



Production of plants with reduced lignin content.

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Jouanin et al.(10) **Pub. No.: US 2012/0192312 A1**(43) **Pub. Date: Jul. 26, 2012**(54) **PRODUCTION OF PLANTS WITH REDUCED
LIGNIN CONTENT**(75) Inventors: **Lise Jouanin**, Noisy Le Roi (FR);
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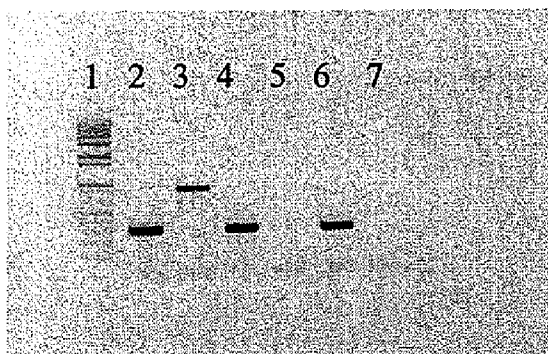
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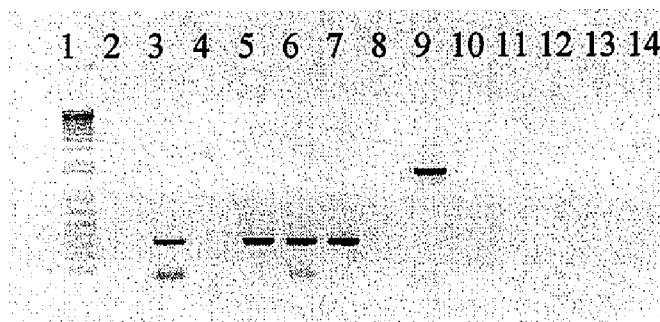
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800/298; 162/100(57) **ABSTRACT**

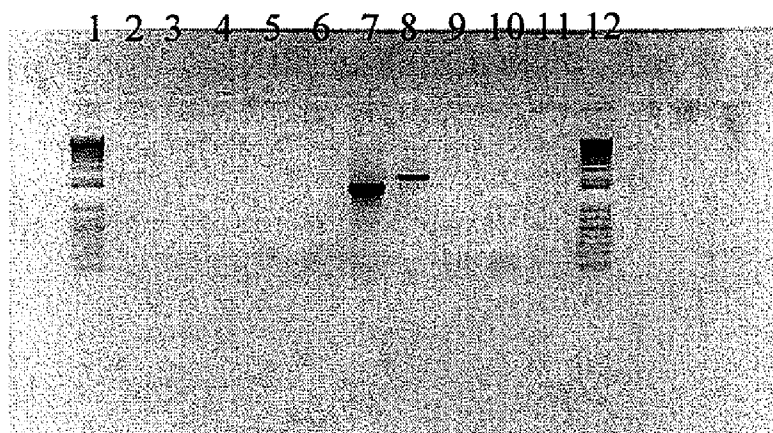
The invention relates to the production of plants having a reduced lignin content and in which the cellulose hydrolysis of the walls is increased, via the total or partial inhibition of the expression and/or the activity of two laccases in said plant.



A



B



C

Figure 1

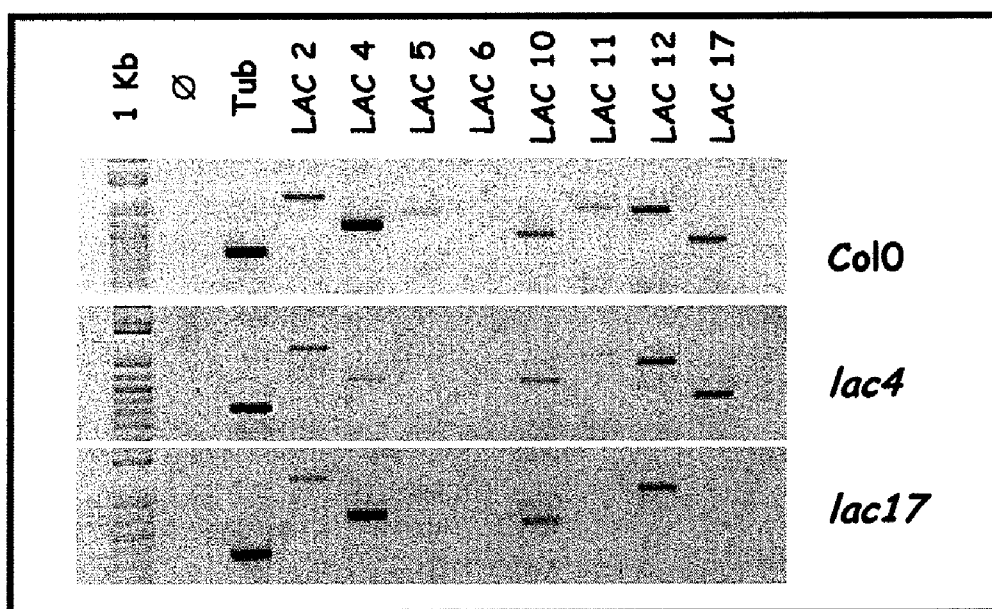


Figure 2

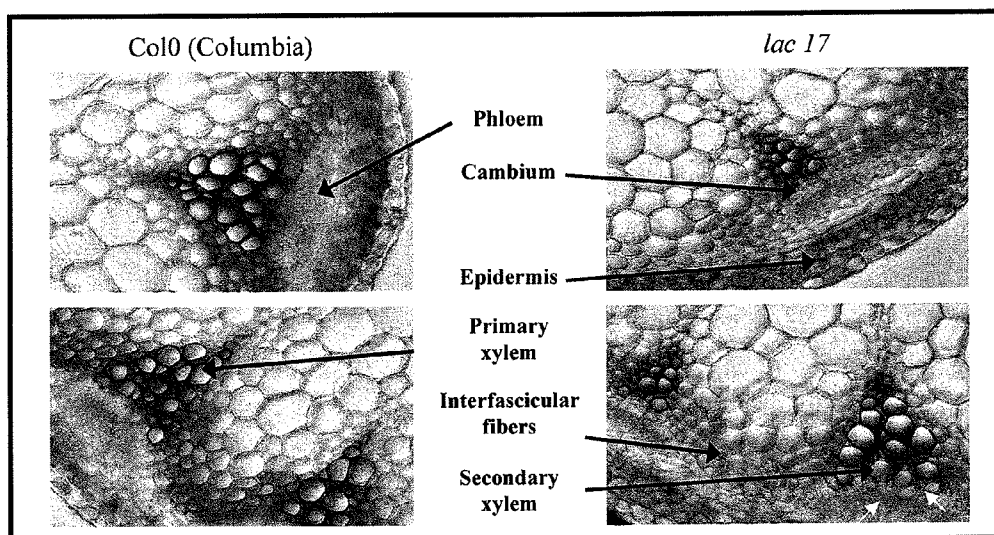


Figure 3

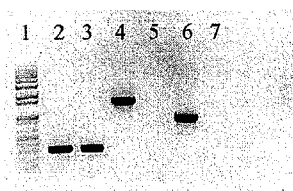


Figure 4

	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	% identity with SEQ ID No. 2	% similarity with SEQ ID No. 2
<i>A. thaliana</i>										
ATLAC17	X	-	X	-	X	-	X		100	100
SEQ ID No. 2										
<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>										
gil113548170	-	X	X	-	-	X	X	-	69	83
gil113534304	X	-	X	-	-	X	-	X	70	82
gil113579298	X	-	X	-	X	-	X	-	69	81
gil113579297	X	-	X	-	X	-	-	X	67	80
gil113594303	-	X	-	X	-	X	X	-	72	84
gil113579295	-	X	X	-	-	X	-	X		
gil255673866	-	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 β -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 β -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 β -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 β -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), caffeoyl 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 Bradi1g74320 (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 of 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 (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 MgCl₂, 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')	T _m (° 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 _m (° 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 ultra-violet 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 β -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 μmol 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 β -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 over-express 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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aac gca tgc cct act tgc aag gcc gga aac gga agc cgt gtc gtg gct	1217
Asn Ala Cys Pro Thr Cys Lys Ala Gly Asn Gly Ser Arg Val Val Ala	
365 370 375	
agc atc aac aat gta acc ttc att atg cct aaa acc gct ttg ctc ccg	1265
Ser Ile Asn Asn Val Thr Phe Ile Met Pro Lys Thr Ala Leu Leu Pro	
380 385 390 395	
gct cat tac ttc aac aca agt gga gtt ttc acg aca gac ttt ccc aag	1313
Ala His Tyr Phe Asn Thr Ser Gly Val Phe Thr Thr Asp Phe Pro Lys	
400 405 410	

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aat cca cca cac gtt ttc aac tac agc gga gga tca gtc acg aac atg	1361
Asn Pro Pro His Val Phe Asn Tyr Ser Gly Gly Ser Val Thr Asn Met	
415 420 425	
gcc aca gaa acc ggc aca agg ctc tac aag cta ccg tat aac gcc act	1409
Ala Thr Glu Thr Gly Thr Arg Leu Tyr Lys Leu Pro Tyr Asn Ala Thr	
430 435 440	
gtt cag ctt gtc ctt caa gat acc ggc gtc ata gcg cca gag aac cat	1457
Val Gln Leu Val Leu Gln Asp Thr Gly Val Ile Ala Pro Glu Asn His	
445 450 455	
cca gta cat ctt cac ggt ttt aac ttt ttt gaa gtc ggt cgt gga tta	1505
Pro Val His Leu His Gly Phe Asn Phe Phe Glu Val Gly Arg Gly Leu	
460 465 470 475	
ggt aac ttc aac tcc acg aaa gac cca aaa aac ttc aat ttg gta gat	1553
Gly Asn Phe Asn Ser Thr Lys Asp Pro Lys Asn Phe Asn Leu Val Asp	
480 485 490	
ccg gtt gag agg aac aca atc gga gtt cca tcc ggt gga tgg gtc gtc	1601
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 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 tcggtttttt ttgctcatgt caaaagtgtg aataatggag	1917
aaaaaagagc attgtattat aataatttgt ttccattata ttcaaattcc 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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515					520					525					
Thr	Trp	Gly	Leu	Lys	Met	Ala	Phe	Leu	Val	Glu	Asn	Gly	Lys	Gly	Pro
530					535					540					
Asn	Gln	Ser	Ile	Leu	Pro	Pro	Pro	Lys	Asp	Leu	Pro	Lys	Cys		
545					550					555					
<210> SEQ ID NO 5															
<211> LENGTH: 587															
<212> TYPE: PRT															
<213> ORGANISM: Zea mays															
<400> SEQUENCE: 5															
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		
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

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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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<210> SEQ ID NO 6

<211> LENGTH: 582

<212> TYPE: PRT

<213> ORGANISM: Zea mays

<400> 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	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

<210> SEQ ID NO 7

<211> LENGTH: 573

<212> TYPE: PRT

<213> ORGANISM: *Saccharum officinarum*

<400> 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

<210> SEQ ID NO 8

<211> LENGTH: 549

<212> TYPE: PRT

<213> ORGANISM: Sorghum bicolor

<400> 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

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

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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

-continued

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	Thr
	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	Val
			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	Thr
			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	Gly
	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						

<210> SEQ ID NO 10

<211> LENGTH: 575

<212> TYPE: PRT

<213> ORGANISM: Sorghum bicolor

<400> 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		

-continued

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

<210> SEQ ID NO 11
 <211> LENGTH: 579
 <212> TYPE: PRT
 <213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 11

Met	Ala	Ile	Ser	Ser	Ala	Leu	Pro	Cys	Ser	Leu	Leu	Met	Ala	Ala	Leu
1				5					10					15	
Met	Leu	Leu	Ala	Ser	Ala	Val	Glu	Val	Gln	Gly	Ile	Thr	Arg	His	Tyr
			20					25					30		
Asp	Phe	Asn	Val	Thr	Met	Ala	Asn	Val	Thr	Arg	Leu	Cys	Ala	Ser	Lys
	35						40					45			
Ser	Ile	Ile	Thr	Val	Asn	Gly	Gln	Phe	Pro	Gly	Pro	Lys	Ile	Val	Ala
	50					55					60				
Arg	Glu	Gly	Asp	Arg	Leu	Val	Ile	Arg	Val	Thr	Asn	His	Ala	Gln	His
65					70				75					80	
Asn	Ile	Ser	Leu	His	Trp	His	Gly	Ile	Arg	Gln	Leu	Arg	Thr	Gly	Trp
			85					90						95	
Ala	Asp	Gly	Pro	Ala	Tyr	Ile	Thr	Gln	Cys	Pro	Ile	Gln	Thr	Gly	Gln
			100					105					110		
Ser	Tyr	Val	Tyr	Asn	Tyr	Thr	Ile	Val	Gly	Gln	Arg	Gly	Thr	Leu	Trp
	115						120					125			
Trp	His	Ala	His	Ile	Ser	Trp	Leu	Arg	Ala	Thr	Val	Tyr	Gly	Pro	Leu
	130					135					140				
Val	Val	Leu	Pro	Lys	Leu	Gly	Val	Pro	Tyr	Pro	Phe	Pro	Ala	Pro	Tyr
145					150					155					160
Lys	Glu	Val	Pro	Val	Ile	Phe	Gly	Glu	Trp	Trp	Leu	Ala	Asp	Thr	Glu
				165					170					175	
Val	Val	Ile	Gln	Gln	Ala	Leu	Gln	Leu	Gly	Ala	Gly	Pro	Asn	Val	Ser
			180					185					190		
Asp	Ala	His	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	Lys	Pro	Gly	Lys	Thr	Tyr	Met
	210					215						220			

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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

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<210> SEQ ID NO 12

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Consensus sequence

<220> FEATURE:

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

<400> SEQUENCE: 12

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 caaatcgga 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

tggttaacttt 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

gttagaaaact 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

ttagggcctt 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

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<400> SEQUENCE: 35

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ccaagaacgc catagcaa

```

18

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

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<400> SEQUENCE: 36

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ttctcttggtg ttctctctct t

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21

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

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<400> SEQUENCE: 37

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gaacttcttt gtgaggttta g

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21

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<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"

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<400> SEQUENCE: 38

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His Trp His Gly Ile Arg Gln Leu
1          5

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<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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-continued

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

<400> SEQUENCE: 39

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

-continued

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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 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

-continued

<400> 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
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
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
Arg Gly Glu Gly	Tyr Pro Phe Pro	Arg Pro Tyr Lys	Glu Val Pro Ile
	165	170	175

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	
						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												

-continued

580	585
<210> SEQ ID NO 47	
<211> LENGTH: 582	
<212> TYPE: PRT	
<213> ORGANISM: Zea mays	
<400> SEQUENCE: 47	
Met Ala Val Gly Arg Arg Leu Ser Pro Ala Cys Leu Leu Leu Leu Arg	
1 5 10 15	
Leu Thr Val Ala Leu Val Val Leu Thr Ala Leu Pro Glu Leu Ala Ala	
20 25 30	
Ala Arg Thr Arg Arg Tyr Thr Phe Asn Val Thr Met Ala Thr Val Thr	
35 40 45	
Arg Leu Cys Val Thr Lys Ser Val Pro Thr Val Asn Gly Gln Phe Pro	
50 55 60	
Gly Pro Arg Leu Val Val Arg Glu Gly Asp Arg Leu Val Val Gln Val	
65 70 75 80	
His Asn Asn Ile Asn Ser Asn Val Thr Phe His Trp His Gly Val Arg	
85 90 95	
Gln Leu Arg Ser Gly Trp Ala Asp Gly Pro Ser Tyr Ile Thr Gln Cys	
100 105 110	
Pro Ile Arg Pro Gly Gln Ser Tyr Ala Tyr Asp Phe Arg Ile Val Gly	
115 120 125	
Gln Arg Gly Thr Leu Trp Trp His Ala His Phe Ser Trp Leu Arg Ala	
130 135 140	
Thr Leu Tyr Gly Pro Leu Val Ile Leu Pro Pro Arg Gly Val Pro Tyr	
145 150 155 160	
Pro Phe Pro Lys Pro Asp Arg Gln Val Thr Leu Met Leu Gly Glu Trp	
165 170 175	
Phe Asn Ala Asp Pro Glu Ala Val Ile Lys Gln Ala Leu Gln Thr Gly	
180 185 190	
Gly Ala Pro Asn Val Ser Asp Ala Tyr Thr Phe Asn Gly Leu Pro Gly	
195 200 205	
Pro Thr Tyr Asn Cys Ser Ser Gly Asp Asp Thr Phe Arg Leu Arg Val	
210 215 220	
Arg Pro Gly Arg 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 Ala Ala Ala Thr Leu Val Ile	
260 265 270	
Ser Pro Gly Gln Thr Met Asp Val Leu Leu Thr Ala Ser Ala Ser Ala	
275 280 285	
Ala Pro Ser Ser Ala Phe Ala Ile Ala Val Ala Pro Tyr Thr Asn Thr	
290 295 300	
Val Gly Thr Phe Asp Asn Thr Thr Ala Val Ala Val Val Glu Tyr Gly	
305 310 315 320	
Pro His Gln Ser Ala Ala Ala Leu Arg Ser Leu Pro Leu Pro Ala Leu	
325 330 335	
Pro Arg Tyr Asn Asp Thr Ala Ala Val Ala Asn Phe Ser Ala Met Phe	
340 345 350	

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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													

<210> SEQ ID NO 48

<211> LENGTH: 572

<212> TYPE: PRT

<213> ORGANISM: Brachypodium distachyon

<400> 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			

-continued

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
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
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
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
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
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

<400> 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					320
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

<210> SEQ ID NO 51

<211> LENGTH: 581

<212> TYPE: PRT

<213> ORGANISM: Brachypodium distachyon

<400> 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
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
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
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
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

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<210> SEQ ID NO 52

<211> LENGTH: 576

<212> TYPE: PRT

<213> ORGANISM: Brachypodium distachyon

<400> SEQUENCE: 52

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

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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

 <210> SEQ ID NO 53
 <211> LENGTH: 580
 <212> TYPE: PRT
 <213> ORGANISM: *Brachypodium distachyon*

 <400> SEQUENCE: 53

 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	

<210> SEQ ID NO 54

<211> LENGTH: 577

<212> TYPE: PRT

<213> ORGANISM: Brachypodium distachyon

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<400> SEQUENCE: 54

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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			415	
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	

Cys

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

<400> SEQUENCE: 55

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 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	
			530		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

<210> SEQ ID NO 56

<211> LENGTH: 578

<212> TYPE: PRT

<213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 56

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Met Gly Ala Arg Cys Leu Ala 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 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				

<210> SEQ ID NO 59

<211> LENGTH: 549

<212> TYPE: PRT

<213> ORGANISM: Oryza sativa

<400> 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
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
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
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
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
Gly	Phe	Asn	Phe	Phe	Val	Val	Gly	Gln	Gly	Phe	Gly	Asn	Phe	Asp	Pro	485	490	495

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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 Met Tyr Ser Glu Pro His Arg Phe Pro Cys Asp Ser
    530                      535                      540

Thr Phe Ala Pro Thr
545

<210> SEQ ID NO 60
<211> LENGTH: 579
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 60

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

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

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

Lys Ser Met Val Thr Val Asn Gly Gln Cys Pro Gly Pro Glu Leu Val
    50                      55                      60

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

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

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

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

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

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

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

Glu Glu Val Val Asn Gln Ala Val Gln Thr Gly Gly Gly Pro Asn Val
   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 Lys Pro Gly Lys Thr Tyr
   210                      215                      220

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

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

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

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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 Pro Ser Asp Leu
 565 570 575
 Pro Lys Cys

<210> SEQ ID NO 61

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Oryza sativa

<400> 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					160
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 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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<210> SEQ ID NO 63
<211> LENGTH: 581
<212> TYPE: PRT
<213> ORGANISM: Populus sp.

<400> 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
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
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
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
			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

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<210> SEQ ID NO 66

<211> LENGTH: 581

<212> TYPE: PRT

<213> ORGANISM: Populus sp.

<400> SEQUENCE: 66

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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					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
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												

<210> SEQ ID NO 67

<211> LENGTH: 581

<212> TYPE: PRT

<213> ORGANISM: Populus sp.

<400> 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	P										

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420					425					430						
Ala	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	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	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																

<210> SEQ ID NO 68

<211> LENGTH: 581

<212> TYPE: PRT

<213> ORGANISM: Populus sp.

<400> SEQUENCE: 68

Met	Gly	Ala	Ser	Leu	Leu	Pro	Pro	Pro	Ala	Phe	Leu	Ala	Val	Phe	Leu
1				5					10					15	
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	Arg	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	Arg	Met	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				
His	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	Ser	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
							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
						535					540				
Cys	His	Leu	Glu</												

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

Cys

<210> SEQ ID NO 70
 <211> LENGTH: 564
 <212> TYPE: PRT
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 70

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

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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

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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             80

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 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            160

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            240

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            320

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

<210> SEQ ID NO 74

<211> LENGTH: 564

<212> TYPE: PRT

<213> ORGANISM: Populus sp.

<400> 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
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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.

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