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Lise Jouanin, Serge Berthet, Catherine Lapierre, Emmanuel Guiderdoni,  
Oumaya Bouchabke-Coussa, Richard Sibout, Jean-Charles Leplé, Julien  
Mazel, Brice Ayangma

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(54) **PRODUCTION OF PLANTS WITH REDUCED LIGNIN CONTENT**

(75) Inventors: **Lise Jouanin**, Noisy Le Roi (FR);  
**Serge Berthet**, Rombas (FR);  
**Catherine Lapierre**, Neauphle Le  
Chateau (FR); **Emmanuel**  
**Guiderdoni**, Aniane (FR); **Oumaya**  
**Bouchabke-Coussa**, Paris (FR);  
**Richard Sibout**, Jouy (FR);  
**Jean-Charles Leple**, Orleans (FR);  
**Julien Mazel**, Courdimanche (FR);  
**Brice Ayangma**, Tours (FR)

(73) Assignees: **INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE**, Paris (FR);  
**GENOPLANTE-VALOR**, Paris (FR)

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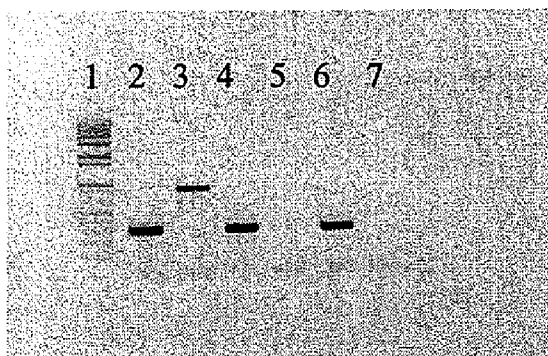
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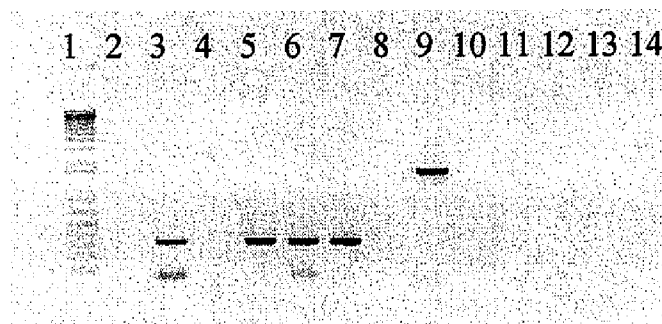
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(57) **ABSTRACT**

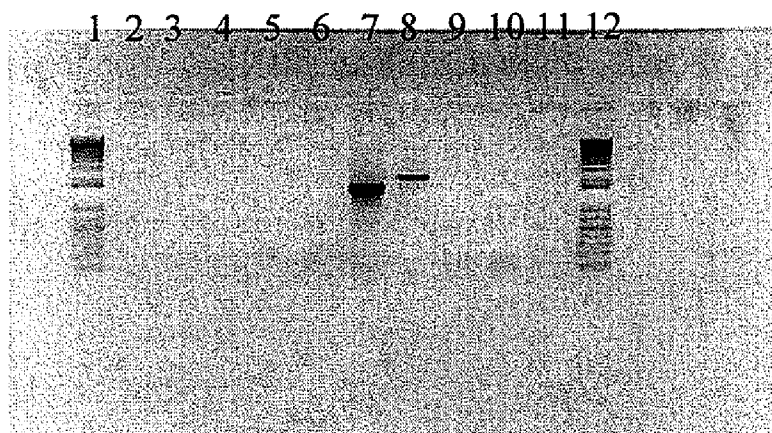
The invention relates to the production of plants having a reduced lignin content and in which the cellulose hydrolysis of the walls is increased, via the total or partial inhibition of the expression and/or the activity of two laccases in said plant.



A



B



C

Figure 1

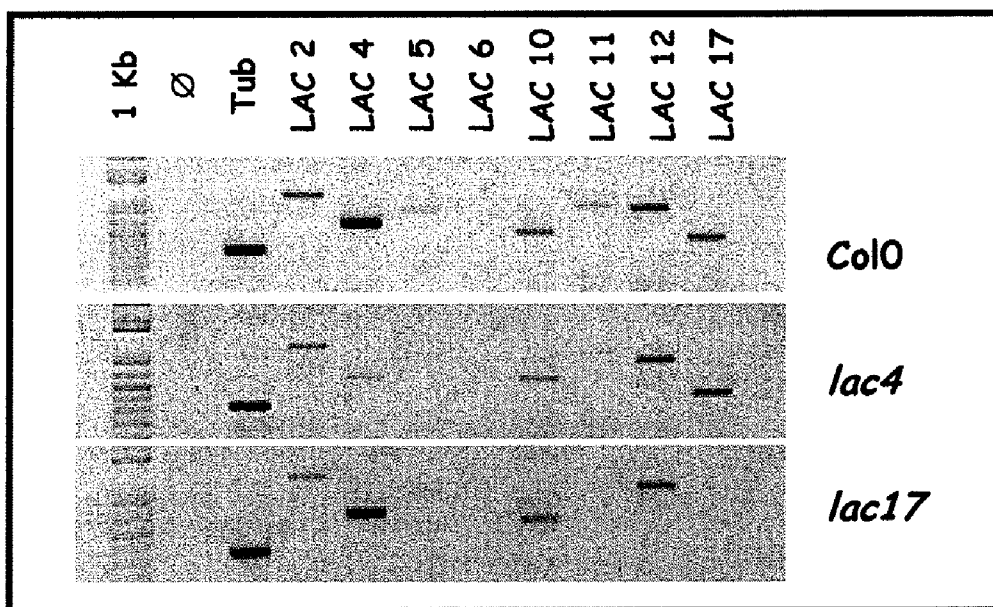


Figure 2

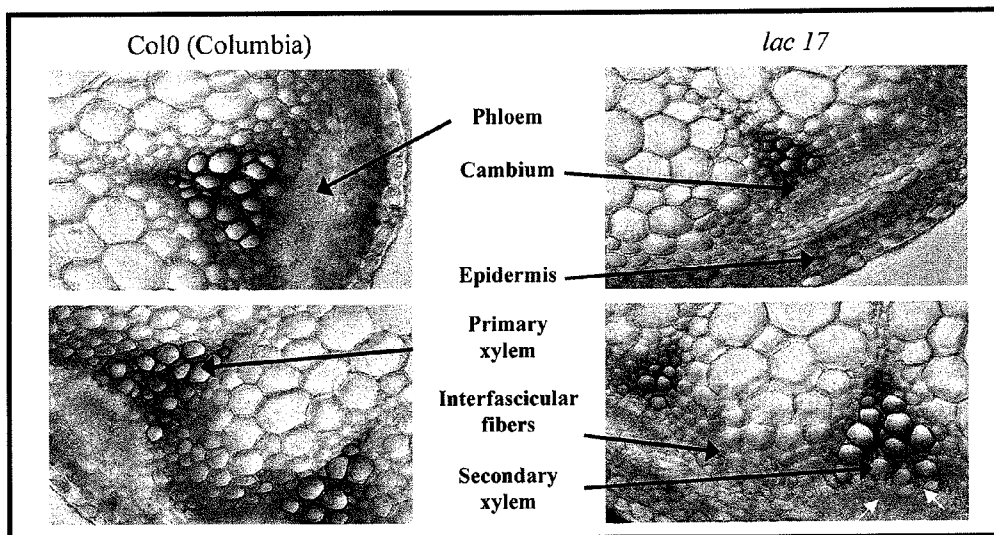


Figure 3

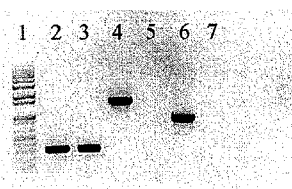


Figure 4

	SEQ ID No. 12	SEQ ID No. 38	SEQ ID No. 13	SEQ ID No. 39	SEQ ID No. 14	SEQ ID No. 40	SEQ ID No. 15	SEQ ID No. 41	% identify with SEQ ID No. 2	% similarity with SEQ ID No. 2
<i>A. thaliana</i>										
ATLAC17	X	-	X	-	X	-	X	-	100	100
<i>Zea mays</i>										
SEQ ID No. 5	X	-	X	-	X	-	X	-	>60	>75
SEQ ID No. 6	X	-	X	-	X	-	X	-	>60	>75
GI:162461426	X	-	X	-	X	-	X	-	72	85
GI:226503958	X	-	X	-	X	-	X	-	73	85
GI:226494660	X	-	X	-	X	-	X	-	72	84
GI:212721074	X	-	X	-	X	-	X	-	70	84
GI:162463584	X	-	X	-	X	-	X	-	62	74
GI:162461268	X	-	X	-	X	-	X	-	62	78
<i>S. officinarum</i>										
SEQ ID No. 7	X	-	X	-	X	-	X	-	>60	>75
<i>Sorghum bicolor</i>										
SEQ ID No. 8	X	-	X	-	X	-	X	-	>60	>75
SEQ ID No. 9	X	-	X	-	X	-	X	-	>60	>75
SEQ ID No. 10	X	-	X	-	X	-	X	-	>60	>75
SEQ ID No. 11	X	-	X	-	X	-	X	-	>60	>75
<i>Brachypodium</i>										
Bradi1g66720	X	-	X	-	X	-	X	-	67	82
Bradi2g54680	-	X	X	-	X	-	X	-	71	83
Bradi1g24910	X	-	X	-	X	-	X	-	67	80
Bradi1g24880	X	-	X	-	X	-	X	-	71	84
Bradi2g54740	X	-	X	-	X	-	X	-	65	78
Bradi2g23370	X	-	X	-	X	-	X	-	63	78
Bradi2g23350	X	-	X	-	X	-	X	-	69	83
Bradi2g54690	X	-	X	-	X	-	X	-	70	83
<i>Poplar</i>										
PLAC1	X	-	X	-	X	-	X	-	78	88
PLAC40	X	-	X	-	X	-	X	-	76	87
PLAC41	X	-	X	-	X	-	X	-	78	88
PLAC6	X	-	X	-	X	-	X	-	78	88
PLAC24	X	-	X	-	X	-	X	-	77	87
PLAC25	X	-	X	-	X	-	X	-	77	88
<i>Rice</i>										
gi 113548170	-	X	X	-	X	-	X	-	69	83
gi 11354304	X	-	X	-	X	-	X	-	70	82
gi 113579298	X	-	X	-	X	-	X	-	69	81
gi 113579297	X	-	X	-	X	-	X	-	67	80
gi 113564303	-	X	X	-	X	-	X	-	72	84
gi 113579295	-	X	X	-	X	-	X	-		
gi 255673866	-	X	X	-	X	-	X	-		

Figure 5

## PRODUCTION OF PLANTS WITH REDUCED LIGNIN CONTENT

[0001] The present invention relates to a method for selecting or producing plants having a reduced lignin content.

[0002] Lignins are insoluble polymers which are located in plant walls and are the result of the polymerization of 3 phenolic monomers (or monolignols), deriving from the phenylpropanoid pathway (Neish, *Constitution and Biosynthesis of Lignin*, publisher New York: Springer Verlag, 1-43, 1968). Their biosynthetic pathway is complex and comprises various steps, one part of which is carried out in the cytoplasm (monolignol synthesis) and another part in the wall (polymerization). *p*-Coumaryl, coniferyl and sinapyl alcohols are the respective precursors for the *p*-hydroxyphenyl (H), guaiacyl (G) and syringyl (S) units constituting lignins. These precursors are oxidized to phenolic radicals which spontaneously couple via various linkages, thereby resulting in the formation of lignins. Among the inter-unit linkages, a distinction is made between labile linkages, called  $\beta$ -O-4 linkages, and resistant linkages. During polymerization, other linkages can also be established with other wall compounds (polysaccharides and proteins) in order to form a complex three-dimensional network. The formation of the phenolic radicals is thought to be catalyzed by oxidases, such as peroxidases, laccases or other oxidases. A large number of these enzymes in combination with regulatory proteins is thought to be necessary for assembly of the H, G and S units (Boudet, *Plant Physiol. Biochem.*, 38, 81-96, 2000; see for review: Ralph et al., *Lignins*, Encyclopedia of Life Sciences, John Wiley & Sons, 2007). However, these enzymes are still poorly identified since they belong to multigene families (Barrière et al., *Genes, Genomes and Genomics*; Global Science Books, 2007, Review).

[0003] Although the mechanisms involved *in vivo* in lignin biosynthesis are not completely elucidated, it is generally considered that laccases could be involved in the first steps of polymerization, for the formation of dimers or trimers, while peroxidases could make it possible to obtain a greater degree of polymerization from the dimers and trimers (Ros Barcelo, *International Review of Cytology*, 176, 87-132, 1997).

[0004] The lignin content of plants has a major influence on their industrial uses. For example, it affects the nutritive value of plants intended for animal feed, and also the performance levels of papermaking processes (yield and quality of the paper pulp obtained) and the production yield for biofuel. Indeed:

[0005] an important component of the nutritional value of fodder plants, such as fodder corn, is the digestibility. Thus, cows fed with varieties that are more digestible show an increase in milk production and better weight gain. In addition, these more digestible varieties enable the animals to reach their potential with a lower level of supplementation, which makes it possible in particular to reduce production costs. An important factor limiting the digestibility of fodder plants is linked to the presence of lignins in the plant cell walls: the lignins establish various types of linkages with the other wall constituents (including polysaccharides) and hinder the accessibility of the digestive enzymes to the polysaccharides (carbohydrates), the main sources of energy for herbivores;

[0006] most paper pulp is obtained by chemical delignification of wood, in order to isolate the plant fibers

consisting mainly of cellulose and linked together by the lignins. However, this delignification step is very demanding in terms of energy and reagents (acids in particular), owing to the resistance of lignins to chemical degradation. In the case of the thermomechanical production of paper pulp, the lignins which are not removed are responsible for light-induced yellowing of the paper. Lignins rich in S units are more sensitive to papermaking delignification processes since the S units are especially linked via  $\beta$ -O-4 linkages (linkages which are targets of these processes). Consequently, in the case of the hardwoods used by the papermaking industries, a higher content of  $\beta$ -O-4-linked S units is sought in the papermaking sector in order to improve the pulp-cooking yield (Guerra et al., *Ind. Eng. Chem. Res.*, 47, 8542-8549, 2008);

[0007] biofuels are formed from bioethanol (a gasoline-miscible product) or from oil (for producing a diesel product). The production of bioethanol, currently carried out from starch or from sucrose, could also be carried out from wood cellulose or straw cellulose. In this case, the production process comprises the following steps: acid pretreatment of the raw material in order to break the interactions between lignins and polysaccharides (this pretreatment facilitates the action of hydrolytic enzymes which convert the wall polysaccharides into simple sugars), followed by a step of fermentation of the simple sugars, resulting in the production of bioethanol. However, the initial acid pretreatment leads to the production of compounds capable of inhibiting the fermentation step. It has therefore been suggested that, if the lignins were modified, the wall polysaccharides would be more accessible to hydrolytic enzymes. This would make it possible not only to eliminate or limit the acid pretreatment and the associated problems of fermentation inhibition, but also to reduce environmental impacts linked to the residues from the acid treatments.

[0008] In this context, the quantitative modification of the lignins in plants is the subject of numerous research studies. The qualitative modification of lignins (modification of their structure or of their interactions with the other wall polymers) is also greatly studied. For example, lignins rich in S units or in  $\beta$ -O-4 linkages are much easier to remove during the chemical production of paper pulp.

[0009] One of the preferred routes for decreasing the lignin content in plants concerns production by genetic engineering of plants. It has thus been proposed to act on the enzymes of the lignin biosynthesis pathway, such as laccases (International Application WO 97/45549), peroxidases (International Application WO 2004/080202), cinnamoyl CoA reductase (CCR; International Applications WO 97/12982 and WO 98/39454), caffeic acid O-methyl transferase (COMT; International Application WO 94/23044; Oba and Allen, *J. Dairy Sci.*, 82, 135-142, 1999), cafeoyl coenzyme A 3-O-methyl transferase (CCoAOMT; Application EP 0516958; Guo et al., *Transgenic Res.* 10, 457-464, 2001), cinnamyl alcohol dehydrogenase (CAD; Lapierre et al., *Plant*

*Physiol.*, 119, 153-164, 1999), and 4-coumarate: coenzyme A ligase (4CL; Hu et al., *Nat. Biotech.* 17, 808-812, 1999).

[0011] With regard more particularly to the laccases, International Application WO 97/45549 describes a tobacco laccase (the sequence of which is, moreover, described by Kiefer-Mayer et al., *Gene*, 178, 205-207, 1996), and proposes

increasing or reducing the amount of lignins produced by a plant by overexpressing said laccase (or a protein having at least 50% of amino acids homologous to those of said laccase), or by inhibiting its expression.

**[0012]** In *Arabidopsis thaliana*, the laccase multigene family comprises 17 members, 7 of which are expressed in the stems, the stem being the most lignified organ. The genes most strongly expressed are LAC4 (At2g38080), LAC17 (At5g60020) and LAC2 (At2g29130). The LAC2 and LAC17 genes belong to the same subclass, and the LAC4 gene belongs to a subclass which is close according to the phylogenetic trees published by Pourcel et al. (Plant Cell, 17, 2966-2980, 2005) and Caparros-Ruiz et al. (Plant Science, 171, 217-225, 2006). The LAC17 gene encodes the LAC17 protein (AtLAC17), the sequence of which is available under accession number NM\_125395 in the Genbank database, and is also reproduced in the appended sequence listing under the identifier SEQ ID No. 2. The LAC4 gene encodes the LAC4 protein (AtLAC4), the sequence of which is available under accession number NM\_129364 in the Genbank database, and is also reproduced in the appended sequence listing under the identifier SEQ ID No. 4. The LAC2 gene encodes the LAC2 protein (AtLAC2), the sequence of which is available under accession number NM\_128470 (GI:186503951) in the Genbank database. In *Arabidopsis*, AtLAC17 is expressed in the interfascicular fibers.

**[0013]** The inventors have thus demonstrated that the proteins that are orthologs of the AtLAC17 protein exhibit at least 60% identity or at least 75% similarity with said protein and comprise, from the N-terminal end to the C-terminal end, at least one of the 4 consensus peptide domains of sequence:

**[0014]** H-W-H-G-I/V-R-Q-L (SEQ ID No. 12; amino acids corresponding to positions 80-87 of the peptide sequence of AtLAC17) or H-W-H-G-I/V-R/L-Q-L/M/V (SEQ ID No. 38),

**[0015]** I/V-N-A-A-L-N-D-E-L-F-F (SEQ ID No. 13; amino acids corresponding to positions 223-233 of the peptide sequence of AtLAC17) or I-N-A/S-A-L-N/E-D/N/E-E-L-F-F (SEQ ID No. 39),

**[0016]** E-S-H-P-L-H-L-H-G-F/Y-N/D-F-F-V-V-G-Q-G-F/Y-G-N-F/Y-D (SEQ ID No. 14; amino acids corresponding to positions 476-498 of the peptide sequence of AtLAC17), or E-S-H-P-L/F-H-L/M-H-G-F/Y-N/D-F/Y-F/Y-V-V/I-G-Q/T/E-G-F/V/T-G-N-F/Y-D/N (SEQ ID No. 40), and

**[0017]** A-D-N-P-G-V-W (SEQ ID No. 15; amino acids corresponding to positions 539-546 of the peptide sequence of AtLAC17), or A/V-D-N-P-G-V/ø-W/ø (SEQ ID No. 41), where "ø" indicates that an amino acid is absent, respectively.

**[0018]** By way of nonlimiting examples of orthologs of the *A. thaliana* LAC17 protein, mention will in particular be made of the laccases of:

**[0019]** corn (*Zea mays*) of sequences SEQ ID Nos. 5 and 6 (sequences also available under accession numbers NM\_001112405.1 and EU957078 in the Genbank database) and the sequences available in the Genbank database under accession numbers GI:162461426 (SEQ ID No. 42), GI:226503958 (SEQ ID No. 43), GI:226494660 (SEQ ID No. 44), GI:212721074 (SEQ ID No. 45), GI:162463584 (SEQ ID No. 46) and GI:162461268 (SEQ ID No. 47),

**[0020]** sugar cane (*Saccharum officinarum*) of sequence SEQ ID No. 7,

**[0021]** sorghum (*Sorghum bicolor*) of sequences SEQ ID Nos. 8, 9, 10 and 11,

**[0022]** *Brachypodium*, such as the sequences Bradi1g66720 (SEQ ID No. 48), Bradi2g54680 (SEQ ID No. 49), Bradi1g24910 (SEQ ID No. 50), Bradi1g24880 (SEQ ID No. 51), Bradi2g54740 (SEQ ID No. 52), Bradi2g23370 (SEQ ID No. 53), Bradi2g23350 (SEQ ID No. 54) and Bradi2g54690 (SEQ ID No. 55),

**[0023]** rice, such as the sequences available in the Genbank database under accession numbers GI:113548170 (SEQ ID No. 56), GI:113534304 (SEQ ID No. 57), GI:113579298 (SEQ ID No. 58), GI:113579297 (SEQ ID No. 59), GI:113534303 (SEQ ID No. 60), GI:113579295 (SEQ ID No. 61), GI:255673866 (SEQ ID No. 62) (these sequences have the domain referenced under accession number IPR017761 in the InterPro database), and

**[0024]** poplar, such as the sequences PtLAC1 (gene POPTR\_0001s14010.1; SEQ ID No. 63), PtLAC40 (POPTR\_0001s41160.1; SEQ ID No. 64), PtLAC41 (POPTR\_0001s41170.1; SEQ ID No. 65), PtLAC6 (POPTR\_0001s41170.1; SEQ ID No. 66), PtLAC24 (POPTR\_0011s12090.1; SEQ ID No. 67) and PtLAC25 (POPTR\_0011s12100.1; SEQ ID No. 68).

**[0025]** The table represented in FIG. 5 shows the presence (noted in the table by the sign "X") of the consensus peptide domains as defined above in the sequences of the orthologs of the AtLAC17 protein in *Zea mays*, *S. officinarum*, *Sorghum bicolor*, *Brachypodium*, poplar and rice, and also the respective percentages of identity and of similarity relative to AtLAC17.

**[0026]** The LAC17 protein exhibits 55.2% identity with the LAC4 protein, and 67.1% identity with the LAC2 protein, but the latter does not comprise the consensus peptide domain of sequence SEQ ID No. 14, and 54.6% identity with the tobacco laccase described in International Application WO 97/45549; the LAC4 protein exhibits 54.0% identity with the LAC2 protein and 75.8% identity with the tobacco laccase described in International Application WO 97/45549 (it appears that said tobacco laccase is the ortholog of the AtLAC4 protein), the percentages of identity being calculated over the entire length of the sequences by means of the needle program (Needleman and Wunsch, J. Mol. Biol., 48, 443-453, 1970) using the default parameters: "Matrix": EBLOSUM62, "Gap penalty": 10.0 and "Extend penalty": 0.5. In *Arabidopsis*, AtLAC4 is expressed in the vessels of the xylem and in the interfascicular fibers.

**[0027]** By way of nonlimiting examples of orthologs of the *A. thaliana* LAC4 protein, mention will in particular be made of the laccases of:

**[0028]** *Brachypodium*, such as the sequence Bradilg74320 (SEQ ID No. 69), which exhibits 67% identity and 83% similarity with the sequence SEQ ID No. 4,

**[0029]** rice, such as the sequence available in the Genbank database under accession number GI:150383842 (QOIQU1; SEQ ID No. 70), which exhibits 69% identity and 83% similarity with the sequence SEQ ID No. 4, and

**[0030]** poplar, the sequences PtLAC14 (POPTR\_0006s09830.1; SEQ ID No. 71, which exhibits 75% identity and 87% similarity with the sequence SEQ ID No. 4), PtLAC15 (POPTR\_0006s09840.1; SEQ ID No.



72, which exhibits 76% identity and 87% similarity with the sequence SEQ ID No. 4), PtLAC32 (POPTR\_0016s11950.1; SEQ ID No. 73, which exhibits 78% identity and 88% similarity with the sequence SEQ ID No. 4) and PtLAC33 (POPTR\_0016s11960.1; SEQ ID No. 74, which exhibits 77% identity and 87% similarity with the sequence SEQ ID No. 4).

**[0031]** *A. thaliana* lines of the SALK collection in the Col0 accession (Columbia) exhibiting T-DNA insertions in the LAC17 (SALK\_016748 line), LAC4 (SALK\_051892 line) and LAC2 (SALK\_025690 line) genes have been identified. The mutants lac4 and lac2 have in particular been described by Brown et al. (Plant Cell, 17, 2281-2295, 2005). These mutants exhibit a greatly reduced or zero expression of the mutated gene, but do not exhibit any particular phenotype under glass.

**[0032]** The inventors have investigated whether these mutations have an effect on the amount of lignins of the mutated plants, and their qualitative (structural) properties. They have noted that the lac2 mutant does not exhibit any notable difference compared with the Col0 wild-type line, but that, on the other hand, the lac4 and lac17 mutants contain an amount of lignins (determined on mature dry stems) that is reduced by 6 to 8% and exhibit a cellulolysis yield that is increased by 17% in the case of lac17 and by 52% in the case of lac4, compared with the Col0 wild-type line (cellulolysis carried out without acid pretreatment).

**[0033]** In addition, the inventors have obtained lac4/lac17 double mutants from the lac4 and lac17 mutants by crossing. They have noted that these double mutants exhibit a very reduced amount of lignins (reduced by approximately 19% compared with the Col0 wild-type line), and a better cellulolysis yield compared with the Col0 wild-type line (+25% to +42%) and with the lac17 single mutant (+6% to +21%) approximately.

**[0034]** Consequently, the subject of the present invention is a method for reducing the lignin content of a plant and increasing the cellulolysis of the walls of said plant, characterized in that the expression and/or the activity in said plant:

**[0035]** a) of a laccase of which the polypeptide sequence has at least 60% identity, and in increasing order of preference at least 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% and 99% identity, or at least 75% similarity, and in increasing order of preference at least 78%, 79%, 80%, 83%, 85%, 90%, 95%, 97%, 98% and 99% similarity with the sequence SEQ ID No. 2 (LAC17), and comprises, from its N-terminal end to its C-terminal end, at least one of the 4, preferably at least 2 of the 4, more preferably at least 3 of the 4 and more preferentially the 4 consensus peptide domains i) to iv), respectively, which follow:

**[0036]** i) the consensus peptide domain of sequence SEQ ID No. 12 or 38,

**[0037]** ii) the consensus peptide domain of sequence SEQ ID No. 13 or 39,

**[0038]** iii) the consensus peptide domain of sequence SEQ ID No. 14 or 40,

**[0039]** iv) the consensus peptide domain of sequence SEQ ID No. 15 or 41, and

**[0040]** b) of a laccase of which the polypeptide sequence comprises at least 65% identity, and in increasing order of preference at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% and 99% identity, with the sequence SEQ ID No. 4 (LAC4),

is totally or partially inhibited.

**[0041]** The term “lignin content” is intended to mean the Klason lignin content. This content can be measured by assaying the acid-insoluble lignin (ASL) fraction present in the parietal residue (PR) of a plant, as described in Example 3 below.

**[0042]** The term “laccase” is intended to mean a copper-comprising enzyme (EC 1.10.3.2) which catalyzes the oxidation of a phenolic substrate using dioxygen as final electron acceptor.

**[0043]** Unless otherwise specified, the percentages of identity indicated herein are established, as indicated above, by means of the needle program using the default parameters.

**[0044]** The present invention applies to dicotyledonous or monocotyledonous plants. By way of nonlimiting examples, it can apply to corn, wheat, barley, rye, triticale, oats, rice, sorghum, sugar cane, poplar and pine.

**[0045]** By way of nonlimiting examples of laccases, as defined in paragraph a) above, mention may be made, in corn (*Zea mays*), of the peptide sequences SEQ ID Nos. 5, 6 and 42 to 47, in sugar cane (*Saccharum officinarum*), of the sequence SEQ ID No. 7, in sorghum (*Sorghum bicolor*), of the peptide sequences SEQ ID Nos. 8 to 11, in *Brachypodium*, of the peptide sequences SEQ ID Nos. 48 to 55, in rice, of the peptide sequences SEQ ID Nos. 56 to 62, and in poplar, of the peptide sequences SEQ ID Nos. 63 to 68.

**[0046]** By way of nonlimiting examples of laccases, of which the polypeptide sequence has at least 60% identity or at least 75% similarity with the sequence SEQ ID No. 2 and comprises, from its N-terminal end to its C-terminal end, the 4 consensus peptide domains of sequence SEQ ID Nos. 12, 13, 14 and 15 respectively, mention may be made, in corn, of the peptide sequences SEQ ID Nos. 5, 6, 42, 43, 44 and 45, in sugar cane, of the peptide sequence SEQ ID No. 7, in sorghum, of the peptide sequences SEQ ID Nos. 8 (partial sequence of the protein), 9, 10 and 11, in *Brachypodium*, of the peptide sequences SEQ ID Nos. 50 and 51, in rice, of the peptide sequence SEQ ID No. 58, and in poplar, of the peptide sequences SEQ ID Nos. 63, 67 and 68.

**[0047]** By way of nonlimiting examples of laccases, of which the polypeptide sequence has at least 65% identity with the sequence SEQ ID No. 4, mention may be made, in *Brachypodium*, of the peptide sequence SEQ ID No. 69, in rice, of the peptide sequence SEQ ID No. 70, and in poplar, of the peptide sequences SEQ ID Nos. 71 to 74.

**[0048]** The total or partial inhibition of the expression and/or of the activity of a laccase as defined above can be obtained in various ways, by methods known per se.

**[0049]** Particularly advantageously, this inhibition can be obtained by intervening upstream of the production of said laccase, by mutagenesis of the gene encoding this protein, or else by inhibition or modification of the transcription or of the translation of this laccase.

**[0050]** The mutagenesis of the gene encoding said laccase can take place at the level of the coding sequence or of the expression-regulating sequences, in particular of the promoter. It is, for example, possible to delete all or part of said gene and/or to insert an exogenous sequence. By way of example, for corn, mention will be made of insertional mutagenesis: a large number of individuals deriving from a plant that is active in terms of the transposition of a transposable element (AC or mutator element) are produced, and the plants in which an insertion has taken place in the gene of said laccase are selected, for example by PCR. This exogenous

sequence can also be a T-DNA (fragment of the *Agrobacterium tumefaciens* Ti plasmid).

[0051] It is also possible to introduce one or more point mutations with physical agents (for example radiation) or chemical agents. These mutations result in the reading frame being shifted and/or in a stop codon being introduced into the sequence and/or in the level of transcription and/or of translation of the gene being modified and/or in the enzyme being made less active than the wild-type protein. The mutated alleles of the gene of said laccase can be identified, for example, by PCR using primers specific for said gene.

[0052] In this context, techniques of "TILLING" type (Targeting Induced Local Lesions IN Genomes; McCallum et al., *Plant Physiol.*, 123, 439-442, 2000) can in particular be used.

[0053] It is also possible to carry out a site-directed mutagenesis targeting the gene encoding said laccase. The inhibition or the modification of the transcription and/or the translation can be obtained via the expression of sense, antisense or double-stranded RNAs derived from the gene of said laccase, or of the cDNA of this protein, or else through the use of interfering RNAs (for review on antisense inhibition techniques see, for example: Watson and Grierson, *Transgenic Plants: Fundamentals and Applications* (Hiatt, A, ed) New York: Marcel Dekker, 255-281, 1992; Chicas and Macino, *EMBO reports*, 21, 992-996, 2001; for review concerning more specifically the use of interfering RNAs, see Hannon, *Nature*, 418, 244-251, 2002).

[0054] The subject of the present invention is also a recombinant DNA construct comprising one or more polynucleotides capable of inhibiting the expression of the two laccases as defined above. By way of nonlimiting examples, said polynucleotides can encode antisense RNAs, interfering RNAs (noncoding double-stranded RNAs approximately 21 to 25 nucleotides in length), micro-RNAs (noncoding, single-stranded RNAs approximately 21 to 25 nucleotides in length) (Ossowski et al., *The Plant Journal*, 53, 674-690, 2008; Schwab et al., *Methods Mol Biol.*, 592, 71-88, 2010; Wei et al., *Funct Integr Genomics.*, 9, 499-511, 2009) or ribozymes targeting the gene encoding a laccase as defined above.

[0055] Preferably, said polynucleotides capable of inhibiting the expression of the LAC4 and LAC17 laccases as defined above are micro-RNAs, such as the micro-RNAs miR397 and miR408, preferably miR397. By way of nonlimiting examples of such micro-RNAs, use may be made of those having the following sequences:

[0056] SEQ ID No. 75 (AtmiR397a) or SEQ ID No. 76 (AtmiR397b), obtained from *Arabidopsis thaliana* (Abdel-Ghany and Pilon, *J Biol Chem.*, 283, 15932-15945, 2008);

[0057] SEQ ID No. 77 (ptc-miR397), obtained from poplar; or

[0058] SEQ ID No. 78 (Bdi-miR397a) or SEQ ID No. 79 (Bdi-miR397b), obtained from *Brachypodium distachyon* (Zhang et al., *BMC Genomics.*, 23, 10:449, 2009; Unver and Budak, *Planta*, 230, 659-669, 2009).

[0059] According to one preferred embodiment of the invention, the recombinant DNA construct is chosen from:

[0060] a DNA construct comprising a fragment of at least 15 consecutive nucleotides, preferably at least 20 consecutive nucleotides of the cDNA of the gene encoding a laccase as defined above,

[0061] a DNA construct of from 200 to 1000 bp, comprising a fragment of the cDNA of the gene encoding a laccase as defined above, or a complementary poly-

nucleotide which, when it is transcribed, forms an RNA hairpin (or ribozyme) targeting said gene;

[0062] a DNA construct capable, when it is transcribed, of forming a micro-RNA targeting the gene encoding a laccase as defined above.

[0063] According to one particular embodiment of the invention, said recombinant DNA construct comprises a fragment of at least 15 consecutive nucleotides, preferably at least 20, and entirely preferably at least 50 consecutive nucleotides of a polynucleotide of sequence SEQ ID No. 1 or SEQ ID No. 3, or of a polynucleotide complementary to a polynucleotide of sequence SEQ ID No. 1 or SEQ ID No. 3.

[0064] These constructs can in particular be:

[0065] expression cassettes comprising one or more recombinant DNA constructs as defined above, under the transcriptional control of a suitable promoter. These expression cassettes can also advantageously comprise other regulatory elements, in particular regulatory elements for transcription, such as terminators, enhancers, etc.;

[0066] recombinant vectors comprising one or more recombinant DNA constructs as defined above, or advantageously an expression cassette as defined above.

[0067] Recombinant DNA constructs in accordance with the invention can also comprise other elements, for example one or more selectable markers.

[0068] Those skilled in the art have at their disposal a very wide choice of elements that can be used for obtaining recombinant DNA constructs in accordance with the invention.

[0069] By way of nonlimiting examples of promoters that can be used in the context of the present invention, mention will be made of:

[0070] constitutive promoters, such as the cauliflower mosaic virus (CaMV) 35S promoter described by Kay et al. (*Science*, 236, 4805, 1987), or derivatives thereof, the cassava vein mosaic virus (CsVMV) promoter described in International Application WO 97/48819, the maize ubiquitin promoter or the rice "actin-intron-actin" promoter (McElroy et al., *Mol. Gen. Genet.*, 231, 150-160, 1991; GenBank accession number S 44221);

[0071] inducible or tissue-specific promoters, in order to modify the lignin content or composition only at certain developmental stages of the plant, under certain environmental conditions, or in certain target tissues, such as, for example, the stems, the leaves, the seeds, the spathes, the cortex or the xylem (e.g., the cinnamyl alcohol dehydrogenase (CAD) promoter or the 4-coumarate-CoA ligase (4CL) promoter).

[0072] By way of nonlimiting examples of other regulatory elements for transcription that can be used in the context of the present invention, mention will be made of terminators, such as the NOS 3' terminator of nopaline synthase (Depicker et al., *J. Mol. Appl. Genet.*, 1, 561-573, 1982), or the CaMV 3' terminator (Franck et al., *Cell*, 21, 285-294, 1980; GenBank accession number V00141).

[0073] By way of nonlimiting examples of selectable marker genes that can be used in the context of the present invention, mention will in particular be made of genes which confer resistance to an antibiotic (Herrera-Estrella et al., *EMBO J.*, 2, 987-995, 1983) such as hygromycin, kanamycin, bleomycin or streptomycin, or to a herbicide (EP 0 242 246) such as glufosinate, glyphosate or bromoxynil, or the NPTII gene which confers resistance to kanamycin (Bevan et al., *Nucleic Acid Research*, 11, 369-385, 1984).

**[0074]** The plants can be transformed using numerous methods, known in themselves to those skilled in the art.

**[0075]** It is, for example, possible to transform plant cells, protoplasts or explants and to regenerate a whole plant from the transformed material. The transformation can thus be carried out, by way of nonlimiting examples:

**[0076]** by transfer of the vectors in accordance with the invention into protoplasts, in particular after incubation of the latter in a solution of polyethylene glycol (PEG) in the presence of divalent cations ( $\text{Ca}^{2+}$ ) according to the method described in the article by Krens et al. (Nature, 296, 72-74, 1982);

**[0077]** by electroporation, in particular according to the method described in the article by Fromm et al. (Nature, 319, 791-793, 1986);

**[0078]** by using a gene gun which makes it possible to discharge, at very high speed, metal particles coated with the DNA sequences of interest, thus delivering genes inside the cell nucleus, in particular according to the technique described in the article by Finer et al. (Plant Cell Report, 11, 323-328, 1992);

**[0079]** by cytoplasmic or nuclear microinjection.

**[0080]** Use may also be made of *Agrobacterium tumefaciens*, in particular according to the methods described in the articles by Bevan et al. (Nucleic Acid Research, 11, 369-385, 1984) and by An et al. (Plant Physiol., 81, 86-91, 1986), or else *Agrobacterium rhizogenes*, in particular according to the method described in the article by Jouanin et al. (Plant Sci., 53, 53-63, 1987). For example, the plant cell transformation can be carried out by transfer of the T region of the *Agrobacterium tumefaciens* tumor-inducing extrachromosomal circular plasmid Ti, using a binary system (Watson et al., publisher De Boeck University, 273-292, 1994). *Agrobacterium tumefaciens* can also be used on whole plants, for example by depositing at the level of the wound of a monocotyledonous plant, the bacterium harboring the DNA to be transferred, in the presence of substances released at the level of the wound of a dicotyledonous plant.

**[0081]** The subject of the present invention is also a plant cell comprising an expression cassette as defined above or a recombinant vector as defined above.

**[0082]** The subject of the present invention is also the plants which can be obtained by means of a method in accordance with the invention, with the exception of the *A. thaliana* mutants SALK\_016748 and SALK\_051892. Said plants can carry mutations which inhibit the LAC4 and LAC17 laccases as defined above or express one or more polynucleotides capable of inhibiting the expression of said LAC4 and LAC17 laccases as defined above. Of course, the present invention encompasses the descendants, in particular the hybrids resulting from crossing involving at least one plant according to the invention, which are obtained by sowing or by vegetative multiplication of the plants directly obtained by means of the method of the invention.

**[0083]** The plant material, such as protoplasts, cells, calluses, leaves, stems, roots, flowers, fruits, cuttings and/or seeds, obtained from the plants in accordance with the invention (with the exception of the *A. thaliana* mutants SALK\_016748 and SALK\_051892), are also part of the subject of the present invention.

**[0084]** The subject of the present invention is also the use of the plants in accordance with the invention or of plant material obtained from said plants, for producing fodder plants, biofuels or paper pulp.

**[0085]** The present invention will be understood more clearly by means of the further description which follows, which refers to nonlimiting examples illustrating the reduction in lignin content and the increase in cellulolysis of the walls of a plant in which the expression of the LAC17 and/or LAC4 laccases is inhibited, and also the appended figures:

**[0086]** FIG. 1: analysis by 1% agarose gel electrophoresis of the PCR products obtained from genomic DNA of the *A. thaliana* lines SALK\_016748 (lac17 mutant) (Figure A), SALK\_051892 (lac4 mutant) (Figure B) and SALK\_025690 (lac2 mutant) (Figure C). A: well 1: 1 Kb+ size marker (Invitrogen); well 2: tubulin of the Col0 wild-type line; well 3: laccase 17 of the wild-type line; wells 4 and 6: tubulin of 2 plants of the SALK\_016748 line (lac17); wells 5 and 7: laccase 17 of 2 plants of the SALK\_016748 line (lac17). B: well 1: 1 Kb+ size marker (Invitrogen), well 2: empty; well 3: tubulin of the Col0 wild-type line; well 4: empty; wells 5 to 7: tubulin of 3 plants of the SALK\_051892 line (lac4); well 8: empty; well 9: laccase 4 of the Col0 wild-type line; well 10: empty; wells 11 to 13: laccase 4 of 3 plants of the SALK\_051892 line (lac4). C: wells 1 and 12: 1 Kb+ size marker (Invitrogen); wells 2 to 6 and 11: empty; well 7: laccase 2 of the Col0 wild-type line (cDNA); well 8: laccase 2 of 1 plant of the Col0 wild-type line (gDNA); well 9: laccase 2 of 1 plant of the SALK\_025690 line; well 10: control, laccase 2 amplified on the RNA of a plant of the Col0 wild-type line having undergone the same treatment as the other plants, with the difference that, during the reverse transcription step, the reverse transcriptase was not added;

**[0087]** FIG. 2: analysis of the expression profile of *A. thaliana* laccases (LAC 2, 4, 5, 6, 10, 11, 12 and 17) by 1% agarose gel electrophoresis, in TAE buffer, of the RT-PCR products obtained from cDNA of the cells of the floral scape of the Col0 wild-type line, of the SALK\_051892 line (lac4) and of the SALK\_016748 line (lac17). Tub=tubulin;

**[0088]** FIG. 3: optical microscope observation (200X magnification) of 70-micron-thick transverse sections primary scape of 20 cm, stained with phloroglucinol-HCl, from the Col0 wild-type line and from the SALK\_016748 line (lac17);

**[0089]** FIG. 4: analysis by 1% agarose gel electrophoresis of the PCR products obtained from genomic DNA of an *A. thaliana* double mutant Kim (lac4/lac17). Well 1: 1 Kb+ size marker (Invitrogen); well 2: tubulin of the wild-type line; well 3: tubulin of the Kim mutant; well 4: laccase 4 of the wild-type line; well 5: laccase 4 of the Kim mutant; well 6: laccase 17 of the wild-type line; well 7: laccase 17 of the Kim mutant.

## EXAMPLE 1

### Selection, Genotyping and Characterization of *Arabidopsis thaliana* lac17, lac4 AND lac2 Mutants

**[0090]** 1) Selection of the *A. thaliana* Laccase Mutants

**[0091]** *A. thaliana* lines of the SALK collection in the Col0 accession exhibiting T-DNA insertions in the LAC17, LAC4 and LAC2 genes (respectively, the SALK\_016748, SALK\_051892 and SALK\_025690 lines) were identified and characterized.

**[0092]** The SALK\_016748 (lac17) mutant contains two T-DNAs inserted in inverted tandem into the promoter of the gene encoding LAC17, 146 base pairs from the ATG start codon.

[0093] The SALK\_051892 (lac4) mutant contains one T-DNA inserted into the promoter of the gene encoding LAC4, 127 base pairs from the ATG start codon.

[0094] The SALK\_025690 (lac2) mutant contains one T-DNA inserted into its coding sequence.

[0095] 2) Genotyping of the *A. thaliana* lac17 (SALK\_016748), lac4 (SALK\_051892) and lac2 (SALK\_025690) Mutants

[0096] a) Materials and Methods

[0097] Primers for the LAC17, LAC4 and LAC2 genes were defined using the OLIGO 4 software (National Biosciences Inc., Plymouth, USA). Their sequences (5'→3') are represented in Table 1 hereinafter:

TABLE 1

	Sense primer sequence	Antisense primer sequence
Primers for LAC17 gene amplification	Lac 17 FST dir: TCG AAG AGG GTC AAA GAG TTT (SEQ ID No. 16)	Lac 17 FST rev: TCT TAG CCA TGA AAT GTG AGC (SEQ ID No. 17)
Primers for LAC4 gene amplification	irx12 FST dir: ATT GTG TAA GCA AAT CGG CAC (SEQ ID No. 18)	irx12 FST rev: TGG CTT GCT TGA GCA TAA TCT (SEQ ID No. 19)
Primers for LAC2 gene amplification	Lac 2 RT dir: GCA AGA CAA AAA CAA TCG TGA (SEQ ID No. 20)	Lac 2 RT rev: GAA ATC TGA GGG TGG AGG AAG (SEQ ID No. 21)

[0098] The DNA of the plants was extracted according to the protocol described by Edwards et al. (Nucleic Acid Research, 19, 1349, 1991).

[0099] The PCRs were carried out in 25 µl on 30 ng of genomic DNA, with 2 mM of MgCl<sub>2</sub>, 0.4 mM of each dNTP, 0.4 mM of each primer, and 1.25 units of Taq DNA polymerase (Invitrogen).

[0100] The PCR cycles for the genotyping of the lac17 mutants are (95° C. 30 sec, 50° C. 30 sec, 72° C. 1 min) 28 times, with a final extension of 10 min at 72° C.

[0101] The PCR cycles for the genotyping of the lac4 mutants are (95° C. 30 sec, 58° C. 30 sec, 72° C. 30 sec) 30 times, with a final extension of 10 min at 72° C.

[0102] The PCR cycles for the genotyping of the lac2 mutants are (95° C. 30 sec, 54° C. 30 sec, 72° C. 1 min 30 sec) 30 times, with a final extension of 10 min at 72° C.

[0103] The PCR products are then separated on 1% agarose gels in TAE buffer.

[0104] b) Results

[0105] 2 plants of the SALK\_016748 line, 3 plants of the SALK\_051892 line and 1 plant of the SALK\_025690 line were tested.

[0106] The genotyping results are represented in FIG. 1:

[0107] the 2 plants of the SALK\_016748 line that were tested are homozygous for the mutation in the LAC17 gene: the presence of the T-DNAs on the two strands coding for this gene prevents the amplification of a fragment of the LAC17 gene (FIG. 1A);

[0108] the 3 plants of the SALK\_051892 line that were tested are homozygous for the mutation in the LAC4 gene: the presence of the T-DNA on the two strands coding for this gene prevents the amplification of a fragment of the LAC4 gene (FIG. 1B);

[0109] the plant of the SALK\_025690 line that was tested is homozygous for the mutation in the LAC2 gene: the presence of the T-DNA on the two strands coding for this gene prevents the amplification of a fragment of the LAC2 gene (FIG. 1C).

[0110] 3) Laccase Expression in the lac17 and lac4 Mutants

[0111] The expression profile of *Arabidopsis* laccases expressed in the floral scape in the wild-type line (Columbia), the lac17 mutant (SALK\_016748) and the lac4 mutant (SALK\_051892) was determined by RT-PCR.

[0112] a) Materials and Methods

[0113] A 26-cycle RT-PCR was performed on cDNAs obtained from 1 µg of RNA extracted using an RNeasy kit (Qiagen), that were treated with a DNase and reverse-transcribed with the SSRTII reverse transcriptase (Invitrogen).

[0114] The primers used are described in Table 2 hereinafter:

TABLE 2

Gene amplified	Name of primer	Sequence (5'→3')	Tm (° C.) of the primer
LAC2	LAC 2RT dir	GCA AGA CAA AAA CAA TCG TGA SEQ ID No. 20	58
LAC2	LAC 2RT rev	GAA ATC TGA GGG TGG AGG AAG SEQ ID No. 21	64
LAC4	lac4 FST dir	AGT AAT GAA CAG TTGCGG TGG SEQ ID No. 22	62
LAC4	lac4 FST rev	TGG TAA CTT TGG ACG ATC AGG SEQ ID No. 23	58
LAC4	LAC 4 RT dir	GTT AGA AAC TGT CCA TCT CAA SEQ ID No. 24	58
LAC4	LAC 4 RT rev	CTC CAC TTG TGT TGA AGT AAT SEQ ID No. 25	58
LAC4	irx 12 FST dir	ATT GTG TAA GCA AAT CGG CAC SEQ ID No. 18	60

TABLE 2-continued

Gene	Name of amplified primer	Sequence (5'→3')	T <sub>m</sub> (° C.) of the primer
LAC4	irx 12 FST rev	TGG CTT GCT TGA GCA TAA TCT SEQ ID No. 19	60
LRC5	LAC 5 RT dir	ATC CGG TTG ATG TGT TGA GA SEQ ID No. 26	58
LAC5	LAC 5 RT rev	AGA GAG ATC GGC TTA TGT TG SEQ ID No. 27	58
LAC6	LAC 6 RT dir	TAT GCC AAA CAA ACG AGA T SEQ ID No. 28	52
LAC6	LAC 6 RT rev	CTG CTG GAG GAG GAG GTC SEQ ID No. 29	60
LAC10	LAC 10 RT dir	TGT AAA GCC GGA AAC TTC TC SEQ ID No. 30	58
LAC10	LAC 10 RT rev	TTA GGG CCT TTA CCA TTC TC SEQ ID No. 31	58
LAC11	LAC 11 RT dir	GAG CTA TTC TTC GGG ATT SEQ ID No. 22	52
LAC11	LAC 11 RT rev	GTC TTT AGG CGG TGG TAG SEQ ID No. 33	56
LAC12	LAC 12 RT dir	GCC GAC GCA TCT TAC CTC SEQ ID No. 34	58
LAC12	LAC 12 RT rev	CCA AGA ACG CCA TAG CAA SEQ ID No. 35	54
LAC17	lac17 FST dir	TCG AAG AGG GTC AAA GAG TTT SEQ ID No. 16	60
LAC17	lac17 FST rev	TCT TAG CCA TGA AAT GTG AGC SEQ ID No. 17	60
LAC17	LAC 17 RT dir	TTC TCT TGT GTT CTT CTT CTT SEQ ID No. 36	56
LAC17	LAC 17 RT rev	GAA CTT CTT TGT GAG GTT TAG SEQ ID No. 37	58

**[0115]** The pairs of primers termed “FST” (for Flanking Sequence Tag) were designed on either side of the T-DNA; they were used for amplifying on gDNA (genomic DNA). The pairs of primers termed “RT” were defined in the coding sequence and make it possible to amplify on cDNAs.

**[0116]** The RT-PCR cycles on the lac17 and lac4 mutants and the wild-type line are (95° C. 30 sec, 50° C. 30 sec, 72° C. 1 min 30) 26 times, with a final extension of 10 min at 72° C. for the laccases 2, 4, 6, 12 and 17 and the tubulins.

**[0117]** The RT-PCR cycles on the lac17 and lac4 mutants and the wild-type line are (95° C. 30 sec, 55° C. 30 sec, 72° C. 1 min 30) 26 times, with a final extension of 10 min at 72° C. for the laccases 5 and 10.

**[0118]** The RT-PCR cycles on the lac17 and lac4 mutants and the wild-type line are (95° C. 30 sec, 58° C. 30 sec, 72° C. 1 min 30) 26 times, with a final extension of 10 min at 72° C. for the laccase 11.

**[0119]** The RT-PCR products are then separated on 1% agarose gels in TAE buffer in order to visualize a difference in intensity of the fragments amplified.

**[0120]** b) Results

**[0121]** The results are represented in FIG. 2. Only the level of the laccase 17 (LAC17) transcripts decreases in the lac17 mutant and that of laccase 4 (LAC4) in the lac4 mutant. The mutants do not overexpress any other laccase for the purpose of compensating for the loss of expression of LAC17 and LAC4.

**[0122]** 4) Cytological Analysis of the lac17 Mutant

**[0123]** a) Materials and Methods

**[0124]** Sections of primary scape of 20 cm were stained with phloroglucinol-HCl according to the protocol described by Sibout et al. (Plant Cell, 17, 2059-2076, 2005). The red coloration observed corresponds to the lignified cell walls.

**[0125]** b) Results

**[0126]** The cytological observation results are represented in FIG. 3. A delay and/or a decrease in the amount of lignin deposited on the cell walls is observed in the lac17 mutant but not in the wild-type line (FIG. 3).

## EXAMPLE 2

Production and Molecular Characterization of an *Arabidopsis thaliana* lac17/lac4 Double Mutant**[0127]** a) Materials and Methods

**[0128]** Plants of the SALK\_016748 line (lac17) were crossed with plants of the SALK\_051892 line (lac4) in order to obtain a lac4/lac17 double mutant (hereinafter referred to as Kim mutant).

**[0129]** The lac4/lac17 double mutant was then characterized by genotyping according to the protocol described in Example 1.a) and using the lac4 FST dir, lac4 FST rev, irx12 FST dir and irx12 FST rev primers.

**[0130]** b) Results

**[0131]** The results of the genotyping for the Kim mutant are represented in FIG. 4: the Kim mutant is homozygous for the mutations in the LAC17 and LAC4 genes. Indeed, the presence of the T-DNAs on the two strands coding for these genes prevents the amplification of a fragment of the LAC17 and LAC4 genes.

**[0132]** The presence of two T-DNAs in the promoter of the LAC17 gene and of one T-DNA in the promoter of the LAC4 gene was confirmed by amplification of the sequences adjacent to the T-DNAs and sequencing of the amplicons.

## EXAMPLE 3

Analysis of the Lignin Content and of the cellulolysis of the *Arabidopsis thaliana* lac17 and lac4 Single Mutant and lac17/lac4 Double Mutant**[0133]** a) Materials and Methods**[0134]** i) Assaying of Lignin Content

**[0135]** The assaying of the lignins was carried out on the stems collected at maturity, ground and subjected to thorough extraction with the solvents ethanol/toluene (2/1, v/v), ethanol, and then water; extractions carried out in a Soxhlet apparatus. The material extracted and dried represents the "parietal residue" or PR (since it consists of the plant walls). The removal of the soluble compounds by extraction with solvent is essential before any assaying of lignins (these compounds possibly interfering with gravimetric or spectrometric assays).

**[0136]** The lignin content was measured by assaying the acid-insoluble lignin fraction present in the PR and called Klason lignin (KL). This KL fraction, assayed by gravimetric analysis by treating the parietal residue with concentrated sulfuric acid (which makes it possible to hydrolyze the polysaccharides and to leave a KL residue which is rinsed, dried and weighed), represents most of the parietal lignins. However, a very small fraction of the lignins may be solubilized during the treatment with sulfuric acid: it is the fraction called acid-soluble lignin (ASL), which is evaluated by measuring the absorbance of the sulfuric supernatant in the ultraviolet range.

**[0137]** These measurements were carried out using the T222 om-83 method, known to those skilled in the art, and developed for wood and derivatives thereof by TAPPI (Technical Association of the Pulp and Paper Industry) (C. W. Dence, The determination of lignin; in: S. Y. Lin, and C. W. Dence, (Eds.). Methods in Lignin Chemistry. Springer-Verlag, pp. 33-61, 1992).

**[0138]** ii) Study of Lignin Structure

**[0139]** The structure of the lignins was evaluated by thioacidolysis. Thioacidolysis of the lignins releases thioethy-

lated monomer products H, G or S from the p-hydroxyphenyl (H), guaiacyl (G) or syringyl (S) units linked only via  $\beta$ -O-4 linkages (major inter-unit linkages in native lignins). These products were analyzed by gas chromatography coupled to mass spectrometry (GC-MS) of their trimethylsilyl (TMS) derivatives. The trimethylsilyl H, G or S monomers were assayed using chromatograms reconstructed respectively on the 239, 269 or 299 ions (the most intense ions of their mass spectrum obtained by electron impact).

**[0140]** The protocol that was used is similar to that described by Lapierre et al. (Res. Chem. Interm., 21, 397-412, 1995) and by Mir Derikvand et al. (Planta 227, 943-956, 2008). The H monomers are most commonly minor (less than 1% of the total monomers) and were therefore not considered (except in the case of mutant plants affected in the formation of the G and S units, or in the case of stress lignins).

**[0141]** iii) Measurement of the Enzymatic Degradability by Cellulolysis in Vitro

**[0142]** The susceptibility of the parietal polysaccharides to enzymatic hydrolysis was evaluated in vitro, by subjecting the walls (i.e. the parietal residue PR) to a preparation of cellulase and hemicellulase enzymes.

**[0143]** The protocol that was used is described by Hoffmann et al. (Plant Cell 16, 1446-1465, 2004), which is a protocol adapted from the method by Rexen (Anim. Feed Sci. Technol., 2, 205-218, 1977). Said enzymatic preparation used was the Cellulase Onozuka R10 preparation extracted from *Trichoderma viride*, 096i/mg (Serva Electrophoresis GmbH, Germany).

**[0144]** b) Results

**[0145]** The results are given in Table 3 (giving the mean values between the 2 analytical repeats and the mean deviation between these repeats, except for the percentage PR for which a single measurement was carried out) hereinafter, in which:

**[0146]** % PR=percentage of parietal residue. This percentage reflects the amount of wall in the dry sample (% by weight of the dry sample); it is given by way of indication;

**[0147]** % KL=amount of Klason lignin expressed as % by weight of the PR;

**[0148]** m.d. KL=mean deviation between 2 independent analytical KL measurement repeats;

**[0149]** % ASL=amount of acid-soluble lignin expressed as % by weight of the PR and measured on the basis of the absorbance at 205 nm of the sulfuric supernatant resulting from the measurement of the Klason lignin (using an absorptivity coefficient of  $110 \text{ l.g}^{-1}.\text{cm}^{-1}$ );

**[0150]** m.d. ASL=mean deviation between 2 independent analytical ASL measurement repeats;

**[0151]** yld thio  $\mu\text{mol/g KL}$ =yield of monomers (G+S) from thioacidolysis, expressed in  $\mu\text{mol per gram of Klason lignin}$  (the H monomers obtained in trace amounts are not considered). When it is calculated on the basis of the Klason lignin content, the total yield of monomers from thioacidolysis reflects the proportion of units linked only via  $\beta$ -O-4 linkages in the lignins. This structural information is important since it reflects the susceptibility of the lignins to industrial delignification processes;

**[0152]** m.d. yld thio=mean deviation of the yield from thioacidolysis between 2 independent analytical thioacidolysis repeats;

- [0153]** S/G thio=molar ratio of the G and S monomers released by thioacidolysis of the lignins. This ratio reflects the proportion of S units and of G units in the native lignins. In angiosperms, the extent of the S units varies according to the developmental stage (the S units being deposited mainly at the end of lignification) and also to the tissues (the fibers are richer in S units than the vessels). Consequently, when a mutant plant has an S/G ratio that is different than that of the control line (cultivated under the same conditions), this difference may be attributable to the fact that the mutation affects lignification over time (at the start or at the end) or in a tissue-specific manner (affects fiber lignification or vessel lignification). It is also possible that the mutation affects more specifically an enzyme involved in the biosynthesis of coniferyl alcohol (precursor of G units) or of sinapyl alcohol (precursor of S units);
- [0154]** m.d. S/G=mean deviation of the thioacidolysis S/G molar ratio between 2 independent analytical thioacidolysis repeats;
- [0155]** % loss by cellulolysis=loss by weight (as %) of the PR treated with a commercial preparation of cellulase and hemicellulase enzymes;
- [0156]** m.d. cellulolysis=mean deviation between 2 independent analytical cellulolysis repeats;
- [0157]** the Kim 1 and Kim 2 mutants are 2 biological repeats of the same line. Kim 1 and Kim 2 were cultivated on 2 separate culture trays, which may explain the variations between these repeats.
- [0158]** It should be noted that the SALK\_025690 mutant (lac2) does not exhibit any decrease in the amount of lignins compared with the wild-type line (Col0).

(approximately 19%). This decrease in lignin content, which does not affect the growth and the development of the plant, is sought-after in the context of the chemical production of paper pulp from angiosperm lignocelluloses. It also facilitates enzymatic hydrolysis, the lignins acting as barriers between the enzymes and the polysaccharides;

- [0162]** the acid-soluble lignin (ASL) content of the mutant lines is lower than the ASL content of the wild-type line. The reduced Klason lignin (or acid-insoluble lignin) content is not therefore compensated for by an increase in acid-soluble lignin;
- [0163]** the yields from thioacidolysis, calculated on the basis of the KL content, are close between the wild-type line and the mutant lines. This result indicates that the lignins of the mutant lines contain as many labile linkages as the lignins of the wild-type lines. The mutations have not therefore accentuated the frequency of the resistant inter-unit linkages, which would be disadvantageous in the perspective of the chemical production of paper pulp, for example;
- [0164]** on the other hand, the single and double mutants exhibiting the lac17 mutation have a higher S/G ratio compared with that of the wild-type line. This result suggests that the lac17 mutation could affect the start of lignification (and therefore the depositing of the G units) and/or the lignification of the vessels (richer in G units than the fibers);
- [0165]** the yield from cellulolysis of the mutant lines is increased compared with that of the wild-type line. The

TABLE 3

Study of the lignins of the scapes of the wild-type line (Col0) and the lines mutant for laccases 4 and/or 17.											
Lines	% PR	% KL	m.d. KL	% ASL	m.d. ASL	yld thio $\mu\text{mol/g}$ KL	m.d. yld thio	S/G thio	m.d. S/G	% loss by cellulolysis	m.d. cellulolysis
Col0 (wild-type)	62.0	16.91	0.16	2.43	0.04	1261	50	0.46	0.00	26.9	1.0
SALK_051892 (lac4)	61.4	15.51	0.07	1.76	0.03	1221	20	0.47	0.00	40.9	1.1
SALK_016748 (lac17)	61.4	15.81	0.08	2.05	0.04	1291	63	0.56	0.01	31.5	1.4
Kim 1 (lac4/lac17)	60.3	13.62	0.12	2.38	0.01	1265	90	0.65	0.01	38.1	1.5
Kim 2 (lac4/lac17)	62.6	13.73	0.09	2.41	0.08	1370	6	0.63	0.00	33.5	1.0

- [0159]** It emerges from the above results that:

**[0160]** the homogeneity of the PR contents (60.3 to 62.6%) indicates that the mutations do not affect the lignocellulose-wall content of the mature stems. Since the mutant lines do not exhibit any reduction in size, this suggests that the mutant plants have the same productivity in terms of lignocellulose biomass that can be exploited as fibers or as biofuel, for example;

**[0161]** on the other hand, all the mutants exhibit a significantly lower Klason lignin content than that of the control: the decrease is moderate for the single mutants (decrease of 8 and 6% for the lac4 and lac17 mutants, respectively) and more marked for the double mutants

decrease in Klason lignin content therefore improves the efficiency of the cellulolysis.

#### EXAMPLE 4

##### Production of Transgenic poplars Overexpressing a Micro-RNA capable of Inhibiting the Expression of Laccases LAC17 and LAC4

**[0166]** Two genetic constructs are prepared in order to overexpress a micro-RNA (called miR397, SEQ ID No. 77) capable of inhibiting the expression of poplar (*Populus*) laccases LAC17 and LAC4, under the control either of the CaMV 2x35S constitutive promoter or of the "lignin-spe-

cific” promoter of Eucalyptus cinnamyl alcohol dehydrogenase 2 (CAD2) (called EuCAD).

[0167] The Gateway pMDC32 binary vector (Curtis and Grossniklaus, Plant Physiology, 133, 462-469, 2003) is used to overexpress the transgenes under the control of the 2x35S constitutive promoter.

[0168] For expression under the control of the EuCAD promoter, the 2x35S promoter is excised from the pMDC32 plasmid above by digestion with the HindIII-KpnI enzymes (unique restriction sites) and replaced with the “lignin-specific” EuCAD promoter.

[0169] The genetic transformation of the poplar is carried out according to the method described in Leplé et al. (Plant Cell Rep. 11, 137-141, 1992), i.e. by coculture of explants of poplar stems with agrobacteria containing a binary vector for the expression of miR397, isolation of transgenic calluses and regeneration of transformed seedlings.

[0170] Transgenic calluses are selected for the regeneration step. Seedlings are regenerated from these different calluses, therefore corresponding to different transformation events. Each seedling is cloned by multiplication.

[0171] An example of each transgenic line is used to:

[0172] study the structure of the lignins by thioacidolysis (see above) on a stem fragment;

[0173] identify spatial variations in amount of lignins, by FTIR-ATR (“Fourier Transform InfraRed Spectroscopy—Attenuated Total Reflectance”) infrared imaging and histochemical staining with phloroglucinol.

[0174] These first phenotyping analyses make it possible to identify the lines which exhibit reductions in the amount of lignins in the wood.

[0175] Lines are then analyzed for the expression of the transgenes and the genes encoding LAC17 and LAC4. These expression analyses are carried out by quantitative RT-PCR (qRT-PCR).

#### EXAMPLE 5

Production of Transgenic *Brachypodium distachyon* Overexpressing a Micro-RNA Capable of Inhibiting the Expression of Laccases LAC17 AND LAC4

[0176] Gateway binary vectors which are compatible and specific for the transformation of monocotyledons, containing a sequence encoding a micro-RNA of sequence SEQ ID No. 78 or 79, under the control either of a constitutive promoter, for example the maize ubiquitin promoter (ZmUbi), or a “lignin-specific” promoter, and a selectable gene such as the pat gene (which confers resistance to basta), are used for the genetic transformation of *Brachypodium distachyon*.

[0177] The analysis of the structure and of the lignin content of the transgenic plants obtained can be carried out using the same methods as for the analysis of the transgenic poplars above.

#### EXAMPLE 6

Production of Transgenic Corn Overexpressing a Micro-RNA Capable of Inhibiting the Expression of Laccases LAC17 AND LAC4

[0178] A vector as described for the genetic transformation of *Brachypodium* can be used for the genetic transformation of corn.

[0179] It is also possible to use the integrative vector L1038 (represented by the sequence SEQ ID No. 80), which contains an expression cassette comprising a herbicide resistance gene (Basta resistance gene), an expression cassette comprising a gene encoding a fluorescent protein for following the transgene without genotyping (gene encoding a GFP under the control of an Actin promoter), and a “triple Gateway” cassette attR4-ccdB-attR3 (where attR4 and attR3 are recombination sites and ccdB is a negative selection gene), which makes it possible to recombine a promoter of choice (attL4-attR1 ends), a gene of choice (attL1-attL2 ends) (in the case in point, a micro-RNA miR397) and a mock (attR1-attL3) (see the instruction manual published by Invitrogen, “MultiSite Gateway Pro”, Version B, Oct. 3, 2006).

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Pro Val Glu Arg Asn Thr Ile Gly Val Pro Ser Gly Gly Trp Val Val	
495 500 505	
atc aga ttc aga gca gat aat ccc ggg gtt tgg ttc atg cat tgt cac	1649
Ile Arg Phe Arg Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His	
510 515 520	
ttg gag gta cac acg acg tgg gga tta aag atg gct ttc ttg gtg gag	1697
Leu Glu Val His Thr Trp Gly Leu Lys Met Ala Phe Leu Val Glu	
525 530 535	
aac ggc aaa gga ccc aat cag tcg att ttg ccg ccg cct aag gat ctt	1745
Asn Gly Lys Gly Pro Asn Gln Ser Ile Leu Pro Pro Pro Lys Asp Leu	
540 545 550 555	
ccc aag tgc taa gtctgcaac taaatagggc gacatatcaa catcacgcca	1797
Pro Lys Cys	
cgccaagaa gactaatgag tgggtattta atgcgtggat ttggctaaca aattgtattt	1857
ttttgagcaa agcaaaaggt tcgggttttt ttgctcatgt caaaagtgtg aataatggag	1917
aaaaaagagc attgtattat aataattgt tttcattata ttcaattcc attcatattt	1977
tttattattg tctctaacac acctcttata tggccaag ttgt	2021
<210> SEQ ID NO 4	
<211> LENGTH: 558	
<212> TYPE: PRT	
<213> ORGANISM: Arabidopsis thaliana	
<400> SEQUENCE: 4	
Met Gly Ser His Met Val Trp Phe Leu Phe Leu Val Ser Phe Phe Ser	
1 5 10 15	
Val Phe Pro Ala Pro Ser Glu Ser Met Val Arg His Tyr Lys Phe Asn	
20 25 30	
Val Val Met Lys Asn Val Thr Arg Leu Cys Ser Ser Lys Pro Thr Val	
35 40 45	
Thr Val Asn Gly Arg Tyr Pro Gly Pro Thr Ile Tyr Ala Arg Glu Asp	
50 55 60	
Asp Thr Leu Leu Ile Lys Val Val Asn His Val Lys Tyr Asn Val Ser	
65 70 75 80	
Ile His Trp His Gly Val Arg Gln Val Arg Thr Gly Trp Ala Asp Gly	
85 90 95	
Pro Ala Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Gln Val Tyr Thr	
100 105 110	

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Tyr Asn Tyr Thr Leu Thr Gly Gln Arg Gly Thr Leu Trp Trp His Ala  
 115 120 125  
 His Ile Leu Trp Leu Arg Ala Thr Val Tyr Gly Ala Leu Val Ile Leu  
 130 135 140  
 Pro Lys Arg Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Asn Glu Lys  
 145 150 155 160  
 Val Ile Val Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Asn Ile Ile  
 165 170 175  
 Asn Glu Ala Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ser His  
 180 185 190  
 Met Ile Asn Gly His Pro Gly Pro Val Arg Asn Cys Pro Ser Gln Gly  
 195 200 205  
 Tyr Lys Leu Ser Val Glu Asn Gly Lys Thr Tyr Leu Leu Arg Leu Val  
 210 215 220  
 Asn Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Val Ala Gly His Ile  
 225 230 235 240  
 Phe Thr Val Val Glu Val Asp Ala Val Tyr Val Lys Pro Phe Lys Thr  
 245 250 255  
 Asp Thr Val Leu Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Leu Thr  
 260 265 270  
 Ala Ser Lys Ser Ala Gly Lys Tyr Leu Val Thr Ala Ser Pro Phe Met  
 275 280 285  
 Asp Ala Pro Ile Ala Val Asp Asn Val Thr Ala Thr Ala Thr Val His  
 290 295 300  
 Tyr Ser Gly Thr Leu Ser Ser Ser Pro Thr Ile Leu Thr Leu Pro Pro  
 305 310 315 320  
 Pro Gln Asn Ala Thr Ser Ile Ala Asn Asn Phe Thr Asn Ser Leu Arg  
 325 330 335  
 Ser Leu Asn Ser Lys Lys Tyr Pro Ala Leu Val Pro Thr Thr Ile Asp  
 340 345 350  
 His His Leu Phe Phe Thr Val Gly Leu Gly Leu Asn Ala Cys Pro Thr  
 355 360 365  
 Cys Lys Ala Gly Asn Gly Ser Arg Val Val Ala Ser Ile Asn Asn Val  
 370 375 380  
 Thr Phe Ile Met Pro Lys Thr Ala Leu Leu Pro Ala His Tyr Phe Asn  
 385 390 395 400  
 Thr Ser Gly Val Phe Thr Thr Asp Phe Pro Lys Asn Pro Pro His Val  
 405 410 415  
 Phe Asn Tyr Ser Gly Gly Ser Val Thr Asn Met Ala Thr Glu Thr Gly  
 420 425 430  
 Thr Arg Leu Tyr Lys Leu Pro Tyr Asn Ala Thr Val Gln Leu Val Leu  
 435 440 445  
 Gln Asp Thr Gly Val Ile Ala Pro Glu Asn His Pro Val His Leu His  
 450 455 460  
 Gly Phe Asn Phe Phe Glu Val Gly Arg Gly Leu Gly Asn Phe Asn Ser  
 465 470 475 480  
 Thr Lys Asp Pro Lys Asn Phe Asn Leu Val Asp Pro Val Glu Arg Asn  
 485 490 495  
 Thr Ile Gly Val Pro Ser Gly Gly Trp Val Val Ile Arg Phe Arg Ala  
 500 505 510  
 Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr





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Asp Ala Pro Arg Pro Ser Ala Ser Ala Gly Ser Phe Asn Glu Ala Leu
      325                      330          335

Pro Leu Tyr Arg Pro Thr Leu Pro Gln Leu Asn Asp Thr Ser Phe Val
      340                      345          350

Gly Asn Phe Thr Ala Lys Leu Arg Ser Leu Ala Thr Pro Arg Tyr Pro
      355                      360          365

Ala Ala Val Pro Arg Thr Val Asp Arg Arg Phe Phe Phe Ala Val Gly
      370                      375          380

Leu Gly Thr His Pro Cys Pro Ala Asn Ala Thr Cys Gln Gly Pro Thr
      385                      390          395          400

Asn Thr Thr Gln Phe Ala Ala Ser Val Asn Asn Val Ser Phe Val Leu
      405                      410          415

Pro Thr Lys Ala Leu Leu His Ser His Phe Thr Gly Leu Ser Ser Gly
      420                      425          430

Val Tyr Ser Pro Asp Phe Pro Val Ala Pro Leu Ala Pro Phe Asn Tyr
      435                      440          445

Thr Gly Thr Pro Pro Asn Asn Thr Asn Val Ala Ser Gly Thr Lys Leu
      450                      455          460

Met Val Val Pro Tyr Gly Ala Asn Val Glu Leu Val Met Gln Gly Thr
      465                      470          475          480

Ser Ile Leu Gly Val Glu Ser His Pro Leu His Leu His Gly Phe Asn
      485                      490          495

Phe Phe Val Val Gly Gln Gly Tyr Gly Asn Tyr Asp Pro Val Asn Asp
      500                      505          510

Pro Ser Lys Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr Val Gly
      515                      520          525

Val Pro Ala Gly Gly Trp Val Ala Ile Arg Phe Leu Ala Asp Asn Pro
      530                      535          540

Gly Val Trp Phe Met His Cys His Leu Glu Ala His Thr Thr Trp Gly
      545                      550          555          560

Leu Arg Met Ala Trp Leu Val Leu Asp Gly Ser Leu Pro His Gln Lys
      565                      570          575

Leu Leu Pro Pro Pro Ser Asp Leu Pro Lys Cys
      580                      585

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&lt;210&gt; SEQ ID NO 6

&lt;211&gt; LENGTH: 582

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Zea mays

&lt;400&gt; SEQUENCE: 6

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Met Ala Thr Pro Tyr Arg Leu Pro Cys Cys Cys Tyr Ala Leu Val Thr
  1      5      10      15

Val Leu Val Leu Phe Phe Ser Val Asp Ala Thr Glu Gly Ala Ile Arg
  20      25      30

Glu Tyr Gln Phe Asp Val Gln Met Thr Asn Val Thr Arg Leu Cys Ser
  35      40      45

Ser Lys Ser Ile Val Thr Val Asn Gly Gln Phe Pro Gly Pro Thr Val
  50      55      60

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

Pro Tyr Asn Met Ser Ile His Trp His Gly Ile Arg Gln Leu Arg Ser
  85      90      95

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Gly Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile Gln Ser  
 100 105 110

Gly Gln Ser Tyr Val Tyr Lys Phe Thr Ile Thr Gly Gln Arg Gly Thr  
 115 120 125

Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val Tyr Gly  
 130 135 140

Pro Ile Val Ile Leu Pro Lys Pro Gly Val Pro Tyr Pro Phe Pro Ala  
 145 150 155 160

Pro Tyr Asp Glu Val Pro Val Leu Phe Gly Glu Trp Trp Thr Ala Asp  
 165 170 175

Thr Glu Ala Val Ile Ser Gln Ala Leu Gln Thr Gly Gly Gly Pro Asn  
 180 185 190

Val Ser Asp Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn  
 195 200 205

Cys Ser Ala Lys Asp Thr Phe Lys Leu Lys Val Lys Pro Gly Lys Thr  
 210 215 220

Tyr Met Leu Arg Ile Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe  
 225 230 235 240

Ser Ile Ala Gly His Pro Leu Thr Val Val Asp Val Asp Ala Val Tyr  
 245 250 255

Ile Lys Pro Ile Thr Val Glu Thr Ile Ile Ile Thr Pro Gly Gln Thr  
 260 265 270

Thr Asn Val Leu Leu Thr Thr Lys Pro Ser Tyr Pro Gly Ala Thr Tyr  
 275 280 285

Tyr Met Leu Ala Ala Pro Tyr Ser Thr Ala Arg Pro Gly Thr Phe Asp  
 290 295 300

Asn Thr Thr Val Ala Gly Ile Leu Glu Tyr Glu Asp Pro Thr Ser Ser  
 305 310 315 320

Pro Pro Pro His Ala Ala Phe Asp Lys Asn Leu Pro Ala Leu Lys Pro  
 325 330 335

Thr Leu Pro Gln Ile Asn Asp Thr Ser Phe Val Ala Asn Tyr Thr Ala  
 340 345 350

Arg Leu Arg Ser Leu Ala Thr Ala Glu Tyr Pro Ala Asp Val Pro Arg  
 355 360 365

Glu Val His Arg Arg Phe Phe Thr Val Gly Leu Gly Thr His Pro  
 370 375 380

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

Ala Ala Ser Val Asn Asn Val Ser Phe Val Leu Pro Thr Thr Ala Leu  
 405 410 415

Leu Gln Ser His Phe Ala Gly Lys Ser Arg Gly Val Tyr Ser Ser Asn  
 420 425 430

Phe Pro Ala Ala Pro Leu Val Pro Phe Asn Tyr Thr Gly Thr Pro Pro  
 435 440 445

Asn Asn Thr Asn Val Ser Asn Gly Thr Lys Leu Val Val Leu Pro Tyr  
 450 455 460

Gly Thr Ser Val Glu Leu Val Met Gln Gly Thr Ser Ile Leu Gly Ala  
 465 470 475 480

Glu Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly  
 485 490 495

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Gln Gly Phe Gly Asn Phe Asp Pro Ala Lys Asp Pro Ala Lys Tyr Asn  
500 505 510

Leu Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro Ala Ala Gly  
515 520 525

Trp Val Ala Ile Arg Phe Arg Ala Asp Asn Pro Gly Val Trp Phe Met  
530 535 540

His Cys His Leu Glu Val His Val Ser Trp Gly Leu Lys Met Ala Trp  
545 550 555 560

Leu Val Leu Asp Gly Asp Arg Pro Asn Glu Lys Leu Leu Pro Pro Pro  
565 570 575

Ser Asp Leu Pro Lys Cys  
580

&lt;210&gt; SEQ ID NO 7

&lt;211&gt; LENGTH: 573

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Saccharum officinarum

&lt;400&gt; SEQUENCE: 7

Met Gly Ala Pro Pro Cys Leu Ala Phe Leu Leu Leu Phe Gly Thr Leu  
1 5 10 15

Leu Ala Leu Leu Gln Ser Ser His Gly Thr Thr Arg Tyr Tyr Thr Phe  
20 25 30

Asn Val Thr Met Gln Asn Val Thr Arg Leu Cys Thr Thr Arg Ala Ile  
35 40 45

Pro Thr Val Asn Gly Lys Phe Pro Gly Pro Lys Ile Val Thr Arg Glu  
50 55 60

Gly Asp Arg Val Val Val Lys Val Val Asn Asn Val Lys Asp Asn Val  
65 70 75 80

Thr Ile His Trp His Gly Val Arg Gln Leu Arg Thr Gly Trp Ser Asp  
85 90 95

Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile Gln Thr Gly Gln Ser Tyr  
100 105 110

Val Tyr Asn Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Leu Trp His  
115 120 125

Ala His Val Ser Trp Met Arg Ala Thr Leu Tyr Gly Pro Ile Val Ile  
130 135 140

Leu Pro Lys Arg Gly Val Pro Tyr Pro Phe Pro Val Lys Pro Tyr Lys  
145 150 155 160

Glu Val Pro Ile Ile Phe Gly Glu Trp Phe Asn Ala Asp Pro Glu Ala  
165 170 175

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

Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys Ser Ser  
195 200 205

Lys Asp Thr Phe Arg Leu Lys Val Leu Pro Gly Lys Trp Tyr Leu Leu  
210 215 220

Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile Ala  
225 230 235 240

Asn His Thr Leu Thr Val Val Asp Val Asp Ala Ala Tyr Val Lys Pro  
245 250 255

Phe His Thr Asp Ile Val Leu Ile Thr Pro Gly Gln Asn Thr Asn Val  
260 265 270

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Leu Leu Arg Ala Glu Pro Asp Ala Gly Cys Pro Ala Ala Thr His Leu  
 275 280 285  
 Met Gln Ala Arg Pro Tyr Gly Thr Gly Gln Pro Gly Thr Phe Asp Asn  
 290 295 300  
 Thr Thr Val Ala Ala Val Leu Glu Tyr Ala Pro Ala Ala Gly His Ile  
 305 310 315 320  
 Lys Ser Leu Pro Leu Phe Arg Pro Trp Leu Pro Ala Leu Asn Asp Thr  
 325 330 335  
 Ala Phe Ala Ala Asn Tyr Thr Ala Arg Leu Arg Ser Leu Ala Thr Pro  
 340 345 350  
 Glu Tyr Pro Ala Ser Val Pro Arg Gly Val Asp Arg Ser Phe Phe Phe  
 355 360 365  
 Ala Val Gly Leu Gly Thr Asn Pro Cys Pro Ala Asn Gln Thr Cys Gln  
 370 375 380  
 Gly Pro Thr Asn Arg Thr Met Phe Thr Ala Ser Met Asn Asn Val Ser  
 385 390 395 400  
 Phe Thr Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Asp Asn Ile  
 405 410 415  
 Ala Gly Val Tyr Thr Thr Asp Phe Pro Val Ala Pro Arg Glu Pro Phe  
 420 425 430  
 Asn Tyr Thr Gly Thr Thr Pro Asn Asn Thr Asn Val Ser Ser Gly Thr  
 435 440 445  
 Lys Val Val Val Leu Glu Tyr Asn Thr Ser Val Glu Val Val Leu Gln  
 450 455 460  
 Gly Thr Ser Ile Leu Gly Ala Glu Ser His Pro Leu His Leu His Gly  
 465 470 475 480  
 Phe Asp Phe Phe Val Val Gly Gln Gly Phe Gly Asn Tyr Asp Ser Ser  
 485 490 495  
 Lys Asp Pro Ala Asn Phe Asn Leu Val Asp Pro Val Gln Arg Asn Thr  
 500 505 510  
 Val Gly Val Pro Ser Ala Gly Trp Val Ala Ile Arg Phe Phe Ala Asp  
 515 520 525  
 Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Ser  
 530 535 540  
 Trp Gly Leu Lys Met Ala Trp Val Val Asn Asp Gly Pro Leu Pro Glu  
 545 550 555 560  
 Gln Lys Leu Met Pro Pro Pro Asp Leu Pro Lys Cys  
 565 570

&lt;210&gt; SEQ ID NO 8

&lt;211&gt; LENGTH: 549

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Sorghum bicolor

&lt;400&gt; SEQUENCE: 8

Val Trp Gln Val Gln Met Thr Ser Val Thr Arg Leu Cys Gly Thr Lys  
 1 5 10 15  
 Gly Ile Val Thr Val Asn Gly Gln Tyr Pro Gly Pro Thr Leu Phe Ala  
 20 25 30  
 Arg Glu Gly Asp His Val Glu Val Asn Val Val Asn Arg Ser Pro Tyr  
 35 40 45  
 Asn Ile Ser Ile His Trp His Gly Val Arg Gln Leu Leu Ser Gly Trp

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50					55					60									
Ala	Asp	Gly	Pro	Ser	Tyr	Ile	Thr	Gln	Cys	Pro	Ile	Gln	Pro	Gly	Gln	65	70	75	80
Ser	Tyr	Val	Tyr	Arg	Tyr	Gln	Ile	Val	Gly	Gln	Arg	Gly	Thr	Leu	Trp	85	90	95	
Trp	His	Ala	His	Ile	Ser	Trp	Leu	Arg	Ala	Thr	Val	Tyr	Gly	Pro	Ile	100	105	110	
Val	Ile	Leu	Pro	Pro	Ala	Gly	Val	Pro	Tyr	Pro	Phe	Pro	Ala	Pro	Asp	115	120	125	
Glu	Glu	Val	Pro	Val	Met	Phe	Gly	Glu	Trp	Trp	Arg	Asn	Asp	Thr	Glu	130	135	140	
Ala	Val	Ile	Ala	Gln	Ala	Leu	Gln	Thr	Gly	Gly	Gly	Pro	Asn	Val	Ser	145	150	155	160
Asp	Ala	Tyr	Thr	Ile	Asn	Gly	Leu	Thr	Gly	Pro	Leu	Tyr	Asn	Cys	Ser	165	170	175	
Ala	Gln	Asp	Thr	Phe	Lys	Leu	Lys	Val	Lys	Pro	Gly	Lys	Thr	Tyr	Met	180	185	190	
Leu	Arg	Leu	Ile	Asn	Ala	Ala	Leu	Asn	Asp	Glu	Leu	Phe	Phe	Ser	Val	195	200	205	
Ala	Asn	His	Thr	Leu	Thr	Val	Val	Asp	Val	Asp	Ala	Leu	Tyr	Val	Lys	210	215	220	
Pro	Phe	Thr	Val	Asp	Thr	Leu	Ile	Ile	Ala	Pro	Gly	Gln	Thr	Ser	Asn	225	230	235	240
Val	Leu	Leu	Ala	Thr	Lys	Pro	Thr	Tyr	Pro	Gly	Ala	Ile	Tyr	Tyr	Met	245	250	255	
Glu	Ala	Arg	Pro	Tyr	Thr	Asn	Thr	Gln	Gly	Thr	Phe	Asp	Asn	Thr	Thr	260	265	270	
Val	Ala	Gly	Val	Leu	Glu	Tyr	Glu	Asp	Pro	Ser	Ser	Ser	Ser	Ser	Ser	275	280	285	
Gly	Glu	Asn	Gln	Ser	Asn	Ser	Asn	Leu	Pro	Val	Phe	Ala	Pro	Thr	Leu	290	295	300	
Pro	Pro	Ile	Asn	Asp	Thr	Ser	Phe	Val	Ala	Asn	Tyr	Thr	Ala	Lys	Leu	305	310	315	320
Arg	Ser	Leu	Ala	Ser	Ala	Glu	Tyr	Pro	Ala	Ala	Val	Pro	Gln	Asp	Val	325	330	335	
Asp	Arg	Arg	Phe	Phe	Phe	Thr	Val	Gly	Leu	Gly	Thr	His	Pro	Cys	Ala	340	345	350	
Gly	Gly	Val	Asn	Gly	Thr	Cys	Gln	Gly	Pro	Asn	Gly	Ser	Arg	Phe	Ala	355	360	365	
Ala	Ser	Ile	Asn	Asn	Val	Ser	Phe	Val	Leu	Pro	Thr	Thr	Ala	Leu	Leu	370	375	380	
Gln	Ala	His	Phe	Ala	Gly	Arg	Ser	Asn	Gly	Val	Tyr	Ala	Thr	Asn	Phe	385	390	395	400
Pro	Ala	Phe	Pro	Pro	Thr	Pro	Phe	Asn	Tyr	Ala	Gly	Thr	Pro	Pro	Asn	405	410	415	
Asn	Thr	Asn	Val	Met	Asn	Gly	Thr	Lys	Val	Ala	Val	Leu	Pro	Phe	Gly	420	425	430	
Thr	Ser	Val	Glu	Leu	Val	Leu	Gln	Asp	Thr	Ser	Ile	Leu	Gly	Ala	Glu	435	440	445	
Ser	His	Pro	Leu	His	Leu	His	Gly	Phe	Asn	Phe	Phe	Val	Val	Gly	Gln	450	455	460	

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Gly Phe Gly Asn Phe Asp Pro Thr Asn Asp Pro Ala Lys Phe Asn Leu  
 465 470 475 480

Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp  
 485 490 495

Val Ala Ile Arg Phe Arg Ala Asp Asn Pro Gly Val Trp Phe Met His  
 500 505 510

Cys His Leu Glu Val His Met Ser Trp Gly Leu Lys Met Ala Trp Leu  
 515 520 525

Val Leu Asp Gly Ser Leu Pro Asn Gln Lys Leu Pro Pro Pro Leu  
 530 535 540

Asp Leu Pro Gln Cys  
 545

<210> SEQ ID NO 9  
 <211> LENGTH: 585  
 <212> TYPE: PRT  
 <213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 9

Met Ala Gly Gly Arg Arg Arg Leu Ser Pro Ala Cys Leu Phe Leu Thr  
 1 5 10 15

Val Ala Leu Val Val Leu Val Ala Leu Pro Glu Leu Ala Ala Ala Arg  
 20 25 30

Thr Arg Arg Tyr Thr Phe Asn Val Thr Met Ala Thr Val Thr Arg Leu  
 35 40 45

Cys Val Thr Lys Ser Ile Pro Thr Val Asn Gly Arg Phe Pro Gly Pro  
 50 55 60

Arg Ile Val Val Arg Glu Gly Asp Arg Leu Val Val Gln Val His Asn  
 65 70 75 80

Asn Ile Asn Asn Asn Val Thr Phe His Trp His Gly Val Arg Gln Leu  
 85 90 95

Arg Ser Gly Trp Ser Asp Gly Pro Ser Phe Ile Thr Gln Cys Pro Ile  
 100 105 110

Arg Pro Gly Gln Ser Tyr Ala Tyr Asp Phe Arg Ile Val Gly Gln Arg  
 115 120 125

Gly Thr Leu Trp Trp His Ala His Phe Ser Trp Leu Arg Ala Thr Leu  
 130 135 140

Tyr Gly Pro Leu Val Ile Leu Pro Pro Arg Gly Val Pro Tyr Pro Phe  
 145 150 155 160

Pro Lys Pro His Ala Glu Val Pro Leu Met Leu Gly Glu Trp Phe Asn  
 165 170 175

Ala Asp Pro Glu Ala Val Ile Lys Gln Ala Leu Gln Thr Gly Gly Gly  
 180 185 190

Pro Asn Val Ser Asp Ala Tyr Thr Phe Asn Gly Leu Pro Gly Pro Thr  
 195 200 205

Tyr Asn Cys Ser Gly Gly Gly Ala Gly Asp Thr Phe Lys Leu Arg Val  
 210 215 220

Lys Pro Gly Lys Thr Tyr Leu Leu Arg Leu Val Asn Ala Ala Leu Asn  
 225 230 235 240

Asp Glu Leu Phe Phe Ala Val Ala Asn His Thr Leu Thr Val Val Gln  
 245 250 255

Ala Asp Ala Ser Tyr Val Lys Pro Phe Thr Ala Asp Thr Leu Val Ile

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260					265					270				
Ser	Pro	Gly	Gln	Thr	Met	Asp	Val	Leu	Leu	Thr	Ala	Ala	Ala	Thr
		275					280					285		
Ala	Pro	Ser	Ser	Thr	Ala	Ala	Tyr	Ala	Ile	Ala	Val	Ala	Pro	Tyr
	290					295					300			
Asn	Thr	Val	Gly	Thr	Phe	Asp	Asn	Thr	Thr	Ala	Ile	Ala	Val	Glu
305					310					315				320
Tyr	Tyr	Gly	Ala	Pro	Pro	Gln	Ser	Ala	Ala	Ala	Leu	Arg	Asn	Pro
				325					330					335
Leu	Pro	Ala	Leu	Pro	Leu	Tyr	Asn	Asp	Thr	Gly	Ala	Val	Ala	Phe
			340						345				350	
Ser	Ala	Lys	Phe	Arg	Ser	Leu	Ala	Ser	Ala	Gln	Tyr	Pro	Ala	Val
		355					360					365		
Pro	Arg	Thr	Val	Asp	Arg	Arg	Phe	Phe	Phe	Ala	Val	Gly	Leu	Ala
		370					375					380		
Asp	Pro	Cys	Gln	Ser	Arg	Val	Asn	Gly	Thr	Cys	Gln	Gly	Pro	Gly
385					390					395				400
Thr	Arg	Phe	Ala	Ala	Thr	Met	Asn	Asn	Val	Ser	Phe	Thr	Met	Lys
				405					410					415
Thr	Ser	Leu	Leu	Gln	Ala	His	Tyr	Gln	Arg	Arg	Tyr	Ser	Gly	Leu
			420					425					430	
Thr	Ala	Asn	Phe	Pro	Gly	Val	Pro	Pro	Thr	Pro	Phe	Asn	Tyr	Gly
		435					440					445		
Thr	Pro	Pro	Asn	Asn	Thr	Phe	Val	Thr	His	Gly	Thr	Arg	Val	Pro
				450			455					460		
Leu	Ser	Phe	Asn	Thr	Thr	Val	Glu	Val	Val	Leu	Gln	Asp	Thr	Ile
465				470						475				480
Leu	Gly	Ala	Glu	Ser	His	Pro	Leu	His	Leu	His	Gly	Tyr	Asp	Phe
				485					490					495
Val	Val	Gly	Gln	Gly	Phe	Gly	Asn	Tyr	Asp	Ala	Gly	Asn	Asp	Ala
			500					505					510	
Lys	Tyr	Asn	Leu	Val	Asp	Pro	Val	Gln	Arg	Asn	Thr	Ile	Ser	Pro
		515					520					525		
Thr	Ala	Gly	Trp	Val	Ala	Ile	Arg	Phe	Val	Ala	Asp	Asn	Pro	Val
				530			535					540		
Trp	Ile	Met	His	Cys	His	Leu	Asp	Val	His	Leu	Ser	Trp	Gly	Ala
545				550						555				560
Met	Ala	Trp	Leu	Val	Asn	Asp	Gly	Pro	Leu	Pro	Asn	Gln	Lys	Pro
565				570					575					
Pro	Pro	Pro	Ser	Asp	Ile	Pro	Arg	Cys						
				580				585						

&lt;210&gt; SEQ ID NO 10

&lt;211&gt; LENGTH: 575

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Sorghum bicolor

&lt;400&gt; SEQUENCE: 10

Met	Ala	Ala	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Leu	Phe	Phe	Gly	Thr	Leu
1				5					10					15	
Leu	Ala	Leu	Pro	Gln	Ser	Ser	His	Gly	Ala	Thr	Arg	Tyr	Tyr	Thr	Phe
			20					25						30	

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Asn	Val	Thr	Met	Gln	Lys	Val	Thr	Arg	Leu	Cys	Thr	Thr	Arg	Ala	Ile
	35						40					45			
Pro	Thr	Val	Asn	Gly	Lys	Phe	Pro	Gly	Pro	Lys	Ile	Val	Thr	Arg	Glu
	50					55					60				
Gly	Asp	Arg	Val	Val	Val	Lys	Val	Val	Asn	Asn	Val	Lys	Asp	Asn	Val
65					70					75					80
Thr	Ile	His	Trp	His	Gly	Val	Arg	Gln	Leu	Arg	Thr	Gly	Trp	Ser	Asp
				85					90					95	
Gly	Pro	Ala	Tyr	Val	Thr	Gln	Cys	Pro	Ile	Gln	Thr	Gly	Gln	Ser	Phe
		100						105					110		
Val	Tyr	Asn	Phe	Thr	Ile	Thr	Gly	Gln	Arg	Gly	Thr	Leu	Phe	Trp	His
	115						120					125			
Ala	His	Val	Ser	Trp	Leu	Arg	Ala	Thr	Leu	Tyr	Gly	Pro	Ile	Val	Ile
	130					135					140				
Leu	Pro	Lys	Arg	Gly	Val	Pro	Tyr	Pro	Phe	Leu	Pro	Val	Lys	Pro	Tyr
145					150					155					160
Lys	Glu	Val	Pro	Ile	Ile	Phe	Glu	Trp	Phe	Asn	Ala	Asp	Pro	Glu	Ala
				165					170					175	
Ile	Ile	Ala	Gln	Ala	Leu	Gln	Thr	Gly	Ala	Gly	Pro	Asn	Val	Ser	Asp
		180						185					190		
Ala	Phe	Thr	Ile	Asn	Gly	Leu	Pro	Gly	Pro	Leu	Tyr	Asn	Cys	Ser	Ser
		195					200					205			
Lys	Asp	Thr	Phe	Lys	Leu	Lys	Val	Leu	Pro	Gly	Lys	Trp	Tyr	Leu	Leu
	210					215					220				
Arg	Leu	Ile	Asn	Ala	Ala	Leu	Asn	Asp	Glu	Leu	Phe	Phe	Ser	Ile	Ala
225					230					235					240
Asn	His	Thr	Leu	Thr	Val	Val	Asp	Val	Asp	Ala	Ser	Tyr	Val	Lys	Pro
			245						250					255	
Phe	His	Thr	Asp	Ile	Val	Leu	Ile	Thr	Pro	Gly	Gln	Thr	Thr	Asn	Val
		260						265					270		
Leu	Leu	Arg	Ala	Glu	Pro	Asp	Ala	Gly	Cys	Ala	Ala	Ala	Thr	His	Leu
		275					280					285			
Met	Leu	Ala	Arg	Pro	Tyr	Gly	Thr	Gly	Gln	Pro	Gly	Thr	Phe	Asp	Asn
	290					295					300				
Thr	Thr	Val	Ala	Ala	Val	Leu	Glu	Tyr	Ala	Pro	Ala	Ala	Ala	Ala	Gly
305					310					315					320
His	Ile	Lys	Ser	Leu	Pro	Leu	Phe	Arg	Pro	Ser	Leu	Pro	Ala	Leu	Asn
				325					330					335	
Asp	Thr	Ala	Phe	Ala	Ala	Asn	Tyr	Ser	Ala	Arg	Leu	Arg	Ser	Leu	Ala
		340						345					350		
Thr	Pro	Glu	Phe	Pro	Ala	Thr	Val	Pro	Arg	Ala	Val	Asp	Arg	Ser	Phe
		355					360					365			
Phe	Phe	Ala	Val	Gly	Leu	Gly	Thr	Asn	Pro	Cys	Pro	Ala	Asn	Gln	Thr
	370					375					380				
Cys	Gln	Gly	Pro	Thr	Asn	Arg	Thr	Lys	Phe	Thr	Ala	Ser	Met	Asn	Asn
385					390					395					400
Val	Ser	Phe	Thr	Met	Pro	Thr	Thr	Ala	Leu	Leu	Gln	Ala	His	Tyr	Asp
				405					410					415	
Asn	Ile	Ala	Gly	Val	Tyr	Thr	Ala	Asp	Phe	Pro	Val	Ala	Pro	Leu	Glu
		420						425					430		
Pro	Phe	Asn	Tyr	Thr	Gly	Thr	Thr	Pro	Asn	Asn	Thr	Asn	Val	Ser	Ser





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Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile  
 225 230 235 240  
 Ala Asn His Ser Leu Thr Val Val Glu Val Asp Ala Val Tyr Val Lys  
 245 250 255  
 Pro Phe Thr Val Asp Thr Leu Val Ile Ala Pro Gly Gln Thr Thr Asn  
 260 265 270  
 Val Leu Leu Ala Ala Lys Pro Phe Tyr Pro Ala Ala Asn Tyr Tyr Met  
 275 280 285  
 Thr Ala Arg Thr Tyr Ser Thr Gly Arg Pro Ala Thr Phe Asp Asn Thr  
 290 295 300  
 Thr Val Ala Gly Ile Leu Glu Tyr Glu Tyr Pro Asp Ala Pro Ser Ala  
 305 310 315 320  
 Ala Ala Ser Phe Asn Lys Ala Leu Pro Leu Tyr Arg Pro Ala Leu Pro  
 325 330 335  
 Gln Leu Asn Asp Thr Ser Phe Val Gly Asn Phe Thr Ala Lys Leu Leu  
 340 345 350  
 Ser Leu Ala Thr Pro Glu Tyr Pro Ala Ala Val Pro Gln Thr Val Asp  
 355 360 365  
 Lys Arg Phe Phe Phe Thr Val Gly Leu Gly Thr His Pro Cys Pro Ala  
 370 375 380  
 Asn Thr Thr Cys Gln Gly Pro Thr Asn Thr Thr Gln Phe Ala Ala Ser  
 385 390 395 400  
 Val Asn Asn Val Ser Phe Val Leu Pro Thr Lys Ala Leu Leu His Ser  
 405 410 415  
 His Phe Ala Gly Leu Ser Ser Gly Val Tyr Glu Ser Asp Phe Pro Val  
 420 425 430  
 Ala Pro Leu Ala Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr  
 435 440 445  
 Asn Val Ala Asn Gly Thr Lys Leu Met Val Ile Pro Tyr Gly Thr Asn  
 450 455 460  
 Val Glu Leu Val Met Gln Gly Thr Ser Ile Leu Gly Ile Glu Ser His  
 465 470 475 480  
 Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln Gly Tyr  
 485 490 495  
 Gly Asn Tyr Asp Pro Val Asn Asp Pro Pro Lys Phe Asn Leu Val Asp  
 500 505 510  
 Pro Val Glu Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala  
 515 520 525  
 Ile Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His  
 530 535 540  
 Leu Glu Val His Thr Thr Trp Gly Leu Arg Met Ala Trp Leu Val Leu  
 545 550 555 560  
 Asp Gly Ser Leu Pro His Gln Lys Leu Leu Pro Pro Pro Ser Asp Leu  
 565 570 575  
 Pro Lys Cys

&lt;210&gt; SEQ ID NO 12

&lt;211&gt; LENGTH: 8

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Consensus sequence

&lt;220&gt; FEATURE:

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<221> NAME/KEY: VARIANT
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: /Replace = "Val"

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<400> SEQUENCE: 12

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```

His Trp His Gly Ile Arg Gln Leu
1           5

```

```

<210> SEQ ID NO 13
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: /Replace = "Val"

```

```

<400> SEQUENCE: 13

```

```

Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe
1           5           10

```

```

<210> SEQ ID NO 14
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: /Replace = "Tyr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: /Replace = "Asp"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: /Replace = "Tyr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (22)..(22)
<223> OTHER INFORMATION: /Replace = "Tyr"

```

```

<400> SEQUENCE: 14

```

```

Glu Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly
1           5           10           15

```

```

Gln Gly Phe Gly Asn Phe Asp
20

```

```

<210> SEQ ID NO 15
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: /Replace = "Asp"

```

```

<400> SEQUENCE: 15

```

```

Met His Cys His Leu Glu Val His
1           5

```

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<210> SEQ ID NO 16  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer  
  
<400> SEQUENCE: 16  
  
tcgaagaggg tcaaagagtt t 21

<210> SEQ ID NO 17  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer  
  
<400> SEQUENCE: 17  
  
tcttagccat gaaatgtgag c 21

<210> SEQ ID NO 18  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer  
  
<400> SEQUENCE: 18  
  
attgtgtaag caaatcgca c 21

<210> SEQ ID NO 19  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer  
  
<400> SEQUENCE: 19  
  
tggettgtt gagcataatc t 21

<210> SEQ ID NO 20  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer  
  
<400> SEQUENCE: 20  
  
gcaagacaaa aacaatcgtg a 21

<210> SEQ ID NO 21  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer  
  
<400> SEQUENCE: 21  
  
gaaatctgag ggtggaggaa g 21

<210> SEQ ID NO 22  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial

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<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 22

agtaatgaac agttgcggtg g 21

<210> SEQ ID NO 23  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 23

tggtacttt ggacgatcag g 21

<210> SEQ ID NO 24  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 24

gtagaaact gtccatctca a 21

<210> SEQ ID NO 25  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 25

ctccacttgt gttgaagtaa t 21

<210> SEQ ID NO 26  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 26

atccggttga tgtgttgaga 20

<210> SEQ ID NO 27  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 27

agagagatcg gcttatgttg 20

<210> SEQ ID NO 28  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 28

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tatgccaaac aaacgagat 19

<210> SEQ ID NO 29  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 29

ctgctggagg aggaggtc 18

<210> SEQ ID NO 30  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 30

tgtaaagccg gaaacttctc 20

<210> SEQ ID NO 31  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 31

ttaggcctt taccattctc 20

<210> SEQ ID NO 32  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 32

gagctattct tcgggatt 18

<210> SEQ ID NO 33  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 33

gtctttaggc ggtggtag 18

<210> SEQ ID NO 34  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 34

gccgacgcat cttacctc 18

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<210> SEQ ID NO 35
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 35

ccaagaacgc catagcaa 18

<210> SEQ ID NO 36
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 36

ttctcttggtg ttcttcttct t 21

<210> SEQ ID NO 37
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 37

gaacttcttt gtgaggttta g 21

<210> SEQ ID NO 38
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: /Replace = "Val"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: /Replace = "Leu"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: /Replace = "Met" or "Val"

<400> SEQUENCE: 38

His Trp His Gly Ile Arg Gln Leu
1 5

<210> SEQ ID NO 39
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: /Replace = "Ser"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: /Replace = "Glu"
<220> FEATURE:

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<221> NAME/KEY: VARIANT
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: /Replace = "Asn" or "Glu"

<400> SEQUENCE: 39

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```

Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe
1           5           10

```

```

<210> SEQ ID NO 40
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: /Replace = "Phe"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: /Replace = "Met"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: /Replace = "Tyr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: /Replace = "Asp"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: /Replace = "Tyr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: /Replace = "Tyr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: /Replace = "Ile"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: /Replace = "Thr" or "Glu"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: /Replace = "Val" or "Thr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (22)..(22)
<223> OTHER INFORMATION: /Replace = "Tyr"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (23)..(23)
<223> OTHER INFORMATION: /Replace = "Asn"

<400> SEQUENCE: 40

```

```

Glu Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly
1           5           10           15

```

```

Gln Gly Phe Gly Asn Phe Asp
20

```

```

<210> SEQ ID NO 41
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: /Replace = "Val"
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: /Replace = no amino acid present
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: /Replace = no amino acid present

<400> SEQUENCE: 41

Ala Asp Asn Pro Gly Val Trp
1                5

<210> SEQ ID NO 42
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 42

Met Ala Ile Ser Ser Ala Leu Pro Cys Ser Ser Leu Leu Met Ala Ala
1                5                10                15

Ala Gln Leu Met Leu Leu Ala Ser Val Val Val Gln Val Gln Gly Ile
20                25                30

Thr Arg His Tyr Asp Phe Asn Val Thr Met Ala Asn Val Thr Arg Leu
35                40                45

Cys Ala Ser Lys Ser Ile Ile Thr Val Asn Gly Gln Phe Pro Gly Pro
50                55                60

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

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

Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile
100               105               110

Gln Thr Gly Gln Ser Tyr Val Tyr Asn Tyr Thr Val Val Gly Gln Arg
115               120               125

Gly Thr Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val
130               135               140

Tyr Gly Pro Leu Val Ile Leu Pro Lys Leu Gly Val Pro Tyr Pro Phe
145               150               155               160

Pro Ala Pro Tyr Lys Glu Val Pro Val Ile Phe Gly Glu Trp Trp Leu
165               170               175

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

Pro Asn Val Ser Asp Ala His Thr Ile Asn Gly Leu Pro Gly Pro Leu
195               200               205

Tyr Asn Cys Ser Ala Lys Asp Thr Tyr Lys Leu Lys Val Lys Pro Gly
210               215               220

Lys Thr Tyr Met Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu
225               230               235               240

Phe Phe Ser Val Ala Asn His Ser Leu Thr Val Val Glu Val Asp Ala
245               250               255

Val Tyr Val Lys Pro Phe Thr Val Asp Thr Leu Leu Ile Ala Pro Gly
260               265               270

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Gln Thr Thr Asn Val Leu Leu Ala Ala Lys Pro Ser Tyr Pro Gly Ala  
 275 280 285  
 Asn Tyr Tyr Met Ser Ala Ala Pro Tyr Ser Thr Ala Arg Pro Ala Thr  
 290 295 300  
 Phe Asp Asn Thr Thr Val Ala Gly Ile Leu Glu Tyr Glu Leu Tyr Pro  
 305 310 315 320  
 Asp Ala Pro Arg Pro Ser Ala Ser Ala Gly Ser Phe Asn Glu Ala Leu  
 325 330 335  
 Pro Leu Tyr Arg Pro Thr Leu Pro Gln Leu Asn Asp Thr Ser Phe Val  
 340 345 350  
 Gly Asn Phe Thr Ala Lys Leu Arg Ser Leu Ala Thr Pro Arg Tyr Pro  
 355 360 365  
 Ala Ala Val Pro Arg Thr Val Asp Arg Arg Phe Phe Phe Ala Val Gly  
 370 375 380  
 Leu Gly Thr His Pro Cys Pro Ala Asn Ala Thr Cys Gln Gly Pro Thr  
 385 390 395 400  
 Asn Thr Thr Gln Phe Ala Ala Ser Val Asn Asn Val Ser Phe Val Leu  
 405 410 415  
 Pro Thr Lys Ala Leu Leu His Ser His Phe Thr Gly Leu Ser Ser Gly  
 420 425 430  
 Val Tyr Ser Pro Asp Phe Pro Val Ala Pro Leu Ala Pro Phe Asn Tyr  
 435 440 445  
 Thr Gly Thr Pro Pro Asn Asn Thr Asn Val Ala Ser Gly Thr Lys Leu  
 450 455 460  
 Met Val Val Pro Tyr Gly Ala Asn Val Glu Leu Val Met Gln Gly Thr  
 465 470 475 480  
 Ser Ile Leu Gly Val Glu Ser His Pro Leu His Leu His Gly Phe Asn  
 485 490 495  
 Phe Phe Val Val Gly Gln Gly Tyr Gly Asn Tyr Asp Pro Val Asn Asp  
 500 505 510  
 Pro Ser Lys Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr Val Gly  
 515 520 525  
 Val Pro Ala Gly Gly Trp Val Ala Ile Arg Phe Leu Ala Asp Asn Pro  
 530 535 540  
 Gly Val Trp Phe Met His Cys His Leu Glu Ala His Thr Thr Trp Gly  
 545 550 555 560  
 Leu Arg Met Ala Trp Leu Val Leu Asp Gly Ser Leu Pro His Gln Lys  
 565 570 575  
 Leu Leu Pro Pro Ser Asp Leu Pro Lys Cys  
 580 585

<210> SEQ ID NO 43  
 <211> LENGTH: 582  
 <212> TYPE: PRT  
 <213> ORGANISM: Zea mays

<400> SEQUENCE: 43

Met Ala Thr Pro Tyr Arg Leu Pro Cys Cys Cys Tyr Ala Leu Val Thr  
 1 5 10 15  
 Val Leu Val Leu Phe Phe Ser Val Asp Ala Thr Glu Gly Ala Ile Arg  
 20 25 30  
 Glu Tyr Gln Phe Asp Val Gln Met Thr Asn Val Thr Arg Leu Cys Ser

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35					40					45					
Ser	Lys	Ser	Ile	Val	Thr	Val	Asn	Gly	Gln	Phe	Pro	Gly	Pro	Thr	Val
50					55					60					
Phe	Ala	Arg	Glu	Gly	Asp	Phe	Val	Val	Ile	Arg	Val	Val	Asn	His	Val
65					70					75					80
Pro	Tyr	Asn	Met	Ser	Ile	His	Trp	His	Gly	Ile	Arg	Gln	Leu	Arg	Ser
				85					90					95	
Gly	Trp	Ala	Asp	Gly	Pro	Ala	Tyr	Ile	Thr	Gln	Cys	Pro	Ile	Gln	Ser
			100					105					110		
Gly	Gln	Ser	Tyr	Val	Tyr	Lys	Phe	Thr	Ile	Thr	Gly	Gln	Arg	Gly	Thr
		115					120					125			
Leu	Trp	Trp	His	Ala	His	Ile	Ser	Trp	Leu	Arg	Ala	Thr	Val	Tyr	Gly
	130					135					140				
Pro	Ile	Val	Ile	Leu	Pro	Lys	Pro	Gly	Val	Pro	Tyr	Pro	Phe	Pro	Ala
145					150					155					160
Pro	Tyr	Asp	Glu	Val	Pro	Val	Leu	Phe	Gly	Glu	Trp	Trp	Thr	Ala	Asp
			165						170					175	
Thr	Glu	Ala	Val	Ile	Ser	Gln	Ala	Leu	Gln	Thr	Gly	Gly	Gly	Pro	Asn
			180					185					190		
Val	Ser	Asp	Ala	Phe	Thr	Ile	Asn	Gly	Leu	Pro	Gly	Pro	Leu	Tyr	Asn
		195					200					205			
Cys	Ser	Ala	Lys	Asp	Thr	Phe	Lys	Leu	Lys	Val	Lys	Pro	Gly	Lys	Thr
	210					215					220				
Tyr	Met	Leu	Arg	Ile	Ile	Asn	Ala	Ala	Leu	Asn	Asp	Glu	Leu	Phe	Phe
225					230					235					240
Ser	Ile	Ala	Gly	His	Pro	Leu	Thr	Val	Val	Asp	Val	Asp	Ala	Val	Tyr
				245					250					255	
Ile	Lys	Pro	Ile	Thr	Val	Glu	Thr	Ile	Ile	Ile	Thr	Pro	Gly	Gln	Thr
			260					265					270		
Thr	Asn	Val	Leu	Leu	Thr	Thr	Lys	Pro	Ser	Tyr	Pro	Gly	Ala	Thr	Tyr
		275					280					285			
Tyr	Met	Leu	Ala	Ala	Pro	Tyr	Ser	Thr	Ala	Arg	Pro	Gly	Thr	Phe	Asp
	290					295					300				
Asn	Thr	Thr	Val	Ala	Gly	Ile	Leu	Glu	Tyr	Glu	Asp	Pro	Thr	Ser	Ser
305					310					315					320
Pro	Pro	Pro	His	Ala	Ala	Phe	Asp	Lys	Asn	Leu	Pro	Ala	Leu	Lys	Pro
				325					330					335	
Thr	Leu	Pro	Gln	Ile	Asn	Asp	Thr	Ser	Phe	Val	Ala	Asn	Tyr	Thr	Ala
			340					345					350		
Arg	Leu	Arg	Ser	Leu	Ala	Thr	Ala	Glu	Tyr	Pro	Ala	Asp	Val	Pro	Arg
		355					360					365			
Glu	Val	His	Arg	Arg	Phe	Phe	Phe	Thr	Val	Gly	Leu	Gly	Thr	His	Pro
	370					375					380				
Cys	Ala	Val	Asn	Gly	Thr	Cys	Gln	Gly	Pro	Thr	Asn	Ser	Ser	Arg	Phe
385					390					395					400
Ala	Ala	Ser	Val	Asn	Asn	Val	Ser	Phe	Val	Leu	Pro	Thr	Thr	Ala	Leu
				405					410					415	
Leu	Gln	Ser	His	Phe	Ala	Gly	Lys	Ser	Arg	Gly	Val	Tyr	Ser	Ser	Asn
			420					425					430		
Phe	Pro	Ala	Ala	Pro	Leu	Val	Pro	Phe	Asn	Tyr	Thr	Gly	Thr	Pro	Pro
		435					440					445			

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Asn Asn Thr Asn Val Ser Asn Gly Thr Lys Leu Val Val Leu Pro Tyr
 450                               455                               460

Gly Thr Ser Val Glu Leu Val Met Gln Gly Thr Ser Ile Leu Gly Ala
465                               470                               475                               480

Glu Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly
 485                               490                               495

Gln Gly Phe Gly Asn Phe Asp Pro Ala Lys Asp Pro Ala Lys Tyr Asn
 500                               505                               510

Leu Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro Ala Ala Gly
 515                               520                               525

Trp Val Ala Ile Arg Phe Arg Ala Asp Asn Pro Gly Val Trp Phe Met
 530                               535                               540

His Cys His Leu Glu Val His Val Ser Trp Gly Leu Lys Met Ala Trp
545                               550                               555                               560

Leu Val Leu Asp Gly Asp Arg Pro Asn Glu Lys Leu Leu Pro Pro Pro
 565                               570                               575

Ser Asp Leu Pro Lys Cys
 580

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<210> SEQ ID NO 44
<211> LENGTH: 584
<212> TYPE: PRT
<213> ORGANISM: Zea mays

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<400> SEQUENCE: 44

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Met Ala Ile Ser Ser Ala Leu Pro Cys Ser Ser Leu Leu Met Ala Ala
 1                               5                               10                               15

Ala Gln Leu Lys Leu Leu Ala Ser Val Val Val Gln Val Gln Gly Ile
 20                               25                               30

Thr Arg His Tyr Asp Phe Asn Val Thr Met Ala Asn Val Thr Arg Leu
 35                               40                               45

Cys Ala Thr Lys Ser Ile Val Thr Val Asn Gly Gln Phe Pro Gly Pro
 50                               55                               60

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

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

Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile
 100                              105                              110

Gln Thr Gly Gln Ser Tyr Val Tyr Asn Tyr Thr Val Ala Gly Gln Arg
 115                              120                              125

Gly Thr Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val
 130                              135                              140

Tyr Gly Pro Leu Val Val Leu Pro Arg Pro Gly Val Pro Tyr Pro Phe
 145                              150                              155                              160

Pro Ala Pro Tyr Lys Glu Val Pro Val Ile Phe Gly Glu Trp Trp Leu
 165                              170                              175

Ala Asp Thr Glu Val Val Val Glu Gln Ala Leu Gln Leu Gly Ala Gly
 180                              185                              190

Pro Asn Val Ser Asp Ala His Thr Ile Asn Gly Leu Pro Gly Pro Leu
 195                              200                              205

Tyr Asn Cys Ser Ala Lys Asp Thr Tyr Lys Leu Lys Val Lys Pro Gly

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210				215				220							
Lys	Thr	Tyr	Met	Leu	Arg	Leu	Ile	Asn	Ala	Ala	Leu	Asn	Asp	Glu	Leu
225					230					235					240
Phe	Phe	Ser	Val	Ala	Asn	His	Ser	Leu	Thr	Val	Val	Glu	Val	Asp	Ala
				245					250					255	
Val	Tyr	Val	Lys	Pro	Phe	Thr	Val	Asp	Thr	Leu	Pro	Ile	Ala	Pro	Gly
			260						265					270	
Gln	Thr	Thr	Asn	Val	Leu	Leu	Ala	Ala	Lys	Pro	Phe	Tyr	Pro	Gly	Ala
			275				280							285	
Asn	Tyr	Tyr	Met	Ser	Ala	Lys	Pro	Tyr	Ser	Thr	Ala	Arg	Pro	Ala	Thr
	290					295						300			
Phe	Asp	Asn	Thr	Thr	Val	Ala	Gly	Ile	Leu	Glu	Tyr	Glu	Tyr	Pro	Asp
305					310					315					320
Ala	Pro	Ser	Ser	Ser	Ala	Ala	Ser	Phe	Asp	Lys	Ala	Leu	Pro	Leu	His
				325					330					335	
Arg	Pro	Thr	Leu	Pro	Gln	Leu	Asn	Asp	Thr	Ser	Phe	Val	Gly	Asn	Phe
			340						345					350	
Thr	Ala	Lys	Leu	Arg	Ser	Leu	Ala	Thr	Pro	Gln	Tyr	Pro	Ala	Ala	Val
		355					360						365		
Pro	Arg	Thr	Val	Asp	Arg	Ala	Phe	Phe	Phe	Thr	Val	Gly	Leu	Gly	Thr
	370					375						380			
His	Pro	Cys	Pro	Gly	Asn	Ala	Thr	Cys	Leu	Gly	Pro	Thr	Asn	Thr	Thr
385					390					395					400
Gln	Phe	Ala	Ala	Ala	Val	Asn	Asn	Val	Ser	Phe	Val	Leu	Pro	Thr	Arg
				405					410					415	
Ala	Leu	Leu	His	Ser	His	Phe	Ala	Gly	Leu	Ser	Ser	Gly	Val	Tyr	Ser
			420						425					430	
Ser	Asp	Phe	Pro	Val	Ala	Pro	Leu	Thr	Pro	Phe	Asn	Tyr	Thr	Gly	Thr
		435					440						445		
Pro	Pro	Asn	Asn	Thr	Asn	Val	Ala	Ser	Gly	Thr	Lys	Leu	Met	Val	Val
		450				455						460			
Pro	Tyr	Gly	Ala	Asn	Val	Glu	Leu	Val	Leu	Gln	Gly	Thr	Ser	Ile	Leu
465					470					475					480
Gly	Val	Glu	Ser	His	Pro	Leu	His	Leu	His	Gly	Phe	Asn	Phe	Phe	Val
				485					490					495	
Val	Gly	Gln	Gly	Tyr	Gly	Asn	Tyr	Asp	Pro	Val	Asn	Asp	Pro	Pro	Lys
			500						505					510	
Phe	Asn	Leu	Val	Asp	Pro	Val	Glu	Arg	Asn	Thr	Val	Gly	Val	Pro	Ala
		515					520						525		
Gly	Gly	Trp	Val	Ala	Ile	Arg	Phe	Leu	Ala	Asp	Asn	Pro	Gly	Val	Trp
		530				535							540		
Phe	Met	His	Cys	His	Leu	Glu	Val	His	Thr	Thr	Trp	Gly	Leu	Arg	Met
545					550					555					560
Ala	Trp	Leu	Val	Leu	Asp	Gly	Ser	Leu	Pro	His	Gln	Lys	Leu	Leu	Pro
				565					570					575	
Pro	Pro	Ser	Asp	Leu	Pro	Lys	Cys								
			580												

<210> SEQ ID NO 45  
 <211> LENGTH: 576  
 <212> TYPE: PRT  
 <213> ORGANISM: Zea mays

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&lt;400&gt; SEQUENCE: 45

Met Gly Ala Ala Pro Pro Ser Ser Trp Leu Ala Phe Ile Leu Phe Phe  
 1 5 10 15  
 Gly Thr Leu Val Ala Leu Pro Gln Ser Ser His Gly Gly Gly Thr Thr  
 20 25 30  
 Arg His Tyr Thr Phe Asn Val Thr Met Lys Lys Val Thr Arg Leu Cys  
 35 40 45  
 Thr Thr Arg Ala Ile Pro Thr Val Asn Gly Gln Phe Pro Gly Pro Lys  
 50 55 60  
 Ile Val Thr Arg Glu Gly Asp Arg Val Val Val Lys Val Leu Asn Asn  
 65 70 75 80  
 Val Lys Asp Asn Val Thr Ile His Trp His Gly Val Arg Gln Leu Arg  
 85 90 95  
 Thr Gly Trp Ser Asp Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile Gln  
 100 105 110  
 Thr Gly Gln Ser Phe Val Tyr Asn Phe Thr Ile Thr Gly Gln Arg Gly  
 115 120 125  
 Thr Leu Phe Trp His Ala His Val Ser Trp Met Arg Ala Thr Leu Tyr  
 130 135 140  
 Gly Ala Ile Val Ile Leu Pro Lys Arg Gly Val Pro Tyr Pro Leu Pro  
 145 150 155 160  
 Val Lys Pro Tyr Lys Asp Val Pro Val Ile Phe Gly Glu Trp Phe Asn  
 165 170 175  
 Ala Asp Pro Glu Thr Ile Val Ala Gln Ala Leu Gln Thr Gly Ala Gly  
 180 185 190  
 Pro Asn Val Ser Asp Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu  
 195 200 205  
 Tyr Asn Cys Ser Ser Lys Asp Thr Phe Lys Leu Lys Val Leu Pro Gly  
 210 215 220  
 Lys Trp Tyr Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu  
 225 230 235 240  
 Phe Phe Ser Ile Ala Asn His Thr Leu Thr Val Val Asp Val Asp Ala  
 245 250 255  
 Ala Tyr Val Lys Pro Phe Arg Thr Asp Ile Val Leu Ile Thr Pro Gly  
 260 265 270  
 Gln Thr Thr Asn Val Leu Leu Arg Ala Glu Pro Asp Ala Gly Cys Pro  
 275 280 285  
 Ala Ala Thr His Leu Met Leu Ala Arg Pro Tyr Gly Thr Gly Gln Pro  
 290 295 300  
 Gly Thr Phe Asp Asn Thr Thr Val Ala Ala Val Leu Glu Tyr Ala Pro  
 305 310 315 320  
 Pro Gly His Ile Arg Ser Leu Pro Leu Phe Arg Pro Ser Leu Pro Ala  
 325 330 335  
 Leu Asn Asp Thr Ala Phe Ala Ala Asn Tyr Ser Ala Arg Leu Arg Ser  
 340 345 350  
 Leu Ala Thr Pro Asp Tyr Pro Ala Asn Val Pro Arg Ala Val Asp Arg  
 355 360 365  
 Ser Phe Phe Phe Ala Val Gly Leu Gly Thr Asn Pro Cys Pro Val Asn  
 370 375 380  
 Gln Thr Cys Gln Gly Pro Asn Gly Thr Met Phe Thr Ala Ser Met Asn

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385                390                395                400
Asn Val Ser Phe Asn Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr
                405                410                415
Gly Ser Val Ala Gly Val Tyr Thr Pro Asp Phe Pro Val Ala Pro Leu
                420                425                430
Glu Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val Ser
                435                440                445
His Gly Thr Lys Val Val Val Leu Asp Tyr Asn Thr Ser Val Glu Val
                450                455                460
Val Leu Gln Ala Thr Ser Ile Leu Gly Ala Glu Ser His Pro Leu His
                465                470                475                480
Leu His Gly Phe Asp Phe Phe Val Val Gly Gln Gly Phe Gly Asn Tyr
                485                490                495
Asp Ser Ser Lys Asp Pro Pro Lys Phe Asn Leu Val Asp Pro Val Gln
                500                505                510
Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala Ile Arg Phe
                515                520                525
Phe Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val
                530                535                540
His Thr Ser Trp Gly Leu Lys Met Ala Trp Val Val Asn Asp Gly Pro
                545                550                555                560
Leu Pro Glu Gln Lys Leu Met Pro Pro Pro Ala Asp Leu Pro Lys Cys
                565                570                575

<210> SEQ ID NO 46
<211> LENGTH: 588
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 46
Met Gly Ala Arg Arg Gly Leu Arg Arg Gly Gln Ala Ala Ala Ala Ala
1                    5                    10                    15
Phe Ser Ala Cys Pro Phe Leu Ala Leu Ala Val Val Leu Leu Ala Leu
20                    25                    30
Pro Glu Leu Ala Ala Gly Asp Thr His Tyr Tyr Thr Phe Asn Val Gln
35                    40                    45
Met Thr Asn Val Thr Arg Leu Cys Val Thr Lys Ser Ile Pro Thr Val
50                    55                    60
Asn Gly Glu Phe Pro Gly Pro Lys Leu Val Val Arg Glu Gly Asp Arg
65                    70                    75                    80
Leu Val Val Lys Val His Asn His Ile Asn Tyr Asn Val Ser Phe His
85                    90                    95
Trp His Gly Val Arg Gln Leu Arg Asn Gly Trp Ala Asp Gly Pro Ser
100                   105                   110
Tyr Ile Thr Gln Cys Pro Ile Gln Gly Gly Gln Ser Tyr Val Tyr Asp
115                   120                   125
Phe Thr Val Thr Gly Gln Arg Gly Thr Leu Trp Trp His Ala His Phe
130                   135                   140
Ser Trp Leu Arg Val His Leu Tyr Gly Pro Leu Val Ile Leu Pro Lys
145                   150                   155                   160
Arg Gly Glu Gly Tyr Pro Phe Pro Arg Pro Tyr Lys Glu Val Pro Ile
165                   170                   175

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Leu	Phe	Gly	Glu	Trp	Phe	Asn	Ala	Asp	Thr	Glu	Ala	Val	Ile	Asn	Gln
			180					185					190		
Ala	Leu	Gln	Thr	Gly	Ala	Gly	Pro	Asn	Val	Ser	Asp	Ala	Tyr	Thr	Phe
		195					200					205			
Asn	Gly	Leu	Pro	Gly	Pro	Thr	Tyr	Asn	Cys	Ser	Ser	Lys	Asp	Thr	Tyr
		210				215					220				
Lys	Leu	Lys	Val	Lys	Ala	Arg	Glu	Gly	Arg	Thr	Cys	Ser	Arg	Leu	His
225					230					235					240
Gln	Leu	Arg	Pro	Gln	Thr	Asn	Glu	Leu	Phe	Phe	Gly	Ile	Ala	Asn	His
				245					250					255	
Thr	Leu	Thr	Val	Val	Glu	Ala	Asp	Ala	Ser	Tyr	Val	Lys	Pro	Phe	Thr
			260					265					270		
Val	Ser	Thr	Leu	Val	Ile	Ser	Pro	Gly	Gln	Thr	Met	Asn	Val	Leu	Leu
		275					280					285			
Thr	Thr	Ala	Pro	Ser	Pro	Ala	Ser	Pro	Ala	Tyr	Ala	Met	Ala	Ile	Ala
		290				295					300				
Pro	Tyr	Thr	Asn	Thr	Gln	Gly	Thr	Phe	Asp	Asn	Thr	Thr	Ala	Ala	Ala
305					310					315					320
Val	Leu	Glu	Tyr	Ala	Pro	Thr	Pro	Pro	Pro	Val	Ala	Thr	Arg	Asn	Asn
				325						330				335	
Thr	Leu	Pro	Pro	Leu	Pro	Ala	Leu	Pro	Leu	Tyr	Asn	Asp	Thr	Gly	Ala
			340				345						350		
Val	Ser	Asn	Phe	Ser	Arg	Asn	Phe	Arg	Ser	Leu	Asn	Ser	Ala	Arg	Tyr
		355					360					365			
Pro	Ala	Arg	Val	Pro	Ala	Ala	Val	Asp	Arg	His	Leu	Leu	Phe	Thr	Val
		370				375					380				
Gly	Leu	Gly	Thr	Asp	Pro	Cys	Pro	Tyr	Thr	Asn	Gln	Thr	Cys	Gln	Gly
385					390					395					400
Pro	Asn	Gly	Thr	Lys	Phe	Ala	Ala	Ser	Val	Asn	Asn	Asn	Ser	Phe	Phe
				405					410					415	
Arg	Pro	Arg	Thr	Ala	Leu	Leu	Glu	Ala	His	Tyr	Arg	Arg	Arg	Tyr	Ala
			420					425					430		
Gly	Val	Leu	Leu	Gly	Asp	Phe	Pro	Thr	Ala	Pro	Pro	His	Pro	Phe	Asn
		435					440					445			
Tyr	Thr	Gly	Thr	Pro	Pro	Asn	Asn	Thr	Phe	Val	Gln	His	Gly	Thr	Arg
		450				455					460				
Val	Val	Pro	Leu	Arg	Phe	Asn	Ala	Ser	Val	Glu	Leu	Val	Leu	Gln	Gly
465					470					475					480
Thr	Ser	Ile	Gln	Gly	Ala	Glu	Ser	His	Pro	Leu	His	Leu	His	Gly	Tyr
			485						490					495	
Asn	Phe	Phe	Val	Val	Gly	Gln	Gly	Phe	Gly	Asn	Phe	Asp	Pro	Val	Asn
			500					505					510		
Asp	Pro	Pro	Gly	Tyr	Asn	Leu	Ala	Asp	Pro	Val	Glu	Arg	Asn	Thr	Ile
		515					520					525			
Ser	Val	Pro	Thr	Ala	Gly	Trp	Val	Ala	Val	Arg	Phe	Leu	Ala	Asp	Asn
		530				535					540				
Pro	Gly	Val	Trp	Leu	Met	His	Cys	His	Phe	Asp	Val	His	Leu	Ser	Trp
545					550					555					560
Gly	Leu	Ser	Met	Ala	Trp	Leu	Val	Asn	Asp	Gly	Pro	Leu	Pro	Asn	Glu
				565					570					575	
Lys	Met	Leu	Pro	Pro	Pro	Ser	Asp	Leu	Pro	Lys	Cys				





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Arg Ser Leu Ala Ser Ala Arg Tyr Pro Ala Arg Val Pro Arg Thr Val  
 355 360 365  
 Asp Arg Arg Phe Phe Phe Thr Val Gly Leu Gly Ala Asp Pro Cys Arg  
 370 375 380  
 Ser Arg Val Asn Gly Thr Cys Gln Gly Pro Asn Gly Thr Arg Phe Ala  
 385 390 395 400  
 Ala Ser Met Asn Asn Val Ser Phe Ala Met Pro Arg Thr Thr Ser Leu  
 405 410 415  
 Leu Gln Ala His Tyr Gln Arg Arg Tyr Ser Gly Val Leu Ala Ala Asn  
 420 425 430  
 Phe Pro Ala Val Pro Pro Thr Arg Phe Asp Tyr Thr Gly Ala Pro Pro  
 435 440 445  
 Asn Asn Thr Phe Val Thr His Gly Thr Arg Val Val Pro Leu Ser Phe  
 450 455 460  
 Asn Thr Thr Val Glu Val Val Leu Gln Asp Thr Ser Val Leu Gly Ala  
 465 470 475 480  
 Glu Ser His Pro Leu His Leu His Gly Tyr Asp Phe Phe Val Val Gly  
 485 490 495  
 Thr Gly Phe Gly Asn Tyr Asp Ala Thr Asn Asp Thr Ala Arg Tyr Asn  
 500 505 510  
 Leu Val Asp Pro Val Gln Arg Asn Thr Val Ser Val Pro Thr Ala Gly  
 515 520 525  
 Trp Val Ala Ile Arg Phe Val Ala Asp Asn Pro Gly Val Trp Ile Met  
 530 535 540  
 His Cys His Leu Asp Val His Leu Thr Trp Gly Leu Ala Met Ala Trp  
 545 550 555 560  
 Leu Val Asn Asp Gly Pro Leu Pro Asn Gln Lys Leu Pro Pro Pro Pro  
 565 570 575  
 Ser Asp Ile Pro Arg Cys  
 580

&lt;210&gt; SEQ ID NO 48

&lt;211&gt; LENGTH: 572

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Brachypodium distachyon

&lt;400&gt; SEQUENCE: 48

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

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Ala His Val Ser Trp Met Arg Ala Thr Leu Tyr Gly Pro Ile Val Ile  
130 135 140

Leu Pro Lys Leu Gly Val Pro Tyr Pro Phe Pro Lys Pro Phe Lys Asp  
145 150 155 160

Val Pro Ile Met Phe Gly Glu Trp Phe Asn Val Asp Pro Glu Ala Ile  
165 170 175

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

Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys Ser Ser Arg  
195 200 205

Asp Thr Phe Lys Leu Lys Val Gln Pro Gly Lys Trp Tyr Leu Leu Arg  
210 215 220

Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile Ala Asn  
225 230 235 240

His Thr Leu Thr Ile Val Asp Val Asp Ala Ser Tyr Val Lys Pro Phe  
245 250 255

Asp Thr Asp Val Val Leu Val Thr Pro Gly Gln Thr Thr Asn Val Leu  
260 265 270

Leu His Ala Lys Pro Asp Glu Gly Cys Gln Pro Ala Thr His Leu Met  
275 280 285

Leu Ala Arg Pro Tyr Ala Thr Ser Arg Pro Gly Thr Tyr Asp Asn Thr  
290 295 300

Thr Val Ala Ala Val Leu Glu Tyr Ser Pro Ser Gly Gln Ile Lys Ser  
305 310 315 320

Arg Pro Leu Phe Arg Pro Thr Leu Pro Val Phe Asn Asp Thr Ser Phe  
325 330 335

Ala Ala Asn Tyr Ser Ala Lys His Arg Ser Leu Ala Ser Ser Glu Tyr  
340 345 350

Pro Ala Asn Val Pro Arg Arg Ile Asp Arg Pro Phe Phe Phe Ala Val  
355 360 365

Gly Leu Gly Thr Thr Pro Cys Pro Thr His Gln Gly Cys Asn Gly Pro  
370 375 380

Thr Asn Asp Thr Lys Phe Ser Ala Ser Met Asn Asn Val Ser Phe Asn  
385 390 395 400

Met Pro Thr Thr Ala Leu Leu Lys Ala His Tyr Asp Gly Asn Thr Ala  
405 410 415

Gly Val Tyr Thr Ala Asp Phe Pro Ala Met Pro Thr Gln Pro Phe Asn  
420 425 430

Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val Ser Asn Gly Thr Lys  
435 440 445

Val Ala Val Leu Pro Tyr Asn Ala Ser Val Glu Val Val Leu Gln Asp  
450 455 460

Thr Ser Ile Gln Gly Ala Glu Ser His Pro Leu His Leu His Gly Phe  
465 470 475 480

Asp Phe Phe Val Val Gly Gln Gly Val Gly Asn Tyr Asn Ala Ser Met  
485 490 495

His Pro Ala Gly Phe Asn Leu Leu Asp Pro Val Gln Arg Asn Thr Val  
500 505 510

Gly Val Pro Ala Gly Gly Trp Val Ala Ile Arg Phe Tyr Ala Asp Asn  
515 520 525

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Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Ser Trp  
 530 535 540

Gly Leu Lys Met Ala Trp Val Val Asn Asp Gly Pro Leu Pro Asp Gln  
 545 550 555 560

Lys Leu Met Pro Pro Pro Ser Asp Leu Pro Lys Cys  
 565 570

<210> SEQ ID NO 49  
 <211> LENGTH: 577  
 <212> TYPE: PRT  
 <213> ORGANISM: Brachypodium distachyon

<400> SEQUENCE: 49

Met Ala Met Ala Ile Ser Ser Gly Leu Pro Ala Cys Ser Val Val Met  
 1 5 10 15

Ala Thr Leu Met Val Leu Ile Ile Gln Ala Gln Gly Ile Thr Arg His  
 20 25 30

Tyr Asp Phe Asp Val Gln Met Ala Lys Val Thr Arg Leu Cys Gly Ser  
 35 40 45

Lys Ser Ile Val Thr Val Asn Gly Gln Phe Pro Gly Pro Glu Leu Val  
 50 55 60

Ala Arg Glu Gly Asp Arg Val His Val Arg Val Thr Asn His Val Ser  
 65 70 75 80

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

Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile Gln Met Gly  
 100 105 110

Gln Thr Tyr Val Tyr Lys Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu  
 115 120 125

Trp Trp His Ala His Ile Ser Trp His Arg Ala Thr Val Tyr Gly Ala  
 130 135 140

Ile Val Ile Leu Pro Lys Leu Gly Val Pro Tyr Pro Phe Ala Ala Pro  
 145 150 155 160

His Lys Glu Val Pro Val Ile Phe Gly Glu Trp Trp Ala Ala Asp Thr  
 165 170 175

Glu Val Val Met Ser Gln Ala Leu Lys Val Gly Gly Ala Pro Asn Ile  
 180 185 190

Ser Asp Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys  
 195 200 205

Ser Ala Gln Asp Thr Phe Lys Leu Lys Val Thr Pro Gly Lys Thr Tyr  
 210 215 220

Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser  
 225 230 235 240

Val Ala Asn His Thr Leu Thr Val Val Glu Val Asp Ala Val Tyr Val  
 245 250 255

Lys Pro Phe Thr Val Lys Thr Ile Val Ile Ser Pro Gly Gln Thr Thr  
 260 265 270

Asn Val Leu Leu Thr Ala Lys Pro Val Asn Pro Lys Ala Asn Phe Tyr  
 275 280 285

Met Ser Ala Ala Pro Tyr Ser Val Ile Arg Pro Gly Thr Phe Asp Asn  
 290 295 300

Thr Thr Val Ala Gly Ile Leu Glu Tyr His Glu Asp Pro Ser Ser Ser  
 305 310 315 320

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Ser Ser Phe Asp Lys Asn Leu Pro Leu Phe Lys Pro Met Leu Pro Arg  
 325 330 335  
 Phe Asn Asp Thr Lys Phe Val Thr Asn Phe Thr Thr Lys Leu Arg Ser  
 340 345 350  
 Leu Ala Thr Thr Lys Tyr Pro Ala Ala Val Pro Gln Thr Val Asp Lys  
 355 360 365  
 Arg Phe Phe Phe Thr Ile Gly Leu Gly Thr Leu Pro Cys Pro Lys Asn  
 370 375 380  
 Met Thr Cys Gln Gly Pro Asn Gly Thr Gln Phe Ala Ala Val Asn  
 385 390 395 400  
 Asn Val Ser Leu Val Leu Pro Thr Lys Ala Leu Leu Gln Ser His Phe  
 405 410 415  
 Thr Gly Leu Thr Thr Gly Val Tyr Ala Ser Asp Phe Pro Ala Met Pro  
 420 425 430  
 Leu Ser Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val  
 435 440 445  
 Ala Thr Gly Thr Lys Leu Leu Ala Leu Pro Phe Asn Thr Ser Val Glu  
 450 455 460  
 Leu Val Met Gln Asp Thr Ser Val Leu Gly Ile Glu Ser His Pro Leu  
 465 470 475 480  
 His Leu His Gly Phe Asn Tyr Phe Val Val Gly Gln Gly Phe Gly Asn  
 485 490 495  
 Tyr Asp Ser Ala Lys Asp Pro Ala Lys Phe Asn Leu Val Asp Pro Val  
 500 505 510  
 Glu Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala Ile Arg  
 515 520 525  
 Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu  
 530 535 540  
 Val His Thr Thr Trp Gly Leu Arg Met Ala Trp Leu Val His Asp Gly  
 545 550 555 560  
 Ser Lys Pro Asn Gln Lys Leu Leu Pro Pro Ser Asp Met Pro Lys  
 565 570 575

Cys

<210> SEQ ID NO 50  
 <211> LENGTH: 599  
 <212> TYPE: PRT  
 <213> ORGANISM: Brachypodium distachyon

&lt;400&gt; SEQUENCE: 50

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

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Gly Trp Ala Asp Gly Pro Ala Tyr Val Ala Gln Cys Pro Ile Gln Ile  
 100 105 110

Gly Gln Ser Tyr Val Tyr Asn Phe Asn Ile Thr Gly Gln Arg Gly Thr  
 115 120 125

Leu Trp Trp His Ala His Ile Ser Trp Ile Arg Ala Thr Val Tyr Gly  
 130 135 140

Ala Ile Val Ile Leu Pro Glu Leu Gly Ile Pro Tyr Pro Leu Ala Ala  
 145 150 155 160

Pro His Glu Glu Val Pro Ile Leu Phe Gly Glu Trp Trp Lys Ala Asn  
 165 170 175

Thr Glu Ala Val Val Lys Gln Ala Leu Gln Thr Gly Gly Ala Pro Asn  
 180 185 190

Ile Ser Asp Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn  
 195 200 205

Cys Ser Ala Lys Gly Met Asn Glu Leu Val Leu Lys Val Glu Ala Gly  
 210 215 220

Lys Thr Tyr Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu  
 225 230 235 240

Phe Phe Val Ile Ala Asn His Lys Leu Thr Val Val Glu Val Asp Ala  
 245 250 255

Val Cys Val Lys Pro Phe Thr Val Asn Thr Leu Val Ile Ser Pro Gly  
 260 265 270

Gln Thr Thr Asn Val Leu Leu Thr Ala Lys Pro Phe Asn Pro Lys Ala  
 275 280 285

Asn Phe Tyr Met Ser Ala Val Pro Tyr Ser Thr Ile Arg Pro Gly Thr  
 290 295 300

Phe Asp Asn Thr Thr Val Thr Gly Ile Leu Glu Tyr His Asn Pro Asn  
 305 310 315

Ser Gly Ser Ala Ser Ser Ser Phe Asp Lys Asp Leu Pro Leu Phe Lys  
 325 330 335

Pro Thr Met Pro Arg Phe Asn Asp Thr Gly Pro Val Thr Asn Phe Thr  
 340 345 350

Thr Lys Leu Arg Ser Leu Ala Thr Ala Thr Tyr Pro Val Ile Val Pro  
 355 360 365

Arg Ser Val Asp Lys Arg Phe Leu Phe Thr Ile Gly Pro Gly Thr Leu  
 370 375 380

Pro Cys Pro Val Asn Met Thr Cys Gln Gly Pro Thr Asn Val Thr Arg  
 385 390 395 400

Phe Ala Ala Ala Met Asn Asn Val Ser Leu Val Phe Pro Ser Thr Ala  
 405 410 415

Leu Leu Gln Ser His Tyr Thr Gly Met Gly Met Ser Lys Gly Val Tyr  
 420 425 430

Ala Ser Asn Phe Pro Thr Ala Pro Leu Thr Pro Phe Ser Tyr Thr Gly  
 435 440 445

Thr Pro Pro Asn Asn Ile Asn Val Ala Lys Gly Thr Arg Leu Leu Val  
 450 455 460

Leu Pro Phe Asn Thr Ser Val Glu Leu Val Met Gln Glu Thr Ser Ile  
 465 470 475 480

Leu Gly Val Glu Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe  
 485 490 495

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Val Val Gly Gln Gly Phe Gly Asn Tyr Asp Ala Val Asn Asp Leu Ala  
500 505 510

Lys Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro  
515 520 525

Ala Ser Gly Trp Val Ala Ile Arg Phe Leu Ala Asp Asn Pro Gly Val  
530 535 540

Trp Phe Met His Cys His Leu Glu Val His Thr Thr Trp Gly Leu Arg  
545 550 555 560

Met Ala Trp Leu Val Leu Asp Gly Ser Leu Ala Asn Gln Lys Leu Asn  
565 570 575

Arg His Leu Ile Phe Pro Asn Ala Ser Arg His Thr Leu Pro Glu Phe  
580 585 590

Val Leu Pro Arg Leu Ile Gly  
595

&lt;210&gt; SEQ ID NO 51

&lt;211&gt; LENGTH: 581

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Brachypodium distachyon

&lt;400&gt; SEQUENCE: 51

Met Ala Ala Ser Pro Gly Leu Pro Ala Pro Trp Ser Leu Phe Met Ala  
1 5 10 15

Thr Leu Val Leu Leu Ile Val Gln Ala Gln Gly Ile Thr Arg His Phe  
20 25 30

Asp Phe Asn Val Gln Met Ala Asn Val Thr Arg Leu Cys Ala Thr Lys  
35 40 45

Ser Ile Val Thr Val Asn Gly Glu Phe Pro Gly Pro Ala Leu Val Ala  
50 55 60

Arg Glu Gly Asp Arg Val Leu Val Arg Val Thr Asn Gln Val Ser His  
65 70 75 80

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

Ala Asp Gly Pro Ala Tyr Val Ala Gln Cys Pro Ile Gln Thr Gly Gln  
100 105 110

Ser Tyr Val Tyr Asn Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Trp  
115 120 125

Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val Tyr Gly Ala Ile  
130 135 140

Val Ile Leu Pro Glu Phe Gly Val Pro Tyr Pro Phe Ala Ala Pro His  
145 150 155 160

Glu Glu Val Pro Ile Leu Phe Gly Glu Trp Trp Lys Ala Asp Thr Glu  
165 170 175

Ala Val Val Lys Gln Ala Leu Gln Thr Gly Gly Ala Pro Asn Ile Ser  
180 185 190

Asp Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys Ser  
195 200 205

Ala Lys Asp Thr Phe Lys Leu Lys Val Gln Pro Gly Lys Thr Tyr Leu  
210 215 220

Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile  
225 230 235 240

Ala Lys His Arg Leu Thr Val Val Glu Val Asp Ala Val Tyr Val Lys  
245 250 255

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Pro Phe Thr Val Asp Thr Leu Val Ile Ser Pro Gly Gln Thr Thr Asn  
 260 265 270  
 Val Leu Leu Thr Ala Lys Leu Phe Tyr Pro Lys Ala Asn Phe Phe Met  
 275 280 285  
 Ser Ala Val Pro Tyr Ser Asn Ile Arg Pro Gly Thr Phe Asp Asn Thr  
 290 295 300  
 Thr Val Ala Gly Ile Leu Glu Tyr His Asn Pro Ser Ser Gly Ser Val  
 305 310 315 320  
 Ser Ser Ser Phe Asn Lys Asp Leu Pro Leu Phe Arg Pro Lys Leu Pro  
 325 330 335  
 Arg Phe Asn Asp Thr Gly Leu Val Thr Lys Phe Thr Ala Lys Leu Arg  
 340 345 350  
 Ser Leu Ala Thr Ala Ser Tyr Pro Ala Ala Val Pro Gln Ser Val Asp  
 355 360 365  
 Lys Arg Phe Phe Phe Thr Ile Gly Leu Gly Thr Leu Pro Cys Pro Thr  
 370 375 380  
 Asn Thr Thr Cys Gln Gly Pro Thr Asn Ile Thr Arg Phe Ala Ala Ala  
 385 390 395 400  
 Val Asn Asn Val Ser Leu Val Leu Pro Ser Thr Ala Leu Leu Gln Ser  
 405 410 415  
 His Tyr Thr Gly Met Gly Met Ser Lys Gly Val Tyr Ala Ser Asn Phe  
 420 425 430  
 Pro Thr Ala Pro Leu Ser Thr Phe Asn Tyr Thr Gly Thr Pro Pro Asn  
 435 440 445  
 Asn Thr Asn Val Ala Gln Gly Thr Arg Leu Leu Val Leu Pro Phe Asn  
 450 455 460  
 Ala Ser Val Glu Leu Val Met Gln Asp Thr Ser Ile Leu Gly Ile Glu  
 465 470 475 480  
 Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln  
 485 490 495  
 Gly Phe Gly Asn Tyr Asp Val Val Asn Asp Pro Ala Gln Phe Asn Leu  
 500 505 510  
 Val Asp Pro Val Glu Arg Asn Thr Val Ala Val Pro Ala Gly Gly Trp  
 515 520 525  
 Val Ala Ile Arg Phe Ile Ala Asp Asn Pro Gly Val Trp Phe Met His  
 530 535 540  
 Cys His Leu Glu Val His Thr Thr Trp Gly Leu Arg Met Ala Trp Leu  
 545 550 555 560  
 Val Arg Asp Gly Ser Leu Pro Asn Gln Lys Leu Leu Pro Pro Pro Ser  
 565 570 575  
 Asp Leu Pro Lys Cys  
 580

&lt;210&gt; SEQ ID NO 52

&lt;211&gt; LENGTH: 576

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Brachypodium distachyon*

&lt;400&gt; SEQUENCE: 52

Met Gly Ala Leu Arg Gly Leu Arg Arg His Ala Ala Ala Ser Ala Cys  
 1 5 10 15

Pro Phe Leu Ala Phe Ala Val Leu Leu Ala Leu Pro Gly Leu Ala Ala



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20					25					30					
Gly	Ile	Thr	Arg	His	Tyr	Thr	Phe	Asp	Val	Gln	Met	Thr	Asn	Val	Thr
		35					40					45			
Arg	Leu	Cys	Ala	Thr	Lys	Ser	Ile	Pro	Thr	Val	Asn	Gly	Gln	Phe	Pro
	50					55					60				
Gly	Pro	Arg	Leu	Val	Ala	Arg	Glu	Gly	Asp	Arg	Leu	Val	Val	Lys	Val
65					70					75				80	
His	Asn	His	Ile	Asn	Tyr	Asn	Val	Ser	Phe	His	Trp	His	Gly	Ile	Arg
				85					90					95	
Gln	Leu	Arg	Asn	Gly	Trp	Ala	Asp	Gly	Pro	Ala	Tyr	Ile	Thr	Gln	Cys
			100					105					110		
Pro	Ile	Gln	Gly	Gly	Gln	Ser	Tyr	Val	Tyr	Asp	Phe	Thr	Ile	Thr	Gly
	115						120					125			
Gln	Arg	Gly	Thr	Leu	Trp	Trp	His	Ala	His	Phe	Ser	Trp	Leu	Arg	Val
	130					135					140				
His	Leu	Tyr	Gly	Pro	Leu	Val	Ile	Leu	Pro	Lys	Arg	Ala	Glu	Gly	Tyr
145					150					155					160
Pro	Phe	Pro	Leu	Pro	Tyr	Lys	Glu	Phe	Pro	Ile	Met	Phe	Gly	Glu	Trp
			165						170					175	
Phe	Lys	Ala	Asp	Ser	Glu	Ala	Val	Ile	Asn	Gln	Ala	Leu	Gln	Thr	Gly
		180						185					190		
Ala	Gly	Pro	Asn	Val	Ser	Asp	Ala	Tyr	Thr	Phe	Asn	Gly	Leu	Ser	Gly
	195						200					205			
Pro	Thr	Tyr	Asn	Cys	Ser	Ser	Lys	Asp	Thr	Tyr	Lys	Leu	Lys	Val	Gln
	210					215					220				
Pro	Gly	Arg	Thr	Tyr	Met	Leu	Arg	Leu	Ile	Asn	Ser	Ala	Leu	Asn	Asn
225					230					235				240	
Glu	Leu	Phe	Phe	Gly	Ile	Ala	Asn	His	Thr	Leu	Thr	Val	Val	Glu	Ala
				245					250					255	
Asp	Ala	Asn	Tyr	Val	Lys	Pro	Phe	Thr	Ser	Lys	Thr	Val	Val	Ile	Ser
		260						265					270		
Pro	Gly	Gln	Thr	Met	Asn	Val	Leu	Leu	Thr	Thr	Ser	Ser	Asn	Pro	Ala
	275						280					285			
Ser	Arg	Ala	Phe	Ala	Met	Ser	Ile	Ala	Pro	Tyr	Thr	Asn	Thr	Gln	Gly
	290					295					300				
Thr	Phe	Asp	Asn	Thr	Thr	Ala	Thr	Ala	Val	Leu	Glu	Tyr	Ala	Ser	Thr
305				310						315					320
Arg	Pro	Ser	Ser	Thr	Gln	Asn	Leu	Ala	Met	Pro	Ala	Leu	Pro	Arg	Tyr
				325					330					335	
Asn	Asp	Thr	Asn	Ala	Val	Ala	Asn	Phe	Ser	Ser	Asn	Phe	Arg	Ser	Leu
		340						345					350		
Ala	Ser	Ala	Gln	Tyr	Pro	Ala	Arg	Val	Pro	Gln	Ala	Val	Asp	Arg	His
	355						360					365			
Val	Leu	Phe	Thr	Val	Gly	Leu	Gly	Thr	Asp	Pro	Cys	Pro	Ser	Asn	Gln
	370					375					380				
Thr	Cys	Gln	Gly	Pro	Asn	Gly	Thr	Lys	Phe	Ala	Ala	Ser	Ile	Asn	Asn
385					390					395				400	
Asn	Ser	Phe	Val	Arg	Pro	Lys	Thr	Ala	Leu	Leu	Glu	Ala	His	Tyr	Gln
			405						410					415	
Ser	Arg	Tyr	Ala	Gly	Val	Leu	Met	Ala	Asn	Phe	Pro	Thr	Thr	Pro	Pro
			420					425						430	

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His Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Lys Thr Phe Val Ala
 435                               440                               445

His Gly Thr Arg Val Val Pro Leu Ser Phe Asn Thr Thr Val Glu Leu
 450                               455                               460

Val Met Gln Gly Thr Ser Ile Gln Gly Ala Glu Ser His Pro Leu His
 465                               470                               475                               480

Met His Gly Phe Asn Phe Phe Val Val Gly Gln Gly Phe Gly Asn Tyr
 485                               490                               495

Asp Pro Val Asn Asp Pro Ala Lys Tyr Asn Leu Ile Asp Pro Val Glu
 500                               505                               510

Arg Asn Thr Val Ser Val Pro Thr Ala Gly Trp Val Ala Val Arg Phe
 515                               520                               525

Leu Ala Asp Asn Pro Gly Val Trp Leu Met His Cys His Phe Asp Val
 530                               535                               540

His Leu Ser Trp Gly Leu Ser Met Ala Trp Leu Val Asn Asp Gly Pro
 545                               550                               555                               560

Leu Pro Asn Gln Lys Met Leu Pro Pro Pro Ser Asp Leu Pro Lys Cys
 565                               570                               575

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&lt;210&gt; SEQ ID NO 53

&lt;211&gt; LENGTH: 580

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Brachypodium distachyon*

&lt;400&gt; SEQUENCE: 53

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Met Gly Gly Ala His His Gly Leu Leu Arg Cys Ala Ser Pro Ala Cys
 1                               5                               10                               15

Leu His Leu Ala Phe Phe Leu Leu Leu Ala Val Glu Pro Gly Leu Thr
 20                               25                               30

Ala Gly Leu Thr Arg Arg Tyr Thr Phe Asn Val Thr Met Ala Thr Val
 35                               40                               45

Thr Arg Leu Cys Leu Thr Lys Ser Ile Pro Thr Val Asn Gly Gln Phe
 50                               55                               60

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

Val His Asn Asn Ile Asn Asn Asn Val Thr Phe His Trp His Gly Val
 85                               90                               95

Arg Gln Leu Arg Ser Gly Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln
 100                              105                              110

Cys Pro Ile Arg Pro Gly Gln Ser Tyr Val Tyr Ser Phe Arg Ile Val
 115                              120                              125

Gly Gln Arg Gly Thr Leu Trp Trp His Ala His Phe Ser Trp Leu Arg
 130                              135                              140

Ala Thr Leu His Gly Pro Met Val Ile Leu Pro Pro Leu Gly Val Pro
 145                              150                              155                              160

Tyr Pro Phe Pro Lys Pro Tyr Arg Glu Val Pro Leu Met Leu Gly Glu
 165                              170                              175

Trp Phe Asn Ala Asp Pro Glu Ala Val Ile Lys Gln Ala Leu Gln Thr
 180                              185                              190

Gly Gly Gly Pro Asn Val Ser Asp Ala Tyr Thr Phe Asn Gly Phe Pro
 195                              200                              205

Gly Pro Thr Tyr Asn Cys Ser Ala Lys Ser Thr Tyr Lys Leu Lys Val

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210	215	220
Lys Pro Gly Arg Thr	Tyr Met Leu Arg Leu	Ile Asn Ala Ala Leu Asn
225	230	235 240
Asp Glu Leu Phe	Phe Ala Val Ala Asn His	Thr Leu Thr Val Val Gln
	245	250 255
Ala Asp Ala Ser	Tyr Val Lys Pro Phe Thr	Ala Asn Thr Leu Val Ile
	260	265 270
Ser Pro Gly Gln Thr	Met Asp Val Leu Leu Thr	Ala Ala Ala Ser Thr
	275	280 285
Ser Ser Ser Ala Phe	Ala Ile Ala Val Ala Pro	Tyr Thr Asn Thr Val
	290	295 300
Gly Thr Phe Asp Asn	Thr Thr Ala Ile Ala Val	Leu Glu Tyr Ser Pro
305	310	315 320
Gln Arg Pro Ser	Met Leu Arg Asn Leu Pro	Ala Pro Ser Leu Pro Leu
	325	330 335
Tyr Asn Asp Thr	Asn Ala Val Thr Asn Phe	Ser Ser Lys Phe Arg Ser
	340	345 350
Leu Asp Asn Ala Arg	Tyr Pro Ala Gln Val Pro	Met Thr Val Asp Arg
	355	360 365
His Phe Phe Phe Thr	Val Gly Leu Gly Ala Asp	Pro Cys Gln Ser Pro
	370	375 380
Ile Asn Gly Thr Cys	Gln Gly Pro Asn Asn Thr	Arg Phe Ala Ala Ser
385	390	395 400
Ile Asn Asn Val Ser	Phe Ile Met Pro Lys Thr	Ser Leu Leu Gln Ala
	405	410 415
His Tyr Gln Arg Met	Tyr Lys Gly Val Leu Met	Ala Asn Phe Pro Thr
	420	425 430
Ala Pro Val Arg Lys	Phe Asn Tyr Thr Gly Thr	Pro Pro Asn Asn Thr
	435	440 445
Phe Val Thr His Gly	Thr Arg Val Val Pro Leu	Ala Phe Asn Thr Thr
	450	455 460
Val Glu Val Val Leu	Gln Asp Thr Ser Ile Gln	Gly Ala Glu Ser His
465	470	475 480
Pro Leu His Leu His	Gly Tyr Asp Phe Tyr Val	Val Gly Thr Gly Phe
	485	490 495
Gly Asn Tyr Asp	Ala Asn Asn Asp Thr	Ala Lys Tyr Asn Leu Val Asp
	500	505 510
Pro Val Lys Arg Asn	Thr Ile Ser Val Pro Thr	Ala Gly Trp Val Ala
	515	520 525
Ile Arg Phe Ile Ala	Asp Asn Pro Gly Val Trp	Ile Met His Cys His
	530	535 540
Leu Asp Val His Leu	Ser Trp Gly Leu Ser Met	Ala Trp Leu Val Asn
545	550	555 560
Asp Gly Pro Leu Pro	Asn Gln Lys Leu Pro Pro	Pro Pro Ala Asp Ile
	565	570 575
Pro Lys Cys Ser		
	580	

&lt;210&gt; SEQ ID NO 54

&lt;211&gt; LENGTH: 577

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Brachypodium distachyon

-continued

&lt;400&gt; SEQUENCE: 54

Met Ala Val Ser Ser Ser Leu Leu Cys Leu Leu Phe Ala Ala Leu Thr  
1 5 10 15  
Ala Thr Leu Val Gly Ala Gln Ala Val Thr Arg Lys Tyr Gln Phe Asp  
20 25 30  
Val Gln Met Thr Ser Val Thr Arg Leu Cys Ser Thr Lys Ser Ile Val  
35 40 45  
Thr Val Asn Gly Gln Tyr Pro Gly Pro Thr Leu Phe Ala Arg Glu Gly  
50 55 60  
Asp His Val Glu Val Asn Val Val Asn Asn Ser Pro Tyr Asn Met Thr  
65 70 75 80  
Ile His Trp His Gly Val Arg Gln Leu Arg Ser Gly Trp Tyr Asp Gly  
85 90 95  
Pro Ala Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Gln Ser Tyr Val  
100 105 110  
Tyr Arg Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Trp Trp His Ala  
115 120 125  
His Val Ser Trp Leu Arg Ala Thr Val His Gly Pro Ile Val Ile Leu  
130 135 140  
Pro Pro Leu Gly Val Pro Tyr Pro Phe Ser Pro Val Pro Tyr Lys Glu  
145 150 155 160  
Val Pro Leu Met Phe Gly Glu Trp Trp Lys Asn Asp Thr Glu Ala Val  
165 170 175  
Ile Ala Gln Ala Leu Gln Thr Gly Gly Gly Pro Asn Ile Ser Asp Ala  
180 185 190  
Phe Thr Met Asn Gly Leu Pro Gly Pro Leu Tyr Asn Val Cys Ser Ser  
195 200 205  
Ala Lys Gly Glu Thr Phe Lys Leu Lys Val Glu Pro Gly Lys Thr Tyr  
210 215 220  
Met Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ala  
225 230 235 240  
Val Ala Asn His Thr Leu Thr Val Val Asp Val Asp Ala Leu Tyr Val  
245 250 255  
Lys Pro Phe Ala Val Glu Ser Leu Val Ile Ala Pro Gly Gln Thr Ser  
260 265 270  
Asn Val Leu Leu Thr Ala Asn Asn Asn Pro Asn Ala Arg Tyr Tyr Met  
275 280 285  
Leu Ala Arg Pro Tyr Thr Asn Thr Gln Gly Thr Phe Asp Asn Thr Thr  
290 295 300  
Val Ala Gly Ile Leu Glu Tyr Glu Asp Thr Ser Asn Gly Lys Ala Pro  
305 310 315 320  
Ser Thr Ser Ser Leu Pro Ile Leu Arg Pro Thr Leu Pro Glu Ile Asn  
325 330 335  
Asp Thr Ser Val Val Ser Asn Tyr Thr Ala Lys Leu Arg Ser Leu Ala  
340 345 350  
Ser Ala Glu Tyr Pro Ala Ser Val Pro Gln Gln Val Asp Arg Glu Phe  
355 360 365  
Phe Phe Thr Val Gly Leu Gly Thr His Pro Cys Gln Ser Leu Ile Asn  
370 375 380  
Gly Thr Cys Gln Gly Pro Asn Asn Thr Arg Phe Ala Ala Ser Ile Asn

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385                390                395                400
Asn Ile Ser Phe Val Leu Pro Thr Thr Ala Leu Leu Gln Ser His Tyr
      405                410
Thr Gly Met Ser Asn Gly Val Tyr Ala Ser Asn Phe Pro Phe Tyr Pro
      420                425                430
Leu Arg Pro Trp Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val
      435                440                445
Met Asn Gly Thr Lys Ala Leu Val Leu Pro Phe Gly Val Ala Val Glu
      450                455                460
Leu Val Met Gln Asp Thr Ser Ile Leu Gly Ala Glu Ser His Pro Leu
      465                470                475                480
His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln Gly Phe Gly Asn
      485                490                495
Tyr Asn Pro Ser Ser Asp Pro Ala Lys Phe Asn Leu Val Asp Pro Val
      500                505                510
Glu Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala Ile Arg
      515                520                525
Phe Arg Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu
      530                535                540
Val His Met Ser Trp Gly Leu Lys Met Ala Trp Val Val Leu Asp Gly
      545                550                555                560
Ala Arg Pro Asp Gln Lys Leu Pro Pro Pro Pro Ala Asp Leu Pro Lys
      565                570                575

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Cys

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<210> SEQ ID NO 55
<211> LENGTH: 578
<212> TYPE: PRT
<213> ORGANISM: Brachypodium distachyon

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&lt;400&gt; SEQUENCE: 55

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

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165					170					175									
Val	Ile	Ser	Gln	Ala	Leu	Gln	Thr	Gly	Gly	Gly	Pro	Asn	Val	Ser	Asp				
			180					185					190						
Ala	Phe	Thr	Ile	Asn	Gly	Leu	Pro	Gly	Pro	Leu	Tyr	Asn	Cys	Ser	Ala				
		195					200					205							
Lys	Asp	Thr	Phe	Lys	Leu	Lys	Val	Lys	Pro	Gly	Lys	Met	Tyr	Met	Leu				
	210					215					220								
Arg	Ile	Ile	Asn	Ser	Ala	Leu	Asn	Asp	Glu	Leu	Phe	Phe	Ser	Ile	Ala				
225					230					235					240				
Gly	His	Leu	Leu	Thr	Val	Val	Asp	Val	Asp	Ala	Val	Tyr	Val	Lys	Pro				
				245					250					255					
Val	Thr	Val	Glu	Thr	Leu	Leu	Ile	Thr	Pro	Gly	Gln	Thr	Thr	Asn	Val				
			260					265						270					
Leu	Leu	Thr	Thr	Lys	Pro	Ser	Tyr	Pro	Gly	Ala	Asn	Tyr	Tyr	Met	Leu				
		275					280					285							
Ala	Ser	Pro	Tyr	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Phe	Asp	Asn	Thr	Thr				
		290				295					300								
Val	Ala	Gly	Ile	Leu	Glu	Tyr	Glu	His	Asp	Glu	Tyr	Pro	Gly	Ser	Ser				
305					310					315					320				
Ala	Ser	Phe	Asn	Lys	Asn	Leu	Pro	Leu	Phe	Lys	Pro	Thr	Met	Pro	Gln				
				325					330					335					
Ile	Asn	Asp	Thr	Ser	Phe	Val	Ser	Asn	Phe	Thr	Ala	Lys	Leu	Arg	Ser				
			340					345						350					
Leu	Ala	Asn	Glu	Asp	Tyr	Pro	Ala	Asp	Val	Pro	Arg	Glu	Val	Asp	Arg				
		355					360					365							
Arg	Phe	Phe	Phe	Thr	Val	Gly	Leu	Gly	Thr	His	Pro	Cys	Ala	Gly	Ala				
	370					375					380								
Asn	Gly	Thr	Cys	Gln	Gly	Pro	Asn	Gly	Ser	Arg	Phe	Ala	Ala	Ala	Val				
385					390					395					400				
Asn	Asn	Val	Ser	Phe	Val	Leu	Pro	Thr	Thr	Ala	Leu	Leu	Gln	Ser	His				
				405					410					415					
Phe	Thr	Gly	Met	Ser	Asn	Gly	Val	Tyr	Glu	Ser	Asn	Phe	Pro	Ala	Met				
			420					425					430						
Pro	Ser	Ser	Pro	Phe	Asn	Tyr	Thr	Gly	Thr	Pro	Pro	Asn	Asn	Thr	Asn				
		435					440					445							
Val	Ser	Asn	Gly	Thr	Lys	Leu	Val	Val	Leu	Ser	Tyr	Gly	Glu	Ser	Val				
		450				455						460							
Glu	Leu	Val	Met	Gln	Gly	Thr	Ser	Ile	Leu	Gly	Ala	Glu	Ser	His	Pro				
465					470					475					480				
Phe	His	Leu	His	Gly	Phe	Asn	Phe	Phe	Val	Val	Gly	Gln	Gly	Phe	Gly				
				485					490					495					
Asn	Phe	Asp	Pro	Met	Ser	Asp	Pro	Ala	Lys	Tyr	Asn	Leu	Val	Asp	Pro				
			500					505					510						
Val	Glu	Arg	Asn	Thr	Val	Gly	Val	Pro	Ala	Ala	Gly	Trp	Val	Ala	Leu				
			515				520						525						
Arg	Phe	Arg	Ala	Asp	Asn	Pro	Gly	Val	Trp	Phe	Met	His	Cys	His	Leu				
						535					540								
Glu	Val	His	Val	Ser	Trp	Gly	Leu	Lys	Met	Ala	Trp	Leu	Val	Gln	Asp				
545					550					555					560				
Gly	Ser	Leu	Ser	Asn	Gln	Lys	Leu	Leu	Pro	Pro	Pro	Ser	Asp	Leu	Pro				
565					570					575									

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Lys Cys

&lt;210&gt; SEQ ID NO 56

&lt;211&gt; LENGTH: 578

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Oryza sativa*

&lt;400&gt; SEQUENCE: 56

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Met Gly Ala Arg Cys Leu Ala Leu Leu Leu Leu Tyr Gly Thr Leu Leu
1          5          10          15

Leu Leu Leu Leu Leu Pro Gln Leu Pro Leu Ala Gly Ala Ala Thr Arg
20          25          30

Tyr Tyr Thr Phe Asn Val Lys Leu Gln Asn Val Thr Arg Leu Cys Asn
35          40          45

Thr Arg Ala Ile Pro Thr Val Asn Gly Lys Phe Pro Gly Pro Lys Ile
50          55          60

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

Lys Asp Asn Ile Thr Ile His Trp His Gly Val Arg Gln Met Arg Thr
85          90          95

Gly Trp Ser Asp Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile Gln Thr
100         105         110

Gly Gln Ser Tyr Val Tyr Asn Phe Thr Ile Asn Gly Gln Arg Gly Thr
115         120         125

Leu Phe Trp His Ala His Val Ser Trp Leu Arg Ser Thr Leu Tyr Gly
130         135         140

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

Pro His Lys Asp Val Pro Ile Ile Phe Gly Glu Trp Phe Asn Ala Asp
165         170         175

Pro Glu Ala Ile Val Ala Gln Ala Leu Gln Thr Gly Gly Gly Pro Asn
180         185         190

Val Ser Asp Ala Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn
195         200         205

Cys Ser Ser Lys Asp Thr Phe Arg Leu Lys Val Gln Pro Gly Lys Met
210         215         220

Tyr Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe
225         230         235         240

Ser Val Ala Asn His Thr Leu Thr Val Val Asp Val Asp Ala Ser Tyr
245         250         255

Val Lys Pro Phe Asp Thr Asp Val Val Leu Ile Thr Pro Gly Gln Thr
260         265         270

Thr Asn Val Leu Leu Arg Ala Lys Pro Thr Ala Glu Ala Ala Gly Ala
275         280         285

Thr His Leu Met Met Ala Arg Pro Tyr Ala Thr Gly Arg Pro Gly Thr
290         295         300

Tyr Asp Asn Thr Thr Val Ala Ala Val Leu Glu Tyr Ala Pro Pro Gly
305         310         315         320

His Ile Lys Ser Leu Pro Leu Leu Arg Pro Ser Leu Pro Ala Leu Asn
325         330         335

Asp Thr Ala Phe Ala Ala Gly Phe Ala Ala Lys Leu Arg Ser Leu Ala
340         345         350

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Cys Pro Asp Tyr Pro Ser Asn Val Pro Arg Arg Val Asp Lys Pro Phe  
 355 360 365  
 Phe Phe Ala Val Gly Leu Gly Thr Thr Pro Cys Pro Gly Ser Asn Asn  
 370 375 380  
 Gln Thr Cys Gln Gly Pro Thr Asn Thr Thr Lys Phe Thr Ala Ser Ile  
 385 390 395 400  
 Asn Asn Val Ser Phe Asp Met Pro Thr Thr Ala Leu Leu Gln Ala His  
 405 410 415  
 Tyr Thr Gly Gln Ser Ala Gly Val Tyr Thr Ala Asp Phe Pro Ala Ser  
 420 425 430  
 Pro Leu Glu Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn  
 435 440 445  
 Val Ser Asn Gly Thr Arg Val Val Val Leu Pro Tyr Asn Ala Ser Val  
 450 455 460  
 Glu Val Val Leu Gln Asp Thr Ser Ile Leu Gly Ala Glu Ser His Pro  
 465 470 475 480  
 Leu His Leu His Gly Phe Asp Phe Phe Val Val Gly Gln Gly Thr Gly  
 485 490 495  
 Asn Tyr Asp Pro Ser Lys His Pro Ala Glu Phe Asn Leu Val Asp Pro  
 500 505 510  
 Val Gln Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala Ile  
 515 520 525  
 Arg Phe Phe Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu  
 530 535 540  
 Glu Val His Thr Thr Trp Gly Leu Lys Met Ala Trp Val Val Asn Asp  
 545 550 555 560  
 Gly Pro Leu Pro Glu Gln Lys Leu Met Pro Pro Ser Asp Leu Pro  
 565 570 575  
 Met Cys

<210> SEQ ID NO 57  
 <211> LENGTH: 577  
 <212> TYPE: PRT  
 <213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 57

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



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Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val Tyr Gly Pro Ile  
 130 135 140

Ile Ile Leu Pro Lys Ala Gly Val Pro Tyr Pro Phe Pro Ala Pro Asp  
 145 150 155 160

Lys Glu Val Pro Val Val Phe Gly Glu Trp Trp Lys Ala Asp Thr Glu  
 165 170 175

Ala Val Ile Ser Gln Ala Thr Gln Thr Gly Gly Gly Pro Asn Val Ser  
 180 185 190

Asp Ala Phe Thr Ile Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys Ser  
 195 200 205

Ala Lys Asp Thr Phe Lys Leu Lys Val Glu Ala Gly Lys Thr Tyr Met  
 210 215 220

Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile  
 225 230 235 240

Ala Gly His Thr Leu Thr Val Val Asp Val Asp Ala Val Tyr Val Lys  
 245 250 255

Pro Phe Thr Val Asp Thr Leu Leu Ile Thr Pro Gly Gln Thr Thr Asn  
 260 265 270

Val Leu Leu Thr Thr Lys Pro Ser Tyr Pro Gly Ala Thr Phe Tyr Met  
 275 280 285

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

Thr Val Ala Gly Ile Leu Glu Tyr Glu Asp Pro Ser Ser His Ser Thr  
 305 310 315 320

Ala Ala Phe Asn Lys Asn Leu Pro Val Leu Arg Pro Thr Leu Pro Gln  
 325 330 335

Ile Asn Asp Thr Ser Phe Val Ser Asn Tyr Thr Ala Lys Leu Arg Ser  
 340 345 350

Phe Ala Thr Ala Glu Tyr Pro Ala Asn Val Pro Gln Gln Val Asp Thr  
 355 360 365

Arg Phe Phe Phe Thr Val Gly Leu Gly Thr His Pro Cys Ala Val Asn  
 370 375 380

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

Asn Val Ser Phe Val Leu Pro Ser Thr Ala Leu Leu Gln Ser His Tyr  
 405 410 415

Thr Gly Arg Ser Asn Gly Val Tyr Ala Ser Asn Phe Pro Ala Met Pro  
 420 425 430

Leu Ser Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val  
 435 440 445

Ser Asn Gly Thr Arg Leu Val Val Leu Pro Tyr Gly Ala Ser Val Glu  
 450 455 460

Leu Val Met Gln Gly Thr Ser Val Leu Gly Ala Glu Ser His Pro Phe  
 465 470 475 480

His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln Gly Phe Gly Asn  
 485 490 495

Phe Asp Pro Val Asn Asp Pro Ala Lys Tyr Asn Leu Val Asp Pro Val  
 500 505 510

Glu Arg Asn Thr Val Gly Val Pro Ala Ala Gly Trp Val Ala Ile Arg  
 515 520 525

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Phe Leu Val Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu  
 530 535 540

Val His Val Ser Trp Gly Leu Lys Met Ala Trp Val Val Gln Asp Gly  
 545 550 555 560

Ser Leu Pro Asn Gln Lys Ile Leu Pro Pro Pro Ser Asp Leu Pro Lys  
 565 570 575

Cys

<210> SEQ ID NO 58  
 <211> LENGTH: 574  
 <212> TYPE: PRT  
 <213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 58

Met Ala Ala Ala Ser Ser Val Leu Arg Cys Cys Leu Leu Val Ala Ala  
 1 5 10 15

Leu Met Thr Leu Ser Ala Met Gly Ala Glu Ala Ile Thr Arg Gln Tyr  
 20 25 30

Leu Phe Asp Val Gln Thr Thr Ser Val Thr Arg Leu Cys Ser Thr Lys  
 35 40 45

Ser Ile Val Thr Val Asn Gly Gln Tyr Pro Gly Pro Thr Leu Phe Ala  
 50 55 60

Arg Glu Gly Asp His Val Glu Val Thr Val Val Asn His Ser Pro Tyr  
 65 70 75 80

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

Ala Asp Gly Pro Ser Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Gly  
 100 105 110

Ser Tyr Val Tyr Arg Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Trp  
 115 120 125

Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val His Gly Pro Met  
 130 135 140

Val Ile Leu Pro Pro Ala Gly Val Gly Tyr Pro Phe Pro Ala Pro His  
 145 150 155 160

Glu Glu Val Pro Ile Met Phe Gly Glu Trp Trp Asn Asn Asp Thr Glu  
 165 170 175

Ala Val Ile Ser Gln Ala Leu Gln Thr Gly Gly Gly Pro Asn Ile Ser  
 180 185 190

Asp Ala Tyr Thr Leu Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys Ser  
 195 200 205

Ala Gln Asp Thr Phe Lys Leu Lys Val Lys Pro Gly Lys Thr Tyr Met  
 210 215 220

Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile  
 225 230 235 240

Ala Asn His Thr Leu Thr Val Val Asp Val Asp Ala Leu Tyr Val Lys  
 245 250 255

Pro Phe Thr Val Asp Thr Leu Ile Ile Ala Pro Gly Gln Thr Ser Asn  
 260 265 270

Val Leu Leu Thr Ala Lys Pro Thr Tyr Pro Gly Ala Ser Tyr Tyr Met  
 275 280 285

Leu Ala Arg Pro Tyr Thr Thr Thr Gln Gly Thr Phe Asp Asn Thr Thr  
 290 295 300

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Val Ala Gly Val Leu Glu Tyr Asp Asp Pro Cys Pro Thr Thr Ala Ala  
 305 310 315 320  
 Gly Lys Ile Val Pro Ile Phe Ser Pro Thr Leu Pro Gln Ile Asn Asp  
 325 330 335  
 Thr Asn Ala Val Ser Asn Phe Thr Ala Lys Leu Arg Ser Leu Ala Ser  
 340 345 350  
 Ala Gly Tyr Pro Ala Ala Val Pro Gln Gln Val Asp His Arg Phe Phe  
 355 360 365  
 Phe Thr Val Gly Leu Gly Thr His Pro Cys Ala Val Asn Gly Thr Cys  
 370 375 380  
 Gln Gly Pro Asn Gly Ser Arg Phe Ala Ala Ser Ile Asn Asn Val Ser  
 385 390 395 400  
 Phe Val Leu Pro Ala Thr Ala Leu Leu Gln Ser His Phe Ala Gly Lys  
 405 410 415  
 Ser Lys Gly Val Tyr Ala Ser Asn Phe Pro Tyr Tyr Pro Leu Asn Pro  
 420 425 430  
 Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val Met Asn Gly  
 435 440 445  
 Thr Lys Val Leu Val Leu Pro Tyr Gly Ala Asn Val Glu Leu Val Met  
 450 455 460  
 Gln Asp Thr Ser Ile Leu Gly Ala Glu Ser His Pro Leu His Leu His  
 465 470 475 480  
 Gly Phe Asn Phe Phe Val Val Gly Gln Gly Phe Gly Asn Phe Asp Pro  
 485 490 495  
 Ile Asn Asp Pro Ala Lys Phe Asn Leu Tyr Asp Pro Val Glu Arg Asn  
 500 505 510  
 Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala Ile Arg Phe His Ala  
 515 520 525  
 Asp Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Met  
 530 535 540  
 Ser Trp Gly Leu Lys Met Ala Trp Leu Val Leu Asp Gly Ser Arg Pro  
 545 550 555 560  
 Asp Gln Lys Leu Pro Pro Pro Pro Leu Asp Leu Pro Lys Cys  
 565 570

&lt;210&gt; SEQ ID NO 59

&lt;211&gt; LENGTH: 549

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Oryza sativa*

&lt;400&gt; SEQUENCE: 59

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

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Ala Asp Gly Pro Ser Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Gly  
100 105 110

Ser Tyr Val Tyr Arg Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Trp  
115 120 125

Trp His Ala His Ile Ser Trp Leu Arg Ala Thr Val His Gly Pro Met  
130 135 140

Val Ile Leu Pro Pro Ala Gly Val Gly Tyr Pro Phe Pro Ala Pro His  
145 150 155 160

Glu Glu Val Pro Ile Met Phe Gly Glu Trp Trp Asn Asn Asp Thr Glu  
165 170 175

Ala Val Ile Ser Gln Ala Leu Gln Thr Gly Gly Gly Pro Asn Ile Ser  
180 185 190

Asp Ala Tyr Thr Leu Asn Gly Leu Pro Gly Pro Leu Tyr Asn Cys Ser  
195 200 205

Ala Gln Asp Thr Phe Lys Leu Lys Val Lys Pro Gly Lys Thr Tyr Met  
210 215 220

Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Ser Ile  
225 230 235 240

Ala Asn His Thr Leu Thr Val Val Asp Val Asp Ala Leu Tyr Val Lys  
245 250 255

Pro Phe Thr Val Asp Thr Leu Ile Ile Ala Pro Gly Gln Thr Ser Asn  
260 265 270

Val Leu Leu Thr Ala Lys Pro Thr Tyr Pro Gly Ala Ser Tyr Tyr Met  
275 280 285

Leu Ala Arg Pro Tyr Thr Thr Thr Gln Gly Thr Phe Asp Asn Thr Thr  
290 295 300

Val Ala Gly Val Leu Glu Tyr Asp Asp Pro Cys Pro Thr Thr Ala Ala  
305 310 315 320

Gly Lys Ile Val Pro Ile Phe Ser Pro Thr Leu Pro Gln Ile Asn Asp  
325 330 335

Thr Asn Ala Val Ser Asn Phe Thr Ala Lys Leu Arg Ser Leu Ala Ser  
340 345 350

Ala Gly Tyr Pro Ala Ala Val Pro Gln Gln Val Asp His Arg Phe Phe  
355 360 365

Phe Thr Val Gly Leu Gly Thr His Pro Cys Ala Val Asn Gly Thr Cys  
370 375 380

Gln Gly Pro Asn Gly Ser Arg Phe Ala Ala Ser Ile Asn Asn Val Ser  
385 390 395 400

Phe Val Leu Pro Ala Thr Ala Leu Leu Gln Ser His Phe Ala Gly Lys  
405 410 415

Ser Lys Gly Val Tyr Ala Ser Asn Phe Pro Tyr Tyr Pro Leu Asn Pro  
420 425 430

Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr Asn Val Met Asn Gly  
435 440 445

Thr Lys Val Leu Val Leu Pro Tyr Gly Ala Asn Val Glu Leu Val Met  
450 455 460

Gln Asp Thr Ser Ile Leu Gly Ala Glu Ser His Pro Leu His Leu His  
465 470 475 480

Gly Phe Asn Phe Phe Val Val Gly Gln Gly Phe Gly Asn Phe Asp Pro  
485 490 495



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Thr Thr Val Ala Gly Ile Leu Glu Tyr Glu Asn Pro Ala Met Ser Pro  
 305 310 315 320  
 Ser Ala Ala Ser Phe Val Lys Gly Leu Pro Leu Phe Lys Pro Thr Leu  
 325 330 335  
 Pro Gln Leu Asn Asp Thr Asp Phe Val Thr Asn Phe Thr Asp Lys Leu  
 340 345 350  
 Arg Ser Leu Ala Thr Pro Glu Tyr Pro Ala Ala Val Pro Gln Ser Val  
 355 360 365  
 Asp Lys Arg Phe Phe Phe Thr Val Gly Leu Gly Thr Leu Pro Cys Pro  
 370 375 380  
 Ala Asn Met Thr Cys Gln Gly Pro Asn Asn Thr Gln Met Ala Ala Ser  
 385 390 395 400  
 Met Asn Asn Val Ser Phe Val Leu Pro Ala Arg Ala Leu Leu Gln Ser  
 405 410 415  
 His Phe Thr Gly Leu Ser Ser Gly Val Tyr Ala Pro Asp Phe Pro Val  
 420 425 430  
 Ala Pro Leu Ser Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn Asn Thr  
 435 440 445  
 Asn Val Lys Thr Gly Thr Lys Leu Leu Val Leu Arg Tyr Asn Thr Ser  
 450 455 460  
 Val Glu Leu Val Met Gln Asp Thr Ser Ile Leu Gly Ile Glu Ser His  
 465 470 475 480  
 Pro Leu His Leu His Gly Phe Asn Phe Phe Val Ile Gly Gln Gly Phe  
 485 490 495  
 Gly Asn Tyr Asp Ala Val Asn Asp Pro Ala Lys Phe Asn Leu Val Asp  
 500 505 510  
 Pro Val Glu Arg Asn Thr Val Gly Val Pro Ala Gly Gly Trp Val Ala  
 515 520 525  
 Ile Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Met His Cys His  
 530 535 540  
 Leu Glu Ala His Thr Thr Trp Gly Leu Arg Met Ala Trp Leu Val Leu  
 545 550 555 560  
 Asp Gly Ser His Pro Asn Gln Lys Leu Leu Pro Pro Ser Asp Leu  
 565 570 575  
 Pro Lys Cys

&lt;210&gt; SEQ ID NO 61

&lt;211&gt; LENGTH: 513

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Oryza sativa*

&lt;400&gt; SEQUENCE: 61

Met Ala Thr Val Thr Arg Leu Cys Val Thr Lys Ser Val Pro Thr Val  
 1 5 10 15  
 Asn Gly Gln Phe Pro Gly Pro Lys Leu Val Val Arg Glu Gly Asp Thr  
 20 25 30  
 Leu Val Ile Arg Val Thr Asn Asn Ile Asn Asn Asn Val Thr Phe His  
 35 40 45  
 Trp His Gly Ile Arg Gln Val Arg Ser Gly Trp Ala Asp Gly Pro Ala  
 50 55 60  
 Tyr Ile Thr Gln Cys Pro Ile Arg Ser Gly Gly Ser Tyr Val Tyr Arg  
 65 70 75 80

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Phe Thr Val Thr Gly Gln Arg Gly Thr Leu Trp Trp His Ala His Phe  
 85 90 95

Ser Trp Leu Arg Ala Thr Leu Tyr Gly Pro Leu Val Ile Leu Pro Pro  
 100 105 110

Arg Gly Val Ala Tyr Pro Phe Pro Lys Pro His Arg Glu Val Pro Leu  
 115 120 125

Leu Leu Gly Glu Trp Phe Asn Ala Asp Pro Glu Ala Val Ile Lys Gln  
 130 135 140

Ala Leu Gln Thr Gly Gly Gly Pro Asn Val Ser Asp Ala Tyr Thr Phe  
 145 150 155

Asn Gly Leu Pro Gly Pro Thr Tyr Asn Cys Ser Ser Ser Asn Asp Thr  
 165 170 175

Phe Lys Leu Arg Val Arg Pro Gly Lys Thr Tyr Leu Leu Arg Leu Ile  
 180 185 190

Asn Ala Ala Leu Asn Asp Glu Leu Phe Phe Gly Val Ala Asn His Thr  
 195 200 205

Leu Met Val Val Gln Ala Asp Ala Ser Tyr Val Lys Pro Phe Ala Ala  
 210 215 220

Thr Ala Leu Val Ile Ser Pro Gly Gln Thr Met Asp Val Leu Leu Thr  
 225 230 235 240

Ala Ala Ala Asn Asn Pro Pro Ser Arg Ser Phe Ala Ile Ala Val Ala  
 245 250 255

Pro Tyr Thr Asn Thr Val Gly Thr Phe Asp Asn Thr Thr Ala Val Ala  
 260 265 270

Val Leu Glu Tyr Tyr Gly Ala Ala Thr Ser Ala Ala Ala Leu Arg Ser  
 275 280 285

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

Asn Phe Ser Ala Ser Phe Arg Ser Leu Ala Ser Ala Gln Tyr Pro Ala  
 305 310 315 320

Arg Val Pro Arg Thr Val Asp Arg His Phe Phe Phe Ala Val Gly Leu  
 325 330 335

Gly Ala Asp Pro Cys Gln Ser Pro Val Asn Gly Thr Cys Gln Gly Pro  
 340 345 350

Asn Asn Thr Arg Phe Ala Ala Ser Met Asn Asn Val Ser Phe Val Met  
 355 360 365

Pro Arg Thr Ser Leu Leu Gln Ala His Tyr Gln Arg Arg Tyr Asn Gly  
 370 375 380

Val Leu Ala Ala Asn Phe Pro Ala Ala Pro Arg Thr Pro Phe Asn Tyr  
 385 390 395 400

Thr Gly Thr Pro Pro Asn Asn Thr Phe Val Thr His Gly Thr Arg Val  
 405 410 415

Val Pro Leu Ser Phe Asn Thr Thr Val Glu Val Val Leu Gln Asp Thr  
 420 425 430

Ser Ile Leu Gly Ala Glu Ser His Pro Leu His Leu His Gly Tyr Asp  
 435 440 445

Phe Tyr Val Val Gly Thr Gly Phe Gly Asn Tyr Asp Ala Ser Asn Asp  
 450 455 460

Thr Ala Lys Tyr Asn Leu Val Asp Pro Val Gln Arg Asn Thr Ile Ser  
 465 470 475 480

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Val Pro Thr Ala Gly Trp Val Ala Ile Arg Phe Val Ala Asp Asn Pro  
                           485                          490                          495

Gly Trp Leu Pro Ala Leu Tyr Leu Tyr Leu His Leu Lys Arg Glu Phe  
                           500                          505                          510

Leu

<210> SEQ ID NO 62  
 <211> LENGTH: 547  
 <212> TYPE: PRT  
 <213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 62

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

Cys Arg Phe Leu Ala Ala Phe Ala Val Leu Leu Ala Leu Pro Thr Leu  
           20                  25                  30

Thr Ala Gly Leu Thr Arg His Tyr Thr Phe Asn Val Gln Met Thr Asn  
       35                  40                  45

Val Thr Arg Leu Cys Val Thr Lys Ser Ile Pro Thr Val Asn Gly Gln  
       50                  55                  60

Phe Pro Gly Pro Lys Leu Val Val Arg Glu Gly Asp Arg Leu Val Val  
       65                  70                  75                  80

Lys Val His Asn His Met Asn Tyr Asn Val Ser Phe His Trp His Gly  
           85                  90                  95

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

Gln Cys Pro Ile Gln Gly Gly Ser Tyr Val Tyr Asp Phe Thr Val  
       115                  120                  125

Thr Gly Gln Arg Gly Thr Leu Trp Trp His Ala His Phe Ser Trp Leu  
       130                  135                  140

Arg Val His Leu Tyr Gly Pro Leu Val Ile Leu Pro Lys Arg Gly Glu  
       145                  150                  155                  160

Gly Phe Pro Phe Pro Arg Pro Tyr Lys Glu Leu Pro Pro Ile Met Phe  
           165                  170                  175

Gly Glu Trp Phe Asn Ala Asp Thr Glu Ala Val Ile Asn Gln Ala Leu  
       180                  185                  190

Gln Thr Gly Ala Gly Pro Asn Ile Ser Asp Ala Tyr Thr Phe Asn Gly  
       195                  200                  205

Leu Pro Gly Pro Thr Tyr Asn Cys Ser Ser Lys Asp Thr Tyr Lys Val  
       210                  215                  220

Lys Val Gln Pro Gly Arg Thr Tyr Leu Leu Arg Leu Ile Asn Ser Ala  
       225                  230                  235                  240

Leu Asn Asp Glu Leu Phe Phe Gly Ile Ala Asn His Thr Leu Thr Val  
           245                  250                  255

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

Val Ile Ser Pro Gly Gln Thr Met Asn Leu Leu Leu Thr Thr Ala Pro  
       275                  280                  285

Asn Pro Gly Ser Pro Val Tyr Ala Met Ala Ile Ala Pro Tyr Thr Asn  
       290                  295                  300

Thr Gln Gly Thr Phe Asp Asn Thr Thr Ala Val Ala Val Leu Glu Tyr  
       305                  310                  315                  320



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Ala Pro Thr Arg Ala Ser Ala Thr Gly Asn Asn Asn Leu Pro Leu Pro  
 325 330 335

Pro Leu Pro Arg Tyr Asn Asp Thr Asn Ala Val Ala Asn Phe Ser Ser  
 340 345 350

Lys Phe Arg Ser Leu Ala Thr Ala Arg Tyr Pro Ala Arg Val Pro Arg  
 355 360 365

Ala Val Asp Arg His Val Leu Phe Thr Val Gly Leu Gly Thr Asp Pro  
 370 375 380

Cys Pro Ser Asn Gln Thr Cys Gln Gly Pro Asn Gly Thr Lys Phe Ala  
 385 390 395 400

Ala Ser Ile Asn Asn Asn Ser Phe Val Arg Pro Arg Val Ala Leu Leu  
 405 410 415

Glu Ala His Cys Gln Arg Arg Val Val Pro Leu Ala Phe Asn Thr Ser  
 420 425 430

Val Glu Leu Val Leu Gln Gly Thr Ser Ile Gln Gly Ala Glu Ser His  
 435 440 445

Pro Leu His Met His Gly Phe Asn Phe Phe Val Val Gly Gln Gly Phe  
 450 455 460

Gly Asn Tyr Asp Pro Val Asn Asp Pro Ala Asn Tyr Asn Leu Val Asp  
 465 470 475 480

Pro Val Glu Arg Asn Thr Val Ser Val Pro Thr Gly Gly Trp Val Ala  
 485 490 495

Val Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Leu Met His Cys His  
 500 505 510

Phe Asp Val His Leu Ser Trp Gly Leu Ser Met Ala Trp Leu Val Asn  
 515 520 525

Asp Gly Pro Leu Pro Ser Gln Lys Met Leu Pro Pro Pro Ser Asp Leu  
 530 535 540

Pro Lys Cys  
 545

&lt;210&gt; SEQ ID NO 63

&lt;211&gt; LENGTH: 581

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Populus sp.

&lt;400&gt; SEQUENCE: 63

Met Gly Val Ser Phe Leu Pro Ser Pro Ala Phe Leu Gly Leu Leu Leu  
 1 5 10 15

Phe Ser Phe Val Thr Leu Ser Leu His Pro Lys Pro Ala Val Ala Thr  
 20 25 30

Thr Arg His Tyr Lys Leu Asp Val Met Leu Gln Asn Val Thr Arg Leu  
 35 40 45

Cys His Thr Lys Ser Met Val Thr Val Asn Gly Lys Phe Pro Gly Pro  
 50 55 60

Arg Ile Val Ala Arg Glu Gly Asp Arg Leu Leu Ile Lys Val Val Asn  
 65 70 75 80

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

Arg Ser Gly Trp Ala Asp Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile  
 100 105 110

Gln Thr Gly Gln Ser Tyr Val Tyr Asn Tyr Thr Ile Val Gly Gln Arg  
 115 120 125

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Gly Thr Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ser Thr Leu  
 130 135 140

Tyr Gly Pro Leu Ile Ile Leu Pro Lys Leu Gly Thr Pro Tyr Pro Phe  
 145 150 155 160

Val Lys Pro Tyr Lys Glu Val Pro Ile Ile Phe Gly Glu Trp Phe Asn  
 165 170 175

Ala Asp Pro Glu Ala Ile Ile Asn Gln Ala Leu Gln Thr Gly Gly Gly  
 180 185 190

Pro Asn Val Ser Asp Ala Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu  
 195 200 205

Tyr Asn Cys Ser Ala Lys Asp Thr Phe Lys Leu Lys Val Lys Pro Gly  
 210 215 220

Lys Thr Tyr Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Asp Glu Leu  
 225 230 235 240

Phe Phe Ser Ile Ala Asn His Thr Phe Thr Val Val Glu Ala Asp Ala  
 245 250 255

Val Tyr Val Lys Pro Phe Asp Thr Lys Thr Leu Leu Ile Ala Pro Gly  
 260 265 270

Gln Thr Thr Asn Val Leu Leu Lys Thr Lys Pro His His Pro Asn Ala  
 275 280 285

Lys Phe Phe Met Thr Ala Arg Pro Tyr Val Thr Gly Gln Gly Thr Phe  
 290 295 300

Asp Asn Ser Thr Val Ala Gly Ile Leu Glu Tyr Glu Glu Ser His Lys  
 305 310 315 320

Thr Ile Gln Ser Ser His Ser Thr Lys Arg Leu Pro Leu Phe Lys Pro  
 325 330 335

Asn Leu Pro Pro Leu Asn Asp Thr Ser Phe Ala Thr Lys Phe Thr Ser  
 340 345 350

Lys Leu Arg Ser Leu Ala Asn Ala Gln Phe Pro Ala Asn Val Pro Gln  
 355 360 365

Lys Val Asp Arg Gln Phe Phe Thr Val Gly Leu Gly Thr His Ser  
 370 375 380

Cys Pro Gln Asn Gln Thr Cys Gln Gly Pro Asn Gly Thr Met Phe Ala  
 385 390 395 400

Ala Ser Val Asn Asn Val Ser Phe Ala Met Pro Thr Thr Ala Leu Leu  
 405 410 415

Gln Ala His His Phe Gly Gln Ser Asn Gly Val Tyr Thr Pro Asp Phe  
 420 425 430

Pro Ile Asn Pro Leu Thr Pro Phe Asn Tyr Thr Gly Asn Pro Pro Asn  
 435 440 445

Asn Thr Met Val Ser Asn Gly Thr Lys Leu Val Val Leu Pro Phe Asn  
 450 455 460

Thr Thr Val Glu Leu Ile Met Gln Asp Thr Ser Ile Leu Gly Ala Glu  
 465 470 475 480

Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln  
 485 490 495

Gly Phe Gly Asn Phe Asp Pro Asn Lys Asp Pro Ala Asn Phe Asn Leu  
 500 505 510

Ile Asp Pro Ile Glu Arg Asn Thr Val Gly Val Pro Ser Gly Gly Trp  
 515 520 525

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Val Ala Ile Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Met His  
 530 535 540

Cys His Leu Glu Val His Thr Ser Trp Gly Leu Lys Met Ala Trp Val  
 545 550 555 560

Val Leu Asp Gly Lys Leu Pro Asn Gln Lys Leu Leu Pro Pro Pro Ala  
 565 570 575

Asp Leu Pro Arg Cys  
 580

<210> SEQ ID NO 64  
 <211> LENGTH: 581  
 <212> TYPE: PRT  
 <213> ORGANISM: Populus sp.

<400> SEQUENCE: 64

Met Gly Val Tyr Leu Leu Pro Ser Pro Ala Ser Leu Ala Val Phe Leu  
 1 5 10 15

Ser Ser Phe Val Thr Leu Phe Val His Pro Arg Pro Ala Ile Ala Ile  
 20 25 30

Thr Arg His Tyr Lys Phe Asp Val Met Leu Gln Asn Val Thr Arg Leu  
 35 40 45

Cys His Thr Lys Ser Met Val Thr Val Asn Gly Lys Phe Pro Gly Pro  
 50 55 60

Cys Ile Val Ala Arg Glu Gly Asp Arg Leu Leu Ile Lys Val Val Asn  
 65 70 75 80

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

Arg Ser Gly Trp Ala Asp Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile  
 100 105 110

Gln Thr Gly Gln Ser Tyr Val Tyr Asn Tyr Thr Ile Val Gly Gln Arg  
 115 120 125

Gly Thr Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ser Thr Leu  
 130 135 140

Tyr Gly Pro Leu Ile Ile Leu Pro Lys Leu Gly Thr Pro Tyr Pro Phe  
 145 150 155 160

Ala Lys Pro Asp Lys Glu Val Pro Ile Ile Phe Gly Glu Trp Phe Asn  
 165 170 175

Ala Asp Pro Glu Ala Ile Ile Asn Gln Ala Met Gln Thr Gly Gly Gly  
 180 185 190

Pro Asn Val Ser Asp Ala Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu  
 195 200 205

Tyr Asn Cys Ser Ala Lys Asn Thr Phe Lys Leu Lys Val Lys Pro Gly  
 210 215 220

Lys Thr Tyr Leu Leu Arg Leu Ile Asn Ala Ala Leu Asn Glu Glu Leu  
 225 230 235 240

Phe Phe Ser Ile Ala Asn His Thr Leu Thr Val Val Gly Val Asp Ala  
 245 250 255

Ile Tyr Val Lys Pro Phe Asp Thr Glu Thr Leu Leu Ile Ala Ser Gly  
 260 265 270

Gln Thr Thr Asp Val Leu Leu Lys Thr Lys Pro His His Pro Asp Ala  
 275 280 285

Lys Phe Phe Met Ser Ala Arg Pro Tyr Val Thr Gly Gln Gly Thr Phe  
 290 295 300

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Asp Asn Ser Thr Val Ala Gly Ile Leu Glu Tyr Glu Val Ala Arg Lys  
 305 310 315 320  
 Thr Ile Gln Ser Ser His Thr Ser Lys Arg Leu Pro Leu Tyr Lys Pro  
 325 330 335  
 Asn Leu Pro Pro Leu Asn Asp Thr Ser Phe Ala Thr Asn Phe Thr Ser  
 340 345 350  
 Lys Leu Arg Ser Leu Ala Ser Ala Glu Phe Pro Ala Asn Val Pro Gln  
 355 360 365  
 Lys Val Asp Arg His Phe Phe Phe Thr Val Gly Leu Gly Thr Asn Pro  
 370 375 380  
 Cys Ser Lys Asn Gln Thr Cys Gln Gly Pro Asn Gly Thr Arg Phe Ala  
 385 390 395 400  
 Ala Ser Val Asn Asn Val Ser Phe Val Met Pro Thr Lys Ala Leu Leu  
 405 410 415  
 Glu Ala His His Phe Gly Gln Ser Lys Gly Val Tyr Ser Pro Asn Phe  
 420 425 430  
 Pro Ile Ser Pro Leu Ile Pro Phe Asp Tyr Thr Gly Thr Pro Gln Asn  
 435 440 445  
 Asn Thr Met Val Ser His Gly Thr Lys Leu Val Met Leu Pro Phe Asn  
 450 455 460  
 Thr Ser Val Glu Leu Ile Met Gln Asp Thr Ser Ile Leu Gly Ala Glu  
 465 470 475 480  
 Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln  
 485 490 495  
 Gly Phe Gly Asn Phe Asp Pro Lys Lys Asp Pro Ala Asn Phe Asn Leu  
 500 505 510  
 Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro Ser Gly Gly Trp  
 515 520 525  
 Val Ala Ile Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Leu His  
 530 535 540  
 Cys His Val Glu Leu His Met Ser Trp Gly Leu Met Met Ala Trp Val  
 545 550 555 560  
 Val Leu Asp Gly Lys Leu Pro Asn His Arg Leu Leu Pro Pro Pro Val  
 565 570 575  
 Asp Leu Pro Lys Cys  
 580

<210> SEQ ID NO 65  
 <211> LENGTH: 581  
 <212> TYPE: PRT  
 <213> ORGANISM: Populus sp.

<400> SEQUENCE: 65

Met Gly Ala Ser Phe Leu Pro Ser Pro Ala Phe Leu Ala Val Phe Leu  
 1 5 10 15  
 Ile Ser Phe Val Thr Leu Ser Ile His Pro Glu Pro Ala Leu Ala Ile  
 20 25 30  
 Thr Arg His Tyr Lys Phe Asp Val Met Leu Gln Asn Val Thr Arg Leu  
 35 40 45  
 Cys His Thr Lys Ser Ile Val Thr Val Asn Gly Lys Phe Pro Gly Pro  
 50 55 60  
 Arg Ile Val Ala Arg Glu Gly Asp Arg Leu Leu Ile Lys Val Val Asn

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65		70				75				80					
His	Val	Gln	Asn	Asn	Ile	Ser	Ile	His	Trp	His	Gly	Ile	Arg	Gln	Leu
			85						90					95	
Arg	Ser	Gly	Trp	Ala	Asp	Gly	Pro	Ala	Tyr	Ile	Thr	Gln	Cys	Pro	Ile
			100					105					110		
Gln	Thr	Gly	Gln	Ser	Tyr	Val	Tyr	Asn	Tyr	Thr	Ile	Val	Gly	Gln	Arg
		115					120					125			
Gly	Thr	Leu	Trp	Trp	His	Ala	His	Ile	Ser	Trp	Leu	Arg	Ser	Thr	Leu
	130					135					140				
Tyr	Gly	Pro	Leu	Ile	Ile	Leu	Pro	Lys	Leu	Gly	Thr	Thr	Tyr	Pro	Phe
145					150					155					160
Ala	Lys	Pro	His	Lys	Glu	Val	Pro	Ile	Ile	Phe	Gly	Glu	Trp	Phe	Asn
				165					170					175	
Ala	Asp	Pro	Glu	Ala	Ile	Ile	Asn	Gln	Ala	Met	Gln	Thr	Gly	Gly	Gly
			180					185					190		
Pro	Asn	Val	Ser	Asp	Ala	Tyr	Thr	Ile	Asn	Gly	Phe	Pro	Gly	Pro	Leu
		195					200						205		
Tyr	Asn	Cys	Ser	Ala	Lys	Asp	Thr	Phe	Lys	Leu	Lys	Val	Lys	Pro	Gly
	210					215					220				
Lys	Thr	Tyr	Leu	Leu	Arg	Met	Ile	Asn	Ala	Ala	Leu	Asn	Asp	Glu	Leu
225					230					235					240
Phe	Phe	Ser	Ile	Ala	Asn	His	Thr	Leu	Thr	Val	Val	Asp	Val	Asp	Ala
				245					250					255	
Ile	Tyr	Val	Lys	Pro	Phe	Asp	Thr	Glu	Thr	Leu	Leu	Ile	Ala	Pro	Gly
			260					265					270		
Gln	Thr	Thr	Asn	Val	Leu	Leu	Lys	Thr	Lys	Pro	His	His	Pro	Asn	Ala
		275					280					285			
Ser	Phe	Phe	Met	Ser	Ala	Arg	Pro	Tyr	Val	Thr	Gly	Gln	Gly	Thr	Phe
	290					295					300				
Asp	Asn	Ser	Thr	Val	Ala	Gly	Ile	Leu	Glu	Tyr	Glu	Glu	Ser	Asn	Lys
305					310					315					320
Thr	Ile	Lys	Ser	Ser	His	Ser	Pro	Lys	Lys	Leu	Pro	Phe	Tyr	Lys	Pro
				325					330					335	
Asn	Leu	Pro	Pro	Leu	Asn	Asp	Thr	Ser	Phe	Ala	Thr	Asn	Phe	Thr	Ser
			340					345					350		
Lys	Leu	Arg	Ser	Leu	Ala	Ser	Ala	Glu	Phe	Pro	Ala	Asn	Val	Pro	Gln
		355					360					365			
Lys	Val	Asp	Arg	Gln	Phe	Phe	Phe	Ser	Val	Ser	Leu	Gly	Thr	Asn	Pro
	370					375					380				
Cys	Ser	Lys	Asn	Lys	Thr	Cys	Gln	Gly	Pro	Asn	Gly	Thr	Met	Phe	Ala
385					390					395					400
Ala	Ser	Val	Asn	Asn	Val	Ser	Phe	Val	Met	Pro	Thr	Lys	Ala	Leu	Leu
				405					410					415	
Gln	Ala	His	His	Phe	Gly	Gln	Ser	Lys	Gly	Val	Tyr	Ser	Pro	Asn	Phe
			420					425					430		
Pro	Ile	Asn	Pro	Leu	Ile	Pro	Phe	Asn	Tyr	Thr	Gly	Thr	Pro	Pro	Asn
		435					440					445			
Asn	Thr	Met	Val	Ser	Asn	Gly	Thr	Lys	Leu	Val	Val	Leu	Pro	Phe	Asn
	450					455					460				
Thr	Ser	Val	Glu	Leu	Ile	Met	Gln	Asp	Thr	Ser	Ile	Leu	Gly	Ala	Glu
465					470					475					480

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Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly Glu  
 485 490 495

Gly Phe Gly Asn Phe Asp Pro Lys Lys Asp Pro Ala Asn Phe Asn Leu  
 500 505 510

Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro Ser Gly Gly Trp  
 515 520 525

Val Ala Ile Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Met His  
 530 535 540

Cys His Leu Glu Val His Thr Ser Trp Gly Leu Lys Met Ala Trp Val  
 545 550 555 560

Val Leu Asp Gly Lys Leu Pro Asn Gln Lys Leu Leu Pro Pro Pro Ala  
 565 570 575

Asp Leu Pro Lys Cys  
 580

&lt;210&gt; SEQ ID NO 66

&lt;211&gt; LENGTH: 581

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Populus sp.

&lt;400&gt; SEQUENCE: 66

Met Gly Ala Ser Phe Leu Pro Ser Pro Ala Phe Leu Ala Val Phe Leu  
 1 5 10 15

Ile Ser Phe Val Thr Leu Ser Ile His Pro Glu Pro Ala Leu Ala Ile  
 20 25 30

Thr Arg His Tyr Lys Phe Asp Val Met Leu Gln Asn Val Thr Arg Leu  
 35 40 45

Cys His Thr Lys Ser Ile Val Thr Val Asn Gly Lys Phe Pro Gly Pro  
 50 55 60

Arg Ile Val Ala Arg Glu Gly Asp Arg Leu Leu Ile Lys Val Val Asn  
 65 70 75 80

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

Arg Ser Gly Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile  
 100 105 110

Gln Thr Gly Gln Ser Tyr Val Tyr Asn Tyr Thr Ile Val Gly Gln Arg  
 115 120 125

Gly Thr Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ser Thr Leu  
 130 135 140

Tyr Gly Pro Leu Ile Ile Leu Pro Lys Leu Gly Thr Thr Tyr Pro Phe  
 145 150 155 160

Ala Lys Pro His Lys Glu Val Pro Ile Ile Phe Gly Glu Trp Phe Asn  
 165 170 175

Ala Asp Pro Glu Ala Ile Ile Asn Gln Ala Met Gln Thr Gly Gly Gly  
 180 185 190

Pro Asn Val Ser Asp Ala Tyr Thr Ile Asn Gly Phe Pro Gly Pro Leu  
 195 200 205

Tyr Asn Cys Ser Ala Lys Asp Thr Phe Lys Leu Lys Val Lys Pro Gly  
 210 215 220

Lys Thr Tyr Leu Leu Arg Met Ile Asn Ala Ala Leu Asn Asp Glu Leu  
 225 230 235 240

Phe Phe Ser Ile Ala Asn His Thr Leu Thr Val Val Asp Val Asp Ala

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245					250					255					
Ile	Tyr	Val	Lys	Pro	Phe	Asp	Thr	Glu	Thr	Leu	Leu	Ile	Ala	Pro	Gly
			260					265					270		
Gln	Thr	Thr	Asn	Val	Leu	Leu	Lys	Thr	Lys	Pro	His	His	Pro	Asn	Ala
			275					280					285		
Ser	Phe	Phe	Met	Ser	Ala	Arg	Pro	Tyr	Val	Thr	Gly	Gln	Gly	Thr	Phe
			290					295					300		
Asp	Asn	Ser	Thr	Val	Ala	Gly	Ile	Leu	Glu	Tyr	Glu	Glu	Ser	Asn	Lys
			305					310					315		320
Thr	Ile	Lys	Ser	Ser	His	Ser	Pro	Lys	Lys	Leu	Pro	Phe	Tyr	Lys	Pro
								325					330		335
Asn	Leu	Pro	Pro	Leu	Asn	Asp	Thr	Ser	Phe	Ala	Thr	Asn	Phe	Thr	Ser
								340					345		350
Lys	Leu	Arg	Ser	Leu	Ala	Ser	Ala	Glu	Phe	Pro	Ala	Asn	Val	Pro	Gln
								355					360		365
Lys	Val	Asp	Arg	Gln	Phe	Phe	Phe	Ser	Val	Ser	Leu	Gly	Thr	Asn	Pro
								370					375		380
Cys	Ser	Lys	Asn	Lys	Thr	Cys	Gln	Gly	Pro	Asn	Gly	Thr	Met	Phe	Ala
								385					390		395
Ala	Ser	Val	Asn	Asn	Val	Ser	Phe	Val	Met	Pro	Thr	Lys	Ala	Leu	Leu
								405					410		415
Gln	Ala	His	His	Phe	Gly	Gln	Ser	Lys	Gly	Val	Tyr	Ser	Pro	Asn	Phe
								420					425		430
Pro	Ile	Asn	Pro	Leu	Ile	Pro	Phe	Asn	Tyr	Thr	Gly	Thr	Pro	Pro	Asn
								435					440		445
Asn	Thr	Met	Val	Ser	Asn	Gly	Thr	Lys	Leu	Val	Val	Leu	Pro	Phe	Asn
								450					455		460
Thr	Ser	Val	Glu	Leu	Ile	Met	Gln	Asp	Thr	Ser	Ile	Leu	Gly	Ala	Glu
								465					470		475
Ser	His	Pro	Leu	His	Leu	His	Gly	Phe	Asn	Phe	Phe	Val	Val	Gly	Glu
								485					490		495
Gly	Phe	Gly	Asn	Phe	Asp	Pro	Lys	Lys	Asp	Pro	Ala	Asn	Phe	Asn	Leu
								500					505		510
Val	Asp	Pro	Val	Glu	Arg	Asn	Thr	Val	Gly	Val	Pro	Ser	Gly	Gly	Trp
								515					520		525
Val	Ala	Ile	Arg	Phe	Leu	Ala	Asp	Asn	Pro	Gly	Val	Trp	Phe	Met	His
								530					535		540
Cys	His	Leu	Glu	Val	His	Thr	Ser	Trp	Gly	Leu	Lys	Met	Ala	Trp	Val
								545					550		555
Val	Leu	Asp	Gly	Lys	Leu	Pro	Asn	Gln	Lys	Leu	Leu	Pro	Pro	Pro	Ala
								565					570		575
Asp	Leu	Pro	Lys	Cys											
								580							

&lt;210&gt; SEQ ID NO 67

&lt;211&gt; LENGTH: 581

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Populus sp.

&lt;400&gt; SEQUENCE: 67

Met	Gly	Ala	Ser	Leu	Leu	Pro	Pro	Pro	Ala	Phe	Leu	Ala	Val	Phe	Leu
1				5					10					15	

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Phe Ser Phe Val Thr Leu Ser Val Asn Pro Glu Pro Ala Leu Ala Ile  
                   20                                  25                                  30  
 Thr Arg His Tyr Lys Phe Asp Val Met Leu Gln Asn Val Thr Arg Leu  
                   35                                  40                                  45  
 Cys His Thr Lys Ser Met Val Thr Val Asn Gly Lys Phe Pro Gly Pro  
                   50                                  55                                  60  
 Arg Ile Val Ala Arg Glu Gly Asp Arg Leu Val Ile Thr Val Val Asn  
   65                                  70                                  75                                  80  
 His Val Gln Asn Asn Ile Ser Ile His Trp His Gly Ile Arg Gln Leu  
                                   85                                  90                                  95  
 Arg Ser Gly Trp Ala Asp Gly Pro Ala Tyr Val Thr Gln Cys Pro Ile  
                   100                                  105                                  110  
 Gln Thr Gly Gln Ser Tyr Val Tyr Asn Tyr Thr Ile Val Gly Gln Arg  
                   115                                  120                                  125  
 Gly Thr Leu Trp Trp His Ala His Ile Ser Trp Leu Arg Ser Thr Leu  
                   130                                  135                                  140  
 Tyr Gly Pro Ile Ile Leu Leu Pro Lys Leu Gly Thr Pro Tyr Pro Phe  
   145                                  150                                  155                                  160  
 Ala Lys Pro Tyr Lys Glu Val Pro Ile Ile Phe Gly Glu Trp Phe Asn  
                   165                                  170                                  175  
 Ala Asp Pro Glu Ala Ile Ile Asn Gln Ala Met Gln Thr Gly Gly Gly  
                   180                                  185                                  190  
 Pro Asn Val Ser Asp Ala Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu  
                   195                                  200                                  205  
 Tyr Asn Cys Ser Ala Lys Asp Thr Phe Lys Leu Lys Val Lys Pro Gly  
                   210                                  215                                  220  
 Lys Thr Tyr Leu Leu Arg Met Ile Asn Ala Ala Leu Asn Asp Glu Leu  
   225                                  230                                  235                                  240  
 Phe Phe Ser Ile Ala Asn His Thr Val Thr Val Val Asp Val Asp Ala  
                   245                                  250                                  255  
 Val Tyr Val Lys Pro Phe Asp Ala Glu Thr Leu Leu Ile Thr Pro Gly  
                   260                                  265                                  270  
 Gln Thr Thr Asn Val Leu Leu Lys Thr Lys Pro Asp Tyr Pro Asn Ala  
                   275                                  280                                  285  
 Gln Phe Phe Met Ser Ala Arg Pro Tyr Ala Thr Gly Gln Gly Thr Phe  
                   290                                  295                                  300  
 Asp Asn Ser Thr Val Ala Gly Ile Leu Glu Tyr Glu Val Pro Asn Lys  
   305                                  310                                  315                                  320  
 Thr Ser Gln Ser Asn His Ser Thr Lys Lys Leu Pro Leu Tyr Lys Pro  
                   325                                  330                                  335  
 Asn Leu Pro Pro Leu Asn Asp Thr Ser Phe Ala Thr Asn Phe Ser Ser  
                   340                                  345                                  350  
 Lys Leu Arg Ser Leu Ala Ser Ala Asp Phe Pro Ala Asn Val Pro Gln  
                   355                                  360                                  365  
 Lys Val Asp Arg Gln Phe Val Phe Thr Val Gly Leu Gly Thr Asn Pro  
                   370                                  375                                  380  
 Cys Ser Lys Asn Gln Thr Cys Gln Gly Pro Asn Gly Thr Arg Phe Ala  
   385                                  390                                  395                                  400  
 Ala Ser Val Asn Asn Val Ser Phe Val Met Pro Ser Thr Ala Leu Leu  
                   405                                  410                                  415  
 Gln Ala His His Phe Gly Gln Ser Arg Gly Val Tyr Ser Pro Tyr Phe





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Pro Asn Val Ser Asp Ala Tyr Thr Ile Asn Gly Leu Pro Gly Pro Leu  
 195 200 205  
 Tyr Asn Cys Ser Ala Lys Asp Thr Phe Lys Leu Lys Val Lys Pro Gly  
 210 215 220  
 Lys Thr Tyr Leu Leu Arg Met Ile Asn Ala Ala Leu Asn Asp Glu Leu  
 225 230 235 240  
 Phe Phe Ser Ile Ala Asn His Thr Val Thr Val Val Asp Val Asp Ala  
 245 250 255  
 Val Tyr Val Lys Pro Phe Asp Ala Glu Thr Leu Leu Ile Thr Pro Gly  
 260 265 270  
 Gln Thr Thr Asn Val Leu Leu Lys Thr Lys Pro Asp Tyr Pro Asn Ala  
 275 280 285  
 Gln Phe Phe Met Ser Ala Arg Pro Tyr Ala Thr Gly Gln Gly Thr Phe  
 290 295 300  
 Asp Asn Ser Thr Val Ala Gly Ile Leu Glu Tyr Glu Val Pro Asn Lys  
 305 310 315 320  
 Thr Ser Gln Ser Asn His Ser Thr Lys Lys Leu Pro Leu Tyr Lys Pro  
 325 330 335  
 Asn Leu Pro Pro Leu Asn Asp Thr Ser Phe Ala Thr Asn Phe Ser Ser  
 340 345 350  
 Lys Leu Arg Ser Leu Ala Ser Ala Asp Phe Pro Ala Asn Val Pro Gln  
 355 360 365  
 Lys Val Asp Arg Gln Phe Phe Phe Thr Val Gly Leu Gly Thr Asn Pro  
 370 375 380  
 Cys Ser Lys Asn Gln Thr Cys Gln Gly Pro Asn Gly Thr Arg Phe Ala  
 385 390 395 400  
 Ala Ser Val Asn Asn Val Ser Phe Val Met Pro Thr Thr Ala Leu Leu  
 405 410 415  
 Gln Ala His His Phe Gly Gln Ser Arg Gly Val Tyr Ser Pro Tyr Phe  
 420 425 430  
 Pro Ile Ser Pro Leu Ile Pro Phe Asn Tyr Thr Gly Thr Pro Pro Asn  
 435 440 445  
 Asn Thr Met Val Ser Asn Gly Thr Lys Leu Val Val Leu Pro Phe Asn  
 450 455 460  
 Thr Ser Val Glu Leu Ile Met Gln Gly Thr Ser Ile Leu Gly Ala Glu  
 465 470 475 480  
 Ser His Pro Leu His Leu His Gly Phe Asn Phe Phe Val Val Gly Gln  
 485 490 495  
 Gly Phe Gly Asn Phe Asp Pro Ser Lys Asp Pro Ala Asn Phe Asn Leu  
 500 505 510  
 Val Asp Pro Val Glu Arg Asn Thr Val Gly Val Pro Ser Gly Gly Trp  
 515 520 525  
 Val Ala Ile Arg Phe Leu Ala Asp Asn Pro Gly Val Trp Phe Met His  
 530 535 540  
 Cys His Leu Glu Val His Thr Ser Trp Gly Leu Lys Met Ala Trp Val  
 545 550 555 560  
 Val Leu Asp Gly Lys Leu Pro Asn Gln Lys Leu Leu Pro Pro Pro Ala  
 565 570 575  
 Asp Leu Pro Lys Cys  
 580

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<210> SEQ ID NO 69
<211> LENGTH: 561
<212> TYPE: PRT
<213> ORGANISM: Brachypodium distachyon

<400> SEQUENCE: 69

Met Pro Arg His Leu Ser Gln Leu Leu Leu Val Val Met Val Asn Cys
1      5      10      15
Val Leu Leu Gln Ala Leu Ser Val His Ala Ile Thr Arg His Tyr Lys
20     25     30
Phe Asn Val Val Met Arg Lys Met Ser Arg Leu Cys Ser Thr Lys Thr
35     40     45
Ile Leu Thr Val Asn Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg
50     55     60
Glu Gly Asp Asn Val Leu Val Lys Val Val Asn His Val Pro His Asn
65     70     75     80
Val Thr Ile His Trp His Gly Val Arg Gln Ile Arg Thr Gly Trp Tyr
85     90     95
Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Ser Ser
100    105   110
Phe Leu Tyr Asn Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Leu Trp
115   120   125
His Ala His Ile Asn Trp Leu Arg Ala Thr Val His Gly Ala Ile Val
130   135   140
Ile Leu Pro Lys Leu Gly Val Pro Tyr Pro Phe Pro Ala Pro His Lys
145   150   155   160
Glu Ala Val Val Val Leu Gly Glu Trp Trp Lys Ala Asp Ile Glu Thr
165   170   175
Ile Ile Asn Arg Ala Met Gln Leu Gly Val Gly Pro Asn Ile Ser Asp
180   185   190
Ser His Thr Ile Asn Gly His Pro Gly Pro Met Ser Asp Cys Ala Ser
195   200   205
Ser Gln Asp Gly Phe Lys Leu Asn Val Glu Ser Gly Lys Thr Tyr Met
210   215   220
Leu Arg Ile Ile Asn Ala Ala Leu Asn Asp Asp Leu Phe Phe Lys Ile
225   230   235   240
Ala Gly His Lys Leu Thr Val Val Glu Val Asp Ala Val Tyr Thr Lys
245   250   255
Pro Tyr Lys Thr Asp Ile Leu Leu Ile Thr Pro Gly Gln Thr Thr Asn
260   265   270
Val Leu Leu Ala Ala Asp Gln Ser Ala Gly Arg Tyr Leu Leu Ser Ile
275   280   285
Ser Pro Phe Met Asp Ala Pro Val Gln Val Asp Asn Thr Thr Gly Thr
290   295   300
Ala Ile Leu His Tyr Thr Asn Thr Val Ser Ala Ala Ala Arg Leu Thr
305   310   315   320
Leu Phe Lys Pro Pro Pro Gln Asn Ala Thr Leu Ile Ala Ser Lys Phe
325   330   335
Ala Asp Ser Leu Arg Ser Leu Asn Ser Lys Glu Tyr Pro Ala Asn Val
340   345   350
Pro Arg Thr Val Asp His Ser Leu Phe Phe Thr Ile Gly Val Gly Val
355   360   365

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His Lys Glu Ala Val Ile Val Leu Gly Glu Trp Trp Lys Glu Asp Thr  
 165 170 175  
 Glu Thr Val Ile Asn Gln Ala Met Gln Leu Gly Val Gly Pro Asn Ile  
 180 185 190  
 Ser Asp Ser His Thr Ile Asn Gly His Pro Gly Pro Leu Ser Glu Cys  
 195 200 205  
 Ala Ser Ser Gln Asp Gly Phe Lys Leu Ser Val Glu Asn Gly Lys Thr  
 210 215 220  
 Tyr Met Leu Arg Ile Ile Asn Ala Ala Leu Asn Asp Asp Leu Phe Phe  
 225 230 235 240  
 Lys Val Ala Gly His Glu Leu Thr Val Val Glu Val Asp Ala Val Tyr  
 245 250 255  
 Thr Lys Pro Phe Lys Thr Asp Thr Leu Leu Ile Thr Pro Gly Gln Thr  
 260 265 270  
 Thr Asn Val Leu Val Arg Ala Asn Gln Gly Ala Gly Arg Tyr Leu Leu  
 275 280 285  
 Ser Val Ser Pro Phe Met Asp Ala Pro Val Gln Val Asp Asn Lys Thr  
 290 295 300  
 Gly Thr Ala Thr Leu His Tyr Ala Asn Thr Val Ser Ser Ser Met Ala  
 305 310 315 320  
 Ser Leu Thr Leu Val Lys Pro Pro Pro Gln Asn Ala Thr His Ile Val  
 325 330 335  
 Ser Lys Phe Thr Asp Ser Leu His Ser Leu Asn Ser Lys Glu Tyr Pro  
 340 345 350  
 Ala Asn Val Pro Gln Thr Val Asp His Ser Leu Leu Leu Thr Val Gly  
 355 360 365  
 Val Gly Val Asn Pro Cys Pro Ser Cys Ile Asn Gly Thr Arg Val Val  
 370 375 380  
 Gly Thr Ile Asn Asn Val Thr Phe Ile Met Pro Ser Thr Pro Ile Leu  
 385 390 395 400  
 Gln Ala His Tyr Tyr Asn Ile Pro Gly Val Phe Thr Glu Asp Phe Pro  
 405 410 415  
 Ala Thr Pro Leu His Lys Phe Asn Tyr Thr Gly Ser Gly Pro Lys Asn  
 420 425 430  
 Leu Gln Thr Met Asn Gly Thr Arg Val Tyr Arg Leu Pro Tyr Asn Ala  
 435 440 445  
 Ser Val Gln Val Val Leu Gln Asp Thr Gly Ile Ile Ser Pro Glu Ser  
 450 455 460  
 His Pro Ile His Leu His Gly Phe Asn Phe Phe Val Val Gly Lys Gly  
 465 470 475 480  
 Val Gly Asn Tyr Asn Pro Arg Thr Ser Pro Ser Thr Phe Asn Leu Ile  
 485 490 495  
 Asp Pro Ile Glu Arg Asn Thr Ile Gly Val Pro Thr Gly Gly Trp Thr  
 500 505 510  
 Ala Ile Arg Phe Arg Ser Asp Asn Pro Gly Val Trp Phe Met His Cys  
 515 520 525  
 His Phe Glu Val His Thr Ser Trp Gly Leu Lys Met Ala Phe Val Val  
 530 535 540  
 Asp Asn Gly Lys Arg Pro Ser Glu Thr Leu Ile Pro Pro Pro Lys Asp  
 545 550 555 560  
 Leu Pro Gln Cys

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<210> SEQ ID NO 71
<211> LENGTH: 558
<212> TYPE: PRT
<213> ORGANISM: Populus sp.

<400> SEQUENCE: 71

Met Glu Tyr Ala Cys Trp Leu Arg Phe Met Leu Leu Ala Val Cys Leu
 1          5          10          15
Phe Pro Ala Leu Val Gln Cys Arg Val Arg His Tyr Lys Phe Asn Val
 20          25          30
Val Met Lys Asn Thr Thr Arg Leu Cys Ser Arg Lys Pro Ile Val Thr
 35          40          45
Val Asn Gly Arg Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp
 50          55          60
Thr Val Leu Val Lys Val Val Asn His Val Lys Tyr Asn Val Ser Ile
 65          70          75          80
His Trp His Gly Ile Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro
 85          90          95
Ala Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Gln Ser Tyr Val Tyr
 100         105         110
Asn Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His
 115         120         125
Ile Leu Trp Leu Arg Ala Thr Val His Gly Ala Leu Val Val Leu Pro
 130         135         140
Lys Arg Gly Ile Pro Tyr Pro Phe Pro Ala Pro His Lys Glu Val Leu
 145         150         155         160
Val Val Leu Ala Glu Trp Trp Lys Ser Asp Thr Glu Ala Val Ile Asn
 165         170         175
Glu Ala Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr
 180         185         190
Ile Asn Gly His Pro Gly Ala Val Ser Thr Cys Ser Ser Gln Gly Gly
 195         200         205
Phe Thr Leu Pro Val Lys Ser Gly Glu Thr Tyr Met Leu Arg Leu Ile
 210         215         220
Asn Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Lys
 225         230         235         240
Leu Thr Val Val Glu Val Asp Ala Thr Tyr Val Lys Pro Phe Lys Thr
 245         250         255
Asp Thr Val Leu Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Val Thr
 260         265         270
Thr Asn Lys Asn Thr Gly Lys Tyr Leu Val Ala Ala Ser Pro Phe Met
 275         280         285
Asp Ser Pro Ile Ala Val Asp Asn Met Thr Ala Thr Ala Thr Leu Gln
 290         295         300
Tyr Ser Gly Ala Leu Ala Asn Ser Pro Thr Thr Leu Thr Thr Pro Pro
 305         310         315         320
Pro Lys Asn Ala Thr Ala Val Ala Asn Gln Phe Thr Asn Ser Leu Arg
 325         330         335
Ser Leu Asn Ser Arg Arg Phe Pro Ala Lys Val Pro Leu Asn Val Asp
 340         345         350
His Asn Leu Phe Phe Thr Val Ser Leu Gly Val Asn Pro Cys Pro Ser

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355					360					365					
Cys	Lys	Ala	Gly	Asn	Gly	Ser	Arg	Val	Val	Ala	Ser	Ile	Asn	Asn	Val
	370					375					380				
Thr	Phe	Val	Met	Pro	Thr	Thr	Ala	Leu	Leu	Gln	Ala	His	Phe	Leu	Asn
	385					390					395				400
Ile	Ser	Gly	Val	Phe	Thr	Thr	Asp	Phe	Pro	Ala	Lys	Pro	Pro	His	Val
				405					410					415	
Phe	Asn	Tyr	Thr	Gly	Thr	Pro	Pro	Thr	Asn	Leu	Gln	Thr	Lys	Ser	Gly
			420					425					430		
Thr	Lys	Val	Tyr	Arg	Leu	Ser	Tyr	Asn	Ser	Thr	Val	Gln	Leu	Val	Met
	435						440					445			
Gln	Asp	Thr	Gly	Ile	Ile	Ser	Pro	Glu	Asn	His	Pro	Ile	His	Leu	His
	450					455					460				
Gly	Phe	Asn	Phe	Phe	Ala	Val	Gly	Arg	Gly	Val	Gly	Asn	Tyr	Asn	Pro
	465					470					475				480
Lys	Thr	Asp	Thr	Lys	Lys	Phe	Asn	Leu	Val	Asp	Pro	Val	Glu	Arg	Asn
				485					490					495	
Thr	Ile	Gly	Val	Pro	Ser	Gly	Gly	Trp	Val	Ala	Ile	Arg	Phe	Arg	Ala
			500					505						510	
Asp	Asn	Pro	Gly	Val	Trp	Phe	Met	His	Cys	His	Leu	Glu	Val	His	Thr
		515					520					525			
Thr	Trp	Gly	Leu	Lys	Met	Ala	Phe	Leu	Val	Asp	Asn	Gly	Lys	Gly	Pro
	530					535					540				
Lys	Glu	Ser	Leu	Leu	Pro	Pro	Pro	Ser	Asp	Leu	Pro	Lys	Cys		
	545					550					555				
<210> SEQ ID NO 72															
<211> LENGTH: 559															
<212> TYPE: PRT															
<213> ORGANISM: Populus sp.															
<400> SEQUENCE: 72															
Met	Glu	Tyr	Ser	Asn	Trp	Leu	Ile	Arg	Phe	Met	Leu	Leu	Ala	Val	Cys
1				5					10					15	
Leu	Leu	Pro	Ala	Leu	Val	Glu	Cys	Arg	Ile	Arg	His	Tyr	Lys	Phe	Asn
		20						25					30		
Val	Val	Met	Lys	Asn	Thr	Thr	Arg	Leu	Cys	Ser	Arg	Lys	Pro	Ile	Val
		35					40					45			
Thr	Val	Asn	Gly	Arg	Phe	Pro	Gly	Pro	Thr	Leu	Tyr	Ala	Arg	Glu	His
	50					55					60				
Asp	Thr	Val	Leu	Val	Lys	Val	Val	Asn	His	Val	Lys	Tyr	Asn	Val	Ser
	65					70					75				80
Ile	His	Trp	His	Gly	Ile	Arg	Gln	Leu	Arg	Thr	Gly	Trp	Ala	Asp	Gly
				85					90					95	
Pro	Ala	Tyr	Ile	Thr	Gln	Cys	Pro	Ile	Gln	Pro	Gly	Gln	Ser	Tyr	Val
			100					105					110		
Tyr	Asn	Phe	Thr	Ile	Thr	Gly	Gln	Arg	Gly	Thr	Leu	Leu	Trp	His	Ala
		115					120					125			
His	Ile	Leu	Trp	Leu	Arg	Ala	Thr	Val	His	Gly	Ala	Leu	Val	Val	Leu
	130					135					140				
Pro	Lys	Arg	Gly	Ile	Pro	Tyr	Pro	Phe	Pro	Ala	Pro	His	Lys	Glu	Val
	145					150					155				160

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Val	Val	Val	Leu	Ala	Glu	Trp	Trp	Lys	Ser	Asp	Thr	Glu	Ala	Val	Ile
			165						170					175	
Asn	Glu	Ala	Leu	Lys	Ser	Gly	Leu	Ala	Pro	Asn	Val	Ser	Asp	Ala	His
			180					185					190		
Thr	Ile	Asn	Gly	His	Pro	Gly	Ala	Val	Ser	Ala	Cys	Ser	Ser	Gln	Gly
		195					200					205			
Gly	Phe	Thr	Leu	Pro	Val	Lys	Ser	Gly	Glu	Thr	Tyr	Met	Leu	Arg	Leu
	210					215					220				
Ile	Asn	Ala	Ala	Leu	Asn	Glu	Glu	Leu	Phe	Phe	Lys	Ile	Ala	Gly	His
225					230					235				240	
Lys	Leu	Thr	Val	Val	Glu	Val	Asp	Ala	Thr	Tyr	Val	Lys	Pro	Phe	Lys
			245						250					255	
Thr	Asp	Thr	Val	Leu	Ile	Ala	Pro	Gly	Gln	Thr	Thr	Asn	Val	Leu	Val
			260					265					270		
Thr	Thr	Asn	Lys	Asn	Thr	Gly	Lys	Tyr	Leu	Val	Ala	Ala	Ser	Pro	Phe
		275					280					285			
Met	Asp	Ala	Pro	Ile	Ala	Val	Asp	Asn	Met	Thr	Ala	Thr	Ala	Thr	Leu
	290					295					300				
Gln	Tyr	Ser	Gly	Ala	Leu	Ala	Asn	Ser	Pro	Thr	Thr	Leu	Thr	Thr	Pro
305					310					315					320
Pro	Pro	Lys	Asn	Ala	Thr	Ala	Val	Ala	Asn	Gln	Phe	Thr	Asn	Ser	Leu
			325						330					335	
Arg	Ser	Leu	Asn	Ser	Arg	Arg	Phe	Pro	Ala	Lys	Val	Pro	Leu	Asn	Val
		340					345						350		
Asp	His	Asn	Leu	Phe	Phe	Thr	Val	Gly	Leu	Gly	Val	Asn	Pro	Cys	Pro
		355					360					365			
Ser	Cys	Lys	Ala	Gly	Asn	Gly	Ser	Arg	Val	Val	Ala	Ser	Ile	Asn	Asn
	370				375						380				
Val	Thr	Phe	Val	Met	Pro	Thr	Thr	Ala	Leu	Leu	Gln	Ala	His	Phe	Leu
385					390					395					400
Asn	Ile	Ser	Gly	Val	Phe	Thr	Thr	Asp	Phe	Pro	Ala	Lys	Pro	Pro	His
			405						410					415	
Val	Phe	Asn	Tyr	Thr	Gly	Thr	Pro	Pro	Thr	Asn	Leu	Gln	Thr	Lys	Ser
		420					425						430		
Gly	Thr	Lys	Val	Tyr	Arg	Leu	Ser	Tyr	Asn	Ser	Thr	Val	Gln	Leu	Val
		435					440					445			
Met	Gln	Asp	Thr	Gly	Ile	Ile	Ser	Pro	Glu	Asn	His	Pro	Ile	His	Leu
	450					455					460				
His	Gly	Phe	Asn	Phe	Phe	Ala	Val	Gly	Arg	Gly	Val	Gly	Asn	Tyr	Asn
465					470					475					480
Pro	Lys	Thr	Asp	Thr	Lys	Lys	Phe	Asn	Leu	Val	Asp	Pro	Val	Glu	Arg
			485						490					495	
Asn	Thr	Ile	Gly	Val	Pro	Ser	Gly	Gly	Trp	Val	Ala	Ile	Arg	Phe	Arg
		500					505						510		
Ala	Asp	Asn	Pro	Gly	Val	Trp	Phe	Met	His	Cys	His	Leu	Glu	Val	His
		515					520					525			
Thr	Thr	Trp	Gly	Leu	Lys	Met	Ala	Phe	Leu	Val	Asp	Asn	Gly	Lys	Gly
	530					535						540			
Pro	Lys	Glu	Ser	Leu	Leu	Pro	Pro	Pro	Ser	Asp	Leu	Pro	Lys	Cys	
545					550					555					



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<210> SEQ ID NO 73
<211> LENGTH: 557
<212> TYPE: PRT
<213> ORGANISM: Populus sp.

<400> SEQUENCE: 73

Met Glu Tyr Ser Trp Phe Arg Phe Met Leu Leu Ala Val Cys Leu Phe
1      5      10      15
Pro Ala Val Val Glu Cys Arg Ile Arg His Tyr Lys Phe Asn Val Val
20     25     30
Met Lys Asn Thr Thr Arg Leu Cys Ser Ser Lys Pro Ile Val Thr Val
35     40     45
Asn Gly Leu Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr
50     55     60
Val Leu Val Lys Val Val Asn Arg Val Lys Tyr Asn Leu Ser Ile His
65     70     75
Trp His Gly Ile Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala
85     90     95
Tyr Ile Thr Gln Cys Pro Ile Gln Pro Gly Gln Ser Tyr Val Tyr Asn
100    105   110
Phe Thr Ile Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Ile
115    120   125
Leu Trp Leu Arg Ala Thr Val His Gly Ala Leu Val Leu Pro Lys
130    135   140
Leu Gly Val Pro Tyr Pro Phe Pro Ala Pro His Lys Glu Val Val Val
145    150   155
Val Leu Ala Glu Trp Trp Lys Ser Asp Thr Glu Ala Val Ile Asn Glu
165    170   175
Ala Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile
180    185   190
Asn Gly His Pro Gly Ala Val Ser Thr Cys Ser Ser Gln Gly Gly Phe
195    200   205
Thr Leu Pro Val Gln Ser Gly Lys Thr Tyr Met Leu Arg Leu Ile Asn
210    215   220
Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Lys Leu
225    230   235
Thr Val Val Glu Val Asp Ala Thr Tyr Val Lys Pro Phe Lys Thr Asp
245    250   255
Thr Val Leu Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Val Thr Thr
260    265   270
Asn Lys Asn Thr Gly Lys Tyr Leu Val Ala Ala Ser Pro Phe Met Asp
275    280   285
Ala Pro Ile Ala Val Asp Asn Met Thr Ala Thr Ala Thr Leu His Tyr
290    295   300
Ser Gly Ala Leu Ser Asn Ser Pro Thr Thr Leu Thr Ile Pro Pro Pro
305    310   315
Lys Asn Ala Thr Ala Ile Ala Asn Gln Phe Thr Asn Ser Leu Arg Ser
325    330   335
Leu Asn Ser Lys Thr Phe Pro Ala Lys Val Pro Leu Thr Val Asp His
340    345   350
Ser Leu Phe Phe Thr Val Gly Leu Gly Ile Asn Pro Cys Pro Thr Cys
355    360   365

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Lys Ala Gly Asn Gly Ser Arg Val Val Ala Ser Ile Asn Asn Val Thr  
 370 375 380

Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Phe Phe Asn Ile  
 385 390 395 400

Ser Gly Val Phe Thr Thr Asp Phe Pro Ala Lys Pro Pro His Val Phe  
 405 410 415

Asn Tyr Thr Gly Thr Pro Pro Thr Asn Leu Gln Thr Thr Ser Gly Thr  
 420 425 430

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

Asp Thr Gly Ile Ile Ser Pro Glu Asn His Pro Ile His Leu His Gly  
 450 455 460

Phe Asn Phe Phe Ala Val Gly Arg Gly Val Gly Asn Tyr Asn Pro Lys  
 465 470 475 480

Thr Asp Pro Lys Lys Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr  
 485 490 495

Ile Gly Val Pro Ser Gly Gly Trp Val Ala Ile Arg Phe Arg Ala Asp  
 500 505 510

Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Thr  
 515 520 525

Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys Gly Pro Asn  
 530 535 540

Glu Ser Leu Leu Pro Pro Pro Ser Asp Leu Pro Lys Cys  
 545 550 555

&lt;210&gt; SEQ ID NO 74

&lt;211&gt; LENGTH: 564

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Populus sp.

&lt;400&gt; SEQUENCE: 74

Met Ile Arg Lys Ser Ala Lys Met Glu Tyr Ser Trp Phe Arg Phe Met  
 1 5 10 15

Leu Leu Ala Val Ser Leu Phe Pro Ala Leu Val Glu Cys Arg Val Arg  
 20 25 30

His Tyr Lys Phe Asn Val Val Met Lys Asn Thr Thr Arg Leu Cys Ser  
 35 40 45

Ser Lys Pro Val Val Thr Val Asn Gly Arg Phe Pro Gly Pro Thr Leu  
 50 55 60

Tyr Ala Arg Glu Asp Asp Thr Val Leu Val Lys Val Val Asn His Val  
 65 70 75 80

Lys Tyr Asn Val Ser Ile His Trp His Gly Ile Arg Gln Leu Arg Thr  
 85 90 95

Gly Trp Ala Asp Gly Pro Ala Tyr Ile Thr Gln Cys Pro Ile Gln Thr  
 100 105 110

Gly Gln Ser Tyr Val Tyr Asn Phe Thr Ile Thr Gly Gln Arg Gly Thr  
 115 120 125

Leu Leu Trp His Ala His Ile Leu Trp Leu Arg Ala Thr Val His Gly  
 130 135 140

Ala Ile Val Val Leu Pro Lys Arg Gly Val Pro Tyr Pro Phe Pro Ala  
 145 150 155 160

Pro His Lys Glu Phe Val Val Val Leu Ala Glu Trp Trp Lys Ser Asp  
 165 170 175

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Thr Glu Ala Val Ile Asn Glu Ala Leu Lys Ser Gly Leu Ala Pro Asn  
 180 185 190  
 Val Ser Asp Ala His Thr Ile Asn Gly His Pro Gly Ala Val Ser Ala  
 195 200 205  
 Cys Pro Ser Gln Gly Gly Phe Thr Leu Pro Val Glu Ser Gly Lys Thr  
 210 215 220  
 Tyr Met Leu Arg Leu Ile Asn Ala Ala Leu Asn Glu Glu Leu Phe Phe  
 225 230 235 240  
 Lys Ile Ala Gly His Lys Leu Thr Leu Val Glu Val Asp Ala Thr Tyr  
 245 250 255  
 Val Lys Pro Phe Lys Thr Asp Thr Val Leu Ile Ala Pro Gly Gln Thr  
 260 265 270  
 Thr Asn Val Leu Val Thr Thr Asn Lys Asn Thr Gly Lys Tyr Leu Val  
 275 280 285  
 Ala Ala Ser Pro Phe Met Asp Ala Pro Ile Ala Val Asp Asn Met Thr  
 290 295 300  
 Ala Thr Ala Thr Leu His Tyr Ser Gly Ala Leu Ser Gly Thr Pro Thr  
 305 310 315 320  
 Thr Leu Thr Ile Pro Pro Pro Lys Asn Ala Thr Ala Val Ala Asn Gln  
 325 330 335  
 Phe Thr Asn Ser Leu Arg Ser Leu Asn Ser Lys Arg Phe Pro Ala Lys  
 340 345 350  
 Val Pro Leu Thr Val Asp His Asn Leu Phe Phe Thr Val Gly Leu Gly  
 355 360 365  
 Ile Asn Pro Cys Pro Thr Cys Lys Ala Gly Asn Gly Ser Arg Val Val  
 370 375 380  
 Ala Ser Ile Asn Asn Val Thr Phe Val Met Pro Thr Thr Ala Leu Leu  
 385 390 395 400  
 Gln Ala His Phe Phe Asn Ile Ser Gly Val Phe Thr Thr Asp Phe Pro  
 405 410 415  
 Ser Lys Pro Pro His Val Phe Asn Tyr Thr Gly Thr Pro Pro Thr Asn  
 420 425 430  
 Leu Gln Thr Thr Ser Gly Thr Lys Val Tyr Arg Leu Arg Tyr Asn Ser  
 435 440 445  
 Thr Val Glu Leu Val Met Gln Asp Thr Gly Ile Ile Ser Pro Glu Asn  
 450 455 460  
 His Pro Ile His Leu His Gly Phe Asn Phe Phe Gly Val Gly Arg Gly  
 465 470 475 480  
 Val Gly Asn Tyr Asn Pro Lys Thr Asp Pro Lys Lys Phe Asn Leu Val  
 485 490 495  
 Asp Pro Val Glu Arg Asn Thr Ile Gly Val Pro Ser Gly Gly Trp Val  
 500 505 510  
 Ala Ile Arg Phe Arg Val Asp Asn Pro Gly Val Trp Phe Met His Cys  
 515 520 525  
 His Leu Glu Val His Thr Thr Trp Gly Leu Lys Met Ala Phe Leu Val  
 530 535 540  
 Asp Asn Gly Lys Gly Pro Asn Glu Ser Leu Leu Pro Pro Pro Ser Asp  
 545 550 555 560  
 Leu Pro Lys Cys

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<210> SEQ ID NO 75
<211> LENGTH: 107
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 75

tgaatgaaca tcattgagtg cagcgttgat gtaatttcgt tttgttttc attggtgaat      60
ggattaaag aatttatacc agcgttgcgc tcaattatgt ttttcta                      107

<210> SEQ ID NO 76
<211> LENGTH: 109
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 76

tgaatgaaca tcattgagtg catcgttgat gtaattttac ttattttatt ccattgttga      60
attaattaa gaagtatata tcagcgttgc attcaattat gtttttcta                    109

<210> SEQ ID NO 77
<211> LENGTH: 120
<212> TYPE: DNA
<213> ORGANISM: Populus sp.

<400> SEQUENCE: 77

tggagaacca tcattgagtg cagcgttgat gaaatcctcc atttgtgct attaaactgt      60
taccaacctt ttatggggca tggcatcatt tcaccagcgc tgcattcaat catgtttttc    120

<210> SEQ ID NO 78
<211> LENGTH: 124
<212> TYPE: DNA
<213> ORGANISM: Brachypodium distachyon

<400> SEQUENCE: 78

gaagaggcgc aaaggcatca ttgagtgcag cgttgatgaa caggggcccag ggcaccggcg      60
gccggtccgg ttcggttca cggcgctgca cacagtgacg cccttgcaat ctctggcccc      120
attc                                                                    124

<210> SEQ ID NO 79
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Brachypodium distachyon

<400> SEQUENCE: 79

agagggcaag gctcattggt gcagcgttgt gaacgggccc accggg                      45

<210> SEQ ID NO 80
<211> LENGTH: 13118
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Integrative vector

<400> SEQUENCE: 80

tttggatgg cttcattcag ctccggttcc caacgatcaa ggcgagttac atgatcccc      60
atgttgtgca aaaaagcggg tagctccttc ggtcctccga tcgttgcag aagtaagtgt      120
gccgcagtgt tatcactcat ggttatggca gcactgcata attctcttac tgtcatgcca      180
tccgtaagat gttttctgt gactgggtgag tactcaacca agtcattctg agaatagtgt      240

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atgcgcgac cgagttgctc ttgcccggcg tcaacacggg ataataccgc gccacatagc 300  
agaactttaa aagtgtcat cattggaaaa cgttcttcgg ggcgaaaact ctcaaggatc 360  
ttaccgctgt tgagatccag ttcgatgtaa cccactcgtg cacccaactg atcttcagca 420  
tcttttactt tcaccagcgt ttctgggtga gcaaaaacag gaaggcaaaa tgccgcaaaa 480  
aagggaataa gggcgacacg gaaatgttga atactcatac tcttcctttt tcaatattat 540  
tgaagcattt atcagggtta ttgtctcatg agcggataca tatttgaatg tatttagaaa 600  
aataaaciaa taggggttcc gcgcacattt ccccgaaaag tgccacctga cgtctaagaa 660  
accattatta tcatgacatt aacctataaa aataggcgtg tcacgaggcc ctttcgtctt 720  
caagaattgg tcgacgatct tgctcgttc ggatattttc gtggagtcc cgccacagac 780  
ccggattgaa ggcgagatcc agcaactcgc gccagatcat cctgtgacgg aactttggcg 840  
cgtgatgact ggccaggacg tcggccgaaa gagcgacaag cagatcacgc ttttcgacag 900  
cgtcggattt gcgatcgagg atttttcggc gctcgcgtac gtcgcgacc gcgttgaggg 960  
atcaagccac agcagcccac tcgaccttct agccgacca gacgagcaa gggatctttt 1020  
tggaatgctg ctccgtcgtc aggctttccg acgtttgggt ggttgaacag aagtcattat 1080  
cgcacggaat gccaaagcact cccgagggga accctgtggt tggcatgcac atacaaatgg 1140  
acgaacggat aaaccttttc acgcccctttt aaatatccga ttattctaata aaacgctctt 1200  
ttctcttagg tttaccgcc aatatatcct gtcaaacact gatagttttg gagctccaac 1260  
tttgtataga aaagttgaac gagaaacgta aatgatata aatatcaata tattaaatta 1320  
gattttgcat aaaaaacaga ctacataata ctgtaaaaca caacatatcc agtcactatg 1380  
gtcgcactgc agactggctg tgtataaggg agcctgacat ttatattccc cagaacatca 1440  
ggttaatggc gtttttgatg tcattttcgc ggtggctgag atcagccact tcttccccga 1500  
taacggagac cggcacactg gccaggggga tcaccatccg tcgccgggc gtgtcaataa 1560  
tactactctg tacatccaca aacagacgat aacggctctc tcttttatag gtgtaaacct 1620  
taaaactgcat ttcaccagcc cctgttctcg tcggcaaaag agccgttcat tcaataaac 1680  
cggcgacact cagccatccc ttcctgattt tccgctttcc agcgttcggc acgcagacga 1740  
cgggcttcat tctgcatggt tgtgcttacc gaaccggaga tattgacatc atatatgctt 1800  
tgagcaactg atagctgtcg ctgtcaactg tcaactgtaat acgctgcttc atagcatacc 1860  
tctttttgac atacttcggg tatacatatc agtatatatt cttataccgc aaaaatcagc 1920  
gcgcaaaata gcatactgtt atctggcttt tagtaagccg gatcctctag attacgcccc 1980  
gcctgccact catcgcagta ctggtgtaat tcattaagca ttctgccgac atggaagcca 2040  
tcacaaacgg catgatgaac ctgaatcgcc agcggcatca gcacctgtc gcettgctga 2100  
taatatttgc ccatggtgaa aacgggggcg aagaagttgt ccatattggc cacgtttaa 2160  
tcaaaactgg tgaactcac ccagggatg gctgagacga aaaacatatt ctcaataaac 2220  
cctttagga aatagccag gttttcaccg taacacgcca catcttgca atatatgtgt 2280  
agaaactgcc ggaatcgtc gtggtattca ctccagagcg atgaaaacgt ttcagtttgc 2340  
tcatgaaaa cgggtgaaca aggtgaaca ctatccata tcaccagctc accgtctttc 2400  
attgccatc ggaattccgg atgagcattc atcaggcggg caagaatgtg aataaaggcc 2460  
ggataaaact tgtgcttatt tttctttacg gtctttaaaa aggccgtaat atccagctga 2520

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acggctcggg tataggtaca ttgagcaact gactgaaatg cctcaaaatg ttctttacga 2580  
tgccattggg atatatcaac ggtggtatat ccagtgattt ttttctccat tttagcttcc 2640  
ttagctcctg aaaatctcga cggatcctaa ctcaaaatcc acacattata cgagccggaa 2700  
gcataaagtg taaagcctgg ggtgcctaat gcggccgcca tagtgactgg atatgttggtg 2760  
ttttacagta ttatgtagtc tgttttttat gcaaaatcta atttaataata ttgatattta 2820  
tatcatttta cgtttctcgt tcaactttat tatacatagt tgataattca ctggccgctc 2880  
ttttacaagc ttgtcggtag cctgaaatca ccagtccttc tctacaaatc tatctctctc 2940  
tattttctcc ataaataatg tgtgagtagt ttcccgataa gggaaattag ggttcttata 3000  
gggtttcgtc catgtgttga gcataataa aacccttagt atgtattgt atttgaataa 3060  
tactctatc aataaaatct ctaattccta aaacccaaat ccagtactaa aatccagatc 3120  
gatgagctca aaacgtatgc cgggcccgtc tagaactaga gaaggtaatt atccaagatg 3180  
tagcatcaag aatccaatgt ttacgggaaa aactatggaa gtattatgtg agctcagcaa 3240  
gaagcagatc aatatcgggc acatatgcaa cctatgttca aaaatgaaga atgtacagat 3300  
acaagatcct atactgccag aatacgaaga agaatacgtg gaaattgaaa aagaagaacc 3360  
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1. A process for reducing the lignin content of a plant and increasing the cellulolysis of the walls of said plant, wherein the expression and/or the activity in said plant:

a) of a laccase of which the polypeptide sequence has at least 60% identity or at least 75% similarity with the sequence SEQ ID No. 2, and comprises, from its N-terminal end to its C-terminal end, at least one of the four consensus peptide domains i) to iv), respectively, which follow:

- i) the consensus peptide domain of sequence SEQ ID No. 12 or 38,
- ii) the consensus peptide domain of sequence SEQ ID No. 13 or 39,
- iii) the consensus peptide domain of sequence SEQ ID No. 14 or 40,
- iv) the consensus peptide domain of sequence SEQ ID No. 15 or 41, and

b) of a laccase of which the polypeptide sequence has at least 65% identity with the sequence SEQ ID No. 4, is totally or partially inhibited.

2. The process as claimed in claim 1, wherein the total or partial inhibition of the expression and/or the activity in said plant of said laccases is obtained by mutagenesis of the gene encoding these laccases, or else by inhibition or modification of the transcription or of the translation of these laccases.

3. The process as claimed in claim 1, wherein said laccase as defined in paragraph a) is:

- in corn (*Zea mays*), chosen from the peptide sequences SEQ ID Nos. 5, 6 and 42 to 47,
- in sugar cane (*Saccharum officinarum*), the sequence SEQ ID No. 7,
- in sorghum (*Sorghum bicolor*), chosen from the peptide sequences SEQ ID Nos. 8 to 11,
- in *Brachypodium*, chosen from the peptide sequences SEQ ID Nos. 48 to 55,

in rice, chosen from the peptide sequences SEQ ID Nos. 56 to 62, and

in poplar, chosen from the peptide sequences SEQ ID Nos. 63 to 68.

4. The process as claimed in claim 1, wherein said laccase as defined in paragraph b) is:

in *Brachypodium*, the peptide sequence SEQ ID No. 69, in rice, the peptide sequence SEQ ID No. 70, and in poplar, chosen from the peptide sequences SEQ ID Nos. 71 to 74.

5. A recombinant DNA construct, comprising one or more polynucleotides capable of inhibiting the expression of a laccase of which the polypeptide sequence has at least 60% identity or at least 75% similarity with the sequence SEQ ID No. 2, and comprises, from its N-terminal end to its C-terminal end, at least one of the 4 consensus peptide domains i) to iv), respectively, which follow:

- i) the consensus peptide domain of sequence SEQ ID No. 12 or 38,
- ii) the consensus peptide domain of sequence SEQ ID No. 13 or 39,
- iii) the consensus peptide domain of sequence SEQ ID No. 14 or 40,
- iv) the consensus peptide domain of sequence SEQ ID No. 15 or 41, and

of a laccase of which the polypeptide sequence has at least 65% identity with the sequence SEQ ID No. 4.

6. The DNA construct as claimed in claim 5, wherein said polynucleotide encodes an antisense RNA, an interfering RNA, a micro-RNA or a ribozyme targeting the genes encoding said laccases.

7. An expression cassette, comprising one or more DNA constructs as defined in claim 5, under the transcriptional control of a suitable promoter.

8. A recombinant vector, comprising one or more DNA constructs as defined in claim 5.

9. A plant cell, comprising an expression cassette as defined in claim 7.

10. A plant which can be obtained by means of the method as claimed in claim 1, with the exception of the *Arabidopsis thaliana* lines SALK\_016748 and SALK\_051892.

11. The use of a plant which can be obtained by means of the method as claimed in claim 1, or of plant material obtained from said plant, for producing fodder plants, biofuel or paper pulp.

12. The process as claimed in claim 1 wherein said laccase as defined in paragraph a) is:

in corn (*Zea mays*), chosen from the peptide sequences SEQ ID Nos. 5, 6, 42, 43, 44 and 45,

in sugar cane (*Saccharum officinarum*), the sequence SEQ ID No. 7,

in sorghum (*Sorghum bicolor*), chosen from the peptide sequences SEQ ID Nos. 8 to 11,

in *Brachypodium*, chosen from the peptide sequences SEQ ID Nos. 50 and 51,

in rice, chosen from the peptide sequence SEQ ID No. 58, and

in poplar, chosen from the peptide sequences SEQ ID Nos. 63, 67 and 68.

13. A recombinant vector comprising an expression cassette as defined in claim 7.

14. A plant cell, comprising a recombinant vector as defined in claim 8.

\* \* \* \* \*