Lys Gln Ser Pro Lys Lys Val
 260 265 270
 Asn Leu Val Ala Ala Leu Val Arg Gly Met Arg Val Glu Asp Ala Leu
 275 280 285
 Ile Gln Leu Gln Val Thr Val Lys Arg Ala Ala Gln Thr Val Tyr Arg
 290 295 300
 Val Ile His Ala Ala Arg Ala Asn Ala Thr His Asn His Gly Leu Asp
 305 310 315 320
 Pro Asp Arg Leu Leu Val Ala Glu Ala Phe Val Gly Lys Gly Leu Phe
 325 330 335
 Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile Ser
 340 345 350
 Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro Glu
 355 360 365
 Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys Lys
 370 375 380
 Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr Ser
 385 390 395 400
 Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser Glu
 405 410 415
 Leu Val Leu Thr Ile Ile Leu Asp Val Thr Cys Val Gly Asn Met Glu
 420 425 430

Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His
 435 440 445
 Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile
 450 455 460
 Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val
 465 470 475 480
 Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser Ala Ile Gly Val Thr
 485 490 495
 Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg
 500 505

<210> 43
 <211> 729
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (26)..(718)

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 Met Phe Ala Asn Lys Phe Pro Gly Val
 1 5
 tac gca gcc act tgt ctc tcc gtc gaa gac gcc gtc aac gct cga tca 100
 Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser
 10 15 20 25
 ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro
 30 35 40
 gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys
 45 50 55
 tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct 244
 Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser
 60 65 70
 tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca 292
 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser
 75 80 85
 acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct 340
 Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser
 90 95 100 105
 tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac 388

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Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp
      110                      115                      120
atc atg ccg gga ggc tcg atg aag atc gtt aga gag acg ccg acg tcg 436
Ile Met Pro Gly Gly Ser Met Lys Ile Val Arg Glu Thr Pro Thr Ser
      125                      130                      135

gcg att gta aga ttc aaa gcg gga agt gtg gaa ccg gcg cat cac cac 484
Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His
      140                      145                      150

aca ttc ggc cat gac ctt gta gtc ata aag gga aag aaa agt gtg tgg 532
Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp
      155                      160                      165

aat ctg agc aag aag gag aga gct gat ctc gtt gac ggc gat tac cta 580
Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu
      170                      175                      180

ttc act ccc gcc ggt gat gtt cac cga gtc aaa tat cac gaa gac act 628
Phe Thr Pro Ala Gly Asp Val His Arg Val Lys Tyr His Glu Asp Thr
      190                      195                      200

gag ttc ttc atc act tgg gat ggc cat tgg gac ata ttc ctt gac gaa 676
Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu
      205                      210                      215

gac ctc gaa act gca aag aaa gcc atc gaa gaa gaa gct tga 718
Asp Leu Glu Thr Ala Lys Lys Ala Ile Glu Glu Glu Ala
      220                      225                      230

aggtgtaaac t 729

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<210> 44
<211> 230
<212> PRT
<213> Arabidopsis thaliana

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Met Phe Ala Asn Lys Phe Pro Gly Val Tyr Ala Ala Thr Cys Leu Ser
  1                      5                      10                      15

Val Glu Asp Ala Val Asn Ala Arg Ser Ile Ser Asn Cys Asn Val Leu
      20                      25                      30

Ala Phe Ser Gly Ile Lys Thr Ser Pro Glu Thr Ala Leu Glu Ile Phe
      35                      40                      45

Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly
      50                      55                      60

Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu
      65                      70                      75                      80

Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr
      85                      90                      95

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Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala
 100 105 110
 Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met
 115 120 125
 Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala
 130 135 140
 Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val
 145 150 155 160
 Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg
 165 170 175
 Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val
 180 185 190
 His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp
 195 200 205
 Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys
 210 215 220
 Ala Ile Glu Glu Glu Ala
 225 230

<210> 45
 <211> 1203
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(1193)

<400> 45
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 Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln
 1 5 10
 cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98
 Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro
 15 20 25
 agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146
 Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys
 30 35 40 45
 tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194
 Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr
 50 55 60
 cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242


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Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp
      65              70              75
gtt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt 290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser
      80              85              90
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat 338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His
      95              100             105
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta 386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val
     110             115             120             125
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct 434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro
      130             135
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct 482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala
      145             150             155
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt 530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly
      160             165             170
ggg ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat 578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His
      175             180             185
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc 626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala
     190             195             200             205
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag 674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu
      210             215             220
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt 722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val
      225             230             235
ggg tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct 770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala
      240             245             250
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg 818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met
     255             260             265
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat 866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His
     270             275             280             285
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata 914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile

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                290                295                300
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg 962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met
                305                310                315

tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg 1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp
                320                325                330

ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct 1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro
                335                340                345

gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc 1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe
                350                355                360                365

ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga 1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly
                370                375                380

att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaata 1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr
                385                390

<210> 46
<211> 393
<212> PRT
<213> Arabidopsis thaliana

<400> 46
Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln Pro Ile Ser
 1                5                10                15

Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro Ser Asn Leu
                20                25                30

Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile
 35                40                45

Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val
 50                55                60

Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly
 65                70                75                80

Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu
                85                90                95

Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr
                100                105                110

Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu
                115                120                125

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Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln
 130 135 140
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile
 145 150 155 160
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser
 165 170 175
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu
 180 185 190
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His
 195 200 205
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys
 210 215 220
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val
 225 230 235 240
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val
 245 250 255
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro
 260 265 270
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu
 275 280 285
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val
 290 295 300
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg
 305 310 315 320
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu
 325 330 335
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala
 340 345 350
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe
 355 360 365
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn
 370 375 380
 Ser Tyr Thr Asp Glu Thr Asp His Thr
 385 390

<210> 47
 <211> 1194
 <212> DNA
 <213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1194)

<400> 47

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atg aga aaa gtt tct tcc gta att tct gtc gtt gat ccc gtt att ttc      48
Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe
   1               5               10               15

cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg      96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro
           20               25               30

caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt      144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg
           35               40               45

aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt      192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly
           50               55               60

att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt      240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val
           65               70               75               80

tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc      288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser
           85               90               95

aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc      336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile
           100              105              110

act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc      384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr
           115              120              125

gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat      432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn
           130              135              140

aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct      480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala
           145              150              155              160

agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg      528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val
           165              170              175

acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca      576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr
           180              185              190

gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att      624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile
           195              200              205

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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggg gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385 390 395

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<210> 48

<211> 397

<212> PRT

<213> Arabidopsis thaliana

<400> 48

Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe

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

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

<210> 49
 <211> 611
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (5)..(601)

<400> 49
 gaaa atg atc gta ctt tct gtt ggt tcc gct tct tca tct ccg atc gtc 49
 Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val
 1 5 10 15
 gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
 Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
 20 25 30
 cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
 Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
 35 40 45
 agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
 Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
 50 55 60
 act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
 Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
 65 70 75
 ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
 Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
 80 85 90 95
 tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
 Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
 100 105 110

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gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385
Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
115 120 125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433
Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
130 135 140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481
Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
145 150 155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529
Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
160 165 170 175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577
Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
180 185 190

gaa tca caa aaa gac gag ctt taa agcaaagtcc 611
Glu Ser Gln Lys Asp Glu Leu
195

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<210> 50
<211> 198
<212> PRT
<213> Arabidopsis thaliana

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<400> 50
Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val Val
1 5 10 15

Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu
20 25 30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser
35 40 45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
50 55 60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
65 70 75 80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
85 90 95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
100 105 110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
115 120 125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
130 135 140

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Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
145                      150                      155                      160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
                      165                      170                      175

Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu
                      180                      185                      190

Ser Gln Lys Asp Glu Leu
                      195

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<210> 51
<211> 1398
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (1)..(1398)

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<400> 51
atg cct cgt cgt cgt acg tgc tgt cgg cgt gaa ttc ggt ccg aca cag 48
Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln
1 5 10 15

cca tgt aga ggc gcg tca atc act gga tct cta cgt gac cgt cga ccg 96
Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
20 25 30

acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144
Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192
Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240
Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
65 70 75 80

caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288
Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
85 90 95

ggg gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336
Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
100 105 110

att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384
Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys
115 120 125

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

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Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr
355                               360                               365

gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152
Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser
370                               375                               380

tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag 1200
Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
385                               390                               395                               400

aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248
Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu
405                               410                               415

cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296
His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
420                               425                               430

ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344
Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
435                               440                               445

cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392
Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg
450                               455                               460

tag taa 1398
465

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<210> 52
 <211> 464
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 52
Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln
1                               5                               10                               15

Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
20                               25                               30

Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
35                               40                               45

Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
50                               55                               60

Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
65                               70                               75                               80

Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
85                               90                               95

Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

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100	105	110
Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys		
115	120	125
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu		
130	135	140
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys		
145	150	155
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val		
165	170	175
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala		
180	185	190
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr		
195	200	205
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val		
210	215	220
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe		
225	230	235
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val		
245	250	255
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser		
260	265	270
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val		
275	280	285
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg		
290	295	300
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu		
305	310	315
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr		
325	330	335
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly		
340	345	350
Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr		
355	360	365
Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser		
370	375	380
Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys		
385	390	395
Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu		

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                                405                410                415
His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
                                420                425                430

Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
                                435                440                445

Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg
                                450                455                460

<210> 53
<211> 771
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(537)

<400> 53
atg ccg cgt aac gtt gct ggt atg tgc gtt gcg tta gaa cga gtc ttc 48
Met Pro Arg Asn Val Ala Gly Met Cys Val Ala Leu Glu Arg Val Phe
1 5 10 15

gac gtc gat gaa att gtc agg tta agg aag agg ttt ttc aag ttg gac 96
Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp
20 25 30

aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct 144
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro
35 40 45

caa gtt agt tcg aac cct ctt cgg atg cgt gag atg cgt aat ttc gat 192
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
50 55 60

aat gat tgc gta ggg agt gtg gat ttt atc gag ttc atc aat gga cgt 240
Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
65 70 75 80

tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca 288
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
85 90 95

ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag 336
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
100 105 110

tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat 384
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
115 120 125

cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac 432
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp

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130          135          140
ggg gat ggt cga ggt gcg aaa aac agc ttt gag gaa ttt tac ggt cgt 480
Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
145          150          155          160

ttg cca gct acc gta cgt cgg cgt ccg tac cgt acg ttg gta agc ggt 528
Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
165          170          175

gat gtg taa agttcagtc accgtgaccg tgagcctgga agcctgaacg 577
Asp Val

ctgacaagcc cttaagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637

ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697

cttgagcctg agcctgagcc tgatcgatca aaaaaaaagg agcctttttt ttttagctaa 757
aaaaaaaaag ctaa 771

<210> 54
<211> 178
<212> PRT
<213> Arabidopsis thaliana

<400> 54
Met Pro Arg Asn Val Ala Gly Met Cys Val Ala Leu Glu Arg Val Phe
1 5 10 15
Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp
20 25 30
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro
35 40 45
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
50 55 60
Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
65 70 75 80
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
85 90 95
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
100 105 110
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
115 120 125
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
130 135 140
Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
145 150 155 160

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Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
 165 170 175

Asp Val

<210> 55

<211> 1617

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (10)..(1557)

<400> 55

cgctacggt atg cgt acg tca aga aca gga ttt cgg atg cca ttg ggg ccc 51
 Met Arg Thr Ser Arg Thr Gly Phe Arg Met Pro Leu Gly Pro
 1 5 10

tgg gcg gtg aac ccc tgc ttc att gct tcc tgt tcc tgt ctc ctc gtt 99
 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val
 15 20 25 30

ggc ttc ggc gac gca atc ttc tac gag tcg ttc gcc ggg gat ttt gat 147
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tcg gat tcg gcc aag 195
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp
 115 120 125

aaa ttt gac agc tcc acc atg ttt ggt gct gct aag tat ggc gcg agg 435
 Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg
 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu
 145 150 155

tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa	531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
160 165 170	
gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat	675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
210 215 220	
ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc	723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
240 245 250	
atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
255 260 265 270	
gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa	867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
305 310 315	
aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa	1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata gcc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	

gaa tat ggg gaa acc ccg ttg aag acc acg tgt acc gtc gag aag cac 1203
 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His
 385 390 395
 agt ttg cag gct caa gag gcg aga acc cgg tca gac gct ggt tca ccc 1251
 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro
 400 405 410
 tac acc agg tac gta tct aaa atc ccc ggg aaa gcc gat aat ccc ttc 1299
 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe
 415 420 425 430
 tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys
 435 440 445
 cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser
 450 455 460
 att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443
 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys
 465 470 475
 aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu
 480 485 490
 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala
 495 500 505 510
 agc tcg ccc agg cgc tga taattaaatc cgatccgtcc tttaaccccc 1587
 Ser Ser Pro Arg Arg
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 gttgttcaat accgtttttt ttttatTTaa 1617

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 Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp Ala Arg
 35 40 45
 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala
 50 55 60

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

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr
 370 375 380
 Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu
 385 390 395 400
 Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr
 405 410 415
 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser
 420 425 430
 Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys
 435 440 445
 Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn
 450 455 460
 Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln
 465 470 475 480
 Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr
 485 490 495
 Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala Ser Ser
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 Pro Arg Arg
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 Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg
 15 20 25
 ggg tgg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147
 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly
 30 35 40 45
 gca tgg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195
 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile
 50 55 60

acg aca agc acc cgc gcg cgg cgc tac gcg gtc tgc gcc aaa ttc ccg	243
Thr Thr Ser Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro	
65 70 75	
aga tta agt aat aag ggc aaa gat tac atg cgt tgc gtc ctc caa tac	291
Arg Leu Ser Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr	
80 85 90	
acc gtc aaa aat gaa caa aaa gtt gat tgt ggt ggc tca tat atc aag	339
Thr Val Lys Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys	
95 100 105	
tta tta cct tgc aaa ttg cgc acg ggt gat ggt gat ggc gtg tca gaa	387
Leu Leu Pro Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu	
110 115 120 125	
tat tca att atg ttt ggt cca gat tgc aca ggt gca tca cgt act gtt	435
Tyr Ser Ile Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val	
130 135 140	
cgt cga gct cgc aat tat aag ggt aaa cgg cat ttg cgg aaa aaa gaa	483
Arg Arg Ala Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu	
145 150 155	
cag aat aaa gtg gaa aca gat caa tta aca cat cag tat act acg agt	531
Gln Asn Lys Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser	
160 165 170	
tgg tca cca gat tgg acc tac aac gtt cta gta gat aat aag gaa tgc	579
Trp Ser Pro Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser	
175 180 185	
caa gca ggg aac ctt gcc gac gac tgc gag tta ctt cca cag aag cga	627
Gln Ala Gly Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg	
190 195 200 205	
atc ttc cga ccc agc tgc cga aaa caa tcc aaa cca gtc acc tgc gta	675
Ile Phe Arg Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val	
210 215 220	
gac gtc aag cac cac gcc ccc cga cga aat gtg aaa ccc gcc ggg cac	723
Asp Val Lys His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His	
225 230 235	
gat gac att cca gcg cga cgg acg acg ccg gaa gcg gtc cgg aaa ggc	771
Asp Asp Ile Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly	
240 245 250	
cgc acg aac gag cga ccg gac cgg acg tgg gcg acc ggg acg acc cca	819
Arg Thr Asn Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro	
255 260 265	
cgg cca cgg cgt tac aag gga gag acg aag gcc aaa aag cac cca cgg	867
Arg Pro Arg Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg	
270 275 280 285	

ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915
 Pro Glu Tyr Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr
 290 295 300
 cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala
 305 310 315
 ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011
 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met
 320 325 330
 ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059
 Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr
 335 340 345
 aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107
 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly
 350 355 360 365
 acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155
 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu
 370 375 380
 aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203
 Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg
 385 390 395
 cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251
 Arg Thr Gly Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu
 400 405 410
 tac gga ccg gaa taa aatcgccctga tgcct 1281
 Tyr Gly Pro Glu
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 35 40 45
 Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser
 50 55 60
 Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser
 65 70 75 80

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

Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg Arg Thr Gly
385 390 395 400

Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu Tyr Gly Pro
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Glu

<210> 59

<211> 416

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<213> Arabidopsis thaliana

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aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca 96
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr
20 25 30

gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac 144
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn
35 40 45

ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg 192
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
50 55 60

aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc 240
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
65 70 75 80

gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg 288
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
85 90 95

atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg 336
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
100 105 110

atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag 384
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu
115 120 125

ttt gtc aag att atg atg gct aag tga tttgat 417
Phe Val Lys Ile Met Met Ala Lys
130 135

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

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<212> DNA
<213> Arabidopsis thaliana

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<400> 61

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                               1           5

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Asn Ser Ser Leu Ser Ser Gly Asn Gly Thr Glu Val Ala Thr Asp Val
    10           15           20

tct tct tgc ttc tat gtt ccc aat ccc tct gga acc gat ttc gat gcc 150
Ser Ser Cys Phe Tyr Val Pro Asn Pro Ser Gly Thr Asp Phe Asp Ala
    25           30           35

gag tcg tct tct ctt cct cct ct gtaagtcttc tttgaatttt taaaaacatt 203
Glu Ser Ser Ser Leu Pro Pro Le
    40           45

cactctcttg ctgctgtctc tgttgatcct tcttctttga aaatttgaaa acattcttag 263

tctctcgctc tgtcacag c tcc cca gct cct caa gtg gca ttg tca att cct 315
u Ser Pro Ala Pro Gln Val Ala Leu Ser Ile Pro
    50           55

gcg gag ctt gcc gcc gcc att ccc ctc atc gat cgc ttc cag gtt gaa 363
Ala Glu Leu Ala Ala Ala Ile Pro Leu Ile Asp Arg Phe Gln Val Glu
    60           65           70

gct ttt ctg cgg cta atg cag aaa caa atc cag tct gct ggg aag cgt 411
Ala Phe Leu Arg Leu Met Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg
    75           80           85           90

ggc ttc ttc tat tcc aaa aag tcc tct ggc tcc aat gtc cgc gag cgc 459
Gly Phe Phe Tyr Ser Lys Lys Ser Ser Gly Ser Asn Val Arg Glu Arg
    95           100           105

ttc aca ttt gag gat atg ctt tgc ttt caa aag gtttttcttt ccccccttt 512
Phe Thr Phe Glu Asp Met Leu Cys Phe Gln Lys
    110           115

cttccccatt gacaatccat tgactg aat atg tct ctc tcc cct tcc ttc ctt 565
Asn Met Ser Leu Ser Pro Ser Phe Leu
    120           125

cag gat cca atc ccc aca tct ctc ctc aag att aac agc gat ctc gtc 613
Gln Asp Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val
    130           135           140

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agc cgt gct acc aag ttg ttt cat ctc atc tta aaa tat atg ggt gtt 661
Ser Arg Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val
      145                150                155

gat tca tct gat cga tct acg cct ccc agt tta gat gaa cgc att gac 709
Asp Ser Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp
      160                165                170

ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg 757
Leu Val Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg
      175                180                185                190

gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac 805
Asp Glu Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp
      195                200                205

agg caa tac ttg atc aaa gct tgg gaa ttg atg tac tta tgt gcc tcc 853
Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser
      210                215                220

tct atg cct cct agc aaa gat atc ggt gga tat cta tct gag tat att 901
Ser Met Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile
      225                230                235

cat aat gtc gca cac gat gca act att gaa ccg gat gct cag gtt ctt 949
His Asn Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu
      240                245                250

gct gtt aac act ttg aaa gct tta aag cgc tct atc aaa gct ggt cct 997
Ala Val Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro
      255                260                265                270

agg cac acc aca cct ggt cgt gaa gaa att gaa gcc ctt ttg acc ggt 1045
Arg His Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly
      275                280                285

aga aag ctc aca acc att gtc ttc ttt ctc gat gaa act ttt gaa gaa 1093
Arg Lys Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu
      290                295                300

att tca tat gac atg gct acc aca gtg tct gat gct gtt gag 1135
Ile Ser Tyr Asp Met Ala Thr Thr Val Ser Asp Ala Val Glu
      305                310                315

gtatcttctt gctttctttt ttcataattt accgctgac atattcttgt ccccttttct 1195

ctcactgcat tgacatctgt ttcaggag cta gct gga aca att aaa cta tca 1247
Leu Ala Gly Thr Ile Lys Leu Ser
      320

gct ttc tct agc ttt agt ttg ttt gaa tgt cgt aaa gtt gtt tca agt 1295
Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys Val Val Ser Ser
      325                330                335                340

tct aaa tca tct gat ccc gga aat g gtatgcttct atagtactgg 1340
Ser Lys Ser Ser Asp Pro Gly Asn G

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345

cttcgtcata tattgtgaag taatacaaca ttatcgatca tttttctatc tgtgcacttg 1400

cag ag gaa tat ata gga ttg gat gat aac aag tat att gga gat ctc 1447
 lu Glu Tyr Ile Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu
 350 355 360

ctc gca gaa ttt aaa gct att aaa gac cga aat aaa gga gag ata cta 1495
 Leu Ala Glu Phe Lys Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu
 365 370 375

cac tgc aaa ctg gta ttt aaa aaa tta ttc cga gag tct gat gaa 1543
 His Cys Lys Leu Val Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu
 380 385 390 395

gct gta aca gat ctg atg ttt gtg caa ctt tgc tat gtt caa 1585
 Ala Val Thr Asp Leu Met Phe Val Gln Leu Ser Tyr Val Gln
 400 405

gtgagcattt tcttcattgg tgacatttat ttccacacaa aaggcttgcc tttcgttgct 1645

gacacacata tatgcag ctg caa cat gac tat ttg cta gga aac tat cct 1695
 Leu Gln His Asp Tyr Leu Leu Gly Asn Tyr Pro
 410 415 420

gtt ggg agg gac gat gct gca cag ctt tgt gcc ttg caa att ctt gtt 1743
 Val Gly Arg Asp Asp Ala Ala Gln Leu Cys Ala Leu Gln Ile Leu Val
 425 430 435

ggg att ggg ttt gtc aat agt cca gag tca tgc at gttagttttc 1788
 Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Il
 440 445

ttaagctccg ccattgactt tatttttagtt gtccgatact ttatttttcc aattttcctc 1848

ccttaacaat atcatttctt ttctcaatgt atcacatatc ag t gat tgg aca tca 1903
 e Asp Trp Thr Ser
 450

ctt ctt gag cgg ttt ttg cca aga caa ata gca ata acc cga gca aag 1951
 Leu Leu Glu Arg Phe Leu Pro Arg Gln Ile Ala Ile Thr Arg Ala Lys
 455 460 465

cgt gaa tgg gaa ttg gat atc ctt gct cgc tac cgt tca atg 1993
 Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg Ser Met
 470 475 480

gtaggaatag ttctatgcat gtggattgtc ttcccccttc tagatacctt tggcaaataa 2053

aaacccattg aagtgatggc atggtaaaat gatatttcgt atgtgtatgt gggcatgtag 2113

gag aac gtg acc aaa gat gat gca aga caa caa ttt cta cgg ata ctg 2161
 Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg Ile Leu
 485 490 495

aag gca ctg cca tac ggg aat tca gtt ttt ttt agc gta cgc aag ata 2209

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Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg Lys Ile
500                               505                               510

gat gat ccg atc ggt ctt tta cct ggg cga atc att ttg ggt atc aac 2257
Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly Ile Asn
515                               520                               525                               530

aaa cgt ggg gttgtctcaa tataaatggt atacattatg actttaaaaa 2306
Lys Arg Gly

aactgttatt gttgtttgga attcaaatct atgttgttgg atttgaattt gttgtttgct 2366

ttctgttag gtt cac ttt ttt cga ccg gtt cct aaa gaa tat ctg cac tct 2417
Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr Leu His Ser
535                               540                               545

gct gaa cta cgt gac atc atg caa ttt ggc agc agt aac act gct gtc 2465
Ala Glu Leu Arg Asp Ile Met Gln Phe Gly Ser Ser Asn Thr Ala Val
550                               555                               560

ttt ttc aaa atg aga gtc gct ggt gtt ctt cac ata ttt cag ttc gag 2513
Phe Phe Lys Met Arg Val Ala Gly Val Leu His Ile Phe Gln Phe Glu
565                               570                               575

aca aaa cag gtttaaacad cactatttgt ggatcattat attatgaagc 2562
Thr Lys Gln
580

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 Ser Leu Met Ser Glu Leu Arg Gly Met Glu Ala Arg Leu Ala
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gag aaa cac cga tta caa ata cca cgt caa aat tta gct gta tat aat Glu Lys His Arg Leu Gln Ile Pro Arg Gln Asn Leu Ala Val Tyr Asn 515 520 525	1584
agt aat cac gat ata tgg aat aat cgc aat aga gat aaa tat att att Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile 530 535 540	1632
agt aac aat cct aat aat agg aat gat aat aat aac act gta tgc gat Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp 545 550 555 560	1680
cta agc agt ggc gag tta ggt gaa agt cgt gag gtt gtg cca gac ggt Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly 565 570 575	1728
atc ggg ttg gag gta ctt cta gat tct atc gta aaa gaa gag gta cga Ile Gly Leu Glu Val Leu Leu Asp Ser Ile Val Lys Glu Glu Val Arg 580 585 590	1776
atg gaa cca tca aca gtt tcg aag gaa ttt agg tcg atc att tct gaa Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu 595 600 605	1824
tgt tta cga aac gat gca act gaa aga caa aca gct tca aac tta gta Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val	1872


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        610                615                620
aat cac gaa ttt gta aag aaa tat caa aag tac aat cgt gaa aaa tgg 1920
Asn His Glu Phe Val Lys Lys Tyr Gln Lys Tyr Asn Arg Glu Lys Trp
625                630                635                640

acc gca gat tta caa agg tgg caa taa aaatcgctt cagcctgat 1967
Thr Ala Asp Leu Gln Arg Trp Gln
645

cgctgacgct cgacgcctgc ccccgacctg cagctcgccc agctcgccca ggctcgccca 2027
gctgcccac cagcctgccc caccgctcca cgcttaaata ataaaaattt ttaaaaaaaa 2087
aaaaaaaaaa aaaccgct 2105

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<211> 648
<212> PRT
<213> Arabidopsis thaliana

<400> 64
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Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp
20 25 30
Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr
35 40 45
Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser
50 55 60
Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
65 70 75 80
Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
85 90 95
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
100 105 110
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
115 120 125
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
130 135 140
Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
145 150 155 160
Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
165 170 175
Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

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

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<210> 65
<211> 920
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (26)..(907)

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                Met Glu Gly Leu Ala Ile Arg Ala Ser
                1                      5

cga ccg tcg gtt ttc tgt tct att cca ggt ctc ggc ggc gat tcc cac 100
Arg Pro Ser Val Phe Cys Ser Ile Pro Gly Leu Gly Gly Asp Ser His
  10                      15                      20                      25

cga aaa cct cca agt gac ggt ttc ctc aag ctg cct gcg tcg tct att 148
Arg Lys Pro Pro Ser Asp Gly Phe Leu Lys Leu Pro Ala Ser Ser Ile
                30                      35                      40

ccg gcg gac agc cga aaa tta gta gcg aat tct act tcc ttt cat cca 196

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Pro Ala Asp Ser Arg Lys Leu Val Ala Asn Ser Thr Ser Phe His Pro
      45              50              55
atc tca gcc gtt aac gtc tct gct caa gct tcc ctc acc gct gat ttt 244
Ile Ser Ala Val Asn Val Ser Ala Gln Ala Ser Leu Thr Ala Asp Phe
      60              65              70
ccc gcc ctt tca gaa act ata ctg aaa gag gga aga aat aac gga aaa 292
Pro Ala Leu Ser Glu Thr Ile Leu Lys Glu Gly Arg Asn Asn Gly Lys
      75              80              85
gag aaa gca gag aac atc gtg tgg cac gag agt tcg ata tgc aga tgc 340
Glu Lys Ala Glu Asn Ile Val Trp His Glu Ser Ser Ile Cys Arg Cys
      90              95              100
gac aga caa caa ctt ctt caa caa aag ggt tgt gtc gtt tgg atc act 388
Asp Arg Gln Gln Leu Leu Gln Gln Lys Gly Cys Val Val Trp Ile Thr
      110              115              120
ggt ctc agt ggt tca ggg aaa agc act gtt gct tgt gca cta agt aaa 436
Gly Leu Ser Gly Ser Gly Lys Ser Thr Val Ala Cys Ala Leu Ser Lys
      125              130              135
gca ttg ttt gaa aga ggc aaa ctt act tac aca ctc gac ggc gac aat 484
Ala Leu Phe Glu Arg Gly Lys Leu Thr Tyr Thr Leu Asp Gly Asp Asn
      140              145              150
gtc cgt cac ggc ctt aac cgt gac ctc act ttc aaa gca gag cac cgc 532
Val Arg His Gly Leu Asn Arg Asp Leu Thr Phe Lys Ala Glu His Arg
      155              160              165
acc gaa aac att aga aga att ggt gag gtg gct aag ttg ttt gct gac 580
Thr Glu Asn Ile Arg Arg Ile Gly Glu Val Ala Lys Leu Phe Ala Asp
      170              175              180
gtc gga gtc att tgt ata gca agt ttg att tct ccg tac cgg aga gac 628
Val Gly Val Ile Cys Ile Ala Ser Leu Ile Ser Pro Tyr Arg Arg Asp
      190              195              200
aga gac gcg tgc cgg tcc ttg tta cct gac ggc gat ttc gtc gag gtc 676
Arg Asp Ala Cys Arg Ser Leu Leu Pro Asp Gly Asp Phe Val Glu Val
      205              210              215
ttc atg gac gtt cct ctt cat gtg tgc gag tcg aga gat cca aag ggg 724
Phe Met Asp Val Pro Leu His Val Cys Glu Ser Arg Asp Pro Lys Gly
      220              225              230
ttg tac aag ctt gca cgt gca ggc aaa atc aaa ggc ttc act gga atc 772
Leu Tyr Lys Leu Ala Arg Ala Gly Lys Ile Lys Gly Phe Thr Gly Ile
      235              240              245
gac gac cct tac gag gca cca gtg aat tgc gag gta gtg ctg aaa cac 820
Asp Asp Pro Tyr Glu Ala Pro Val Asn Cys Glu Val Val Leu Lys His
      250              255              260
aca gga gac gac gag tcg tgt tcg cca cgt cag atg gct gag aac atc 868
Thr Gly Asp Asp Glu Ser Cys Ser Pro Arg Gln Met Ala Glu Asn Ile

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270 275 280

atc tct tac ctg caa aac aaa ggt tat ctt gag ggc taa gtcaaagtcg 917
 Ile Ser Tyr Leu Gln Asn Lys Gly Tyr Leu Glu Gly
 285 290

gaa 920

<210> 66
 <211> 293
 <212> PRT
 <213> Arabidopsis thaliana

<400> 66
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 Ile Pro Gly Leu Gly Gly Asp Ser His Arg Lys Pro Pro Ser Asp Gly
 20 25 30
 Phe Leu Lys Leu Pro Ala Ser Ser Ile Pro Ala Asp Ser Arg Lys Leu
 35 40 45
 Val Ala Asn Ser Thr Ser Phe His Pro Ile Ser Ala Val Asn Val Ser
 50 55 60
 Ala Gln Ala Ser Leu Thr Ala Asp Phe Pro Ala Leu Ser Glu Thr Ile
 65 70 75 80
 Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
 85 90 95
 Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
 100 105 110
 Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
 115 120 125
 Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
 130 135 140
 Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
 145 150 155 160
 Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
 165 170 175
 Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
 180 185 190
 Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
 195 200 205
 Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
 210 215 220

Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala
 225 230 235 240
 Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro
 245 250 255
 Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys
 260 265 270
 Ser Pro Arg Gln Met Ala Glu Asn Ile Ile Ser Tyr Leu Gln Asn Lys
 275 280 285
 Gly Tyr Leu Glu Gly
 290

<210> 67
 <211> 1257
 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (13)..(1245)

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 Met Gly Ile Cys Leu Ser Ala Gln Val Lys Ala Glu Ser
 1 5 10

tca gga gcg agt acg aag tat gac gcc aaa gat ata gga agt ctt ggg 99
 Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly
 15 20 25

agc aag gct tcg tct gtg tct gta aga cca agc cct cga act gag ggt 147
 Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly
 30 35 40 45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt 195
 Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu
 50 55 60

aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt 243
 Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
 65 70 75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act 291
 Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr
 80 85 90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac 339
 Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn
 95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387
 Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr

110	115	120	125	
ctt ggt cag ttt tct cac cgt cac ctt gtg aag ctg att ggt tat tgc				435
Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys	130	135	140	
cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt				483
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa cgg tta				531
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt				579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag				627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys	190	195	200	205
act tct aat atc ctt ctt gac tgc gag tac aac gca aag ctt tct gat				675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp	210	215	220	
ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct				723
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca				771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc				819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca				867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac				915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac				963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc				1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tgc cac				1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

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ctc gaa cac att cag tct tta aat gct gct ata gga gga aat atg gat 1107
Leu Glu His Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp
350          355          360          365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
          370          375          380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
          385          390          395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga 1245
Val Ala Tyr Pro Arg Pro Ser Ala Ser Pro Leu Tyr Val
          400          405          410

atagggttaa ac 1257

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<210> 68
<211> 410
<212> PRT
<213> Arabidopsis thaliana

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

Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly Glu Ile Leu
          35          40          45

Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
          50          55          60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
          65          70          75          80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
          85          90          95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
          100          105          110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
          115          120          125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
          130          135          140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
          145          150          155          160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

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	165		170		175
Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu Ala Phe Leu					
180		185		190	
His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn					
195		200		205	
Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu					
210		215		220	
Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser Thr Arg Val					
225		230		235	240
Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His					
	245		250		255
Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu					
	260		265		270
Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro Ser Gly Glu					
	275		280		285
Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn Lys Arg Lys					
	290		295		300
Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr Ser Met Glu					
305		310		315	320
Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu Thr Thr Glu					
	325		330		335
Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His Leu Glu His					
	340		345		350
Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp Lys Thr Asp					
	355		360		365
Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys Lys Val Asn					
	370		375		380
Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val Val Ala Tyr					
385		390		395	400
Pro Arg Pro Ser Ala Ser Pro Leu Tyr Val					
	405		410		

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 <211> 3240
 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (69)..(236)

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 <222> (2196) .. (2243)

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 <222> (2734) .. (2818)

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 <222> (2928) .. (2984)

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 <222> (3079) .. (3191)

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 gagcgaat atg cta gag aaa aaa tta gct gct gca gaa gtc tct gag gaa 110
 Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu
 1 5 10
 gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158
 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr
 15 20 25 30
 atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

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Met Arg Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu
      35              40              45
aca atg att ggg aag ggt gca ttc gga gag gtaacatctc ttttatagat 256
Thr Met Ile Gly Lys Gly Ala Phe Gly Glu
      50              55
catagtctgt tactctgttt tctcagcctc tcattggcat gcatcatctt gaaatgttct 316
ctgtgatgca tccttcttga aaggtcttct taggccattt tttttaccac agctaatttt 376
tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt 431
                        Val Arg Ile Cys
                        60
agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys
      65              70              75
tct gag atg ctt cgc aga ggc cag gta tttaaattcc ttcaagtggc 526
Ser Glu Met Leu Arg Arg Gly Gln Val
      80              85
tttcgtttga catttggtta gttggttgat gtgaatgtgg aatctgattt tcag gtg 583
                        Val
gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn
      90              95              100
tgc att gtc aaa ctg tat tgt tct ttc caa gat gaa gag tac ttg tat 679
Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr
      105              110              115
ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg 727
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met
      120              125              130
agg aaa gac acc ctc act gaa gac gag gcc agg ttt tat att ggg gaa 775
Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu
      135              140              145              150
act gtc ctg gct att gag tcc att cat aag cac aac tac att cac ag 822
Thr Val Leu Ala Ile Glu Ser Ile His Lys His Asn Tyr Ile His Ar
      155              160              165
gtcagtgaag cagaatatat gatttagttc tagctcccat tggtattttg ttctaaacgt 882
ctttttttct ccaatgtgat acag a gat atc aag cct gat aat ctg cta ctt 934
                        g Asp Ile Lys Pro Asp Asn Leu Leu Leu
                        s              170              175
gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca 982
Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro
      180              185              190
tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac 1030

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Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn
195 200 205
gtt agt ggg gct tta caa agt gat ggt cgc cct gtg gcg aca aga cgc 1078
Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg
210 215 220
acc caa caa gag caa tta cta aac tgg cag aga aat aga agg atg ctt 1126
Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu
225 230 235
gtaagtttca cttattcctc atcttttctt ccagagatgt ggagtagtcc acagtatcca 1186
gtatatttcg ttattgaaag caaattctct ccattgatat agacatctat gttagatatg 1246
acttactagg ttaagggtcat tacttttcag gct tat tcc aca gtt ggc act cct 1299
Ala Tyr Ser Thr Val Gly Thr Pro
240 245
gac tat att gcc cca gaa gtt ctg ttg aaa aaa gga tat gga atg gaa 1347
Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu
250 255 260
tgt gat tg gtaggtgaag ccaacctatt cctatttctg gtcttttgatt tctttggtgt 1405
Cys Asp Tr
265
aaataaataa tatgggtgaa taatcttgag atttag g tgg tct ctt ggc gcc att 1460
p Trp Ser Leu Gly Ala Ile
270
atg tat gaa atg ctt gtg ggg ttt ccg ccc ttt tat tca gat gac cca 1508
Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro
275 280 285
atg aca act tgt agg aag gtaattaatc cattcctttt tgaatctttc 1556
Met Thr Thr Cys Arg Lys
290
attttaatat tgaaggcaga ctggcgattt caagtcttac atttaatttt agtctttttg 1616
tatctctttg gtaattctaa tgtggaaact tacctcttct cgattcatta tcttccccct 1676
tatgcag ata gta aat tgg aga aat tac ttg aaa ttc cca gat gag gtt 1725
Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val
295 300 305
aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat 1773
Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn
310 315 320
gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815
Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys
325 330 335
gtgtgtatg cgttgttcaa ctttgagatt caaagttccc ttatgtaaga tcattgtgtg 1875

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caattcttaa aaacgatttg actggtttct ttcag ggt cac cct tgg ttt aga 1928
                                Gly His Pro Trp Phe Arg
                                340

ggc aca gaa tgg gga aaa ttg tat caa atg aaa gct gcc ttt att ccc 1976
Gly Thr Glu Trp Gly Lys Leu Tyr Gln Met Lys Ala Ala Phe Ile Pro
345                                350                                355                                360

caa gtt aat gat gag ttg gac acc caa aat ttt gag aaa ttt gaa gag 2024
Gln Val Asn Asp Glu Leu Asp Thr Gln Asn Phe Glu Lys Phe Glu Glu
                                365                                370                                375

gtaacacact gatactatca gctaagatg tctatagtga aatattggtg caatatatgc 2084

caccaaata tgtggcatga tgtatatact gaaatattgg tatcacagat gatttttatg 2144

ctcttgataa ggaaaataat gtatactctt ctttgattcc ttctggaaca g act gac 2201
                                Thr Asp

aag caa gtt cca aag tca gcc aag tca ggt cca tgg aga aag 2243
Lys Gln Val Pro Lys Ser Ala Lys Ser Gly Pro Trp Arg Lys
380                                385                                390

gtacagcata agcactgact ttttggcatt atgtaccatc aagctttttt tttttatcta 2303

atagaagagt gatcatactt caaaatttat ctataagtgg gttccttgag atatgttgtt 2363

ctttgatgat actacagacg tagcttaaaa tattacatgc aacaaagagc tcagaatgat 2423

gaaattggct cagtttctgt cacaggcggt tctatctttg tactatattc acaaaaacgt 2483

gattcactct tttaggttca aattttctta tggtaattta gaatttggag ctgattggga 2543

tgctactaac agaattatgt tgtaaatctg ccagttctgc atgttgacgt gtgtagatag 2603

aatcacttat ctttttggac caacatgata taacttagaa cctgttctgt caatagaatt 2663

tatgtcatga accaaaagga ttcttgtgaa ttccataaca tgacgctggc tttctttttt 2723

ttttctccag atg ctc tca tcc aaa gac att aac ttt gtt ggt tat act 2772
                                Met Leu Ser Ser Lys Asp Ile Asn Phe Val Gly Tyr Thr
                                395                                400                                405

tac aag aac gta gaa atc gta aat gat gac caa ata cca ggg ata g 2818
Tyr Lys Asn Val Glu Ile Val Asn Asp Asp Gln Ile Pro Gly Ile A
                                410                                415                                420

gtaattcact taacccccct tccgttgctg aggaagaagc aacaatacta gattaccttg 2878

tgattatcat cgcattgttg ctgcatttgt aatttgtttt attgtgcag ct gag ttg 2935
                                la Glu Leu
                                G

aag aag aag agc aat aag cca aaa agg ccg tct att aaa tct ctc ttt g 2984
Lys Lys Lys Ser Asn Lys Pro Lys Arg Pro Ser Ile Lys Ser Leu Phe G
425                                430                                435                                440

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<210> 70
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<212> PRT
<213> Arabidopsis thaliana
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151

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

<210> 71
 <211> 979
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (28)..(843)

<400> 71

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acgaaaacca ccgtagcta taggctg atg ata tgt agg atc cga ctc ggg tgg 54
Met Ile Cys Arg Ile Arg Leu Gly Ser
      1              5

atg aac ggt gac gaa tgc gcg aac gtt gcg acg tgc tgg gtt act tct 102
Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
      10              15              20              25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
      30              35              40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
      45              50              55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
      60              65              70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
      75              80              85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
      90              95              100              105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
      110              115              120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
      125              130              135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
      140              145              150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
      155              160              165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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170          175          180          185
aaa gtg tgg aat gtc aat gga aag aaa tgt agg acg ccg cta aaa aag 630
Lys Val Trp Asn Val Asn Gly Lys Lys Cys Arg Thr Pro Leu Lys Lys
          190          195          200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta 678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
          205          210          215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt 726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
          220          225          230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa 774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
          235          240          245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga 822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250          255          260          265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacggtgaa aaagtcgacc 873
Ser Leu Ser Gln Thr Trp
          270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agcttttttag gcctttcgct 933

ttttttgaag aaaaaaggct cgcgaaaaaa aaaaagctcg aaatca 979

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<210> 72
 <211> 271
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 72
Met Ile Cys Arg Ile Arg Leu Gly Ser Met Asn Gly Asp Glu Cys Ala
  1          5          10          15

Asn Val Ala Thr Cys Trp Val Thr Ser Leu Ala Cys Val Val Asp Ala
          20          25          30

Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
          35          40          45

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
          50          55          60

Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
          65          70          75          80

Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
          85          90          95

Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
          100          105          110

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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp
 115 120 125
 Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro
 130 135 140
 Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp
 145 150 155 160
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu
 165 170 175
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly
 180 185 190
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr
 195 200 205
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser
 210 215 220
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys
 225 230 235 240
 Ile Asn Gln Glu Asn Pro Ile Asn Gln Ile Ala Phe Ser Pro Ser Pro
 245 250 255
 Phe Val Val Thr Cys Gln Thr Glu Arg Ser Leu Ser Gln Thr Trp
 260 265 270

<210> 73
 <211> 1260
 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (101)..(155)

<220>
 <221> CDS
 <222> (254)..(660)

<220>
 <221> CDS
 <222> (750)..(1193)

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 taaagaaaaa gctggagtag aactatttta aagtgatcgc atg aag aga cta agc 115
 Met Lys Arg Leu Ser
 1 5

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agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165
Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
      10                      15

ccatctttgt tctttctact ttttgcta at gtcagacaaa acccatgtga tcctttcttc 225
actttccact gttttcttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
      sp Ser Phe Gly Tyr Thr Thr Asp Glu
      20                      25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
      30                      35                      40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
      45                      50                      55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
      60                      65                      70                      75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471
Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
      80                      85                      90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
      95                      100                      105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
      110                      115                      120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
      125                      130                      135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
      140                      145                      150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720
ggtttgattt ttaaagtttt tggttgacag att agt aaa atc aaa gct aag gta 773
      Ile Ser Lys Ile Lys Ala Lys Val
      155                      160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
      165                      170                      175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
      180                      185                      190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr
195                200                205                210

gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct 965
Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser
                215                220                225

tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013
Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser
                230                235                240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061
Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe
                245                250                255

tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109
Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu
                260                265                270

agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157
Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser
275                280                285                290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203
Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
                295                300

tcaaattggt gctctgttta gtctcaatgg gaaaacagag aagagggcaa aggtgga 1260

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<210> 74
 <211> 301
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 74
Met Lys Arg Leu Ser Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr
 1                5                10                15

Ser Thr Asp Ser Phe Gly Tyr Thr Thr Asp Glu Gln Ser Pro Arg Gly
                20                25                30

Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala
                35                40                45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser
                50                55                60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys
                65                70                75                80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu
                85                90                95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln
                100                105                110

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Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly
 115 120 125
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu
 130 135 140
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala
 145 150 155 160
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu
 165 170 175
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser
 180 185 190
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser
 195 200 205
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala
 210 215 220
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr
 225 230 235 240
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly
 245 250 255
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp
 260 265 270
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro
 275 280 285
 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
 290 295 300

<210> 75
 <211> 1122
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (22)..(1122)

<400> 75
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 Met Asn Gln Arg Ala Asp Arg Asp Arg Ala
 1 5 10
 agc tcg atc cgt tgg ttt gcc aac cga tta gtg agt ggt agc ctg tta 99
 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu
 15 20 25
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu Cys Ala Asn Ala Tyr Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala	
30 35 40	
tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt	195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg	
45 50 55	
gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt	243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
60 65 70	
tat aga ctt gca cgc ctc gat aac cgc gct ctt gca caa ttg ttg cac	291
Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc	339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat	387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
110 115 120	
tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt	435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
125 130 135	
gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct	483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
140 145 150	
gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc	531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
155 160 165 170	
tac gtc tac atc gtg tgg cgg gaa tcc gaa cga tcg aaa tta gag gcg	579
Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa	723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
220 225 230	
caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc	771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct	819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

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                255                260                265
atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac 867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn
                270                275                280

gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga 915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly
                285                290                295

cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att 963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile
                300                305                310

ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc 1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr
                315                320                325                330

gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct 1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala
                335                340                345

cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac 1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr
                350                355                360

ggg gca gcg cca tga
Gly Ala Ala Pro
                365

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<210> 76
<211> 366
<212> PRT
<213> Arabidopsis thaliana

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<400> 76
Met Asn Gln Arg Ala Asp Arg Asp Arg Ala Ser Ser Ile Arg Trp Phe
  1              5              10              15

Ala Asn Arg Leu Val Ser Gly Ser Leu Leu Leu Cys Ala Asn Ala Tyr
  20              25              30

Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala Leu Gln Gln Met Asn Arg
  35              40              45

Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser
  50              55              60

Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu
  65              70              75              80

Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu
  85              90              95

Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu
 100              105              110

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

<210> 77
 <211> 1650
 <212> DNA
 <213> Arabidopsis thaliana
 <220>


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actagtagca tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671
      Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe
      130                               135

ggt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro
      140                               145                               150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr
      155                               160                               165                               170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala
      175                               180                               185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868
Leu Thr Ala Phe Ile Phe Gly Ar
      190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044
      g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg
      195                               200                               205                               210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr
      215                               220                               225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly
      230                               235                               240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His
      245                               250                               255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu
      260                               265                               270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly
      275                               280                               285                               290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile
      295                               300                               305

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gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428
Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg
      310                      315                      320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476
Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr
      325                      330                      335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524
Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile
      340                      345                      350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572
Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn
      355                      360                      365                      370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625
Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
      375                      380

ctttgtgaga ctattgccaa gttag 1650

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<210> 78
<211> 380
<212> PRT
<213> Arabidopsis thaliana

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<400> 78
Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val Leu Glu Gly Asp Phe
  1                      5                      10                      15

Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile Asp Thr Leu Glu Asn
      20                      25                      30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu
      35                      40                      45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp
      50                      55                      60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu
      65                      70                      75                      80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe
      85                      90                      95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly
      100                      105                      110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp
      115                      120                      125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu
      130                      135                      140

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

<210> 79
 <211> 589
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (18)..(575)

<400> 79

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atctttttcc gataact atg gct gag gaa atc aag aat gtt cct gaa cag 50
      Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln
      1          5          10

gag gtg cca aag gta gca aca gag gaa tca tgc gca gag gtt aca gat 98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
      15          20          25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca 146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
      30          35          40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca 194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
      45          50          55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac 242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
      60          65          70          75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat 290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
      80          85          90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa 338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
      95          100          105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa 386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
      110          115          120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct 434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
      125          130          135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg 482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
      140          145          150          155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac 530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
      160          165          170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa 575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
      175          180          185

gaagattatc attaa 590

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<210> 80

<211> 185

<212> PRT

<213> Arabidopsis thaliana

<400> 80

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

<210> 81
 <211> 1376
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (20)..(1366)

<400> 81
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 Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala
 1 5 10
 gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa 100
 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys
 15 20 25
 tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

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Ser Gly Gly Ala Asp Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr
   30                               35                               40
gaa cat cca ccg gag caa gat agg ccc ggt gtg ata ggt tca gtg ttc 196
Glu His Pro Pro Glu Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe
   45                               50                               55
agg gct gtc caa gga acg tat gag cat gcg aga gac gct gta gtt gga 244
Arg Ala Val Gln Gly Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly
   60                               65                               70                               75
aaa acc cac gaa gcg gct gag tct acc aaa gaa gga gct cag ata gct 292
Lys Thr His Glu Ala Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala
   80                               85                               90
tca gag aaa gcg gtt gga gca aag gac gca acc gtc gag aaa gct aag 340
Ser Glu Lys Ala Val Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys
   95                               100                               105
gaa acc gct gat tat act gcg gag aag gtg ggt gag tat aaa gac tat 388
Glu Thr Ala Asp Tyr Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr
  110                               115                               120
acg gtt gat aaa gct aaa gag gct aag gac aca act gca gag aag gcg 436
Thr Val Asp Lys Ala Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala
  125                               130                               135
aag gag act gct aat tat act gcg gat aag gcg gtg gaa gca aag gat 484
Lys Glu Thr Ala Asn Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp
  140                               145                               150                               155
aag acg gcg gag aag att ggt gag tac aaa gac tat gcg gtg gat aag 532
Lys Thr Ala Glu Lys Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys
  160                               165                               170
gca gta gaa gct aaa gat aag aca gcg gag aag gcg aag gag act tcg 580
Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser
  175                               180                               185
aat tat acg gcg gat aag gct aaa gag gct aag gac aag acg gct gag 628
Asn Tyr Thr Ala Asp Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu
  190                               195                               200
aag gtt ggt gag tat aag gat tac acg gtg gac aag gcc gtg gaa gct 676
Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala
  205                               210                               215
agg gat tac aca gcg gag aag gct att gaa gca aag gat aag aca gct 724
Arg Asp Tyr Thr Ala Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala
  220                               225                               230                               235
gag aag act gga gag tat aag gac tat acg gtg gag aag gcg acg gag 772
Glu Lys Thr Gly Glu Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu
  240                               245                               250
ggg aaa gat gtt acg gtg agt aag cta gga gag ctg aag gat agt gcc 820
Gly Lys Asp Val Thr Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala

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255	260	265	
ggt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag			868
Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu			
270	275	280	
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac			916
Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn			
285	290	295	
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga			964
Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg			
300	305	310	315
ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag			1012
Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Glu Glu			
320	325	330	
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc			1060
Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala			
335	340	345	
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg			1108
Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly			
350	355	360	
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa			1156
Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys			
365	370	375	
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag			1204
Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu			
380	385	390	395
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca			1252
His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser			
400	405	410	
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc			1300
Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr			
415	420	425	
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa			1348
Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys			
430	435	440	
gat aag gga aag ctg tga gaatactaga			1376
Asp Lys Gly Lys Leu			
445			

<210> 82

<211> 448

<212> PRT

<213> Arabidopsis thaliana

<400> 82

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

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<210> 83
<211> 561
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (18)..(548)
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		Met	Asn	Glu	Met	Ser	Phe	Phe	Gly	Tyr	Ser	Phe					
		1				5					10						
atc	gta	gta	gca	tta	ttc	ttc	gat	tta	act	caa	gcc	tat	cgt	cac	act	98	
Ile	Val	Val	Ala	Leu	Phe	Phe	Asp	Leu	Thr	Gln	Ala	Tyr	Arg	His	Thr		
			15					20					25				
ccc	gct	caa	ccg	cca	aaa	gca	aac	gca	aac	ggt	gat	gtc	aaa	ccg	caa	146	
Pro	Ala	Gln	Pro	Pro	Lys	Ala	Asn	Ala	Asn	Gly	Asp	Val	Lys	Pro	Gln		
		30					35					40					
gaa	acg	ctc	gtg	gtt	cac	aac	aag	gcc	cga	gcc	atg	gtc	gga	gtc	gga	194	
Glu	Thr	Leu	Val	Val	His	Asn	Lys	Ala	Arg	Ala	Met	Val	Gly	Val	Gly		
	45					50					55						
cca	atg	gtg	tgg	aac	gaa	act	ctt	gcg	acc	tat	gca	cag	agc	tac	gca	242	
Pro	Met	Val	Trp	Asn	Glu	Thr	Leu	Ala	Thr	Tyr	Ala	Gln	Ser	Tyr	Ala		

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggt caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

<210> 84

<211> 176

<212> PRT

<213> Arabidopsis thaliana

<400> 84

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

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Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp
   115                               120               125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg
   130                               135               140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val
   145                               150               155               160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr
   165                               170               175

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<210> 85
 <211> 988
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(977)

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      Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe
        1                               5               10

tta gtt ttg ttg ttt gct caa gcc aat tgc caa ggt ttg aaa gta ggt 98
Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly
   15                               20               25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146
Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val
   30                               35               40               45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194
Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu
        50                               55               60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242
Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
        65                               70               75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290
Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn
   80                               85               90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338
Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu
   95                               100              105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386
Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu
  110                               115              120              125

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gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val
130 135 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn
145 150 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530
Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg
160 165 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His
175 180 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn
190 195 200 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala
210 215 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Ala Leu
225 230 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr
240 245 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu
255 260 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His
270 275 280 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly
290 295 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys
305 310 315

cgg tct gct aat taa gagatataga aa 989
Arg Ser Ala Asn
320

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<210> 86

<211> 321

<212> PRT

<213> Arabidopsis thaliana

<400> 86

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Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu
 1           5           10           15

Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser
 20           25           30

Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp
 35           40           45

Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe
 50           55           60

Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp
 65           70           75           80

Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu
 85           90           95

Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val
 100          105          110

Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg
 115          120          125

Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly
 130          135          140

Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser
 145          150          155          160

Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly
 165          170          175

Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly
 180          185          190

Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly
 195          200          205

Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu
 210          215          220

Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp
 225          230          235          240

Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala
 245          250          255

Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser
 260          265          270

Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met
 275          280          285

Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

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                290                295                300
Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
305                310                315                320
Asn

<210> 87
<211> 650
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (8)..(634)

<400> 87
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      Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu
        1                5                10

tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc 97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro
15                20                25                30

cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct 145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala
        35                40                45

tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag 193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu
        50                55                60

ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt 241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe
        65                70                75

gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct 289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala
        80                85                90

aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt 337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg
        95                100                105                110

gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt 385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val
        115                120                125

aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt 433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe
        130                135                140

gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc 481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr

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145          150          155
ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg 529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser
160          165          170

cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa 577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu
175          180          185          190

aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc 625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser
195          200          205

aag cgt taa gagttttata tatcat 650
Lys Arg

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<210> 88
<211> 208
<212> PRT
<213> Arabidopsis thaliana

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<400> 88
Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe
1          5          10          15

Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro Arg Ala
20          25          30

Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu
35          40          45

Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val
50          55          60

Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala
65          70          75          80

Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val
85          90          95

Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala
100         105         110

Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val
115         120         125

Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys
130         135         140

Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly
145         150         155         160

Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu
165         170         175

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Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg
 195 200 205

<210> 89
 <211> 1223
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (16)..(1215)

<400> 89
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 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala
 1 5 10

gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195
 Pro Lys Gly Ala Ser Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro
 385 390 395

ctt aag caa taa gcttttag 1223
 Leu Lys Gln
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<210> 90
 <211> 399
 <212> PRT
 <213> Arabidopsis thaliana

<400> 90
 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala Glu Met Ala Arg
 1 5 10 15
 Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly Gln Leu Lys Ala
 20 25 30
 Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala
 35 40 45
 Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg
 50 55 60
 Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr
 65 70 75 80
 Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr
 85 90 95
 Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln
 100 105 110
 Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly
 115 120 125
 Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu
 130 135 140
 Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr
 145 150 155 160
 Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln
 165 170 175
 Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr
 180 185 190
 Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His
 195 200 205
 Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys
 225 230 235 240

Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val
 245 250 255

Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu
 260 265 270

Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly
 275 280 285

Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp
 290 295 300

Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp
 305 310 315 320

Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala
 325 330 335

Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu
 340 345 350

Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys
 355 360 365

Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala
 370 375 380

Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln
 385 390 395

<210> 91
 <211> 536
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(524)

<400> 91
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 Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe
 1 5 10

gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu
 15 20 25

tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr
 30 35 40 45

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aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
          50                      55                      60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
          65                      70                      75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
          80                      85                      90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
          95                      100                     105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
        110                      115                      120                     125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
          130                      135                      140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
          145                      150                     155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
          160                      165                      170

agaagttgtt ta 536

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<210> 92
 <211> 170
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 92
Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe Val Tyr Gly
 1          5                      10                      15

Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
          20                      25                      30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
          35                      40                      45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
          50                      55                      60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
          65                      70                      75                      80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

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85 90 95

Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val Trp Ala Asn
100 105 110

Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp Lys
115 120 125

Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu
130 135 140

Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe
145 150 155 160

Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
165 170

<210> 93
<211> 293
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (16)..(71)

<220>
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<222> (197)..(278)

<400> 93
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Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys
1 5 10

aaa tgt ggt gat tgc tgc ag gtaaacacctta gattctctct tcattaactt 101
Lys Cys Gly Asp Ser Cys Se
15

atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161

tcttataactt ctgttggtttt tttggtatga caaag t tgc gag aag aac tac aac 215
r Cys Glu Lys Asn Tyr Asn
20 25

aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263
Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser
30 35 40

agc tgt aac tgt tga agaaattatc agcat 293
Ser Cys Asn Cys
45

<210> 94

<211> 45
 <212> PRT
 <213> Arabidopsis thaliana

<400> 94
 Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys Lys Cys Gly Asp
 1 5 10 15
 Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser
 20 25 30
 Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys
 35 40 45

<210> 95
 <211> 880
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (14)..(868)

<400> 95
 cacaccaaca cca atg tct gct tct tct tta ttt aat ctc cca ttg att 49
 Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile
 1 5 10
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe
 15 20 25
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe
 30 35 40
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met
 45 50 55 60
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val
 65 70 75
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His
 80 85 90
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser
 95 100 105
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser
 110 115 120

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aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
205 210 215 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
270 275 280

tga acatcttttt tt 880
285

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<210> 96
<211> 284
<212> PRT
<213> Arabidopsis thaliana

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<400> 96
Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
1 5 10 15
Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
20 25 30

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

<210> 97
 <211> 831
 <212> DNA
 <213> Arabidopsis thaliana
 <220>

<221> CDS

<222> (18)..(821)

<400> 97

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tgcactactc aacctca atg gcc gcc tca aca atg gct ctc tcc tcc cct 50
               Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro
                 1                 5                 10

gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc 98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
              15                20                25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag 146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
              30                35                40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg 194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
              45                50                55

ggt cca ttc tct ggc gaa tca cgg agc tac ctt acc gga gag ttc ccc 242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
              60                65                70                75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca 290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
              80                85                90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg 338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
              95                100               105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga 386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
              110               115               120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc 434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
              125               130               135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct 482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
              140               145               150               155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc 530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
              160               165               170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag 578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
              175                180               185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc 626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
              190                195               200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga 674

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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly
 205                210                215
aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722
Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val
220                225                230                235
act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770
Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro
                240                245                250
gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818
Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
                255                260                265
tga gccaaagtttt 831

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<210> 98
 <211> 267
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 98
Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro Ala Phe Ala Gly Lys
 1                5                10                15
Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val Leu Gly Ser Gly Arg
                20                25                30
Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser
                35                40                45
Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly
                50                55                60
Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp
                65                70                75                80
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg
                85                90                95
Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
                100                105                110
Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu
                115                120                125
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu
                130                135                140
Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala
                145                150                155                160
Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg
                165                170                175

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Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro
      180                      185                      190
Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe
      195                      200                      205
Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe
      210                      215                      220
Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro
      225                      230                      235                      240
Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala
      245                      250                      255
Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
      260                      265

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<210> 99
<211> 855
<212> DNA
<213> Arabidopsis thaliana

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<220>
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<222> (15)..(164)

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<220>
<221> CDS
<222> (257)..(305)

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<220>
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<222> (416)..(843)

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<400> 99
cacagtatta acaa atg gca gga atc aaa gtt ttc ggt cac cca gct tcc 50
          Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser
          1                      5                      10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98
Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp
      15                      20                      25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146
Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu
      30                      35                      40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194
Pro Phe Ile Leu Arg Asn
      45                      50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

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ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att    301
  Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile
                    55                                60                                65

ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt    355
Phe G

atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa    462
lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys
                    70                                75                                80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg    510
Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met
                    85                                90                                95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt    558
Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu
                    100                               105                               110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa    606
Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys
                    115                               120                               125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt    654
Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val
                    130                               135                               140                               145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc    702
Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe
                    150                               155                               160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga    750
Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly
                    165                               170                               175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg    798
Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp
                    180                               185                               190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa    843
Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
                    195                               200                               205

gtgaatctca aa                                                    855

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<210> 100

<211> 208

<212> PRT

<213> Arabidopsis thaliana

<400> 100

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Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser Thr Ala Thr Arg
  1              5              10              15

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

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<210> 101
<211> 512
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (12)..(67)

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<220>
<221> CDS
<222> (241)..(309)

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<220>
<221> CDS
<222> (417)..(492)

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<400> 101
tatctgaaaa a atg tca gag acc aac aag aat gcc ttc caa gcc ggt cag 50

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Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln
  1           5           10
acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact 97
Thr Ala Gly Lys Ala Gl
  15
cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157
actagaaaatt tcagttactt gtttaattta gtttgcgta attatgtaat tgatgatttt 217
atggittacaa tggttgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268
u Glu Lys Ser Asn Val Leu Leu Asp Lys
  20           25
gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl
  30           35           40
ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagctttacat 379
gtacgcagat ttctgatatg gttatgtata tgttata g gcg gga aag agt gta 432
n Ala Gly Lys Ser Val
  45
tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480
Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
  50           55           60
ctg aac aag tag agattcgggt caaatttggg 512
Leu Asn Lys
  65

<210> 102
<211> 66
<212> PRT
<213> Arabidopsis thaliana

<400> 102
Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly
  1           5           10           15
Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
  20           25           30
Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser
  35           40           45
Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
  50           55           60
Asn Lys
  65

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<210> 103
 <211> 1138
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (11)..(1123)

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<400> 103
aaaacaaaa atg gcg act ttg gtt gat cct cct aat ggg ata agg aat   49
          Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn
            1              5              10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac   97
Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
  15              20              25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt  145
Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
  30              35              40              45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag   193
Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
          50              55              60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt   241
Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
          65              70              75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct   289
Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
      80              85              90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt   337
Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
  95              100              105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag   385
Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
 110              115              120              125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag   433
Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
          130              135              140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga   481
Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
          145              150              155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag   529
Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
          160              165              170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc   577
Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
          175              180              185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
190 195 200 205

ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
210 215 220

tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
225 230 235

gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
240 245 250

aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
255 260 265

att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
270 275 280 285

ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
290 295 300

ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
305 310 315

tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009
Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
320 325 330

cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
335 340 345

gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
350 355 360 365

tta aac act gag ctc tga gctcaagtct tggtt 1138
Leu Asn Thr Glu Leu
370

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<210> 104
 <211> 370
 <212> PRT
 <213> Arabidopsis thaliana

<400> 104
 Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn Glu Gly Lys

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

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<210> 105
<211> 445
<212> DNA
<213> Arabidopsis thaliana
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<220>  
<221> CDS  
<222> (20) .. (430)
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[illegible]

cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430
 His Ile His Lys Ser Leu Ile Asn Lys Thr Thr Lys Glu
 125 130 135

tgtgtagctt tttat 445

<210> 106
 <211> 136
 <212> PRT
 <213> Arabidopsis thaliana

<400> 106
 Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala Ala Lys Thr Met Ala
 1 5 10 15
 Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Pro Ile Ser Arg Ser
 20 25 30
 Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
 35 40 45
 Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
 50 55 60
 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
 65 70 75 80
 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
 85 90 95
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
 100 105 110
 Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
 115 120 125
 Leu Ile Asn Lys Thr Thr Lys Glu
 130 135

<210> 107
 <211> 930
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (14)..(916)

<400> 107
 gccctccttg ctt atg tac tta cca aaa cgt ggc aat ttg ttc gaa ctc 49
 Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu
 1 5 10

tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
tggt gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat	529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

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Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg
      240                      245                      250
ctt cgt ttt aat gtc aag cgt tgt gta tca tat tgc ctt gat gaa gag 817
Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
      255                      260                      265
agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865
Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
      270                      275                      280
att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913
Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
      285                      290                      295                      300
tga agataaaaagt aatg 930

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<210> 108
 <211> 300
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 108
Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu Tyr Asp Pro Leu
  1                      5                      10                      15
His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu Ala Lys Ser Thr
      20                      25                      30
Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser
      35                      40                      45
Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val
      50                      55                      60
Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
      65                      70                      75                      80
Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
      85                      90                      95
Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr
      100                     105                     110
Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His
      115                     120                     125
Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln
      130                     135                     140
Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
      145                     150                     155                     160
Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
      165                     170                     175

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Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly
 180 185 190
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His
 195 200 205
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp
 210 215 220
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn
 225 230 235 240
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn
 245 250 255
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro
 260 265 270
 Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro Ile Glu Asn Leu
 275 280 285
 Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
 290 295 300

<210> 109
 <211> 2640
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (145)..(981)
 <220>
 <221> CDS
 <222> (1439)..(1727)

<220>
 <221> CDS
 <222> (1817)..(2126)

<220>
 <221> CDS
 <222> (2204)..(2330)

<220>
 <221> CDS
 <222> (2405)..(2518)

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gatacctaaa ccaaattccaa ttca atg gcg gaa gaa gca aaa tcc aaa gga 171
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      1 5

aac gca gct ttc tct tcc ggc gat tac gcc acc gca ata acc cat ttc 219
Asn Ala Ala Phe Ser Ser Gly Asp Tyr Ala Thr Ala Ile Thr His Phe
10 15 20 25

aca gaa gca atc aac ctt tca cca acc aat cac atc ctc tac tca aac 267
Thr Glu Ala Ile Asn Leu Ser Pro Thr Asn His Ile Leu Tyr Ser Asn
30 35 40

aga tcc gct tct tac gct tct ctc cac cgt tac gaa gaa gct tta tca 315
Arg Ser Ala Ser Tyr Ala Ser Leu His Arg Tyr Glu Glu Ala Leu Ser
45 50 55

gac gcg aag aag act ata gag ctt aaa cct gat tgg tct aaa gga tat 363
Asp Ala Lys Lys Thr Ile Glu Leu Lys Pro Asp Trp Ser Lys Gly Tyr
60 65 70

agc cga tta ggt gct gcg ttt att gga ttg tcc aag ttt gat gaa gcg 411
Ser Arg Leu Gly Ala Ala Phe Ile Gly Leu Ser Lys Phe Asp Glu Ala
75 80 85

gtt gat tcg tat aag aaa gga tta gag att gat ccg agt aat gag atg 459
Val Asp Ser Tyr Lys Lys Gly Leu Glu Ile Asp Pro Ser Asn Glu Met
90 95 100 105

ctt aaa tcg gga tta gct gat gct tcg aga tct agg gtt tcg tca aag 507
Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser Lys
110 115 120

tcg aat cct ttt gtt gat gcg ttt caa ggg aag gag atg tgg gag aag 555
Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu Lys
125 130 135

ttg acg gcg gat ccg ggg act agg gtt tat ttg gag cag gat gat ttt 603
Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp Phe
140 145 150

gtt aag acg atg aag gag att cag agg aac cct aat aat ctt aat ttg 651
Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn Leu
155 160 165

tat atg aag gat aag aga gtt atg aag gct tta ggg gtt ttg ttg aat 699
Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn
170 175 180 185

gtg aag ttt ggt gga tct agt ggt gaa gat act gag atg aag gag gct 747
Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala
190 195 200

gat gag agg aaa gag cct gaa ccg gag atg gaa cct atg gag ttg acg 795
Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr
205 210 215

gag gag gag agg cag aag aag gag aga aag gag aag gct ttg aag gag 843

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Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu
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 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala
 235 240 245
 gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg 939
 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser
 250 255 260 265
 tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag 981
 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys
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 Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys
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 Met Ala Arg Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln
 320 325 330
 aaa gct ctt aca gag cat cgt aat cca gat aca ttg aag aaa ctg aac 1648
 Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn
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 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp
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 cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag 1747
 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G
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 ly Asn Gly Phe Phe Lys Glu Gln Lys Tyr Pro Glu Ala Val
 380 385
 aag cat tat tca gaa gca atc aaa aga aac ccg aac gac gtg agg gca 1905
 Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro Asn Asp Val Arg Ala
 390 395 400 405
 tat agc aac aga gct gct tgt tac aca aag tta gga gca tta cca gag 1953
 Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu Gly Ala Leu Pro Glu
 410 415 420
 gga ttg aaa gat gct gaa aaa tgc att gag ctg gac cca agt ttc acg 2001
 Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu Asp Pro Ser Phe Thr
 425 430 435
 aaa gga tac agt aga aaa gga gct att caa ttt ttc atg aag gaa tac 2049
 Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe Phe Met Lys Glu Tyr
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 Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu Lys His Asp Pro Lys
 455 460 465
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 Asn Gln Glu Phe Leu Asp Gly Val Arg Ar
 470 475
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 tgt gtg gaa cag ata aac aaa gcg agc cgt ggt gat ctg act cca gaa 2252
 Cys Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu
 480 485 490 495
 gaa ttg aag gag aga caa gca aag gca atg caa gat cct gaa gtt cag 2300
 Glu Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln
 500 505 510
 aac ata tta tcg gat cca gtg atg aga cag gtaaaagcag tggcaagcat 2350
 Asn Ile Leu Ser Asp Pro Val Met Arg Gln
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 Val
 cta gtg gac ttt caa gag aat ccg aaa gct gca caa gag cat atg aag 2455
 Leu Val Asp Phe Gln Glu Asn Pro Lys Ala Ala Gln Glu His Met Lys
 525 530 535
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 Asn Pro Met Val Met Asn Lys Ile Gln Lys Leu Val Ser Ala Gly Ile
 540 545 550
 gtt cag gtc cgg taa attggttatg ctaaaccgga gtggtatatt gaatcaaacc 2558

Val Gln Val Arg
555

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

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225                230                235                240
Tyr Lys Lys Lys Asp Phe Gly Arg Ala Val Glu His Tyr Thr Lys Ala
      245                250                255
Met Glu Leu Asp Asp Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala
      260                265                270
Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp
      275                280                285
Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile
      290                295                300
Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg
      305                310                315                320
Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu
      325                330                335
Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu
      340                345                350
Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile
      355                360                365
Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys
      370                375                380
Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro
      385                390                395                400
Asn Asp Val Arg Ala Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu
      405                410                415
Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu
      420                425                430
Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe
      435                440                445
Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu
      450                455                460
Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys
      465                470                475                480
Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu
      485                490                495
Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln Asn
      500                505                510
Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu
      515                520                525
Asn Pro Lys Ala Ala Gln Glu His Met Lys Asn Pro Met Val Met Asn

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atcaagaaa atg gga aga gca ccg tgt tgt gat aag gcc aac gtg aag aaa 171
      Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys
          1             5             10

ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag 219
Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu
15             20             25             30

aat agt ggc aca gga ggc aac tgg att gct ttg cct cag aaa att g 265
Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G
35             40             45

gtatgtatta cttaaaactc acttttgatt taaaattggc actgagaggtt tccaaatagt 325
actttgagac cgtggtcgtg ttaaatttgt gtgttgatga tattttattta catggtatag 385

gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432
ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr
50             55             60

ttg aga cca aac atc aaa cat ggt ggc ttc tcc gag gaa gaa gac aac 480
Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn
65             70             75

atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525
Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar
80             85

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cttacatata tatcatcata tgcattgatg aatattatta attgacacac ttattcttga 585
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                                     g Trp Ser Ile Ile Ala Ala
                                     90                      95

caa ttg ccg gga aga acc gac aac gat atc aaa aac tat tgg aac acg 688
Gln Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr
                                     100                      105                      110

agg ctg aag aag aag ctt ctg aac aaa caa agg aaa gag ttc caa gaa 736
Arg Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu
                                     115                      120                      125

gcg cga atg aag caa gag atg gtg atg atg aaa agg caa caa caa gga 784
Ala Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly
                                     130                      135                      140

caa gga caa ggt caa agt aat ggt agt acg gat ctt tat ctt aac aac 832
Gln Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn
                                     145                      150                      155

atg ttt gga tca tca cca tgg cca tta cta cca caa ctt cct cct cca 880
Met Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro
160                      165                      170                      175

cat cat caa ata cct ctt gga atg atg gaa cca aca agc tgt aac tac 928
His His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr
180                      185                      190

tac caa acg aca ccg tct tgt aac cta gaa caa aag cca ttg atc aca 976
Tyr Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr
195                      200                      205

ctc aag aac atg gtc aag att gaa gaa gaa cag gaa agg aca aac cct 1024
Leu Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro
210                      215                      220

gat cat cat cat caa gat tct gtc aca aac cct ttt gat ttc tct ttc 1072
Asp His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe
225                      230                      235

tct cag ctt ttg tta gat ccc aat tac tat ctg gga tca gga ggg gga 1120
Ser Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly
240                      245                      250                      255

gga gaa gga gat ttt gct atc atg agc agc agc aca aac tca cca tta 1168
Gly Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu
260                      265                      270

cca aac aca agt agt gat caa cat cca agt caa cag caa gag att ctt 1216
Pro Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu
275                      280                      285

caa tgg ttt ggg agc agt aac ttt cag aca gaa gca atc aac gat atg 1264
Gln Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met
290                      295                      300

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aca aaa gtc tat gga gac gcc tca gta gcc gga gcc gct gtc cga gca 1360
Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala
320 325 330 335

gct ttg ggc gga ggg aca acg agt aca tcg gcg gat caa agt aca ata 1408
Ala Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile
340 345 350

agt tgg gag gat ata act tct cta gtt aat tcc gaa gat gca agt tac 1456
Ser Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr
355 360 365

ttc aat gcg cca aat cat gtg taa cttttgttt aaaactttat ttgtacttaa 1510
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Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile Gly Leu Arg
35 40 45

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

Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn Ile Ile Cys
65 70 75 80

Asn Leu Tyr Val Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln
85 90 95

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

Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu Ala
115 120 125

Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly Gln
130 135 140

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Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn Met
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 165 170 175
 His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr
 180 185 190
 Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr Leu
 195 200 205
 Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro Asp
 210 215 220
 His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser
 225 230 235 240
 Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly Gly
 245 250 255
 Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro
 260 265 270
 Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu Gln
 275 280 285
 Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met Phe
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 Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn Thr
 305 310 315 320
 Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala Ala
 325 330 335
 Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile Ser
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Gly Ser Ser Val Ala Lys Leu Ala Ile Arg Arg Thr Leu Ser Gln Ser
      10           15           20

cgt tgt ggt tca tat gcc act aga aca agg gtt ttg cct tgt caa acc 151
Arg Cys Gly Ser Tyr Ala Thr Arg Thr Arg Val Leu Pro Cys Gln Thr
      25           30           35

aga tgt ttt cac tct aca ata ctc aaa tca aag gca gag tct gct gca 199
Arg Cys Phe His Ser Thr Ile Leu Lys Ser Lys Ala Glu Ser Ala Ala
      40           45           50

cct gtt cca cgt cct gtc cca ctt tct aag cta act gat agc ttc tta 247
Pro Val Pro Arg Pro Val Pro Leu Ser Lys Leu Thr Asp Ser Phe Leu
      55           60           65

gat gga aca agc agt gtg tat cta gag gag tta caa aga gct tgg gag 295
Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu Leu Gln Arg Ala Trp Glu
      75           80           85

gct gat ccc aac agt gtt gat gag tcg tgg gat aac ttt ttt agg aat 343
Ala Asp Pro Asn Ser Val Asp Glu Ser Trp Asp Asn Phe Phe Arg Asn
      90           95           100

ttt gtg ggt cag gct tct aca tcg cct ggt atc tcg ggg caa acc att 391
Phe Val Gly Gln Ala Ser Thr Ser Pro Gly Ile Ser Gly Gln Thr Ile
      105           110           115

caa gaa agc atg cgt ttg ttg ttg cta gtt aga gct tac cag gtt aat 439

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Gly	His	Met	Lys	Ala	Lys	Leu	Asp	Pro	Leu	Gly	Leu	Glu	Lys	Arg	Glu		
135					140					145					150		
att	cca	gag	gat	ctc	acg	cca	ggt	ctt	tat	ggg	ttt	act	gag	gct	gat	535	
Ile	Pro	Glu	Asp	Leu	Thr	Pro	Gly	Leu	Tyr	Gly	Phe	Thr	Glu	Ala	Asp		
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ctt	gat	cgg	gaa	ttc	ttt	ctg	ggt	gta	tgg	agg	atg	tcg	ggt	ttt	ctc	583	
Leu	Asp	Arg	Glu	Phe	Phe	Leu	Gly	Val	Trp	Arg	Met	Ser	Gly	Phe	Leu		
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Glu	Gln	Ala	Tyr	Cys	Gly	Thr	Ile	Gly	Tyr	Glu	Tyr	Met	His	Ile	Ala		
		200				205						210					
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Asp	Arg	Asp	Lys	Cys	Asn	Trp	Leu	Arg	Asp	Lys	Ile	Glu	Thr	Pro	Thr		
215					220					225				230			
cct	cga	cag	tac	aat	agt	gag	cgt	cgg	atg	gtt	att	tat	gat	agg	ctt	775	
Pro	Arg	Gln	Tyr	Asn	Ser	Glu	Arg	Arg	Met	Val	Ile	Tyr	Asp	Arg	Leu		
				235					240					245			
acc	tgg	agc	aca	cag	ttt	gag	aat	ttc	ttg	gct	act	aag	tgg	acc	acg	823	
Thr	Trp	Ser	Thr	Gln	Phe	Glu	Asn	Phe	Leu	Ala	Thr	Lys	Trp	Thr	Thr		
			250					255					260				
gct	aaa	agg	ttt	gga	ctg	gaa	ggt	gct	gaa	tct	ttg	att	cct	ggc	atg	871	
Ala	Lys	Arg	Phe	Gly	Leu	Glu	Gly	Ala	Glu	Ser	Leu	Ile	Pro	Gly	Met		
		265					270					275					
aag	gag	atg	ttc	gat	agg	tct	gca	gat	ctc	ggg	gta	gag	aac	ata	gtt	919	
Lys	Glu	Met	Phe	Asp	Arg	Ser	Ala	Asp	Leu	Gly	Val	Glu	Asn	Ile	Val		
		280				285					290						
atc	ggt	atg	ccc	cat	agg	ggt	cga	ctt	aat	gtt	ttg	ggt	aat	gtt	gtt	967	
Ile	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Gly	Asn	Val	Val		
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aga	aaa	cct	cta	cgc	caa	ata	ttc	agc	gag	ttt	agc	ggt	ggt	act	agg	1015	
Arg	Lys	Pro	Leu	Arg	Gln	Ile	Phe	Ser	Glu	Phe	Ser	Gly	Gly	Thr	Arg		
				315					320					325			
cca	gta	gat	gaa	gtt	ggg	ctt	tac	acc	gga	aca	ggt	gat	gtg	aaa	tac	1063	
Pro	Val	Asp	Glu	Val	Gly	Leu	Tyr	Thr	Gly	Thr	Gly	Asp	Val	Lys	Tyr		
			330					335					340				
cac	ttg	ggt	aca	tct	tat	gat	cgt	cca	act	aga	gga	ggc	aaa	cat	ctc	1111	
His	Leu	Gly	Thr	Ser	Tyr	Asp	Arg	Pro	Thr	Arg	Gly	Gly	Lys	His	Leu		

345	350	355	
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gtt gtg ata ggt aaa acc aga gcg aaa caa tat tac acg aaa gac gag Val Val Ile Gly Lys Thr Arg Ala Lys Gln Tyr Tyr Thr Lys Asp Glu 375 380 385 390			1207
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gcc gga caa gga gtg gtg tat gaa act ctc cat ctt agt gca ctt cct Ala Gly Gln Gly Val Val Tyr Glu Thr Leu His Leu Ser Ala Leu Pro 410 415 420			1303
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gac att gaa gca gta gtg cat gct tgt gag ctt gct gct gag tgg cgc Asp Ile Glu Ala Val Val His Ala Cys Glu Leu Ala Ala Glu Trp Arg 475 480 485			1495
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Gln Lys Lys Val Ser Ser Ile Leu Asn Glu Glu Tyr Glu Ala Ser Lys
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 Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile Arg Asn Thr Gl
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 y Val Lys Pro Glu Ile
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 cca cac aga gga gtt aaa aga gtt tat gaa caa cgt gct caa atg att 2163
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 Ala Thr Leu Val Val Glu Gly Asn His Val Arg Leu Ser Gly Gln Asp
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 Val Glu Arg Gly Thr Phe Ser His Arg His Ser Val Leu His Asp Gln
 670 675 680
 gaa acc ggg gag gaa tat tgt ccc ctc gat cac cta atc aaa aac caa 2355
 Glu Thr Gly Glu Glu Tyr Cys Pro Leu Asp His Leu Ile Lys Asn Gln
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 gac cct gaa atg ttc act gtc agc aac ag gtatgcattt ttttttaatc 2404
 Asp Pro Glu Met Phe Thr Val Ser Asn Se
 700 705
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 cag c tcc ctt tca gaa ttt ggt gtt ctc ggt ttc gaa ctg ggt tat tgc 2513
 r Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu Gly Tyr Se
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 r Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln Phe Gly As
 725 730 735
 ttt gct aat ggc gca caa gtt atg ttt gat cag ttc ata agc agt ggg 2609
 p Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile Ser Ser Gl

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y Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu Leu Pro Hi
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gga tat gat ggt cag ggt cct gaa cat tcc agt gga aga ttg gaa cgt 2705
s Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg Leu Glu Ar
775              780              785
ttc ctt cag gtatattata tgaccgatac ttaccggttaa gattctctcc 2754
g Phe Leu Gln
actttttgta ttgttttccc tctcatttga aaatttttaac tgcag atg agt gat gac 2811
Met Ser Asp As
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aat cct tac gtt atc cct gag atg gac cca act ctt cga aag cag att 2859
p Asn Pro Tyr Val Ile Pro Glu Met Asp Pro Thr Leu Arg Lys Gln Il
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r Phe His Val Leu Arg Arg Gln
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aatgttgta ctttaatttc gtattcttca cactcacatg ctgatatca tccatttgca 3018
g ata cac agg gac ttt cgc aag cct ctt ata gtg atg gcc ccc aaa aac 3067
Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys As
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850              855              860
gtt aaa gga cat cct gga ttt gac aag caa gga act cga ttt aaa cgg 3163
p Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys Ar
865              870              875              880
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g Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu A
885              890
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Val Leu Pro Cys Gln Thr Arg Cys Phe His Ser Thr Ile Leu Lys Ser
              35              40              45
Lys Ala Glu Ser Ala Ala Pro Val Pro Arg Pro Val Pro Leu Ser Lys
              50              55              60
Leu Thr Asp Ser Phe Leu Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu
  65              70              75              80
Leu Gln Arg Ala Trp Glu Ala Asp Pro Asn Ser Val Asp Glu Ser Trp
              85              90              95
Asp Asn Phe Phe Arg Asn Phe Val Gly Gln Ala Ser Thr Ser Pro Gly
              100              105              110
Ile Ser Gly Gln Thr Ile Gln Glu Ser Met Arg Leu Leu Leu Val
              115              120              125
Arg Ala Tyr Gln Val Asn Gly His Met Lys Ala Lys Leu Asp Pro Leu
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Gly Leu Glu Lys Arg Glu Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr
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 Gly Phe Thr Glu Ala Asp Leu Asp Arg Glu Phe Phe Leu Gly Val Trp
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 Arg Met Ser Gly Phe Leu Ser Glu Asn Arg Pro Val Gln Thr Leu Arg
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 Ser Ile Leu Ser Arg Leu Glu Gln Ala Tyr Cys Gly Thr Ile Gly Tyr
 195 200 205
 Glu Tyr Met His Ile Ala Asp Arg Asp Lys Cys Asn Trp Leu Arg Asp
 210 215 220
 Lys Ile Glu Thr Pro Thr Pro Arg Gln Tyr Asn Ser Glu Arg Arg Met
 225 230 235 240
 Val Ile Tyr Asp Arg Leu Thr Trp Ser Thr Gln Phe Glu Asn Phe Leu
 245 250 255
 Ala Thr Lys Trp Thr Thr Ala Lys Arg Phe Gly Leu Glu Gly Ala Glu
 260 265 270
 Ser Leu Ile Pro Gly Met Lys Glu Met Phe Asp Arg Ser Ala Asp Leu
 275 280 285
 Gly Val Glu Asn Ile Val Ile Gly Met Pro His Arg Gly Arg Leu Asn
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 Val Leu Gly Asn Val Val Arg Lys Pro Leu Arg Gln Ile Phe Ser Glu
 305 310 315 320
 Phe Ser Gly Gly Thr Arg Pro Val Asp Glu Val Gly Leu Tyr Thr Gly
 325 330 335
 Thr Gly Asp Val Lys Tyr His Leu Gly Thr Ser Tyr Asp Arg Pro Thr
 340 345 350
 Arg Gly Gly Lys His Leu His Leu Ser Leu Val Ala Asn Pro Ser His
 355 360 365
 Leu Glu Ala Val Asp Pro Val Val Ile Gly Lys Thr Arg Ala Lys Gln
 370 375 380
 Tyr Tyr Thr Lys Asp Glu Asn Arg Thr Lys Asn Met Gly Ile Leu Ile
 385 390 395 400
 His Gly Asp Gly Ser Phe Ala Gly Gln Gly Val Val Tyr Glu Thr Leu
 405 410 415
 His Leu Ser Ala Leu Pro Asn Tyr Cys Thr Gly Gly Thr Val His Ile
 420 425 430
 Val Val Asn Asn Gln Val Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg
 435 440 445

Ser Ser Gln Tyr Cys Thr Asp Val Ala Lys Ala Leu Ser Ala Pro Ile
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 545 550 555 560
 Glu Tyr Glu Ala Ser Lys Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu
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 Ala Ser His Trp Thr Gly Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile
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 Arg Asn Thr Gly Val Lys Pro Glu Ile Leu Lys Asn Val Gly Lys Ala
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 Val Tyr Glu Gln Arg Ala Gln Met Ile Glu Ser Gly Glu Gly Ile Asp
 625 630 635 640
 Trp Gly Leu Gly Glu Ala Leu Ala Phe Ala Thr Leu Val Val Glu Gly
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 660 665 670
 His Arg His Ser Val Leu His Asp Gln Glu Thr Gly Glu Glu Tyr Cys
 675 680 685
 Pro Leu Asp His Leu Ile Lys Asn Gln Asp Pro Glu Met Phe Thr Val
 690 695 700
 Ser Asn Ser Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu
 705 710 715 720
 Gly Tyr Ser Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln
 725 730 73
 Phe Gly Ap Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile
 740 745 750

Ser Ser Gy Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu
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 770 775 780
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 785 790 795
 Glu Met Asp Pro Thr Leu Arg Lys Gln Ile Gln Glu Cys Asn Trp Gln
 800 805 810
 Val Val Asn Val Thr Thr Pro Ala Asn Trp Phe His Val Leu Arg Arg
 815 820 825
 Gln Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys
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 845 850 855
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 Arg Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu
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 890 895 900
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Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
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cgt caa atg gaa gac gga aaa gct atc cag ctg gtc ctt gat cag agc 147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
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act g gtacaccaac gccacagtta tatttttaaa cggaacatt ttgaaattaa 201
Thr G

tggtgttttt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga 258
ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg 306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
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aag atc aaa ctg att ccc gga gac tct gcc ggt acg gtc acc gct ttc 354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
60 65 70 75

tac gtaagtctat cattttactc cactagtttt gaaattttac acattcacac 407
Tyr

aataaaaaat aacattttct tgaaacacta acgggtcaaatt cattgatatg tctatag 464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc 512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
80 85 90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt 560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
95 100 105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac 608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
110 115 120

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Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
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Ile Val

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gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn
145 150 155

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Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val
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tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta 917
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu
175 180 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
190 195 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg 1013
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser
205 210 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc 1061
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala
220 225 230

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Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr
240 245 250

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Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile
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 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp
 65 70 75 80
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg
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 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys
 100 105 110
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 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr
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 Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly
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 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp
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Tyr Leu Ser Thr Ala Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
30           35           40

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Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
45           50           55

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Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
60           65           70

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Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
75           80           85

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Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
90           95           100           105

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Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
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Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
125           130           135

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Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
140           145           150

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Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
155           160           165

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Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
170           175           180           185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg 627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
190           195           200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att 675
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Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
270 275 280	
ggt cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att	915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
285 290 295	
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat	963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
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gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
315 320 325	
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga	1059
Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
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1399

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caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg 193
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gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc 241
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Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe
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Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu
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Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu	
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Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile	
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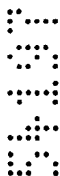
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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated polynucleic acid encoding an HSP 17.6A protein, or part of said polynucleic acid encoding the active domain of said HSP 17.6A protein when used to produce a transgenic plant having an enhanced tolerance or resistance to an environmental stress condition.
2. The isolated polynucleic acid according to claim 1 comprising a nucleotide sequence selected from the group consisting of:
 - (a) SEQ ID NO: 3 or the complementary strand thereof;
 - (b) a nucleotide sequence which hybridizes to the sequence defined in (a) or a fragment thereof;
 - (c) a nucleotide sequence that is degenerate with (a) or (b) as a result of the genetic code;
 - (d) a nucleotide sequence that is at least 50% identical to SEQ ID NO: 3, or a fragment thereof;
 - (e) a nucleotide sequence encoding a protein that has substantially the same biological activity as a protein having the amino acid sequence of SEQ ID NO: 4; and
 - (f) a nucleotide sequence encoding a fragment of a protein encoded by any one of (a) to (e).
3. The isolated polynucleic acid according to claim 1 or 2 wherein said polynucleic acid is derived from a plant.
4. The isolated polynucleic acid of claim 3 wherein the plant is *Arabidopsis thaliana*.
5. A recombinant or isolated polypeptide encoded by the polynucleic acid as defined in any one of claims 1 to 4, or a functional fragment thereof, when



used to produce a plant having an enhanced tolerance or resistance to environmental stress conditions.

6. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising transiently introducing into a plant cell a recombinant DNA comprising the isolated polynucleic acid as defined in any one of claims 1 to 4 suitable for expression in said plant cell in an amount effective to confer enhanced tolerance or resistance to environmental stress.
7. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising stably introducing into a plant cell a recombinant DNA comprising the isolated polynucleic acid as defined in any one of claims 1 to 4 suitable for expression in said plant cell in an amount effective to confer enhanced tolerance or resistance to environmental stress.
8. The method according to claim 6 or 7 wherein the recombinant DNA is introduced into the genome of the plant cell and comprises:
 - (i) the polynucleic acid as defined in any one of claims 1 to 4; and
 - (ii) a plant operable promoter,and wherein said polynucleic acid is in the same transcriptional unit and under the control of said plant operable promoter.
9. The method according to claim 6 or 7, wherein the recombinant DNA is introduced into the genome of the plant cell and comprises:

- (i) DNA encoding a protein which when expressed in said plant cell at an effective amount modulates the expression of an endogenous polynucleic acid as defined in any one of claims 1 to 4 or modulates the activity of a polypeptide as defined in claim 5; and

(ii) a plant operable promoter,

and wherein said DNA is in the same transcriptional unit and under the control of said plant operable promoter.

10. The method of claim 9 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme that modulates the expression of the polynucleic acid as defined in any one of claims 1 to 4 in the plant cell.
11. The method according to any one of claims 6 to 9 wherein the polynucleic acid as defined in any one of claims 1 to 4 is overexpressed in the plant cell thereby enhancing resistance of said plant cell to the environmental stress.
12. The method according to claim 11 wherein the polynucleic acid as defined in any one of claims 1 to 4 is overexpressed in the plant cell and wherein the environmental stress is salt stress.
13. The method according to any one of claims 6 to 9, 11 or 12 wherein the polynucleic acid as defined in any one of claims 1 to 4 is overexpressed in the plant cell thereby enhancing the yield of the plant under the environmental stress conditions.
14. The method according to any one of claims 6 to 9, 11 or 12 wherein the polynucleic acid as defined in any one of claims 1 to 4 is overexpressed in the plant cell thereby enhancing the growth of the plant under the environmental stress conditions.
15. The method according to any one of claims 6 to 9, 11 or 12 wherein the polynucleic acid as defined in any one of claims 1 to 4 is overexpressed in the plant cell thereby enhancing the development of the plant under the environmental stress conditions.
16. The method according to any one of claims 6 to 9, 11 or 12 wherein the polynucleic acid as defined in any one of claims 1 to 4 is overexpressed in

the plant cell thereby enhancing the productivity of the plant under the environmental stress conditions.

17. A recombinant polynucleic acid comprising:

- (i) the polynucleic acid as defined in any of claims 1 to 4; and
- (ii) a plant operable promoter,

wherein said polynucleic acid is in the same transcriptional unit and under the control of said plant operable promoter,

when used to produce a transgenic plant having an enhanced tolerance or resistance to an environmental stress condition.

18. A recombinant polynucleic acid comprising:

- (i) a DNA encoding a protein which when expressed in said plant cell at an effective amount modulates the expression of an endogenous polynucleic acid as defined in any one of claims 1 to 4 or modulates the activity of a polypeptide as defined in claim 5; and

- (ii) a plant operable promoter,

wherein said DNA is in the same transcriptional unit and under the control of said plant operable promoter,

when used to produce a transgenic plant having an enhanced tolerance or resistance to an environmental stress condition.

19. The recombinant polynucleic acid of claim 18 wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant modulates the expression of an endogenous polynucleic acid as defined in any of claims 1 to 4 or which modulates the activity of a protein of claim 5.

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20. The recombinant polynucleic acid according to any one of claims 17 to 19 wherein said plant operable promoter is a constitutive promoter.
21. The recombinant polynucleic acid according to any one of claims 17 to 19 wherein said plant operable promoter is a stress-inducible promoter or organ-specific promoter or tissue-specific promoter.
22. The recombinant polynucleic acid according to any one of claims 17 to 20 wherein said plant operable promoter is the CaMV 35S promoter. .
23. The recombinant polynucleic acid according to any one of claims 17 or 20 to 22 comprising at least part of the nucleotide sequence of SEQ ID NO: 3.
24. The recombinant polynucleic acid according to any one of claims 17 to 22 comprising at least part of the coding sequence of a gene encoding a protein comprising the amino acid sequence set forth in SEQ ID NO: 4.
25. A host cell comprising the polynucleic acid as defined in any one of claims 1 to 4 or the recombinant polynucleic acid according to any one of claims 17 to 24, or comprising a polypeptide according to claim 5.
26. The host cell of claim 25 which is a plant cell.
27. A transgenic plant or tissue consisting essentially of the host cell of claim 26.
28. A transgenic plant according to claim 27, said plant having an enhanced tolerance or resistance to an environmental stress condition.
29. A callus consisting essentially of the host cell of claim 26.
30. The callus of claim 29 when used to produce a whole plant.
31. The callus of claim 29 when used to produce a plant suspension culture.

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32. The callus of claim 31 wherein the suspension culture produces a secondary plant metabolite.
33. A harvestable part, organ, tissue or propagation material of a plant that comprise the isolated polynucleic acid according to any one of claims 1 to 4 or the recombinant polynucleic acid according to any one of claims 17 to 24, said part, organ, tissue or propagation material comprising said polynucleic acid.
34. A probe comprising a part of the polynucleic acid as defined in any one of claims 1 to 4 and which hybridizes specifically with said polynucleic acid or the complement thereof, when used as part of a pharmaceutical or agrochemical composition to enhance stress tolerance of a cell or organism.
35. A primer which is part of the polynucleic acid as defined in any one of claims 1 to 4 and which specifically amplifies said polynucleic acid or the complement thereof, when used as part of a pharmaceutical or agrochemical composition to enhance stress tolerance of a cell or organism.
36. A composition comprising the polynucleic acid as defined in any one of claims 1 to 4 and/or the polypeptide as defined in claim 5 or the probe as defined in claim 33, and/or a primer as defined in claim 34.
37. The composition as defined in claim 35 when used to enhance stress tolerance of a cell or organism.

Dated this 30th day of April 2003

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EDITORIAL NOTE

APPLICATION NUMBER - 54197/99

This specification does not contain drawing pages 1 to 10 or 12.

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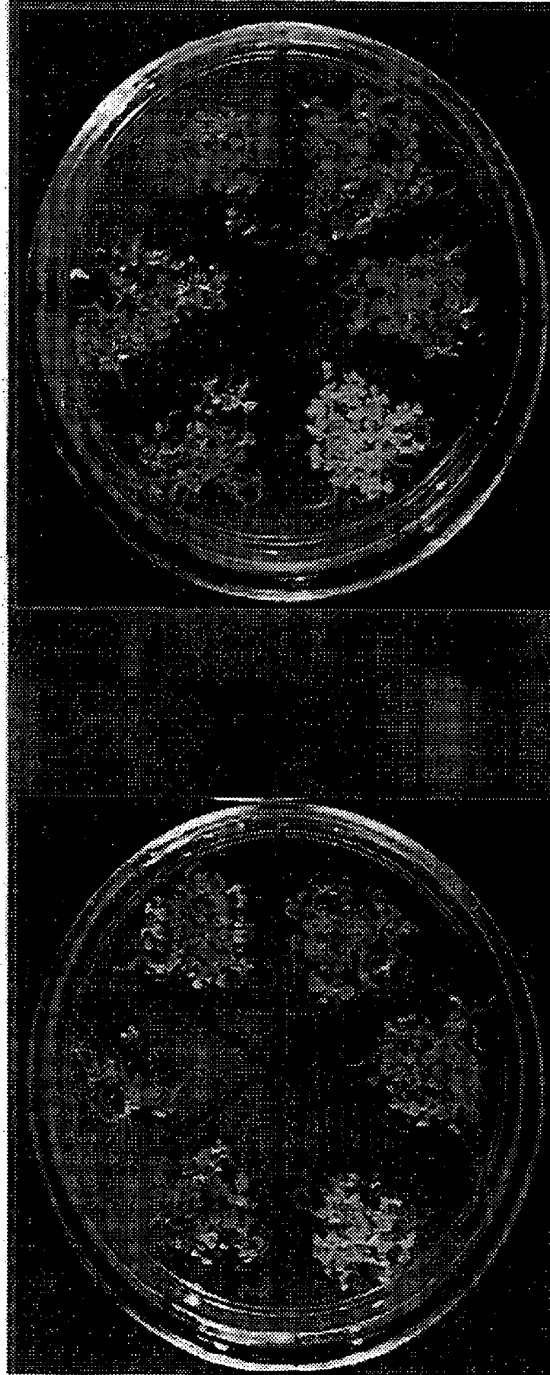


FIGURE 11

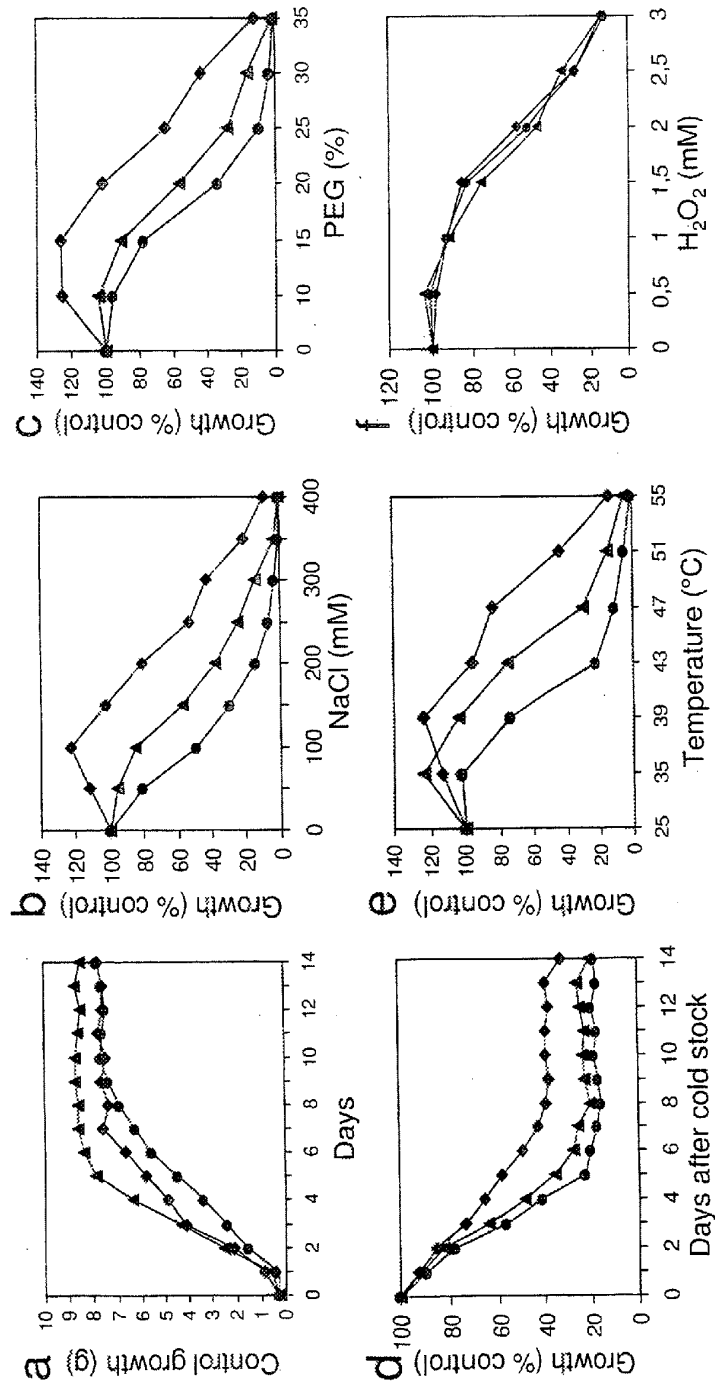


FIGURE 12B



FIGURE 13



FIGURE 14