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(54) Title: WOOD AND CELL WALL GENE MICROARRAY

(57) Abstract: The invention provides polynucleotide and polypeptide sequences isolated from *P. radiate* and *E. grandis* that are involved in wood and cell wall biosynthesis. Methods for using the sequences, along with constructs and transgenic plants, are provided also.

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WOOD AND CELL WALL GENE MICROARRAY

FIELD OF INVENTION

[0001] The present invention relates to polynucleotide sequences isolated from plants that encode wood and cell wall proteins. In particular, this invention relates to polynucleotide and polypeptide sequences isolated from *Eucalyptus* and *Pinus* and the use of such sequences for regulating cell wall biosynthesis and wood development.

BACKGROUND OF THE INVENTION

[0002] Plant cells, unlike animal cells, are surrounded by a relatively thin but mechanically strong cell wall. The plant cell wall is essential for many processes in plant physiology and plant development. Because of its tough outer coating, the plant cell wall provides a cellular exoskeleton that controls cell shape and allows a high turgor pressure.

[0003] Plant cell walls are composed of a complex mixture of polysaccharides and other polymers that are organized into a network linked by covalent and noncovalent bonds. Plant cell walls also contain structural proteins, enzymes, phenolic compounds, and other materials that can modify the wall's chemical and physical structure. While the appearance and architecture of cell walls varies greatly among different cell types, cell walls are commonly classified into two major types: primary walls and secondary walls.

[0004] Primary cell walls are formed by growing cells and are generally unspecialized. Primary cell walls have a similar structure and composition that is present throughout diverse cell types; generally, primary walls are composed of approximately 25% cellulose, 25% hemicellulose, 35% pectin, and about 10% structural protein. In the primary cell wall, cellulose microfibrils, which contribute to the wall's strength, are embedded in a matrix. The individual cellulose chains that comprise the microfibril are closely aligned and form a crystalline structure that is relatively inaccessible to enzymatic digestion. Thus, cellulose is very stable and only degrades during specific developmental stages, such as abscission and senescence. The cell wall matrix is composed of two polysaccharide types, hemicellulose and

pectin, along with a small concentration of structural proteins. The matrix is generally well-hydrated, and the matrix hydration state determines the physical properties of the wall.

[0005] Secondary cell walls form after cessation of cell growth and enlargement. Unlike primary cell walls, secondary cell walls can adopt highly specialized structures and compositions. For example, xylem cells, such as those found in wood, have thickened secondary walls that are strengthened by lignin.

[0006] Recently, several plant cell wall proteins have been identified. For example, polynucleotide sequences encoding the following plant cell wall proteins have been identified: α-amylase, Arabinogalactan, Brassinosteroid-regulated Protein Precursor, β-1,3-endoglucanase, β -1,3-glucanase, β-D-glucan exohydrolase, β-glucosidase, β-xylosidase, Calnexin, Calreticulin, Cellulase, Cellulose synthase, Chitinase, Dirigent, Expansin, Extensin, Galacturan 1,4- α-galacturonidase, Glucose-1-phosphate adenyltransferase, Glycosyl transferase, Glycosyl hydrolase, Glycoside hydrolase, Hexose pyrophoshorylase, Hydroxyproline-rich proteins, Mannose-6-Phosphate Isomerase, Mannose-1-Phosphate Guanylyltransferase, Nucleotidyl transferase, Pectins, Pectin Methylesterase, Phosphomannomutase, Plant disease resistance response protein, Polygalacturonase, Pollen allergen/expansin, Starch Branching Enzyme, Starch Synthase, Sucrose-phosphate synthase, Sucrose synthase, Syringolide-induced protein, UTP-glucose-1-phosphate uridylyltransferase, Xyloglucan endotransglycosylase, Xyloglucan synthase, Xyloglucan: xyloglucosyl transferase, and Yieldin.

[0007] While much is known about the structure and metabolic regulation of various cell wall proteins, very little is known about their functions and intercellular interactions. Additionally, the multigenic control of a plant phenotype presents difficulties in determining the genes responsible for a given phenotype. One major obstacle to identifying genes and gene expression differences that contribute to phenotype in plants is the difficulty with which the expression of more than a handful of genes can be studied concurrently. Another difficulty in identifying and understanding gene expression and the interrelationship of the genes that contribute to

plant phenotype is the high degree of sensitivity to environmental factors that plants demonstrate.

[0008] There have been recent advances using genome-wide expression profiling. In particular, the use of DNA microarrays has been useful to examine the expression of a large number of genes in a single experiment. Several studies of plant gene responses to developmental and environmental stimuli have been conducted using expression profiling. For example, microarray analysis was employed to study gene expression during fruit ripening in strawberry, Aharoni *et al., Plant Physiol.* 129:1019-1031 (2002), wound response in *Arabidopsis*, Cheong *et al., Plant Physiol.* 129:661-7 (2002), pathogen response in *Arabidopsis*, Schenk *et al., Proc. Nat'l Acad. Sci.* 97:11655-60 (2000), and auxin response in soybean, Thibaud-Nissen *et al., Plant Physiol.* 132:118. Whetten *et al., Plant Mol. Biol.* 47:275-91 (2001) discloses expression profiling of cell wall biosynthetic genes in *Pinus taeda L.* using cDNA probes. Whetten *et al.* examined genes which were differentially expressed between differentiating juvenile and mature secondary xylem. Additionally, to determine the effect of certain environmental stimuli on gene expression, gene expression in compression wood was compared to normal wood. A total of 156 of the 2300 elements examined showed differential expression. Whetten, *supra* at 285. Comparison of juvenile wood to mature wood showed 188 elements as differentially expressed. *Id.* at 286.

[0009] Although expression profiling and, in particular, DNA microarrays provide a convenient tool for genome-wide expression analysis, their use has been limited to organisms for which the complete genome sequence or a large cDNA collection is available. *See* Hertzberg *et al., Proc. Nat'l Acad. Sci.* 98:14732-7 (2001a), Hertzberg *et al., Plant J.*, 25:585 (2001b). For example, Whetten, *supra,* states, "A more complete analysis of this interesting question awaits the completion of a larger set of both pine and poplar ESTs." Whetten *et al.* at 286. Furthermore, microarrays comprising cDNA or EST probes may not be able to distinguish genes of the same family because of sequence similarities among the genes. That is, cDNAs or ESTs, when used as microarray probes, may bind to more than one gene of the same family.

[0010] Methods of manipulating gene expression to yield a plant with a more desirable phenotype would be facilitated by a better understanding of cell wall gene expression in various types of plant tissue, at different stages of plant development, and upon stimulation by different environmental cues. The ability to control plant architecture and agronomically important traits would be improved by a better understanding of how cell wall development effects plant cell development and morphology.

[0011] Accordingly, there exists a need for efficiently identifying genes that regulate plant cell wall synthesis and development.

SUMMARY OF THE INVENTION

[0012] In one embodiment, the current invention is to an isolated polynucleotide comprising a nucleic acid sequence that encodes a polypeptide that regulates cell wall development. In other embodiments, the isolated polynucleotide functions in a plant cell or the isolated polynucleotide comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-230. For SEQ ID NO: 1-230, the polynucleotide is normally expressed in a species of *Eucalyptus* or *Pinus*. In other embodiments, the Eucalyptus in Eucalyptus grandis and the Pinus is Pinus radiata.

[0013] In other embodiments, the polynucleotide of the current invention is normally expressed in a species of conifer. In other embodiments, the conifer may be selected from the group consisting of Eastern white pine, Western white, Sugar pine, Red pine, Pitch pine, Jack pine, Longleaf pine, Shortleaf pine, Loblolly pine, Slash pine, Virginia pine, Ponderosa pine, Jeffrey pine, and Lodgepole pine, Radiata pine and hybrid crosses thereof. In other embodiments, the conifer is selected from the group consisting of *Abies firma, Cedrus deodara, Cedrus deodara 'Albospica', Cedrus deodara 'Aurea', Cedrus deodara 'Kashmir', Cedrus deodara 'Shalimar', Cedrus deodara 'Silver Mist', Cedrus deodara 'White Imp', Cedrus libani (ssp. atlantica) glauca, Cedrus libani(ssp.atlantica)glauca pendula, Cedrus libani 'Nana', Cedrus libani pendula, Cedrus libani brevifolia, Cedrus libani var. stenacoma, , Chamaecyparis lawsoniana, Chamaecyparis nootkatensis 'Pendula', Chamaecyparis*

obtusa 'Crippsii', Chamaecyparis pisifera 'Boulevard', Chamaecyparis pisifera 'Filifera Aurea', Chamaecyparis thyoides 'Blue Sport', Cryptomeria japonica 'Sekkan Sugi', Cryptomeria japonica 'Vilmoriniana', Cunninghamia lanceolata 'Glauca', Cuppressus arizonica var. glabra 'Blue Ice', Cuppressus arizonica 'Blue Sapphire', Ginkgo biloba, Ginkgo biloba 'Autumn Gold', Glyptostrobus pensilis, Juniperus chinensis 'Torulosa', Juniperus scopulorum 'Tollesons', Juniperus virginiana, Larix kaempferi, Metasequoia glyptostroboides, Picea abies, Picea abies Pendula, Picea abies 'Remontii', Picea glauca 'Sanders Blue', Pinus x hakkodensis, Pinus nigra var. nigra, Picea omorika, Pinus densiflora 'Umbraculifera', Pinus elliottii, Pinus flexilis 'Vanderwolf Pyramid', Pinus pinea, Pinus massoniana, Pinus strobus, Pinus strobus 'Pendula', Pinus sylvestris 'French Blue', Pinus sylvestris 'Mitsch Weeping', Pinus taeda, Pinus radiata, Pinus Pinascer, Pinus thunbergiana, Pinus virginiana, Pseudotsuga menziesii, *Pseudolarix amabilis, Sequoia sempervirens, Taxodium ascendens, Taxodium distichum, Thuja occidentalis 'Filiformis', Tsuga Canadensis 'Golden Splendor', x Cuppressocyparis leylandii, x Cuppressocyparis leylandii 'Post Sentinal', x Cuppressocyparis leylandii 'Caslewellan', x Cuppressocyparis leylandii 'Naylors Blue'*, and hybrid crosses thereof.

[0014] In another emobidment of the current invention, the conifer is a Southern Yellow pine tree. In further embodiments, the Southern Yellow pine is selected from the group consisting of *Pinus taeda, Pinus serotina, Pinus palustris*, and *Pinus elliottii and hybrids*.

[0015] In other embodiments, the isolated polynucleotide of the current invention is normally expressed in a tree selected from the group consisting of chestnut, ash, beech, basswood, birch, black cherry, black walnut/butternut, chinkapin, cottonwood, elm, eucalyptus, hackberry, hickory, holly, locust, magnolia, maple, oak, poplar, acacia, aspen, teak, red alder, royal paulownia, sassafras, sweetgum, sycamore, tupelo, willow, and yellow-poplar, and intra- and inter-species hybrid crosses thereof.

[0016] In other embodiments, the isolated polynucleotide of the current invention is normally expressed in a gymnosperm or an angiosperm.

[0017] In other embodiments, the isolated polynucleotide of the current invention expresses a polypeptide that is capable of regulating cell wall synthesis in a monocotyledenous plant. In further embodiments, monocotyledenous plant is selected from the group consisting of turfgrass, wheat, maize, rice, oat, barley, orchid, iris, lily, onion, sugarcane, and sorghum. In other embodiments, the turfgrass is selected from the group consisting of *Agrostis spp.*, *Poa pratensis*, *Lolium spp.*, Kentucky Bluegrass And Perennial Ryegrass Mix; *Festuca arundinacea*, *Festuca rubra commutata*, *Cynodon dactylon*, *Pennisetum clandestinum*, *Stenotaphrum secundatum*, *Zoysia japonica*, and *Dichondra micrantha*.

[0018] In other embodiments, the isolated polynucleotide of the current invention expresses a polypeptide that is is capable of regulating cell wall synthesis in a dicotyledenous plant. In further embodiments, the dicotyledenous plant is selected from the group consisting of cotton, tobacco, *Arabidopsis*, tomato, potato, aspen, eucalyptus, Sweetgum, acacia, poplar, willow, teak, mahogany, chestnut, elm, sugar beet, broccoli, cassava, sweet potato, pepper, poinsettia, legumes, alfalfa, soybean, carrot, strawberry, lettuce, oak, maple, walnut, rose, mint, squash, daisy, geranium and cactus.

[0019] In other embodiments, the isolated polynucleotide of the current invention is capable of upregulating or downregulating cell wall biosynthesis in a plant. In further embodiments, the polynucleotide is from a gene that is endogenous to the plant genome. In other embodiments, the phenotype of a plant which expresses the isolated polynucleotide in at least one cell, is different from the phenotype of a plant of the same species that does not express the isolated polynucleotide in any of its cells. In other embodiments, the phenotype of the plant expressing the isolated polynucleotide comprises a difference in lignin quality compared to a plant of the same species that does not express the isolated polynucleotide. In other embodiemtns, the difference in lignin quality is characterized by change in the structure of the lignin molecule. In other embodiments, the phenotype of the plant expressing the isolated polynucleotide comprises a difference in wood composition compared to a plant of the same species that does not express the isolated polynucleotide. In other embodiments, the

phenotype of the plant expressing the isolated polynucleotide comprises a difference in fiber composition compared to a plant of the same species that does not express the isolated polynucleotide. In other embodiments, the phenotype of the plant expressing the isolated polynucleotide comprises a difference in plant cell division compared to a plant of the same species that does not express the isolated polynucleotide. In other embodiments, the phenotype of the plant expressing the isolated polynucleotide comprises a difference in plant cell development compared to a plant of the same species that does not express the isolated polynucleotide. In other embodiments, the phenotype of the plant expressing the isolated polynucleotide comprises a difference in height, volume, or yield compared to a plant of the same species that does not express the isolated polynucleotide.

[0020] In other embodiments, the isolated polynucleotide of the current invention, comprises the sequence of any one of SEQ ID NOs: 1-230, or variant thereof. In other embodiments, the variant encodes a polypeptide that is capable of regulating cell wall development in a plant. In other embodiments, the variant has a sequence identity that is greater than or equal to 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 79%, 78%, 77%, 76%, 75%, 74%, 73%, 72%, 71%, 70%, 69%, 68%, 67%, 66%, 65%, 64%, 63%, 62%, 61%, or 60% in sequence to any one of SEQ ID NOs: 1-230.

[0021] In other embodiments, the plant cell wall protein of the current ivnetion, comprises the amino acid sequence of any one of SEQ ID NOs: 1-230, or variant thereof, wherein said cell wall protein is capable of regulating cell wall development in a plant. In other embodiments, the variant has a sequence identity that is greater than or equal to 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 79%, 78%, 77%, 76%, 75%, 74%, 73%, 72%, 71%, 70%, 69%, 68%, 67%, 66%, 65%, 64%, 63%, 62%, 61%, or 60% in sequence to any one of SEQ ID NOs: 1-230.

[0022] In other embodiments, a DNA construct of the current invention comprises (i) at least one polynucleotide that has the sequence of any one of SEQ ID NOs: 1-230, and (ii) a promoter, wherein said promoter and said polynucleotide are operably

linked. In other embodiments, the promoter is selected from the group consisting of a constitutive promoter, a strong promoter, or an inducible promoter. In other embodiments, the inducible promoter is regulated by any one of wounding, methyl jasmonate or salicylic acid. In other embodiments, the polynucleotide produces an RNA transcript. In other embodiments, RNA transcript has an antisense sequence of a gene that is endogenous to a plant cell or the RNA transcript induces RNA interference of a gene that is normally expressed in a plant cell.

[0023] In another embodiment, a plant cell of the current inventon comprises a DNA construct that comprises (i) at least one polynucleotide that has the sequence of any one of SEQ ID NOs: 1-230 and (ii) a promoter, wherein said polynucleotide encodes a protein that regulates cell wall development, and wherein said promoter and said polynucleotide are operably linked. In another embodiment the current invention is to a transgenic plant comprising such a plant cell.

[0024] In other embodiments, a plant cell of the current invention comprises a DNA construct that comprises (i) at least one polynucleotide that has the sequence of any one of SEQ ID NOs: 1-230 and (ii) a promoter, wherein said polynucleotide encodes a protein that regulates wood development, and wherein said promoter and said polynucleotide are operably linked. In another embodiment the current invention is to a transgenic plant comprising such a plant cell.

[0025] In other embodiments, the current invention is to a method for producing a transgenic plant, comprising (a) transforming a plant cell with a DNA construct that comprises (i) at least one polynucleotide that has the sequence of any one of SEQ ID NOs: 1-230 and (ii) a promoter, wherein said polynucleotide encodes a protein that regulates cell wall development; (b) culturing said transformed plant cell under conditions that promote growth of a plant, and (c) selecting a transgenic plant that exhibits a phenotype that is different from a plant of the same species that does not contain said DNA construct. In other embodiments, the phenotype of the plant expressing the polynucleotide and the desired nucleic acid is characterized by a difference in lignin quality compared to a plant of the same species that does not contain the DNA construct. In other embodiments, the difference in lignin quality is

characterized by change in the structure of the lignin molecule. In other embodiments of the current method, the phenotype of the plant expressing the polynucleotide and the desired nucleic acid is characterized by a difference in wood composition compared to a plant of the same species that does not contain the DNA construct. In other embodiments of the current method, the phenotype of the plant expressing the polynucleotide is characterized by a difference in fiber yield compared to a plant of the same species that does not contain the DNA construct. In other embodiments of the current method, the method of claim 44, wherein the phenotype of the plant expressing the polynucleotide is characterized by a difference in plant cell division compared to a plant of the same species that does not contain the DNA construct. In other embodiments of the current method, the phenotype of the plant expressing the polynucleotide is characterized by a difference in plant cell development compared to a plant of the same species that does not contain the DNA construct. In other embodiments, the phenotype of the plant expressing the polynucleotide is characterized by a difference in starch synthesis compared to a plant of the same species that does not contain the DNA construct. In other embodiments, the phenotype of the plant expressing the polynucleotide and the desired nucleic acid is characterized by a difference in height, volume, or yield, compared to a plant of the same species that does not contain the DNA construct.

[0026] In another embodiment, the current invention is to wood pulp obtained from a transgenic tree expressing a polypeptide comprising an amino acid sequence of any one of SEQ ID NOs. 1-230.

[0027] In another embodiment, transgenic plant of the current invetion expresses a polypeptide comprising an amino acid sequence of any one of SEQ ID NOs: 1-230, wherein said amino acid confers a trait to the plant selected from the group consisting of increased drought tolerance, reduced or increased height, reduced or increased volume, reduced or increased branching, enhanced cold and frost tolerance, improved vigor, enhanced color, enhanced health and nutritional characteristics, improved storage, enhanced yield, enhanced salt tolerance, enhanced heavy metal tolerance, increased disease tolerance, increased insect tolerance, increased water-stress

tolerance, enhanced sweetness, improved taste, improved texture, decreased phosphate content, increased germination, increased micronutrient uptake, improved starch composition, improved flower longevity, and production of novel proteins or peptides.

[0028] In other embodiments, the current invention is to a transgenic plant expressing a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1-230, wherein said plant has a reduced or increased period of juvenality compared to a wild-type plant of the same species.

[0029] In other embodiments, the current invention is to a transgenic plant expressing a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1-230, wherein said plant has self-absicing branches.

[0030] In other embodiments, the current invention is to an isolated nucleotide sequence having the nucleotide sequence of any of SEQ ID NO: 1-230, and nucleotide sequences having 60% sequence identity with the nucleotide sequence of SEQ ID NO: 1-230and which are capable of regulating plant cell wall development.

[0031] In other embodiments, the current invention is to an isolated nucleotide sequence having the nucleotide sequence of any of SEQ ID NO: 1-230, and nucleotide sequences having 65% sequence identity with any of the nucleotide sequences of SEQ ID NO: 1-230 and which are involved in wood development.

[0032] In other embodiments, the current invention is to an isolated nucleotide sequence having the nucleotide sequence of any of SEQ ID NO: 1-230 and nucleotide sequences having 70% sequence identity with any of the nucleotide sequences of SEQ ID NO: 1-230 and which regulate cell wall biogenesis.

[0033] In other embodiments, the current invention is to a method of correlating polynucleotide expression in two different samples, comprising:

detecting a level of expression of one or more polynucleotides encoding a product encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230 and conservative variants thereof in a first sample;

detecting a level of expression of the one or more polynucleotides in a second sample;

comparing the level of expression of the one or more polynucleotides in the first sample to the level of expression of the one or more polynucleotides in the second sample; and

correlating a difference in expression level of the one or more polynucleotides between the first and second samples. In other embodiments, the first sample and the second sample are each from a different type of plant tissue. In other embodiments, the first sample and the second sample are from the same tissue, and wherein the first sample and the second sample are each harvested during a different season of the year. In other embodiments, the first sample and the second sample are obtained from plants in different stages of development.

[0034] In other embodiments, the current invention is to a method of correlating the possession of a plant phenotype to the level of polynucletide expression in the plant of one or more polynucleotides comprising:

detecting a level of expression of one or more polynucleotides encoding a product encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230 and conservative variants thereof in a first plant possessing a phenotype;

detecting a level of expression of the one or more polynucleotides in a second plant lacking the phenotype;

comparing the level of expression of the one or more polynucleotides in the first plant to the level of expression of the one or more polynucleotides in the second plant; and

correlating a difference in expression level of the one or more polynucleotides between the first and second plants to possession of the phenotype. In other embodiments, the first and second samples are both obtained from a plant tissue selected from the group consisting of vascular tissue, apical meristem, vascular cambium, xylem, phloem, root, flower, cone, fruit, and seed. In other embodiments, the plant tissue of the first sample and second sample are each obtained from a different type of tissue. In other embodiments, the first and second samples are each

obtained from a plant tissue in a different stage of development. In other embodiments, both the first and second plants or plant cells are of a same species selected from Eucalyptus and Pinus species. In other embodiments, the first and second plants or plant cells are of a species selected from Eucalyptus grandis or Pinus radiata. In other embodiments, the step of detecting is effected using one or more polynucleotides capable of hybridizing to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230 under standard hybridization conditions. In other embodiments, the step of detecting is effected using one or more polynucleotides capable of hybridizing to a polynucleotide expression product encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230 under standard hybridization conditions. In other embodiments, the step of detecting is affected by hybridization to a labeled nucleic acid. In other embodiments, he one or more polynucleotides are labeled with a detectable label. In other embodiments, at least one of the one or more polynucleotides hybridizes to a 3' untranslated region of one of the one or more polynucleotides. In other embodiments, at least one of the one or more polynucleotides hybridizes to the 3' untranslated region of one of the one or more polynucleotides. In other mebodiments, the one or more polynucleotides comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, the one or more polynucleotides comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, the one or more polynucleotides is selected from the group consisting of DNA and RNA. In other embodiments, prior to the detecting steps, the step of amplifying the one or more polynucleotides in the first and second plant or plant cells is provided. In other embodiments, prior to the detecting steps, the step of labeling the one or more polynucleotides in the first and second plant or plant cells with a detectable label is provided.

[0035] In other embodiments, the current invention is to a combination for detecting expression of one or more polynucleotides, comprising two or more oligonucleotides, wherein each oligonucleotide is capable of hybridizing to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 461-690. In other embodiments,

the two or more oligonucleotides hybridizes to a different one of the nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, at least one of the two or more oligonucleotides hybridizes to a 3' untranslated region of a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, each of the two or more oligonucleotides are comprised of fewer than about 100 nucleotide bases. In other embodiments, at least one of the two or more oligonucleotides comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 461-690. In other embodiments, each of the two or more oligonucleotides hybridizes to a gene encoding a protein selected from the group consisting of α-amylase, Arabinogalactan, Calnexin, Calreticulin, Cellulose synthase, Dirigent, Expansin, Extensin, Galacturan 1,4- β-galacturonidase, Glucose-1-phosphate adenyltransferase, Glycosyl transferase, Glycosyl hydrolase, Glycoside hydrolase, Hydroxyproline-rich proteins, Mannose-6-Phosphate Isomerase, Mannose-1-Phosphate Guanylyltransferase, Nucleotidyl transferase, Pectins, Pectin Methylesterase, Phosphomannomutase, Plant disease resistance response protein, Polygalacturonase, Pollen allergen/expansin, Starch Branching Enzyme, Starch Synthase, Sucrose-phosphate synthase, Sucrose synthase, UTP-glucose-1-phosphate uridylyltransferase, Xyloglucan synthase, Xyloglucan: xyloglucosyl transferase, and Yieldin. In other embodiments, each of the two or more oligonucleotides hybridizes to a gene encoding a different one of the proteins. In other embodiments, each of the two or more oligonucleotides hybridizes to a different gene. In other mebodiments, the combination comprises from about 2 to about 5000 of the two or more oligonucleotides. In other embodiments, each of the two or more oligonucleotides is labeled with a detectable label.

[0036] In other embodiments, the current invention is to a combination for detecting expression of one or more polynucleotides, comprising two or more oligonucleotides, wherein each oligonucleotide is capable of hybridizing to a polynucleotide expression product encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, the two or more oligonucleotides hybridizes to a nucleotide sequence encoded by a different one of the nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-230. In other

embodiments, at least one of the two or more oligonucleotides hybridizes to nucleic acid sequence that is complementary to a 3' untranslated region of a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, each of the two or more oligonucleotides are comprised of fewer than about 100 nucleotide bases. In other embodiments, at least one of the two or more oligonucleotides comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 461-690. In other embodiments, each of the two or more oligonucleotides hybridizes to a nucleic acid sequence encoded by a gene encoding a protein selected from the group consisting of α-amylase, Arabinogalactan, Calnexin, Calreticulin, Cellulose synthase, Dirigent, Expansin, Extensin, Galacturan 1,4- β-galacturonidase, Glucose-1-phosphate adenyltransferase, Glycosyl transferase, Glycosyl hydrolase, Glycoside hydrolase, Hydroxyproline-rich proteins, Mannose-6-Phosphate Isomerase, Mannose-1-Phosphate Guanylyltransferase, Nucleotidyl transferase, Pectins, Pectin Methylesterase, Phosphomannomutase, Plant disease resistance response protein, Polygalacturonase, Pollen allergen/expansin, Starch Branching Enzyme, Starch Synthase, Sucrose-phosphate synthase, Sucrose synthase, UTP-glucose-1-phosphate uridylyltransferase, Xyloglucan synthase, Xyloglucan: xyloglucosyl transferase, and Yieldin. In other embodiments, each of the two or more oligonucleotides hybridizes to a nucleic acid sequence encoded by a gene encoding a different one of the proteins. In other embodiments, each of the two or more oligonucleotides hybridizes to a nucleic acid sequence encoded by a different gene. In other mebodiments, the combination comprises from about 2 to about 5000 of the two or more oligonucleotides. In other embodiments, each of the two or more oligonucleotides is labeled with a detectable label.

[0037] In other embodiments, the current invention is to a microarray comprising the above combination provided on a solid support, wherein each of said two or more oligonucleotides occupies a unique location on said solid support. In other embodiments, the current invention is to a kit for detecting gene expression comprising the above microarray together with one or more buffers or reagents for a nucleotide hybridization reaction.

[0038] In other embodiments, the current invention is to a method for detecting one or more polynucleotides in a sample, comprising:

contacting the sample with two or more oligonucleotides, wherein each oligonucleotide is capable of hybridizing to a gene comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230 under standard hybridization conditions; and

detecting the one or more polynucleotides of interest which are hybridized to the one or more oligonucleotides. In other embodiments, each of the two or more oligonucleotides hybridizes to a gene comprising a different one of the nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, at least one of the two or more oligonucleotides hybridizes to a 3' untranslated region of a gene comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs 1-230. In other embodiments, each of the two or more oligonucleotides are comprised of fewer than about 100 nucleotide bases. In other embodiments, at least one of the two or more oligonucleotides comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs 461-690. In other embodiments, each of the two or more oligonucleotides hybridizes to a gene encoding a protein selected from the group consisting of α-amylase, Arabinogalactan, Calnexin, Calreticulin, Cellulose synthase, Dirigent, Expansin, Extensin, Galacturan 1,4-β-galacturonidase, Glucose-1-phosphate adenyltransferase, Glycosyl transferase, Glycosyl hydrolase, Glycoside hydrolase, Hydroxyproline-rich proteins, Mannose-6-Phosphate Isomerase, Mannose-1-Phosphate Guanylyltransferase, Nucleotidyl transferase, Pectins, Pectin Methylesterase, Phosphomannomutase, Plant disease resistance response protein, Polygalacturonase, Pollen allergen/expansin, Starch Branching Enzyme, Starch Synthase, Sucrose-phosphate synthase, Sucrose synthase, UTP-glucose-1-phosphate uridylyltransferase, Xyloglucan synthase, Xyloglucan: xyloglucosyl transferase, and Yieldin. In other embodiments, each of the two or more oligonucleotides hybridizes to a gene encoding a different one of the proteins. In another embodiments, the two or more oligonucleotides are provided on a solid support, wherein each of the two of more oligonucleotides occupy a unique location on the solid support. In other embodiments, the solid support comprises from about 2

to about 5000 of the two or more oligonucleotides. In other embodiments, the current method further comprises, prior to the contacting step, the step of amplifying the one or more polynucleotides or nucleic acid sequences in the sample. In other embodiments, the current method further comprises prior to the contacting step, the step of labeling the one or more polynucleotides or nucleic acid sequences in the sample with a detectable label.

[0039] In other embodiments, the current invention is to a method for detecting one or more nucleic acid sequences encoded by one or more polynucleotides in a sample, comprising:

contacting the sample with two or more oligonucleotides, wherein each oligonucleotide is capable of hybridizing to a nucleic acid sequence encoded by a gene comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230 under standard hybridization conditions; and

detecting the one or more nucleic acid sequences which are hybridized to the one or more oligonucleotides. In other embodiments, each of the two or more oligonucleotides hybridizes to a nucleic acid sequence encoded by a gene comprising a different one of the nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, at least one of the two or more oligonucleotides hybridizes to a nucleic acid sequence that is complementary to a 3' untranslated region of a gene comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-230. In other embodiments, each of the two or more oligonucleotides are comprised of fewer than about 100 nucleotide bases. In other embodiments, at least one of the two or more oligonucleotides comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 461-690. In other embodiments, each of the two or more oligonucleotides hybridizes to a nucleic acid sequence encoded by a gene encoding a protein selected from the group consisting of α-amylase, Arabinogalactan, Calnexin, Calreticulin, Cellulose synthase, Dirigent, Expansin, Extensin, Galacturan 1,4-β-galacturonidase, Glucose-1-phosphate adenyltransferase, Glycosyl transferase, Glycosyl hydrolase, Glycoside hydrolase, Hydroxyproline-rich proteins, Mannose-6-Phosphate Isomerase, Mannose-1-Phosphate Guanylyltransferase, Nucleotidyl transferase, Pectins, Pectin

Methylesterase, Phosphomannomutase, Plant disease resistance response protein, Polygalacturonase, Pollen allergen/expansin, Starch Branching Enzyme, Starch Synthase, Sucrose-phosphate synthase, Sucrose synthase, UTP-glucose-1-phosphate uridylyltransferase, Xyloglucan synthase, Xyloglucan: xyloglucosyl transferase, and Yieldin. In other embodiments, each of the two or more oligonucleotides hybridizes to a nucleic acid sequence encoded by a gene encoding a different one of the proteins. In another embodiments, the two or more oligonucleotides are provided on a solid support, wherein each of the two of more oligonucleotides occupy a unique location on the solid support. In other embodiments, the solid support comprises from about 2 to about 5000 of the two or more oligonucleotides. In other embodiments, the current method further comprises, prior to the contacting step, the step of amplifying the one or more polynucleotides or nucleic acid sequences in the sample. In other embodiments, the current method further comprises prior to the contacting step, the step of labeling the one or more polynucleotides or nucleic acid sequences in the sample with a detectable label.

BRIEF DESCRIPTION OF THE FIGURES

[0040] Figure 1 shows the annotated amino acid sequence of SEQ ID NO: 231.

[0041] Figure 2 shows the annotated amino acid sequence of SEQ ID NO: 232.

[0042] Figure 3 shows the annotated amino acid sequence of SEQ ID NO: 234.

[0043] Figure 4 shows the annotated amino acid sequence of SEQ ID NO: 235.

[0044] Figure 5 shows the annotated amino acid sequence of SEQ ID NO: 236.

[0045] Figure 6 shows the annotated amino acid sequence of SEQ ID NO: 237.

[0046] Figure 7 shows the annotated amino acid sequence of SEQ ID NO: 238.

[0047] Figure 8 shows the annotated amino acid sequence of SEQ ID NO: 239.

[0048] Figure 9 shows the annotated amino acid sequence of SEQ ID NO: 240.

[0049] Figure 10 shows the annotated amino acid sequence of SEQ ID NO: 241.

[0050] Figure 11 shows the annotated amino acid sequence of SEQ ID NO: 242.

[0051] Figure 12 shows the annotated amino acid sequence of SEQ ID NO: 243.

[0052] Figure 13 shows the annotated amino acid sequence of SEQ ID NO: 244.

[0053] Figure 14 shows the annotated amino acid sequence of SEQ ID NO: 245.

[0054] Figure 15 shows the annotated amino acid sequence of SEQ ID NO: 246.

[0055] Figure 16 shows the annotated amino acid sequence of SEQ ID NO: 248.

[0056] Figure 17 shows the annotated amino acid sequence of SEQ ID NO: 249.

[0057] Figure 18 shows the annotated amino acid sequence of SEQ ID NO: 250.

[0058] Figure 19 shows the annotated amino acid sequence of SEQ ID NO: 251.

[0059] Figure 20 shows the annotated amino acid sequence of SEQ ID NO: 252.

[0060] Figure 21 shows the annotated amino acid sequence of SEQ ID NO: 253.

[0061] Figure 22 shows the annotated amino acid sequence of SEQ ID NO: 254.

[0062] Figure 23 shows the annotated amino acid sequence of SEQ ID NO: 255.

[0063] Figure 24 shows the annotated amino acid sequence of SEQ ID NO: 256.

[0064] Figure 25 shows the annotated amino acid sequence of SEQ ID NO: 257.

[0065] Figure 26 shows the annotated amino acid sequence of SEQ ID NO: 259.

[0066] Figure 27 shows the annotated amino acid sequence of SEQ ID NO: 260.

[0067] Figure 28 shows the annotated amino acid sequence of SEQ ID NO: 261.

[0068] Figure 29 shows the annotated amino acid sequence of SEQ ID NO: 262.

[0069] Figure 30 shows the annotated amino acid sequence of SEQ ID NO: 263.

[0070] Figure 31 shows the annotated amino acid sequence of SEQ ID NO: 264.

[0071] Figure 32 shows the annotated amino acid sequence of SEQ ID NO: 265.

[0072] Figure 33 shows the annotated amino acid sequence of SEQ ID NO: 266.

[0073] Figure 34 shows the annotated amino acid sequence of SEQ ID NO: 267.

[0074] Figure 35 shows the annotated amino acid sequence of SEQ ID NO: 268.

[0075] Figure 36 shows the annotated amino acid sequence of SEQ ID NO: 269.

[0076] Figure 37 shows the annotated amino acid sequence of SEQ ID NO: 270.

[0077] Figure 38 shows the annotated amino acid sequence of SEQ ID NO: 271.

[0078] Figure 39 shows the annotated amino acid sequence of SEQ ID NO: 272.

[0079] Figure 40 shows the annotated amino acid sequence of SEQ ID NO: 273.

[0080] Figure 41 shows the annotated amino acid sequence of SEQ ID NO: 274.

[0081] Figure 42 shows the annotated amino acid sequence of SEQ ID NO: 275.

[0082] Figure 43 shows the annotated amino acid sequence of SEQ ID NO: 276.

[0083] Figure 44 shows the annotated amino acid sequence of SEQ ID NO: 277.

[0084] Figure 45 shows the annotated amino acid sequence of SEQ ID NO: 278.

[0085] Figure 46 shows the annotated amino acid sequence of SEQ ID NO: 279.

[0086] Figure 47 shows the annotated amino acid sequence of SEQ ID NO: 280.

[0087] Figure 48 shows the annotated amino acid sequence of SEQ ID NO: 281.

[0088] Figure 49 shows the annotated amino acid sequence of SEQ ID NO: 282.

[0089] Figure 50 shows the annotated amino acid sequence of SEQ ID NO: 283.

[0090] Figure 51 shows the annotated amino acid sequence of SEQ ID NO: 284.

[0091] Figure 52 shows the annotated amino acid sequence of SEQ ID NO: 285.

[0092] Figure 53 shows the annotated amino acid sequence of SEQ ID NO: 286.

[0093] Figure 54 shows the annotated amino acid sequence of SEQ ID NO: 287.

[0094] Figure 55 shows the annotated amino acid sequence of SEQ ID NO: 288.

[0095] Figure 56 shows the annotated amino acid sequence of SEQ ID NO: 289.

[0096] Figure 57 shows the annotated amino acid sequence of SEQ ID NO: 290.

[0097] Figure 58 shows the annotated amino acid sequence of SEQ ID NO: 291.

[0098] Figure 59 shows the annotated amino acid sequence of SEQ ID NO: 292.

[0099] Figure 60 shows the annotated amino acid sequence of SEQ ID NO: 293.

[0100] Figure 61 shows the annotated amino acid sequence of SEQ ID NO: 294.

[0101] Figure 62 shows the annotated amino acid sequence of SEQ ID NO: 295.

[0102] Figure 63 shows the annotated amino acid sequence of SEQ ID NO: 296.

[0103] Figure 64 shows the annotated amino acid sequence of SEQ ID NO: 297.

[0104] Figure 65 shows the annotated amino acid sequence of SEQ ID NO: 298.

[0105] Figure 66 shows the annotated amino acid sequence of SEQ ID NO: 299.

[0106] Figure 67 shows the annotated amino acid sequence of SEQ ID NO: 300.

[0107] Figure 68 shows the annotated amino acid sequence of SEQ ID NO: 301.

[0108] Figure 69 shows the annotated amino acid sequence of SEQ ID NO: 302.

[0109] Figure 70 shows the annotated amino acid sequence of SEQ ID NO: 303.

[0110] Figure 71 shows the annotated amino acid sequence of SEQ ID NO: 304.

[0111] Figure 72 shows the annotated amino acid sequence of SEQ ID NO: 305.

[0112] Figure 73 shows the annotated amino acid sequence of SEQ ID NO: 306.

[0113] Figure 74 shows the annotated amino acid sequence of SEQ ID NO: 307.

[0114] Figure 75 shows the annotated amino acid sequence of SEQ ID NO: 308.

[0115] Figure 76 shows the annotated amino acid sequence of SEQ ID NO: 309.

[0116] Figure 77 shows the annotated amino acid sequence of SEQ ID NO: 310.

[0117] Figure 78 shows the annotated amino acid sequence of SEQ ID NO: 311.

[0118] Figure 79 shows the annotated amino acid sequence of SEQ ID NO: 312.

[0119] Figure 80 shows the annotated amino acid sequence of SEQ ID NO: 313.

[0120] Figure 81 shows the annotated amino acid sequence of SEQ ID NO: 314.

[0121] Figure 82 shows the annotated amino acid sequence of SEQ ID NO: 315.

[0122] Figure 83 shows the annotated amino acid sequence of SEQ ID NO: 316.

[0123] Figure 84 shows the annotated amino acid sequence of SEQ ID NO: 317.

[0124] Figure 85 shows the annotated amino acid sequence of SEQ ID NO: 318.

[0125] Figure 86 shows the annotated amino acid sequence of SEQ ID NO: 319.

[0126] Figure 87 shows the annotated amino acid sequence of SEQ ID NO: 320.

[0127] Figure 88 shows the annotated amino acid sequence of SEQ ID NO: 321.

[0128] Figure 89 shows the annotated amino acid sequence of SEQ ID NO: 322.

[0129] Figure 90 shows the annotated amino acid sequence of SEQ ID NO: 323.

[0130] Figure 91 shows the annotated amino acid sequence of SEQ ID NO: 324.

[0131] Figure 92 shows the annotated amino acid sequence of SEQ ID NO: 325.

[0132] Figure 93 shows the annotated amino acid sequence of SEQ ID NO: 326.

[0133] Figure 94 shows the annotated amino acid sequence of SEQ ID NO: 327.

[0134] Figure 95 shows the annotated amino acid sequence of SEQ ID NO: 328.

[0135] Figure 96 shows the annotated amino acid sequence of SEQ ID NO: 329.

[0136] Figure 97 shows the annotated amino acid sequence of SEQ ID NO: 330.

[0137] Figure 98 shows the annotated amino acid sequence of SEQ ID NO: 331.

[0138] Figure 99 shows the annotated amino acid sequence of SEQ ID NO: 332.

[0139] Figure 100 shows the annotated amino acid sequence of SEQ ID NO: 333.

[0140] Figure 101 shows the annotated amino acid sequence of SEQ ID NO: 334

[0141] Figure 102 shows the annotated amino acid sequence of SEQ ID NO: 335.

[0142] Figure 103 shows the annotated amino acid sequence of SEQ ID NO: 336.

[0143] Figure 104 shows the annotated amino acid sequence of SEQ ID NO: 337.

[0144] Figure 105 shows the annotated amino acid sequence of SEQ ID NO: 338.

[0145] Figure 106 shows the annotated amino acid sequence of SEQ ID NO: 339.

[0146] Figure 107 shows the annotated amino acid sequence of SEQ ID NO: 340.

[0147] Figure 108 shows the annotated amino acid sequence of SEQ ID NO: 341.

[0148] Figure 109 shows the annotated amino acid sequence of SEQ ID NO: 342.

[0149] Figure 110 shows the annotated amino acid sequence of SEQ ID NO: 343.

[0150] Figure 111 shows the annotated amino acid sequence of SEQ ID NO: 344.

[0151] Figure 112 shows the annotated amino acid sequence of SEQ ID NO: 345.

[0152] Figure 113 shows the annotated amino acid sequence of SEQ ID NO: 346.

[0153] Figure 114 shows the annotated amino acid sequence of SEQ ID NO: 347.

[0154] Figure 115 shows the annotated amino acid sequence of SEQ ID NO: 348.

[0155] Figure 116 shows the annotated amino acid sequence of SEQ ID NO: 349.

[0156] Figure 117 shows the annotated amino acid sequence of SEQ ID NO: 350

[0157] Figure 118 shows the annotated amino acid sequence of SEQ ID NO: 351.

[0158] Figure 119 shows the annotated amino acid sequence of SEQ ID NO: 352.

[0159] Figure 120 shows the annotated amino acid sequence of SEQ ID NO: 353.

[0160] Figure 121 shows the annotated amino acid sequence of SEQ ID NO: 354.

[0161] Figure 122 shows the annotated amino acid sequence of SEQ ID NO: 355.

[0162] Figure 123 shows the annotated amino acid sequence of SEQ ID NO: 356.

[0163] Figure 124 shows the annotated amino acid sequence of SEQ ID NO: 357.

[0164] Figure 125 shows the annotated amino acid sequence of SEQ ID NO: 358.

[0165] Figure 126 shows the annotated amino acid sequence of SEQ ID NO: 359.

[0166] Figure 127 shows the annotated amino acid sequence of SEQ ID NO: 360.

[0167] Figure 128 shows the annotated amino acid sequence of SEQ ID NO: 361.

[0168] Figure 129 shows the annotated amino acid sequence of SEQ ID NO: 362.

[0169] Figure 130 shows the annotated amino acid sequence of SEQ ID NO: 363.

[0170] Figure 131 shows the annotated amino acid sequence of SEQ ID NO: 364.

[0171] Figure 132 shows the annotated amino acid sequence of SEQ ID NO: 365.

[0172] Figure 133 shows the annotated amino acid sequence of SEQ ID NO: 366.

[0173] Figure 134 shows the annotated amino acid sequence of SEQ ID NO: 367.

[0174] Figure 135 shows the annotated amino acid sequence of SEQ ID NO: 368

[0175] Figure 136 shows the annotated amino acid sequence of SEQ ID NO: 369.

[0176] Figure 137 shows the annotated amino acid sequence of SEQ ID NO: 370.

[0177] Figure 138 shows the annotated amino acid sequence of SEQ ID NO: 371

[0178] Figure 139 shows the annotated amino acid sequence of SEQ ID NO: 372.

[0179] Figure 140 shows the annotated amino acid sequence of SEQ ID NO: 373.

[0180] Figure 141 shows the annotated amino acid sequence of SEQ ID NO: 374.

[0181] Figure 142 shows the annotated amino acid sequence of SEQ ID NO: 375.

[0182] Figure 143 shows the annotated amino acid sequence of SEQ ID NO: 376.

[0183] Figure 144 shows the annotated amino acid sequence of SEQ ID NO: 377.

[0184] Figure 145 shows the annotated amino acid sequence of SEQ ID NO: 378.

[0185] Figure 146 shows the annotated amino acid sequence of SEQ ID NO: 380. family 17 signature is in bold.

[0186] Figure 147 shows the annotated amino acid sequence of SEQ ID NO: 381.

[0187] Figure 148 shows the annotated amino acid sequence of SEQ ID NO: 382.

[0188] Figure 149 shows the annotated amino acid sequence of SEQ ID NO: 383.

[0189] Figure 150 shows the annotated amino acid sequence of SEQ ID NO: 384.

[0190] Figure 151 shows the annotated amino acid sequence of SEQ ID NO: 385.

[0191] Figure 152 shows the annotated amino acid sequence of SEQ ID NO: 386.

[0192] Figure 153 shows the annotated amino acid sequence of SEQ ID NO: 387.

[0193] Figure 154 shows the annotated amino acid sequence of SEQ ID NO: 388.

[0194] Figure 155 shows the annotated amino acid sequence of SEQ ID NO: 389.

[0195] Figure 156 shows the annotated amino acid sequence of SEQ ID NO: 390.

[0196] Figure 157 shows the annotated amino acid sequence of SEQ ID NO: 391.

[0197] Figure 158 shows the annotated amino acid sequence of SEQ ID NO: 392.

[0198] Figure 159 shows the annotated amino acid sequence of SEQ ID NO: 393

[0199] Figure 160 shows the annotated amino acid sequence of SEQ ID NO: 394.

[0200] Figure 161 shows the annotated amino acid sequence of SEQ ID NO: 395.

[0201] Figure 162 shows the annotated amino acid sequence of SEQ ID NO: 396.

[0202] Figure 163 shows the annotated amino acid sequence of SEQ ID NO: 397.

[0203] Figure 164 shows the annotated amino acid sequence of SEQ ID NO: 398.

[0204] Figure 165 shows the annotated amino acid sequence of SEQ ID NO: 399.

[0205] Figure 166 shows the annotated amino acid sequence of SEQ ID NO: 400.

[0206] Figure 167 shows the annotated amino acid sequence of SEQ ID NO: 401.

[0207] Figure 168 shows the annotated amino acid sequence of SEQ ID NO: 402.

[0208] Figure 169 shows the annotated amino acid sequence of SEQ ID NO: 403.

[0209] Figure 170 shows the annotated amino acid sequence of SEQ ID NO: 404.

[0210] Figure 171 shows the annotated amino acid sequence of SEQ ID NO: 405.

[0211] Figure 172 shows the annotated amino acid sequence of SEQ ID NO: 406.

[0212] Figure 173 shows the annotated amino acid sequence of SEQ ID NO: 407.

[0213] Figure 174 shows the annotated amino acid sequence of SEQ ID NO: 408.

[0214] Figure 175 shows the annotated amino acid sequence of SEQ ID NO: 409.

[0215] Figure 176 shows the annotated amino acid sequence of SEQ ID NO: 410.

[0216] Figure 177 shows the annotated amino acid sequence of SEQ ID NO: 411.

[0217] Figure 178 shows the annotated amino acid sequence of SEQ ID NO: 412.

[0218] Figure 179 shows the annotated amino acid sequence of SEQ ID NO: 413.

[0219] Figure 180 shows the annotated amino acid sequence of SEQ ID NO: 414.

[0220] Figure 181 shows the annotated amino acid sequence of SEQ ID NO: 415.

[0221] Figure 182 shows the annotated amino acid sequence of SEQ ID NO: 416.

[0222] Figure 183 shows the annotated amino acid sequence of SEQ ID NO: 417.

[0223] Figure 184 shows the annotated amino acid sequence of SEQ ID NO: 418.

[0224] Figure 185 shows the annotated amino acid sequence of SEQ ID NO: 419.

[0225] Figure 186 shows the annotated amino acid sequence of SEQ ID NO: 420.

[0226] Figure 187 shows the annotated amino acid sequence of SEQ ID NO: 421.

[0227] Figure 188 shows the annotated amino acid sequence of SEQ ID NO: 422.

[0228] Figure 189 shows the annotated amino acid sequence of SEQ ID NO: 423.

[0229] Figure 190 shows the annotated amino acid sequence of SEQ ID NO: 424.

[0230] Figure 191 shows the annotated amino acid sequence of SEQ ID NO: 425.

[0231] Figure 192 shows the annotated amino acid sequence of SEQ ID NO: 426.

[0232] Figure 193 shows the annotated amino acid sequence of SEQ ID NO: 427.

[0233] Figure 194 shows the annotated amino acid sequence of SEQ ID NO: 428.

[0234] Figure 195 shows the annotated amino acid sequence of SEQ ID NO: 429.

[0235] Figure 196 shows the annotated amino acid sequence of SEQ ID NO: 430.

[0236] Figure 197 shows the annotated amino acid sequence of SEQ ID NO: 431.

[0237] Figure 198 shows the annotated amino acid sequence of SEQ ID NO: 432.

[0238] Figure 199 shows the annotated amino acid sequence of SEQ ID NO: 433.

[0239] Figure 200 shows the annotated amino acid sequence of SEQ ID NO: 434.

[0240] Figure 201 shows the annotated amino acid sequence of SEQ ID NO: 435.

[0241] Figure 202 shows the annotated amino acid sequence of SEQ ID NO: 436.

[0242] Figure 203 shows the annotated amino acid sequence of SEQ ID NO: 437.

[0243] Figure 204 shows the annotated amino acid sequence of SEQ ID NO: 438.

[0244] Figure 205 shows the annotated amino acid sequence of SEQ ID NO: 439.

[0245] Figure 206 shows the annotated amino acid sequence of SEQ ID NO: 440.

[0246] Figure 207 shows the annotated amino acid sequence of SEQ ID NO: 441.

[0247] Figure 208 shows the annotated amino acid sequence of SEQ ID NO: 442.

[0248] Figure 209 shows the annotated amino acid sequence of SEQ ID NO: 443.

[0249] Figure 210 shows the annotated amino acid sequence of SEQ ID NO: 444.

[0250] Figure 211 shows the annotated amino acid sequence of SEQ ID NO: 445.

[0251] Figure 212 shows the annotated amino acid sequence of SEQ ID NO: 446.

[0252] Figure 213 shows the annotated amino acid sequence of SEQ ID NO: 447.

[0253] Figure 214 shows the annotated amino acid sequence of SEQ ID NO: 448.

[0254] Figure 215 shows the annotated amino acid sequence of SEQ ID NO: 449.

[0255] Figure 216 shows the annotated amino acid sequence of SEQ ID NO: 450.

[0256] Figure 217 shows the annotated amino acid sequence of SEQ ID NO: 451.

[0257] Figure 218 shows the annotated amino acid sequence of SEQ ID NO: 452.

[0258] Figure 219 shows the annotated amino acid sequence of SEQ ID NO: 453.

[0259] Figure 220 shows the annotated amino acid sequence of SEQ ID NO: 454.

[0260] Figure 221 shows the annotated amino acid sequence of SEQ ID NO: 455.

[0261] Figure 222 shows the annotated amino acid sequence of SEQ ID NO: 458.

[0262] Figure 223 shows the annotated amino acid sequence of SEQ ID NO: 459.

[0263] Figure 224 shows the annotated amino acid sequence of SEQ ID NO: 460.

[0264] Figure 225 shows the schematic representation of pWVK223.

[0265] Figure 226 shows the schematic representation of pOX1.

[0266] Figure 227 shows the schematic representation of pOX16.

[0267] Figure 228 shows the schematic representation of pOX2.

DETAILED DESCRIPTION OF THE INVENTION

[0268] The present invention provides isolated polynucleotides that encode wood and cell wall proteins.

[0269] Transformation of a plant with a polynucleotide sequence encoding a protein involved in wood and/or cell wall development can be employed to modify properties such as cellulose synthesis, lignin deposition, aspects of wood development, flower development, root development, branching, seasonal responses such as light and cold controls on meristem identity, and disease resistance. To this end, the present invention provides a polynucleotide sequence encoding a polypeptide sequence having a function in plant cell wall synthesis and/or development. The present invention also provides a DNA construct having a promoter operably linked to a polynucleotide sequence, wherein said polynucleotide sequence encodes a protein involved in the development of the plant cell wall. Additionally, the invention provides methods for assaying the expression of a protein involved in plant cell wall development, methods for using a plant cell wall protein for modifying growth, wood development and/or fiber composition in a plant.

[0270] The present invention uses terms and phrases that are well known to those practicing the art. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Generally, the nomenclature used herein and the laboratory procedures in cell culture, molecular genetics, and nucleic acid chemistry and hybridization described herein are those well known and commonly employed in the art. Standard techniques are used for recombinant nucleic acid methods, polynucleotide synthesis, microbial culture, cell culture, tissue culture, transformation, transfection, transduction, analytical chemistry, organic synthetic chemistry, chemical syntheses, chemical analysis, and pharmaceutical formulation and delivery. Generally, enzymatic reactions and purification and/or isolation steps are performed according to the manufacturers' specifications. The techniques and procedures are generally performed according to conventional methodology

(Molecular Cloning, A Laboratory Manual, 3rd. edition, edited by Sambrook & Russel Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001).

A. Plant Wood and Cell Wall Genes and Proteins

[0271] Alpha-amylase: Alpha-amylase functions as a major starch hydrolase and hydrolyzes alpha-1,4-glucan bonds. Alpha-amylase transcription occurs in response to a variety of hormonal, metabolic, and environmental signals. Sequence analysis of cloned alpha-amylases reveals that these fall into two major classes and three subfamilies, reviewed by Mitsui and Itoh, *Trends in Plant Science* 2 (7), 255-261 (1997), they are important in the mobilization of endosperm storage compounds during germination to supply the embryo with nutriments.

[0272] Agrobacterium: as is well known in the field, *Agrobacteria* that are used for transforming plant cells are disarmed and virulent derivatives of, usually, *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* that contain a vector. The vector typically contains a desired polynucleotide that is located between the borders of a T-DNA.

[0273] Angiosperm: vascular plants having seeds enclosed in an ovary. Angiosperms are seed plants that produce flowers that bear fruits. Angiosperms are divided into dicotyledonous and monocotyledonous plants.

[0274] Arabinogalactan: Arabinogalactan proteins (AGPs) are a family of cell wall proteins that are glycosylated hydroxyproline-rich glycoproteins and are thought to have important roles in various aspects of plant growth and development. Reviewed by Showalter, A.M. *Cell Mol Life Sci.* 58(10):1399-417 (2001). Specifically, AGPs are involved during vegetative, reproductive, and cellular growth and development, as well as programmed cell death and cell signaling.

[0275] Brassinosteroid-regulated Protein: Brassinosteroids are a class of steroid hormones that regulate plant growth and development. Brassinosteroid-regulated Protein (BRU) is a brassinosteroid-induced protein that functions as a xyloglucan endotransferase (XET). Zurek, D.M., and Clouse, S.D. *Plant Physiol.* 104 (1) 161-

170 (1994). Subsequently, similar Brassinolide-induced XETs have been characterized in Arabidopsis (Xu et al., *Plant J.* 9, 879–889 (1996)), rice (Uozu et al., *Plant Physiol.* 122, 853–859 (2000)), and tomato (Koka et al., *Plant Physiol.* **122,** 85–98 (2000)), demonstrating that the induction of XETs correlates with cell wall loosening during Brassinolide-induced growth

[0276] β-1,3-endoglucanase: β-1,3-endoglucanase (EC 3.2.1.39) are characterized as pathogenesis-related (PR) proteins because expression in a plant is often induced upon pathogen attack. They have an important role in plant defence, either directly through the degradation of β-1,3/1,6-glucans in the pathogen cell wall, or indirectly by releasing oligosaccharide elicitors that induce additional plant defenses (Kauffmann et al. (1987) *The Embo Journal* 6(11) 3209 – 3212, Bowles et al. (1990) *Annu. Rev. Biochem.* 59, 873 – 907 , Rose et al. (2002) *The Plant Cell* 14, 1329 – 1345)). The overexpression of β-1,3-endoglucanases has been shown to be useful for the protection of plants against pathogens, as demonstrated by the transformation of a soybean β-1,3-endoglucanase in tobacco (Borkowska M et al. *Z Naturforsch [C].* (1998) 53(11-12):1012-10166. Although major interest in β-1,3-endoglucanases stems from their role in plant defense they have also been implicated in a number of physiological and developmental processes in the uninfected plant including cell division, microsporogenesis, pollen germination and tube growth, fertilization, embryogenesis, fruit ripening, seed germination, mobilization of storage reserves in the endosperm of cereal grains, bud dormancy and response to wounding, cold, ozone and UV B (for review see Leubner-Metzer and Meins in *Pathogensis-related proteins in plants*. Datta and Muthukrishnan (eds) CRC Press LLC, Boco Raton, Florida, pp 49-76 (1999)).

[0277] β -1,3-glucanase; another name for β-1,3-endoglucanase (EC 3.2.1.39)

[0278] β-D-glucan exohydrolase: are widely distributed among yeast and filamentous fungi. Like β-1,3-endoglucanase, exo-1,3-β-glucanases (EC 3.2.1.58) hydrolyze the *O*-glyco-sidic linkages of 1,3-β-linked glucans. While β-1,3-endoglucanase cleave internal 1,3- β-linkages at random sites along the polysaccharide chain, releasing short oligosaccharides exo-1,3-β-glucanases

sequentially release alpha-glucose residues from the non-reducing terminus of 1,3-β-D-glucans. In Saccharomyces cerevisiae there is evidence to suggest that they participate in cell wall modifications or in sporulation (Muthukumar et al. (1993) *Journal of Bacteriology* 175(2) 386-396).

[0279] β-glucosidase: (EC 3.2.1.21) is responsible for the hydrolysis of terminal, non-reducing β-D-glucose residues with the release of β-D-glucose. The enzyme has been found in plants, animals, bacteria and fungi. In plants, β-glucosidases are reported to function in phytohormone metabolism (Smith and van Staden (1978) *J. Exp. Bot.* 29: 1067-1073), defence against pathogens and herbivours (Poulton (1990) *Plant Physiol.* 94: 401-405 (1990), Li et al. (2005) *Acta Biochim Biophys Sin* (Shanghai). Jun;37(6):363-70), and lignification (Hahlbrock and Grsebach (1979) *Ann. Rev. Plant Phyiol.* 30: 105-130).

[0280] β-xylosidase: (EC 3.2.1.37) also known as xylan 1,4-β-xylosidase catalyses the hydrolysis of 1,4- β-D-xylans, to remove successive D-xylose residues from the non-reducing termini. They have been reported to occur widely in micro-organisms, fungi, animals and recently in plants. In *Arabidopsis* it has been proposed that β-xylosidase has a role in secondary cell wall metabolism and plant development (Goujon et al. (2003) *Plant J* 33:677-690, Minic et al. (2005) *Plant Physiology* 135: 867-878).

[0281] Calnexin: Calnexin is an endoplasmic reticulum membrane-bound molecule. Calnexin specifically binds to monoglucosylated N-linked glycans and is thought to play a role in cell wall biosynthesis. It has been demonstrated in yeast that calnexin is required for cell wall biosynthesis and development. For example, a *S. cerevisiae* calnexin strain (designated CNE1$^-$) displayed abnormal cell wall development. Thus, it has been suggested that calnexin plays a role in both protein secretion and cell wall synthesis.

[0282] Calreticulin: Calreticulin is a multifunctional calcium-binding protein found in the endoplasmic reticulum of most eukaryotic cells. In mammalian cells, the trimming of glucoses is connected to a molecular chaperone cycle involving two lectin-

like chaperones, calnexin and calreticulin. Similar to calnexin, calreticulin is believed to play a role in cell wall biosynthesis.

[0283] **Cellulase:** Cellulase refers to any and all enzymes which catalyze the cleavage of cellulosic or lignocellulosic materials. Various genes encoding cellulases have also been isolated and characterized. For instance, genes encoding endoglucanases from the fungus *Trichoderma reesei* are known and have been successfully incorporated and expressed in yeast. Pentilla et al. *Yeast* 3:175-185 (1987). Cellulases are catagorized into two large sub-groups based upon whether they catalyze cleavage from the cellulose chain ends (exocellulases) or if they catalyze cleavage in the middle of the cellulose chain (endocellulases).

[0284] **Cellulose synthase:** Cellulose synthase is thought to reside in the plasma membrane as a multisubunit complex, called a rosette, and extrudes β-1,4-glucan into the extracellular matrix. Close proximity of subunits in the rosette complex presumably facilitates the hydrogen bonding of individual glucan chains into tight bundles of characteristic diameter of cellulose microfibrils.

[0285] Higher plants contain a large number of closely related genes, the CesA family, that encode a catalytic component of cellulose synthase. It is unknown whether other polypeptides are required to form an active cellulose synthase, and little is known about the regulation of its activity. However, because the deposition of cellulose microfibrils is typically oriented relative to the axis of cellular expansion, an interaction between cellulose synthase and the cortical cytoskeleton has been proposed. A temperature-sensitive mutation in one of the CesA genes, rsw1, leads to a mutant phenotype characterized by swollen cells that are thought to reflect the inability of the cells to resist or direct turgor-mediated expansion. Sugimoto K, Williamson RE, Wasteneys GO. *Protoplasma.* 215(1-4):172-83 (2001). Similar phenotypes have been generated with chemical inhibitors of cellulose biosynthesis, indicating that cellulose in the primary cell wall is required for normal growth. (Delmer, D.P., and Amor, Y. (1995). *Plant Cell* 7, 987–1000; Scheible, W.R., Eshed, R., Richmond, T., Delmer, D., and Somerville, C.R. (2001). *Proc. Natl. Acad. Sci. USA* 98, 10079–10084).

[0286] Chitinase: Chitinases catalyze the hydrolysis of *N*-acetyl-β-D-glucsaminide 1,4-β-linkages in chitin. Although chitin is not a constituent of plants, many plants do synthesize chitinases. These chitinases play a role in plant resistance against pathogens by hydrolyzing chitin which is a common component of fungal cell walls. This is also supported by research that shows that the expression of chitinase in plants led to a reduction in damage caused by pathogens (Broglie et al. (1991) Science 254:1194-1197). It has also been suggested that chitinases have a role in plant development and growth, for a review see Kasprzewska, A (2003) (*Cellular & Molecular Biology Letters* 8: 809-824).

[0287] Desired Polynucleotide: a desired polynucleotide of the present invention is a genetic element, such as a promoter, enhancer, or terminator, or gene or polynucleotide that is to be transcribed and/or translated in a transformed cell that comprises the desired polynucleotide in its genome. If the desired polynucleotide comprises a sequence encoding a protein product, the coding region may be operably linked to regulatory elements, such as to a promoter and a terminator, that bring about expression of an associated messenger RNA transcript and/or a protein product encoded by the desired polynucleotide. Thus, a "desired polynucleotide" may comprise a gene that is operably linked in the 5'- to 3'- orientation, a promoter, a gene that encodes a protein, and a terminator. Alternatively, the desired polynucleotide may comprise a gene or fragment thereof, in a "sense" or "antisense" orientation, the transcription of which produces nucleic acids that may affect expression of an endogenous gene in the plant cell. A desired polynucleotide may also yield upon transcription a double-stranded RNA product upon that initiates RNA interference of a gene to which the desired polynucleotide is associated. A desired polynucleotide of the present invention may be positioned within a T-DNA, such that the left and right T-DNA border sequences flank or are on either side of the desired polynucleotide. The present invention envisions the stable integration of one or more desired polynucleotides into the genome of at least one plant cell. A desired polynucleotide may be mutated or a variant of its wild-type sequence. It is understood that all or part of the desired polynucleotide can be integrated into the genome of a plant. It also is understood that the term "desired polynucleotide" encompasses one or more of such

polynucleotides. Thus, a T-DNA of the present invention may comprise one, two, three, four, five, six, seven, eight, nine, ten, or more desired polynucleotides.

[0288] Dicotyledonous plant (dicot): a flowering plant whose embryos have two seed halves or cotyledons, branching leaf veins, and flower parts in multiples of four or five. Examples of dicots include but are not limited to, *Eucalyptus, Populus, Liquidamber, Acacia,* teak, mahogany, cotton, tobacco, *Arabidopsis,* tomato, potato sugar beet, broccoli, cassava, sweet potato, pepper, poinsettia, bean, alfalfa, soybean, carrot, strawberry, lettuce, oak, maple, walnut, rose, mint, squash, daisy, geranium, avocado, and cactus.

[0289] Dirigent: Dirigent proteins are a unique class of plant proteins that control free-radical coupling during lignin formation and lignification. Gang, D.R. et al. *Chem Biol.* 6(3):143-51 (1999). Lignification is a very precise process and moves from the outer wall of the cell inward towards the plasma membrane, and it has been shown that lignification sites in the outer wall house dirigent proteins. Davin, N.B. and N.G. Lewis. *Plant Physiol.* 123(2):453-62 (2000). Dirigent immunolocalization studies reveal cross-reactivity with particular regions of the lignified cell walls, these being coincident with the known sites of initiation of lignin deposition. Burlat, V. et al. *Phytochemistry* 57(6):883-97 (2001).

[0290] Endogenous refers to a gene that is native to a plant genome.

[0291] Expansin: Expansins are a class of proteins that regulate cell wall extension during growth. McQueen-Mason et al. *Plant Cell* 4: 1425-1433 (1992). In addition to their role during wall loosening, expansins are thought to play roles in cell wall extension, pollination, and fruit ripening. Cosgrove, D.J. *Proc Natl Acad Sci U S A.* 27;94(11):5504-5 (1997). Expansins are commonly encoded by several gene families and have classically been divided into two subfamilies, **alpha-** and **beta-expansins**. **Alpha-expansins** are a highly conserved group of proteins hypothesized to control cell wall enlargement and other developmental processes including cell wall disassembly and cell separation. **Beta-expansins**, previously known as **group-1 grass pollen allergens**, are secreted by grass pollen and impart wall loosening effects

on grass cell walls. Beta-expansins are found in non-pollen tissues and may play a developmental role in wall-loosening.

[0292] Extensin: Extensins refer to a class of **hydroxyproline-rich glycoproteins** found in the cell walls of higher plants. Extensins are thought to reinforce the cell wall by inter- and intramolecule interactions. Merkouropoulos, G. et al. *Planta* 208(2):212-9 (1999). Extensins are normally expressed in the root and silent in the leaf; however, wounding reverses this pattern, turning on the gene in the leaf and repressing it in the root. *Id.* Because extensins are activated by several stress-inducing signals, including wounding, methyl jasmonate, salicylic acid, and abscisic acid, extensins are thought to play a defense role by reinforcing and strengthening the cell wall.

[0293] Fiber composition: as used herein, fiber composition refers to trait that can be modified to change the structure, appearance, or use of fiber. While not limiting, traits that determine fiber composition include fiber length, coarseness, strength, color, cross-sectional, and fiber density. For example, it is known that fiber length imparts strength, whereas fiber coarseness determines texture and flexibility.

[0294] Foreign: "foreign," with respect to a nucleic acid, means that that nucleic acid is derived from non-plant organisms, or derived from a plant that is not the same species as the plant to be transformed or is not derived from a plant that is not interfertile with the plant to be transformed, does not belong to the species of the target plant. According to the present invention, foreign DNA or RNA represents nucleic acids that are naturally occurring in the genetic makeup of fungi, bacteria, viruses, mammals, fish or birds, but are not naturally occurring in the plant that is to be transformed. Thus, a foreign nucleic acid is one that encodes, for instance, a polypeptide that is not naturally produced by the transformed plant. A foreign nucleic acid does not have to encode a protein product.

[0295] Galacturan 1,4-alpha-galacturonidase: Galacturan 1,4-alpha-galacturonidase (also called **exopolygalacturonase** or **ExoPG**) is a pectin degrading enzyme. ExoPG degrades pectin by removing galacturonate monomers from the

polygalacturonate chain component of pectin. Using immunochemistry and in situ hybridization, it has been shown that in addition to its presence in pollen, ExoPG is also present in sporophytic tissues, such as the tapetum and mesophyll cells. Dubald, M. et al. *Plant J.* 4(5):781-91 (1993). ExoPG is also though to play a role during fungal pathogenesis; for example, a novel ExoPG was identified as the causative agent responsible for foot crown and root rot disease in tomato plants. De las Heras, A. *J Appl Microbiol.*94(5):856-64 (2003). These results suggest a general function for ExoPG in cell wall degradation.

[0296] **Gene:** A gene is a segment of a DNA molecule that contains all the information required for synthesis of a product, polypeptide chain or RNA molecule that includes both coding and non-coding sequences.

[0297] **Genetic element:** a "genetic element" is any discreet nucleotide sequence such as, but not limited to, a promoter, gene, terminator, intron, enhancer, spacer, 5'-untranslated region, 3'-untranslated region, or recombinase recognition site.

[0298] **Genetic modification:** stable introduction of DNA into the genome of certain organisms by applying methods in molecular and cell biology.

[0299] **Glucose-1-phosphate adenyltransferase:** Glucose-1-phosphate adenyltransferase (**AGP**) catalyzes one of the first committed steps in the starch biosynthesis pathway, the production of ADP-Glucose from Glucose-1-phosphate and ATP. AGP regulates starch accumulation, as AGP mutants have decreased starch accumulation. Wang S-M, Chu B, Lue W-L, Yu T-S, Eimert K, Chen J (1997). Plant J **11**: 1121–1126.

[0300] **Glycoside hydrolase:** Glycoside hydrolases are one of two major classes of carbohydrate-active enzymes, glycoside hydrolases and glycosyltransferases. They frequently display a modular structure: a catalytic domain, responsible for a hydrolysis reaction breaking down a glycoside, and a cellulose-binding module, devoid of catalytic activity but promoting adsorption of the enzyme onto insoluble crystalline cellulose. They are related in structure to chitinases and concanavalin A. Bernard Henrissat and Gideon J. Davies. Glycoside Hydrolases and

Glycosyltransferases. Families, Modules, and Implications for Genomics. Plant Physiol, December 2000, Vol. 124, pp. 1515-1519.

[0301] **Glycosyl hydrolase**: Glycosyl hydrolases are a general class of enzymes that break bonds between sugar moieties. This class includes alpha-amylase, alpha-galactosidase, endo and exo-beta-glucanases, etc.

[0302] **Glycosyl transferase:** Glycosyltransferases are one of two major classes of carbohydrate-active enzymes, glycoside hydrolases and glycosyltransferases. They frequently display a modular structure: a catalytic domain, responsible for a reaction adding a glycoside moiety, and a cellulose-binding module, devoid of catalytic activity but promoting adsorption of the enzyme onto insoluble crystalline cellulose. They are related in structure to chitin synthases. Bernard Henrissat and Gideon J. Davies. Glycoside Hydrolases and Glycosyltransferases. Families, Modules, and Implications for Genomics. Plant Physiol, December 2000, Vol. 124, pp. 1515-1519.

[0303] **Gymnosperm:** as used herein, refers to a seed plant that bears seed without ovaries. Examples of gymnosperms include conifers, cycads, ginkgos, and ephedras.

[0304] **Hexose Pyrophosphorylase**: Hexose Pyrophosphorylases (EC 2.7.7.28) are a class of enzymes that have tranferase activity transferring phosphorous containing groups. They catalyze the reaction: hexose 1-phosphate + nucleoside triphosphate = NDP-hexose + diphosphate (Verachtert et al. (1966) *Journal Biol. Chem.* 241(9) 2007- 2013).

[0305] **Hydroxyproline-rich proteins**: Hydroxyproline-rich proteins (**HRGPs**) are a large class of plant cell wall proteins and are the best studied cell wall proteins. While the precise function of HRGPs remains unknown, HRGPs are induced by wounding and pathogen infection, suggesting a role in reinforcing and strengthening the cell wall. Additionally, HRGPs may also provide nucleating sites for lignification during secondary wall formation. Vignols, F. *Plant Mol Biol.* 39(5):945-52 (1999).

[0306] **Introduction:** as used herein, refers to the insertion of a nucleic acid sequence into a cell, by methods including infection, transfection, transformation or transduction.

[0307] **Juvenility:** describes a physiological difference between a young tree and a mature tree. In the present invention, juvenility refers to differences in microfibril angle, wood density, cellulose yield, regenerability, and reproductive ability between a young tree and a mature tree. For example, it has been shown that as a plant tissue matures, the tissue loses its ability to regenerate.

[0308] **Lignin:** as used herein, refers to a polymeric composition composed of phenylpropanoid units, including polymerized derivatives of monolignols coniferyl, coumaryl, and sinapyl alcohol. Lignin quality refers to the ability of a lignin composition to impart strength to cell wall matrices, assist in the transport of water, and/or impede degradation of cell wall polysaccharides. Lignin compositon or lignin structure may be changed by altering the relative amounts of each of monolignols or by altering the type of lignin. For example, guaiacyl lignins (derived primarily from ferulic acid) are prominent in softwood species, whereas guaiacyl-syringyl lignins (derived from both ferulic acid and sinapic acid) are characteristic of hardwood species. The degradation of lignin from softwoods, such as pine, requires substantially more alkali and longer incubations, compared with the removal of lignin from hardwoods. Additionally, lignin composition may be regulated by either up-regulation or down-regulation of enzymes involved lignin biosynthesis. For example, key lignin biosynthsesis enzymes include 4-coumaric acid: coenzyme A ligase (4CL), Cinnamyl Alcohol dehydrogenase (CAD), and Sinapyl Alcohol Dehydrogenase (SAD).

[0309] **Mannose-6-phosphate isomerase:** Mannose-6-phosphate isomerase catalyzes the interconversion of mannose-6-phosphate to fructose-6-phosphate. There is a distinct lack of literature regarding plant mannose-6-phosphate isomerases, as it has not been identified in many plants.

[0310] Mannose-1-phosphate guanylyltransferase: Mannose-1-phosphate guanylytransferase catalyzes the biosynthesis of GDP-mannose from mannose-6-phosphate and plays a role in cell wall biosynthesis. Specifically, mannose-1-phosphate guanylytransferase is thought to represent the first committed step in the formation of all plant guanosin-containing sugar nucleotides, which are precursors for cell wall biosynthesis. For example, *Arabidopsis cyt1* mutants are deficient in mannose-1-phosphate guanylytransferase and display a severe defect in cell wall biogenesis. Lukowitz, N. et al. *Proc Natl Acad Sci U S A.*; 98(5):2262-7 (2001). Notably, cyt1 mutants display ectopic callose accumulation, incomplete cell walls, and a 5-fold decrease in cellulose content. *Id.*

[0311] Monocotyledonous plant (monocot): a flowering plant having embryos with one cotyledon or seed leaf, parallel leaf veins, and flower parts in multiples of three. Examples of monocots include, but are not limited to turfgrass, maize, rice, oat, wheat, barley, sorghum, orchid, iris, lily, onion, and palm. Examples of turfgrass include, but are not limited to *Agrostis spp.* (bentgrass species including colonial bentgrass and creeping bentgrasses), *Poa pratensis* (kentucky bluegrass), *Lolium spp.* (ryegrass species including annual ryegrass and perennial ryegrass), *Festuca arundinacea* (tall fescue) *Festuca rubra commutata* (fine fescue), *Cynodon dactylon* (common bermudagrass varieties including Tifgreen, Tifway II, and Santa Ana, as well as hybrids thereof); *Pennisetum clandestinum* (kikuyugrass), *Stenotaphrum secundatum* (st. augustinegrass), *Zoysia japonica* (zoysiagrass), and *Dichondra micrantha.*

[0312] Nucleotidyl transferase: [EC 2.7.7] any member of a sub-subclass of enzymes of the transferase class that catalyze the transfer of a nucleotidyl group from a nucleoside di- or triphosphate donor group to an acceptor group. Nucleotidyl transferases are involved in a variety of biological processes including replication and repair, transcription, RNA processing and viral replication (Aravind and Koonin (1999) *Nucleic Acid Research* 27(7) 1609-1618).

[0313] Operably linked: combining two or more molecules in such a fashion that in combination they function properly in a plant cell. For instance, a promoter is

operably linked to a structural gene when the promoter controls transcription of the structural gene.

[0314] Pectins: Pectins are complex polymers and they are thought to perform many functions, such as determining cell wall porosity and providing charged surfaces for modulating cell wall pH and ion balance. Additionally, pectins may play a role in cell signaling by recognizing compounds and then relaying a response in a developmental cascade.

[0315] Pectin methylesterase: Pectin methlyesterase catalyzes the hydrolysis of pectin into pectate and methanol, and plays an important role during fruit ripening. Specifically, pectin methlyesterase is thought to play a role in cell wall metabolism. Additionally, several plant pathogens use pectinesterases to macerate and soft-rot plant tissues. The *Arabidopsis* genome contains at least 12 pectin methylesterase related genes. Micheli et al. *Gene* 5;220(1-2):13-20 (1998).

[0316] Phenotype: phenotype is a distinguishing feature or characteristic of a plant, which may be altered according to the present invention by integrating one or more "desired polynucleotides" and/or screenable/selectable markers into the genome of at least one plant cell of a transformed plant. The "desired polynucleotide(s)" and/or markers may confer a change in the phenotype of a transformed plant, by modifying any one of a number of genetic, molecular, biochemical, physiological, morphological, or agronomic characteristics or properties of the transformed plant cell or plant as a whole. Thus, expression of one or more, stably integrated desired polynucleotide(s) in a plant genome, may yield a phenotype selected from the group consisting of, but not limited to, increased drought tolerance, enhanced cold and frost tolerance, improved vigor, enhanced color, enhanced health and nutritional characteristics, improved storage, enhanced yield, enhanced salt tolerance, enhanced heavy metal tolerance, increased disease tolerance, increased insect tolerance, increased water-stress tolerance, enhanced sweetness, improved vigor, improved taste, improved texture, decreased phosphate content, increased germination, increased micronutrient uptake, improved starch composition, and improved flower longevity.

[0317] Phosphomannomutase: Phosphomannomutase 2 catalyzes the isomerization of mannose 6-phosphate to mannose 1-phosphate. Popova TN, Matasova LV, Lapot'ko AA. Purification, separation and characterization of phosphoglucomutase and phosphomannomutase from maize leaves. Biochem Mol Biol Int. 1998 Oct;46(3):461-70.

[0318] Plant disease resistance response protein: Plant disease resistance genes have been exhaustively investigated in terms of their structural organization, sequence evolution and genome distribution. This has been well reviewed in Lehmann P *J Appl Genet.*; 43(4):403-14(2002). Most plant disease resistance (R) proteins contain a series of leucine-rich repeats (LRRs), a nucleotide-binding site (NBS), and a putative amino-terminal signaling domain. They are termed NBS-LRR proteins. The LRRs of a wide variety of proteins from many organisms serve as protein interaction platforms, and as regulatory modules of protein activation. Genetically, the LRRs of plant R proteins are determinants of response specificity, and their action can lead to plant cell death in the form of the familiar hypersensitive response (HR). The partners or R proteins remain unclear but current knowledge is reviewed in Belkhadir Y, *et al, Curr Opin Plant Biol.* 7(4):391-9 (2004).

[0319] Plant tissue: a "plant" is any of various photosynthetic, eukaryotic, multicellular organisms of the kingdom *Plantae* characteristically producing embryos, containing chloroplasts, and having cellulose cell walls. A part of a plant, *i.e.*, a "plant tissue" may be treated according to the methods of the present invention to produce a transgenic plant. Many suitable plant tissues can be transformed according to the present invention and include, but are not limited to, somatic embryos, pollen, leaves, stems, calli, stolons, microtubers, and shoots. Thus, the present invention envisions the transformation of angiosperm and gymnosperm plants such as turfgrass, wheat, maize, rice, barley, oat, sugar beet, potato, tomato, tobacco, alfalfa, lettuce, carrot, strawberry, cassava, sweet potato, geranium, soybean, oak, pine, fir, acacia, eucalyptus, walnut, and palm. According to the present invention "plant tissue" also encompasses plant cells. Plant cells include suspension cultures, callus, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes,

pollen, seeds and microspores. Plant tissues may be at various stages of maturity and may be grown in liquid or solid culture, or in soil or suitable media in pots, greenhouses or fields. A plant tissue also refers to any clone of such a plant, seed, progeny, propagule whether generated sexually or asexually, and descendents of any of these, such as cuttings or seed. Of particular interest are conifers such as pine, fir and spruce, monocots such as Kentucky bluegrass, creeping bentgrass, maize, and wheat, and dicots such as cotton, tomato, lettuce, *Arabidopsis*, tobacco, and geranium.

[0320] Plant transformation and cell culture: broadly refers to the process by which plant cells are genetically modified and transferred to an appropriate plant culture medium for maintenance, further growth, and/or further development. Such methods are well known to the skilled artisan.

[0321] Polygalacturonase: Polygalacturonase **(Pectin depolymerase, pectinase, PG)** degrades the plant cell wall by depolymerizing **pectin**. Polygalacturonase depolymerizes pectin during a variety of developmental processes, including pollination and fruit ripening. Additionally, many plant pathogens secrete polygalacturonase during host infection, thereby degrading the host cell wall.

[0322] Progeny: a "progeny" of the present invention, such as the progeny of a transgenic plant, is one that is born of, begotten by, or derived from a plant or the transgenic plant. Thus, a "progeny" plant, *i.e.*, an "F1" generation plant is an offspring or a descendant of the transgenic plant produced by the inventive methods. A progeny of a transgenic plant may contain in at least one, some, or all of its cell genomes, the desired polynucleotide that was integrated into a cell of the parent transgenic plant by the methods described herein. Thus, the desired polynucleotide is "transmitted" or "inherited" by the progeny plant. The desired polynucleotide that is so inherited in the progeny plant may reside within a T-DNA construct, which also is inherited by the progeny plant from its parent. The term "progeny" as used herein, also may be considered to be the offspring or descendants of a group of plants.

[0323] Promoter: promoter is intended to mean a nucleic acid, preferably DNA that binds RNA polymerase and/or other transcription regulatory elements. As with

any promoter, the promoters of the current invention will facilitate or control the transcription of DNA or RNA to generate an mRNA molecule from a nucleic acid molecule that is operably linked to the promoter. As stated earlier, the RNA generated may code for a protein or polypeptide or may code for an RNA interfering, or antisense molecule.

[0324] **A plant promoter** is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria such as *Agrobacterium* or *Rhizobium* which comprise genes expressed in plant cells. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as xylem, leaves, roots, or seeds. Such promoters are referred to as **tissue-preferred promoters**. Promoters which initiate transcription only in certain tissues are referred to as **tissue-specific promoters**. A **cell type- specific promoter** primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An **inducible** or **repressible promoter** is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute the class of **non-constitutive promoters**. A **constitutive promoter** is a promoter which is active under most environmental conditions, and in most plant parts.

[0325] **Pollen allergen/expansin**: Group I allergens are the major allergens of grass pollen and they have been shown to be structurally related to expansin (Cosgrove DJ et al, *Proc Natl Acad Sci U S A.* 1997 Jun 10;94(12):6559-64). Expansins are now generally accepted to be key regulators of wall extension during growth. Their exact mode of function is unclear, but in plants, expansins probably increase solubilisation of wall polymers during wall breakdown. There is evidence that expansins enhance growth by mediating cell wall loosening (Choi D, Lee Y, Cho HT, Kende H *Plant Cell.* 2003 Jun;15(6):1386-98), have a role in plant morphogenesis (Pien S, Wyrzykowska J, McQueen-Mason S, Smart C, Fleming A.

Proc *Natl Acad Sci USA*. 2001 Sep 25;98(20):11812-7) and are important in cell wall breakdown or softening in processes such as fruit ripening, pollination, germination and abscission (Li Y, Jones L, McQueen-Mason S, *Curr Opin Plant Biol*. 2003 Dec;6(6):603-10).

[0326] **Polynucleotide** is a nucleotide sequence, comprising a gene coding sequence or a fragment thereof, (comprising at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 50 consecutive nucleotides), a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker or the like. The polynucleotide may comprise single stranded or double stranded DNA or RNA. The polynucleotide may comprise modified bases or a modified backbone. The polynucleotide may be genomic, an RNA transcript (such as an mRNA) or a processed nucleotide sequence (such as a cDNA). The polynucleotide may comprise a sequence in either sense or antisense orientations.

[0327] An **isolated polynucleotide** is a polynucleotide sequence that is not in its native state, e.g., the polynucleotide is comprised of a nucleotide sequence not found in nature or the polynucleotide is separated from nucleotide sequences with which it typically is in proximity or is next to nucleotide sequences with which it typically is not in proximity.

[0328] **Regenerability**: as used herein, refers to the ability of a plant to redifferentiate from a de-differentiated tissue.

[0329] **Seed:** a "seed" may be regarded as a ripened plant ovule containing an embryo, and a propagative part of a plant, as a tuber or spore. Seed may be incubated prior to *Agrobacterium*-mediated transformation, in the dark, for instance, to facilitate germination. Seed also may be sterilized prior to incubation, such as by brief treatment with bleach. The resultant seedling can then be exposed to a desired strain of *Agrobacterium*.

[0330] **Selectable/screenable marker:** a gene that, if expressed in plants or plant tissues, makes it possible to distinguish them from other plants or plant tissues that do

not express that gene. Screening procedures may require assays for expression of proteins encoded by the screenable marker gene. Examples of such markers include the beta glucuronidase (*GUS*) gene and the luciferase (*LUX*) gene. Examples of selectable markers include the neomycin phosphotransferase (*NPTII*) gene encoding kanamycin and geneticin resistance, the hygromycin phosphotransferase (*HPT* or *APHIV*) gene encoding resistance to hygromycin, acetolactate synthase (*als*) genes encoding resistance to sulfonylurea-type herbicides, genes (*BAR* and/or *PAT*) coding for resistance to herbicides which act to inhibit the action of glutamine synthase such as phosphinothricin (Liberty or Basta), or other similar genes known in the art.

[0331] Sequence identity: as used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a specified region. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g. charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, *e.g.*, according to the algorithm of Meyers and Miller, *Computer Applic. Biol. Sci.*, 4: 11-17 (1988) *e.g.*, as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

[0332] As used herein, percentage of sequence identity means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0333] "Sequence identity" has an art-recognized meaning and can be calculated using published techniques. See COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, *ed.* (Oxford University Press, 1988), BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, *ed.* (Academic Press, 1993), COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin & Griffin, *eds.*, (Humana Press, 1994), SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, Von Heinje *ed.*, Academic Press (1987), SEQUENCE ANALYSIS PRIMER, Gribskov & Devereux, *eds.* (Macmillan Stockton Press, 1991), and Carillo & Lipton, *SIAM J. Applied Math.* 48: 1073 (1988). Methods commonly employed to determine identity or similarity between two sequences include but are not limited to those disclosed in GUIDE TO HUGE COMPUTERS, Bishop, *ed.*, (Academic Press, 1994) and Carillo & Lipton, *supra.* Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include but are not limited to the GCG program package (Devereux *et al.*, *Nucleic Acids Research* 12: 387 (1984)), BLASTP, BLASTN, FASTA (Atschul *et al.*, *J. Mol. Biol.* 215: 403 (1990)), and FASTDB (Brutlag *et al.*, *Comp. App. Biosci.* 6: 237 (1990)).

[0334] **Starch**: Starch is an insoluble stable carbohydrate reserve present in almost all plants. Starch is synthesized from triose phosphate generated from the Calvin cycle and starch synthesis occurs in the chloroplast. Starch polymers are composed of two different types of glucan polymers, **amylase** and **amylopectin**.

[0335] Starch Branching Enzyme: Starch Branching Enzyme (**SBE**) is one of the key enzymes involved in starch synthesis. SBE introduces alpha- 1,6 glucan branches and is thought to influence amylopectin structure. All higher plants have two classes of SBE, referred to as **BEI** and **BEII** in maize, rice, wheat, and barley; and as B-type and A-type in pea, kidney bean, and potato. Biochemical analyses with maize revealed that BEI preferentially branches amylose-type fewer branched polyglucans, whereas BEII has a higher capacity for branching amylopectin-type highly brached alpha-glucans. Guan, H.P and Preiss, J. *Plant Physiol* 102: 1269–1273 (1993). These data strongly suggest that BEI and BEII play distinct roles in amylopectin synthesis. Nakamura, Y. *Plant Cell Physiol* 43: 718–725 (2002).

[0336] Starch Synthase: Starch synthase is thought to elongate both amylase and amylopectin polymers by adding an ADP-glucose molecule to the nascent polymer. Starch synthase occurs in 2 different forms: soluble starch synthase and granule-bound starch synthase. Starch synthase proteins share a common KXGG motif, which is thought to provide an ADP-glucose binding site. Knight, M.E. et al. *Plant J* 14(5):613-22 (1998).

[0337] Sucrose synthase: Sucrose synthase plays an important role partitioning sucrose between cell wall biosynthesis and glycolysis. Several reports demonstrate that sucrose synthase acts as a metabolic channel for transferring glucose, derived from sucrose, to a growing cellulose chain. For example, in the roots of wheat (*Triticum aestivum* L. cv. Alcedoroot), elevated sugar content is used for synthesizing cellulose for secondary wall thickening. Albrecht, G. and Mustoph, A. *Planta* 217(2):252-60 (2003). Additionally, suppression of sucrose synthase gene (Sus) in the ovule epidermis of cotton led to a fiberless phenotype. Ruan et al. *Plant Cell* 15(4):952-64 (2003). The level of Sus suppression correlated strongly with the degree of inhibition of fiber initiation and elongation. Ruan et al. *Plant Cell* 15(4):952-64 (2003). Furthermore, it has been shown that antisense repression of sucrose synthase in carrot (*Daucus carota* L.) affects growth rather than sucrose partitioning. Tang GQ and Sturm A. *Plant Mol Biol.* 41(4):465-79 (1999).

[0338] **Sucrose-phosphate synthase (SPS)** catalyzes a reversible reaction in the pathway of sucrose synthesis, the formation of sucrose-6-phosphate from fructose-6-phosphate (Fru6P) and UDPGlucose (UDPG1c), and is the major limiting enzyme for sucrose synthesis. Additionally, sucrose-phosphate synthase plays a role during cell growth. For example, a gene underlying a quantitative trait locus (QTL) controlling plant height in rice (*Oryza sativa* L.) suggests that a putative sucrose phosphate synthase gene controls plant height by enabling higher amounts of sucrose to be translocated in leaves. Ishimaru et al. *Planta* 218(3):388-95 (2004). Transgenic rice plants with a maize SPS gene that had about 3 times the SPS activity of control plants and were significantly taller than control plants. *Id.*

[0339] Several studies have demonstrated that SPS regulates photosynthetic partitioning in the plant. For example, tomato plants expressing a maize SPS showed 2-3-fold increases in SPS activity, increased partitioning of photoassimilate to sucrose, and up to 58% higher maximal rates of photosynthesis. Lunn, J.E. et al. *J Exp Bot.* 54(381):223-37 (2003). Increased SPS expression correlated with altered shoot:root dry weight ratio, favoring the shoot. Galtier, N. *Plant Physiol.* 101(2):535-543 (1993). Accordingly, regulating SPS expression may allow for increased photosynthetic rates during unfavorable conditions. *Id.*

[0340] **Syringolide-induced Protein**: Syringolide is produced by the bacterial plant pathogen *Pseudomonas syringae* and is believed to enter the plant through passive diffusion (Ji et al. (1998) *Proc. Natl. Acad. Sci. USA* 95: 3306-3311). In soybean leaf tissue, it induces *Rpg4*-specific hypersentive cell death but very little is know about signaling in the syringolide/soybean system.

[0341] **Transcription factor**: Transcription factor refers to a polypeptide sequence that regulates the expression of a gene or genes by either directly binding to one or more nucleotide sequences associated with a gene coding sequence or indirectly affecting the activity of another polypeptide(s) that binds directly to one or more nucleotide sequences associated with a gene coding sequence. A transcription factor may **activate (up-regulate)** or **repress (down-regulate)** expression of a gene or genes. A transcription factor may contain a DNA binding domain, an activation

domain, or a domain for protein-protein interactions. In the present invention, a transcription factor is capable of at least one of (1) binding to a nucleic acid sequence or (2) regulating expression of a gene in a plant. Additionally, the inventive polynucleotide sequences and the corresponding polypeptide sequences function as transcription factors in any plant species, including angiosperms and gymnosperms.

[0342] Transcription and translation terminators: The expression DNA constructs of the present invention typically have a transcriptional termination region at the opposite end from the transcription initiation regulatory region. The transcriptional termination region may be selected, for stability of the mRNA to enhance expression and/or for the addition of polyadenylation tails added to the gene transcription product. Translation of a nascent polypeptide undergoes termination when any of the three chain-termination codons enters the A site on the ribosome. Translation termination codons are UAA, UAG, and UGA.

[0343] Transfer DNA (T-DNA): an *Agrobacterium* T-DNA is a genetic element that is well-known as an element capable of integrating a nucleotide sequence contained within its borders into another genome. In this respect, a T-DNA is flanked, typically, by two "border" sequences. A desired polynucleotide of the present invention and a selectable marker may be positioned between the left border-like sequence and the right border-like sequence of a T-DNA. The desired polynucleotide and selectable marker contained within the T-DNA may be operably linked to a variety of different, plant-specific (*i.e.*, native), or foreign nucleic acids, like promoter and terminator regulatory elements that facilitate its expression, *i.e.*, transcription and/or translation of the DNA sequence encoded by the desired polynucleotide or selectable marker.

[0344] Transformation of plant cells: A process by which a nucleic acid is stably inserted into the genome of a plant cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of nucleic acid sequences into a prokaryotic or eukaryotic host cell, including *Agrobacterium*-mediated transformation

protocols, viral infection, whiskers, electroporation, microinjection, polyethylene glycol-treatment, heat shock, lipofection and particle bombardment.

[0345] Transgenic plant: a transgenic plant of the present invention is one that comprises at least one cell genome in which an exogenous nucleic acid has been stably integrated. According to the present invention, a transgenic plant is a plant that comprises only one genetically modified cell and cell genome, or is a plant that comprises some genetically modified cells, or is a plant in which all of the cells are genetically modified. A transgenic plant of the present invention may be one that comprises expression of the desired polynucleotide, *i.e.*, the exogenous nucleic acid, in only certain parts of the plant. Thus, a transgenic plant may contain only genetically modified cells in certain parts of its structure.

[0346] UTP-glucose-1-phosphate uridylyltransferase: UTP-glucose-1-phosphate uridylyltransferase (UGP) catalyzes the conversion of alpha-D-glucose-1-phosphate and UTP to diphosphate and UDP-glucose. UDP-glucose is a key component of polysaccharide biosynthesis and can be combined with D-fructose for sucrose synthesis.

[0347] Variant: a "variant," as used herein, is understood to mean a nucleotide or amino acid sequence that deviates from the standard, or given, nucleotide or amino acid sequence of a particular gene or protein. The terms, "isoform," "isotype," and "analog" also refer to "variant" forms of a nucleotide or an amino acid sequence. An amino acid sequence that is altered by the addition, removal or substitution of one or more amino acids, or a change in nucleotide sequence, may be considered a "variant" sequence. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties, *e.g.*, replacement of leucine with isoleucine. A variant may have "nonconservative" changes, *e.g.*, replacement of a glycine with a tryptophan. Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted may be found using computer programs well known in the art such as Vector NTI Suite (InforMax, MD) software. "Variant" may also refer to a "shuffled gene" such as those described in Maxygen-assigned patents.

For instance, a variant of the present invention may include variants of sequences and desired polynucleotides that are modified according to the methods and rationale disclosed in U.S. 6,132,970, which is incorporated herein by reference.

[0348] Wood composition, as used herein, refers to trait that can be modified to change the structure, appearance, or use of wood. While not limiting, traits that determine wood composition include cell wall thickness, cell length, cell density, microfibril angle, tensile strength, tear strength, wood color, and length and frequency of cell division.

[0349] Wood pulp refers to fiber generated from wood having varying degrees of purification. Wood pulp can be used for producing paper, paper board, and chemical products.

[0350] The invention provides methods of obtaining wood, wood pulp, paper, and oil from a plant transformed with a construct of the present invention. Methods for transforming and selecting a transgenic plant are are known in the art. For example, pine can be cultured and grown as described in U.S. Patent Application Publication No. 2002/0100083. Eucalyptus can be cultured and grown as in, for example, Rydelius, et al., Growing Eucalyptus for Pulp and Energy, presented at the Mechanization in Short Rotation, Intensive Culture Forestry Conference, Mobile, AL, 1994. Wood, wood pulp, paper, and oil can be obtained from the plant by any means known in the art.

[0351] As noted above, the wood and wood pulp obtained in accordance with this invention may demonstrate improved characteristics including, but not limited to any one or more of lignin composition, lignin structure, wood composition, cellulose polymerization, fiber dimensions, ratio of fibers to other plant components, plant cell division, plant cell development, number of cells per unit area, cell size, cell shape, cell wall composition, rate of wood formation, aesthetic appearance of wood, formation of stem defects, rate of growth, rate of root formation ratio of root to branch vegetative development, leaf area index, and leaf shape include increased or decreased lignin content, increased accessibility of lignin to chemical treatments,

improved reactivity of lignin, increased or decreased cellulose content increased dimensional stability, increased tensile strength, increased shear strength, increased compression strength, increased shock resistance, increased stiffness, increased or decreased hardness, decreased spirality, decreased shrinkage, and differences in weight, density, and specific gravity.

[0352] Phenotype can be assessed by any suitable means. The plants can be evaluated based on their general morphology. Transgenic plants can be observed with the naked eye, can be weighed and their height measured. The plant can be examined by isolating individual layers of plant tissue, namely phloem and cambium, which is further sectioned into meristematic cells, early expansion, late expansion, secondary wall formation, and late cell maturation. *See, e.g.,* Hertzberg, *supra.* The plants also can be assessed using microscopic analysis or chemical analysis.

[0353] Microscopic analysis includes examining cell types, stage of development, and stain uptake by tissues and cells. Fiber morphology, such as fiber wall thickness and microfibril angle of wood pulp fibers can be observed using, for example, microscopic transmission ellipsometry. *See* Ye and Sundström, *Tappi J.*, 80:181 (1997). Wood strength, density, and grain slope in wet wood and standing trees can be determined by measuring the visible and near infrared spectral data in conjunction with multivariate analysis. *See,* U.S. Patent Application Publication Nos. 2002/0107644 and 2002/0113212. Lumen size can be measured using scanning electron microscopy. Lignin structure and chemical properties can be observed using nuclear magnetic resonance spectroscopy as described in Marita *et al., J. Chem. Soc., Perkin Trans. I* 2939 (2001).

[0354] The biochemical characteristic of lignin, cellulose, carbohydrates and other plant extracts can be evaluated by any standard analytical method known including spectrophotometry, fluorescence spectroscopy, HPLC, mass spectroscopy, and tissue staining methods.

[0355] **Xyloglucan Endotransglycosylase:** Xyloglucan Endotransglycosylase (XET) can cut and rejoin xyloglucan (XG) chains and thus has been implicated in

many aspects of cell wall biosynthesis. It is considered to be a key agent in regulating cell expansion (Darley et al (2001) *Plant Mol. Biol.* 47: 179-195, Wu et al. (2005) *Planta*. 220(4):593-601), has been implicated in wall degradation needed for fruit ripening, lisogenous aerenchyma, abscission and the wall strengthening that takes place during movement of a plant (reviewed by Nishitani (1997) *Int. Rev. Cytol.* 173: 157-206 and Campbell and Braam (1999(*Trends Plant Sci.* 4: 361-366).

[0356] Several studies have demonstrated roles for XET during cell wall formation. For example, XET activity has been shown in cell wall formation in a diverse array of vascular plants, including club mosses, ferns, gymnosperms, monocots, and dicots. Vissenberg, K. et al. *J. Exp Bot* 54 (381):335-44 (2003). In addition to its role during primary cell wall formation, an in situ XET activity assay in poplar stems has demonstrated XET activity in xylem and phloem fibers during secondary wall formation. Borquin, N. *Plant Cell* 14(12):3073-88 (2002).

[0357] **Xyloglucan Synthase:** xyloglucan synthase is an enzyme system of xyloglucan 4-glucosyltransferase and xyloglucan 6-xylosyltransferase. Xyloglucan synthase catalyses the formation of xyloglucan from UDP-xylose and UDP-glucose, concurrent transfers of glucose and xylose are necessary for this synthesis. Xyloglucan 6-xylosyltransferase transfers an α-D-xylosyl residue from UDP-D-xylose to a glucose residue in xyloglucan, forming an α-1,6-D-xylosyl-D-glucose linkage. Xyloglucan 4-glucosyltransferase, transfers a β-D-glucosyl residue from UDP-glucose on to a glucose residue in xyloglucan, forming a β-1,4-D-glucosyl-D-glucose linkage (Hayashi, T. and Matsuda, K. J. Biol. Chem. 256 (1981) 11117-11122, Hayashi, T. and Matsuda, K. Plant Cell Physiol. 22 (1981) 517-523).

[0358] **Yieldin** is a cell wall protein that regulates the yield threshold of the cell wall. Okamoto-Nakazato A. *Plant Res.*115(4):309-13 (2002). Yieldin is believed to play a role in regulating cell wall yielding during elongation growth. For example, it has been shown that yieldin is differentially expressed during cell elongation in etiolated cowpea seedlings; yieldin localizes to areas of elongation and disappears

with the ceasing of cell elongation. Okamoto-Nakazato A et al. *Plant Cell Physiol.* 42(9):952-8 (2001).

[0359] It is understood that the present invention is not limited to the particular methodology, protocols, vectors, and reagents, etc., described herein, as these may vary. It is also to be understood that the terminology used herein is used for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention. It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a gene" is a reference to one or more genes and includes equivalents thereof known to those skilled in the art and so forth. Indeed, one skilled in the art can use the methods described herein to express any native gene (known presently or subsequently) in plant host systems.

Polynucleotide Sequences

[0360] The present invention relates to an isolated nucleic molecule comprising a polynucleotide having a sequence selected from the group consisting of any of the polynucleotide sequences of SEQ ID NOs: 1-230. The invention also provides functional fragments of the polynucleotide sequences of SEQ ID NOs: 1-230. The invention further provides complementary nucleic acids, or fragments thereof, to any of the polynucleotide sequences of SEQ ID NOs: 1-230, as well as a nucleic acid, comprising at least 15 contiguous bases, which hybridizes to any of the polynucleotide sequences of SEQ ID NOs: 1-230.

[0361] The present invention also relates to an isolated polypeptide sequence comprising a polypeptide having a sequence selected from the group consisting of any of the polypeptide sequences of SEQ ID NOs: 231-460. The invention also provides functional fragments of the polypeptide sequences of SEQ ID NOs: 231-460.

[0362] By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a DNA construct are considered isolated

for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include in vitro RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules, according to the present invention, further include such molecules produced synthetically.

[0363] Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA or RNA may be double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

[0364] Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc.) and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 95% identical, more typically at least about 96% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence may be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

[0365] Each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G, C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U) where each thymidine deoxynucleotide (T) in the specified deoxynucleotide sequence in is replaced by the ribonucleotide uridine (U).

[0366] The present invention is also directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the polynucleotide sequences shown in of SEQ ID NOs: 461-690 is intended DNA fragments at least 15 nucleotides, and more preferably at least 20 nucleotides, still more preferably at least 30 nucleotides in length, which are useful as diagnostic probes and primers is discussed in more detail below. Of course larger nucleic acid fragments of up to the entire length of the nucleic acid molecules of the present invention are also useful diagnostically as probes, according to conventional hybridization techniques, or as primers for amplification of a target sequence by the polymerase chain reaction (PCR), as described, for instance, in Molecular Cloning, A Laboratory Manual, 3rd. edition, edited by Sambrook & Russel., (2001), Cold Spring Harbor Laboratory Press, the entire disclosure of which is hereby incorporated herein by reference. By a fragment at least 20 nucleotides in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of SEQ ID NOs: 1-230. The nucleic acids containing the nucleotide sequences listed in SEQ ID NOs: 1-230 can be generated using conventional methods of DNA synthesis which will be routine to the skilled artisan. For example, restriction endonuclease cleavage or shearing by sonication could easily be used to generate fragments of various sizes. Alternatively, the DNA fragments of the present invention could be generated synthetically according to known techniques.

[0367] In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the

invention described above. By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides, and more preferably at least about 20 nucleotides, and still more preferably at least about 30 nucleotides, and even more preferably more than 30 nucleotides of the reference polynucleotide. These fragments that hybridize to the reference fragments are useful as diagnostic probes and primers. A probe, as used herein is defined as at least about 100 contiguous bases of one of the nucleic acid sequences set forth in of SEQ ID NOs: 1-230. For the purpose of the invention, two sequences hybridize when they form a double-stranded complex in a hybridization solution of 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100μg of non-specific carrier DNA. See Ausubel *et al.*, section 2.9, supplement 27 (1994). Sequences may hybridize at "moderate stringency," which is defined as a temperature of 60 °C in a hybridization solution of 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100μg of non-specific carrier DNA. For "high stringency" hybridization, the temperature is increased to 68 °C. Following the moderate stringency hybridization reaction, the nucleotides are washed in a solution of 2X SSC plus 0.05% SDS for five times at room temperature, with subsequent washes with 0.1X SSC plus 0.1% SDS at 60 °C for 1h. For high stringency, the wash temperature is increased to 68 °C. For the purpose of the invention, hybridized nucleotides are those that are detected using 1 ng of a radiolabeled probe having a specific radioactivity of 10,000 cpm/ng, where the hybridized nucleotides are clearly visible following exposure to X-ray film at -70 °C for no more than 72 hours.

[0368] The present application is directed to such nucleic acid molecules which are at least 60 %, 65 %, 70 %, 75 %, 80 %, 85 %, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to a nucleic acid sequence described in of SEQ ID NOs: 1-230. Preferred, however, are nucleic acid molecules which are at least 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequence shown in of SEQ ID NOs: 1-230. Differences between two nucleic acid sequences may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

[0369] As a practical matter, whether any particular nucleic acid molecule is at least 95%, 96%, 97%, 98% or 99% identical to a reference nucleotide sequence refers to a comparison made between two molecules using standard algorithms well known in the art and can be determined conventionally using publicly available computer programs such as the BLASTN algorithm. *See* Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997).

[0370] Polynucleotides may be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTX and BLASTP programs are available from the National Center for Biotechnology Information (NCBI) National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894, USA. The BLASTN algorithm Version 2.0.4 [Feb-24-1998] and Version 2.0.6 [Sept-16-1998], set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The computer algorithm FASTA is available from the University of Virginia by contacting David Hudson, Assistance Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA. Version 2.0u4 [February 1996], set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.

[0371] The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotide sequences: Unix running command: blastall -p blastn -d embldb -e 10 –G0 -E0 -r 1 -v 30 -b 30 -i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation

value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; and -o BLAST report Output File [File Out] Optional.

[0372] The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of polypeptide sequences: blastall –p blastp –d swissprotdb –e 10 -G 0 -E 0 –v 30 –b 30 –i queryseq –o results; wherein the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

[0373] The "hits" to one or more database sequences by a queried sequence produced by BLASTN, FASTA, BLASTP or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

[0374] The BLASTN, FASTA and BLASTP algorithms also produce "Expect" values for alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database, such as the preferred EMBL database, indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the polynucleotide sequences then have a probability of 90% of

being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN or FASTA algorithm.

[0375] According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN, FASTA, or BLASTP algorithms set at parameters described above.

[0376] Alternatively, variant polynucleotides of the present invention hybridize to the polynucleotide sequences recited in of SEQ ID NOs: 1-230, or complements, reverse sequences, or reverse complements of those sequences, under stringent conditions.

[0377] The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the degeneracy of the genetic code, encode a polypeptide which is the same as that encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in of SEQ ID NOs: 1-230; or complements, reverse sequences, or reverse complements thereof, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in of SEQ ID NOs: 1-230, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in of SEQ ID NOs: 231-460, as a result of amino acid

substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention. In certain embodiments, variants of the inventive polypeptides possess biological activities that are the same or similar to those of the inventive polypeptides. Such variant polypeptides function during cell wall biosynthesis and development and/or wood development.

[0378] In addition to having a specified percentage identity to an inventive polynucleotide or polypeptide sequence, variant polynucleotides and polypeptides preferably have additional structure and/or functional features in common with the inventive polynucleotide or polypeptide. Polypeptides having a specified degree of identity to a polypeptide of the present invention share a high degree of similarity in their primary structure and have substantially similar functional properties. In addition to sharing a high degree of similarity in their primary structure to polynucleotides of the present invention, polynucleotides having a specified degree of identity to, or capable of hybridizing to an inventive polynucleotide preferably have at least one of the following features: (i) they contain an open reading frame or partial open reading frame encoding a polypeptide having substantially the same functional properties as the polypeptide encoded by the inventive polynucleotide; or (ii) they have domains in common.

Promoters

[0379] The polynucleotides of the present invention can be used for specifically directing the expression of polypeptides or proteins in the tissues of plants. The nucleic acids of the present invention can also be used for specifically directing the expression of antisense RNA, or RNA involved in RNA interference (RNAi) such as small interfering RNA (siRNA), in the tissues of plants, which can be useful for inhibiting or completely blocking the expression of targeted genes. As used herein, vascular plant tissue refers to xylem, phloem or vascular cambium tissue. Preferably, the promoters of the invention are either "xylem-preferred," "cambium-preferred" or "phloem-preferred" and direct expression of an operably linked nucleic acid segment in the xylem, cambium or phloem, respectively. As used herein, "coding product" is

intended to mean the ultimate product of the nucleic acid that is operably linked to the promoters. For example, a protein or polypeptide is a coding product, as well as antisense RNA or siRNA which is the ultimate product of the nucleic acid coding for the antisense RNA. The coding product may also be non-translated mRNA. The terms polypeptide and protein are used interchangeably herein. Xylem-preferred, for example, is intended to mean that the nucleic acid molecules of the current invention are more active in the xylem than in any other plant tissue. Most preferably, the nucleic acids of the current invention are promoters that are active specifically in the xylem, cambium or phloem, meaning that the promoters are only active in the xylem, cambium or phloem tissue of plants, respectively. In other words, a "xylem-specific" promoter, for example, drives the expression of a coding product such that detectable levels of the coding product are expressed only in xylem tissue of a plant. However, because of solute transport in plants, the coding product that is specifically expressed in the xylem, phloem or cambium may be found anywhere in the plant and thus its presence is not necessarily confined to xylem tissue. A vascular-preferred promoter, on the other hand can be preferentially active is any of the xylem, phloem or cambium tissues, or in at least two of the three tissue types. A vascular-specific promoter is specifically active in any of the xylem, phloem or cambium, or in at least two of the three.

[0380] As used herein, promoter is intended to mean a nucleic acid, preferably DNA that binds RNA polymerase and/or other transcription regulatory elements. As with any promoter, the promoters of the current invention will facilitate or control the transcription of DNA or RNA to generate an mRNA molecule from a nucleic acid molecule that is operably linked to the promoter. The RNA may code for a protein or polypeptide or may code for an RNA interfering, or antisense molecule. As used herein, "operably linked" is meant to refer to the chemical fusion, ligation, or synthesis of DNA such that a promoter-nucleic acid sequence combination is formed in a proper orientation for the nucleic acid sequence to be transcribed into an RNA segment. The promoters of the current invention may also contain some or all of the 5' untranslated region (5' UTR) of the resulting mRNA transcript. On the other hand,

the promoters of the current invention do not necessarily need to possess any of the 5' UTR.

[0381] A promoter, as used herein, may also include regulatory elements. Conversely, a regulatory element may also be separate from a promoter. Regulatory elements confer a number of important characteristics upon a promoter region. Some elements bind transcription factors that enhance the rate of transcription of the operably linked nucleic acid. Other elements bind repressors that inhibit transcription activity. The effect of transcription factors on promoter activity may determine whether the promoter activity is high or low, i.e. whether the promoter is "strong" or "weak."

[0382] In another embodiment, a constitutive promoter may be used for expressing the inventive polynucleotide sequences. Examples of constitutive plant promoters which may be useful for expressing a cell wall or wood biosynthesis gene: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (Odel et al. *Nature* 313:810(1985)); the nopaline synthase promoter (An et al. *Plant Physiol.* 88:547 (1988)); and the octopine synthase promoter (Fromm et al., *Plant Cell* 1: 977 (1989)).

[0383] In another embodiment, a variety of inducible plant gene promoters can be used for expressing the inventive polynucleotide sequences. Inducible promoters regulate gene expression in response to environmental, hormonal, or chemical signals. Examples of hormone inducible promoters include auxin-inducible promoters (Baumann et al. *Plant Cell* 11:323-334(1999)), cytokinin-inducible promoter (Guevara-Garcia *Plant Mol. Biol.* 38:743-753(1998)), and gibberellin-responsive promoters (Shi et al. *Plant Mol. Biol.* 38:1053-1060(1998)). Additionally, promoters responsive to heat, light, wounding, pathogen resistance, and chemicals such as methyl jasmonate or salicylic acid, may be used for expressing the inventive polynucleotide sequences.

DNA Constructs

[0384] The present invention provides DNA constructs comprising the isolated nucleic acid molecules and polypeptide sequences of the present invention. In one embodiment, the DNA constructs of the present invention are Ti-plasmids derived from *A. tumefaciens.*

[0385] In developing the nucleic acid constructs of this invention, the various components of the construct or fragments thereof will normally be inserted into a convenient cloning vector, e.g., a plasmid that is capable of replication in a bacterial host, e.g., *E. coli.* Numerous vectors exist that have been described in the literature, many of which are commercially available. After each cloning, the cloning vector with the desired insert may be isolated and subjected to further manipulation, such as restriction digestion, insertion of new fragments or nucleotides, ligation, deletion, mutation, resection, etc. to tailor the components of the desired sequence. Once the construct has been completed, it may then be transferred to an appropriate vector for further manipulation in accordance with the manner of transformation of the host celi.

[0386] A recombinant DNA molecule of the invention typically includes a selectable marker so that transformed cells can be easily identified and selected from non-transformed cells. Examples of such markers include, but are not limited to, a neomycin phosphotransferase (*nptII*) gene (Potrykus et al., *Mol. Gen. Genet.* 199:183-188 (1985)), which confers kanamycin resistance. Cells expressing the *nptII* gene can be selected using an appropriate antibiotic such as kanamycin or G418. Other commonly used selectable markers include the bar gene, which confers bialaphos resistance; a mutant EPSP synthase gene (Hinchee et al., *Bio/Technology* 6:915-922 (1988)), which confers glyphosate resistance; and a mutant acetolactate synthase gene (ALS), which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204, 1985).

[0387] Additionally, vectors may include an origin of replication (replicons) for a particular host cell. Various prokaryotic replicons are known to those skilled in the

art, and function to direct autonomous replication and maintenance of a recombinant molecule in a prokaryotic host cell.

[0388] The vectors will preferably contain selectable markers for selection in plant cells. Numerous selectable markers for use in selecting transfected plant cells including, but not limited to, kanamycin, glyphosate resistance genes, and tetracycline or ampicillin resistance for culturing in *E. coli, A. tumefaciens* and other bacteria.

[0389] For secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

[0390] In one embodiment, a DNA construct of the current invention is designed in a manner such that a polynucleotide sequence described herein is operably linked to a tissue-specific promoter. Preferably, the polynucleotide encodes a polypeptide involved in wood or cell wall biosynthesis. Polynucleotides encoding many of the enzymes involved in wood or cell wall biosynthesis include, but are not limited to, cinnamyl alcohol dehydrogenase (CAD), cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate: CoA ligase (4CL) and peroxidase (POX) from pine. U.S. Pat. No. 6,204,434. Other enzymes include coniferin β-glucosidase (CBG), and caffeic acid 3-O-methyltransferase (COMT). U.S. Pat. No. 5,451,514, WO 94/23044, and Dharmawardhana *et al.*, *Plant Mol. Biol.* 40: 365-72 (1999).

[0391] In another embodiment, the coding sequence operably linked to the promoter may code for a gene product that inhibits the expression or activity of enzymes involved in wood or cell wall biosynthesis. For example, of particular interest for control of lignin biosynthesis is an antisense gene encoding a 4CL, CAD, LIM, TED2, or a COMT.

[0392] In a further embodiment, the DNA constructs of the current invention are designed such that the polynucleotide sequences of the current invention are operably linked to DNA or RNA that encodes antisense RNA or interfering RNA, which corresponds to genes that code for polypeptides of interest, resulting in a decreased expression of targeted gene products. Preferably the gene products targeted for suppression are enzymes involved in lignin biosynthesis. The use of RNAi inhibition of gene expression is described in U.S. Patent No. 6,506,559, and the use of RNAi to inhibit gene expression in plants is specifically described in WO 99/61631, both of which are herein incorporated by reference.

[0393] The use of antisense technology to reduce or inhibit the expression of specific plant genes has been described, for example in European Patent Publication No. 271988. Reduction of gene expression led to a change in the phenotype of the plant, either at the level of gross visible phenotypic difference, for example a lack of lycopene synthesis in the fruit of tomato leading to the production of yellow rather than red fruit, or at a more subtle biochemical level, for example, a change in the amount of polygalacturonase and reduction in depolymerisation of pectins during tomato fruit ripening (Smith et. al., *Nature*, 334:724-726 (1988); Smith et. al., *Plant Mol. Biol.*, 14:369-379 (1990)). Thus, antisense RNA has been demonstrated to be useful in achieving reduction of gene expression in plants.

[0394] In one embodiment an inventive polynucleotide sequence is capable of being transcribed inside a plant to yield an antisense RNA transcript is introduced into the plant, e.g., into a plant cell. The inventive polynucleotide can be prepared, for example, by reversing the orientation of a gene sequence with respect to its promoter. Transcription of the exogenous DNA in the plant cell generates an intracellular RNA transcript that is "antisense" with respect to that gene.

[0395] The invention also provides host cells which comprise the DNA constructs of the current invention. As used herein, a host cell refers to the cell in which the coding product is ultimately expressed. Accordingly, a host cell can be an individual cell, a cell culture or cells as part of an organism. The host cell can also be a portion of an embryo, endosperm, sperm or egg cell, or a fertilized egg.

[0396] Accordingly, the present invention also provides plants or plant cells, comprising the DNA constructs of the current invention. Preferably the plants are angiosperms or gymnosperms. The expression construct of the present invention may be used to transform a variety of plants, both monocotyledonous (e.g. grasses, corn, grains, oat, wheat and barley), dicotyledonous (e.g., *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and Gymnosperms (e.g., Scots pine; see Aronen, *Finnish Forest Res. Papers*, Vol. 595, 1996), white spruce (Ellis *et al.*, *Biotechnology* 11:84-89, 1993), and larch (Huang *et al.*, *In Vitro Cell* 27:201-207, 1991).

[0397] In a preferred embodiment, the inventive expression vectors are employed to transform woody plants, herein defined as a tree or shrub whose stem lives for a number of years and increases in diameter each year by the addition of woody tissue. Preferably the target plant is selected from the group consisting of eucalyptus and pine species, most preferably from the group consisting of *Eucalyptus grandis* and its hybrids, and *Pinus taeda*. Also preferred, the target plant is selected from the group consisting of *Pinus banksiana, Pinus brutia, Pinus caribaea, Pinus clasusa, Pinus contorta, Pinus coulteri, Pinus echinata, Pinus eldarica, Pinus ellioti, Pinus jeffreyi, Pinus lambertiana, Pinus massoniana, Pinus monticola, Pinus nigra, Pinus palustrus, pinus pinaster, Pinus ponderosa, Pinus radiata, Pinus resinosa, Pinus rigida, Pinus serotina, Pinus strobus, Pinus sylvestris, Pinus taeda, Pinus virginiana, Abies amabilis, Abies balsamea, Abies concolor, Abies grandis, Abies lasiocarpa, Abies magnifica, Abies procera, Chamaecyparis lawsoniona, Chamaecyparis nootkatensis, Chamaecyparis thyoides, Juniperus virginiana, Larix decidua, Larix laricina, Larix leptolepis, Larix occidentalis, Larix siberica, Libocedrus decurrens, Picea abies, Picea engelmanni, Picea glauca, Picea mariana, Picea pungens, Picea rubens, Picea sitchensis, Pseudotsuga menziesii, Sequoia gigantea, Sequoia sempervirens, Taxodium distichum, Tsuga canadensis, Tsuga heterophylla, Tsuga mertensiana, Thuja occidentalis, Thuja plicata, Eucalyptus alba, Eucalyptus bancroftii, Eucalyptus botryoides, Eucalyptus bridgesiana, Eucalyptus calophylla, Eucalyptus camaldulensis, Eucalyptus citriodora, Eucalyptus cladocalyx, Eucalyptus coccifera, Eucalyptus curtisii, Eucalyptus dalrympleana, Eucalyptus deglupta, Eucalyptus delagatensis, Eucalyptus diversicolor, Eucalyptus dunnii, Eucalyptus ficifolia,*

Eucalyptus globulus, Eucalyptus gomphocephala, Eucalyptus gunnii, Eucalyptus henryi, Eucalyptus laevopinea, Eucalyptus macarthurii, Eucalyptus macrorhyncha, Eucalyptus maculata, Eucalyptus marginata, Eucalyptus megacarpa, Eucalyptus melliodora, Eucalyptus nicholii, Eucalyptus nitens, Eucalyptus nova-angelica, Eucalyptus obliqua, Eucalyptus occidentalisEucalyptus obtusiflora, Eucalyptus oreades, Eucalyptus pauciflora, Eucalyptus polybractea, Eucalyptus regnans, Eucalyptus resinifera, Eucalyptus robusta, Eucalyptus rudis, Eucalyptus saligna, Eucalyptus sideroxylon, Eucalyptus stuartiana, Eucalyptus tereticornis, Eucalyptus torelliana, Eucalyptus urnigera, Eucalyptus urophylla, Eucalyptus viminalis, Eucalyptus viridis, Eucalyptus wandoo, and Eucalyptus youmanni.

[0398] In particular, the transgenic plant may be of the species *Eucalyptus grandis* or its hybrids, *Pinus radiata, Pinus taeda* L (loblolly pine), *Populus nigra, Populus deltoides, Populus alba,* or *Populus* hybrids, *Acacia mangium,* or *Liquidamber styraciflua.* Beyond the ordinary meaning of plant, the term "plants" is also intended to mean the fruit, seeds, flower, strobilus etc. of the plant. The plant of the current invention may be a direct transfectant, meaning that the DNA construct was introduced directly into the plant, such as through *Agrobacterium,* or the plant may the progeny of a transfected plant. The second or subsequent generation plant may or may not be produced by sexual reproduction, i.e., fertilization. Furthermore, the plant can be a gametophyte (haploid stage) or a sporophyte (diploid stage).

[0399] In one embodiment, the present invention provides isolated polynucleotides encoding, or partially encoding, plant wood and cell wall proteins that are involved in cell wall biosynthesis. The polynucleotides of the present invention were isolated from *Eucalyptus grandis* and *Pinus radiata,* but may be isolated from any plant species or synthesized using conventional synthesis techniques.

[0400] In specific embodiments, isolated polynucleotides of the present invention comprise a sequence selected from the group consisting of sequences identified as SEQ ID NOS: 1-230 complements of the sequences identified as SEQ ID NOS: 1-230; reverse complements of the sequences identified as SEQ ID NOS: 1-230, , reverse sequences of the sequences identified as SEQ ID NOS: 1-230; sequences

comprising at least a specified number of contiguous residues (*x*-mers) of any of the above-mentioned polynucleotides; extended sequences corresponding to any of the above polynucleotides; antisense sequences corresponding to any of the above polynucleotides; and variants of any of the above polynucleotides, as that term is described in this specification.

[0401] In another aspect, the present invention provides isolated polypeptides encoded by the polynucleotides of SEQ ID NOS: 231-460.

[0402] *Eucalyptus grandis* and *Pinus radiata* cDNA expression libraries were prepared from mature shoot buds, early wood phloem, floral tissue, leaf tissue, feeder roots, structural roots, xylem or early wood xylem. cDNA sequence from positive clones containing inserts were obtained using methods known in the art. The determined cDNA sequences were compared with known sequences in the public databases (EMBL) using the computer algorithms FASTA and/or BLASTN. Multiple alignments of redundant sequences were used to build reliable consensus sequences. The determined cDNA sequences are provided in SEQ ID NOS: 1-230. The predicted polypeptide sequences are provided in SEQ ID NOS: 231-460.

[0403] Based on similarity to known sequences from other plant species, the isolated polynucleotide sequences were identified as encoding wood and cell wall proteins, as detailed in Tables 1 and 2. The polypeptide sequences were analyzed with publicly available annotation software. EMBL's publicly available "InterPro Scan" was used for identifying motifs and domains in the present polypeptide sequences. InterPro is a database of protein families, domains and functional sites in which identifiable features found in known proteins can be applied to unknown protein sequences. Mulder, N. J. *et al.* 2003, *Nucl Acid Res.* 31: 315-318.

[0404] As shown in Tables 1 and 2, the polynucleotides of the invention encode wood and cell wall proteins. These polynucleotides can be used for regulating cell wall biosynthesis and development.

TABLE 1: Cell Wall Proteins isolated from *P. radiata*

Protein Family	Polynucleotide SEQ ID NO	Polypeptide SEQ ID NO
1,3-beta-D-glucanase	3-29	233-259
Alpha-expansin	111-130	341-360
Calnexin	1-2	231-232
Dirigent	91-110	321-340
Endo-1,4-beta-xylanase	30	260
Exo-1,4-beta-xylanase	31-37	261-267
Glucan 1,3-beta-glucosidase	38-44	268-274
Licheninase	45-52	275-282
Mannose-6-Phosphate Isomerase	58	288
Mannose-1-Phosphate Guanylyltransferase	53-57	283-287
Sucrose-phosphate synthase	59-60	289-290
Xyloglucan: xyloglucosyl transferase	61-90	291-320
Yieldin	131	361

TABLE 2: Wood and Cell Wall Proteins isolated from *E. grandis*

Protein Family	Polynucleotide SEQ ID NO	Polypeptide SEQ ID NO
1,3-beta-D-glucanase	142-158	372-388
Alpha-expansin	217-228	447-458
Calnexin	132-136	362-366
Dirigent	208-216	438-446
Endo-1,4-beta-xylanase	159-161	389-391
Exo-1,4-beta-xylanase	162-165	392-395
Glucan 1,3-beta-glucosidase	166-172	396-402
Licheninase	173-179	403-409
Mannose-6-Phosphate Isomerase	183	413
Mannose-1-Phosphate Guanylyltransferase	180-182	410-412
Sucrose-phosphate synthase	184-186	414-416
Sucrose synthase	137-141	367-371
Xyloglucan: xyloglucosyl transferase	187-207	417-437
Yieldin	229-230	459-460

[0405] Polypeptides encoded by the polynucleotides of the present invention may be expressed and used in various assays to determine their biological activity. Such polypeptides may be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

Plant Transformation and Regeneration

[0406] The present polynucleotides and polypeptides may be introduced into a host plant cell by standard procedures known in the art for introducing recombinant

sequences into a target host cell. Such procedures include, but are not limited to, transfection, infection, transformation, natural uptake, electroporation, biolistics and *Agrobacterium*. Methods for introducing foreign genes into plants are known in the art and can be used to insert a construct of the invention into a plant host, including, biological and physical plant transformation protocols. See, for example, Miki *et al.*, 1993, "Procedure for Introducing Foreign DNA into Plants", In: Methods in Plant Molecular Biology and Biotechnology, Glick and Thompson, eds., CRC Press, Inc., Boca Raton, pages 67-88. The methods chosen vary with the host plant, and include chemical transfection methods such as calcium phosphate, microorganism-mediated gene transfer such as *Agrobacterium* (Horsch *et al.*, Science 227:1229-31, 1985), electroporation, micro-injection, and biolistic bombardment.

[0407] Accordingly, the present invention also provides plants or plant cells, comprising the polynucleotides or polypeptides of the current invention. In one embodiment, the plants are angiosperms or gymnosperms. In another embodiment, the plants are selected from *Eucalyptus* and *Pinus* species. In particular, the transgenic plant may be of the species *Eucalyptus grandis* and hybrids, *Pinus radiata*, *Pinus taeda* L (loblolly pine), *Populus nigra*, *Populus deltoides*, or *Liquidamber styraciflua*. Beyond the ordinary meaning of plant, the term "plants" is also intended to mean the fruit, seeds, flower, strobilus etc. of the plant. The plant of the current invention may be a direct transfectant, meaning that the vector was introduced directly into the plant, such as through *Agrobacterium*, or the plant may be the progeny of a transfected plant. The progeny may also be obtained by asexual reproduction of a transfected plant. The second or subsequent generation plant may or may not be produced by sexual reproduction, i.e., fertilization. Furthermore, the plant can be a gametophyte (haploid stage) or a sporophyte (diploid stage).

[0408] Methods for transforming tree species are well known in the art. By no means limiting, explant refers to plant tissue that is a target for transformation and may include leaf, petiole, floral, and internodal tissues harvested from plants grown in vivo and/or *in vitro*. For example, a tree can be transformed as follows. For increased transformation efficiency, a tree explant can be harvested and cultured on a

pre-culture medium before transformation. A pre-culture medium, as shown in Table 3, is a nutrient medium upon which plant explants are cultured before transformation with *Agrobacterium* and is needed for increasing transformation efficiency and plant regeneration. The pre-culture medium comprises an *Agrobacterium* inducer, such as acetosyringone. The pre-culture medium may optionally comprise plant growth regulators, including auxin and cytokinin. Alternatively, other pre-culture media and time periods of culture may be used.

Table 3. Plant Pre-Culture Medium

Medium	Amount per Liter
WPM salts	1 package (Sigma)
$Ca(NO_3)_2 \cdot 4H_2O$	3.7 g
$MgSO_4 \cdot 4H_2O$	0.37 g
Nicotinic Acid	0.5 mg
Thiamine HCl	0.5 mg
Pyridoxin HCl	0.5 mg
D-Pantothenic Acid	1.0 mg
Myo-inositol	0.1 g
BA	0.1 – 1 mg
Bacto-agar	5 – 8 g
Acetosyringone	5-200 mg
NAA	0.2-3 mg
zeatin	1-6 mg

[0409] In the present invention, plant explants were pre-cultured for four days in the dark on the pre-culture medium displayed in Table 3. Woody Plant Medium (WPM) salts (Loyd and McCown, 1980) were used in the present pre-culture medium; however, other salt media, such as MS medium (Murashige and Skoog 1962) or Lepoivre medium, may be used. While the present pre-culture medium comprises acetosyringone, other *Agrobacterium* inducers may be used. Optionally, the instant

pre-culture medium contained both auxin and cytokinin. Other pre-culture media and other culture time periods may be used.

[0410] Induced *Agrobacterium* culture was prepared by methods known in the art. The induced culture was dripped onto each explant by pipette. Sufficient *Agrobacterium* culture was dripped to ensure that all edges were covered with bacterial solution. Alternatively, the explants may be transformed by vacuum infiltration, floral dip, and other methods of *Agrobacterium*-mediated transformation. Following transformation, explants covered with *Agrobacterium* culture were placed in the dark for four days of co-cultivation. Alternatively, the explants may be co-cultivated with *Agrobacterium* under light conditions. Additionally, the explants may be co-cultivated with *Agrobacterium* under light or dark conditions for 2-10 days, preferably 4 days. Following co-cultivation, the explants were transferred to regeneration medium (Table 4) with 400 mg/l timentin. There is no need to wash explants. Explants were cultured on this medium for four days before transfer to a selection medium. In the present example, the selection medium is the regeneration medium supplemented with both timentin and an herbicide selection agent.

Table 4. Regeneration Medium

Components for 1 Liter of Medium	Grams
KNO_3	1
$NH_4H_2PO_4$	0.25
$MgSO_4 \cdot 7H_2O$	0.25
$CaCl_2.2H_2O$	0.10
$FeSO_4.7H_2O$	0.0139
$Na_2EDTA.2H_2O$	0.01865
MES (Duchefa m1501)	600.0
MS Micro (1/2 strength)	
$MnSO_4.H_2O$	0.00845
$ZnSO_4.7H_2O$	0.0043
$CuSO_4.5H_2O$	0.0000125
$CoCl_2.6H_2O$	0.0000125
KI	0.000415
H_3BO_3	0.0031
$Na_2MoO_4.2H_2O$	0.000125
Zeatin	
NAA.(naphthalene acetic acid)	
Glucose/Sucrose	20.0
Myo-inositol	0.100
Nicotinic Acid	0.010
Thiamine	0.010
Ca Pantothenate	0.001
Pyridoxine	0.001
Biotin	0.00001
Ascorbic Acid	0.050
L-glutamine	0.1
Arginine	0.0258
Glycine	0.00199
Lysine	0.0508
Methionine	0.0132
Phenylalanine	0.0257
Serine	0.00904
Threonine	0.00852
Tryptophan	0.0122

Tyrosine	0.0127
Gelrite	3.0

[0411] Shoot clumps that survive selection are maintained on regeneration medium containing herbicide and timentin, and they are transferred every 3 weeks until shoots proliferate and initially elongate. For transformation experiments with a reporter gene, such as GUS, leaf and stem tissues from the regenerated shoots are stained for GUS expression as soon as the shoots are developed. While any reporter gene may be used, such as GFP or luciferase, GUS expression was assayed in the present invention by methods known in the art.

[0412] GUS staining was performed to monitor the frequency of *Agrobacterium* infection and to ensure that the selected shoots are not escapes or chimeras. Leaf and stem tissues from the regenerated shoots were stained for GUS expression immediately upon shoot development. To determine GUS activity, the explants were incubated in a substrate comprising 100 mM phosphate buffer (pH 7.0), 0.05% dimethyl suphoxide, 0.05% Triton X-100, 10 mM EDTA, 0.5 mM potassium ferrocyanide, and 1.5 mg/ml 5-bromo-4-chloro-3-indolyl-β-D-glucuronide (X-gluc). The explants were subjected to 10 minutes of vacuum before an overnight incubation at 37°C. Following overnight incubation, GUS foci were counted.

B. Expression Profiling of Plant Cell Wall Polynucleotides

[0413] The present invention also provides methods and tools for performing expression profiling of plant cell wall polynuecleotides. Expression profiling is useful in determining whether polynucleotides are transcribed or translated, comparing transcript levels for particular polynucleotide in different tissues, genotyping, estimating DNA copy number, determining identity of descent, measuring mRNA decay rates, identifying protein binding sites, determining subcellular localization of gene products, correlating polynucleotide expression to a phenotype or other phenomenon, and determining the effect on other polynucleotides of the manipulation of a particular gene. Expression profiling is particularly useful for identifying polynucleotide expression in complex, multigenic events. For this reason, expression

profiling is useful in correlating polynuceotide expression to plant phenotype and formation of plant.

[0414] Only a small fraction of the genes of a plant's genome are expressed at a given time in a given tissue sample, and all of the expressed genes may not affect the plant phenotype. To identify polynucleotides capable of affecting a phenotype of interest, the present invention provides methods and tools for determining, for example, a polynucleotide expression profile at a given point in plant development and a gene expression profile a given tissue sample. The invention also provides methods and tools for inventive polynucleotides whose expression can be manipulated to alter plant phenotype or to alter the biological activity of other transcription and translation products. In support of these methods, the invention also provides methods and tools that distinguish expression of different polynucloetides of the same family.

[0415] As used herein, "polynucleotide expression," refers to the process of transcription of a DNA sequence into an RNA sequence, followed by translation of the RNA into a protein, which may or may not undergo post-translational processing. Thus, the relationship between phenotype and/or developmental stage and polynucleotide expression can be observed by detecting, quantitatively or qualitatively, changes in the level of an RNA or a protein. As used herein, the term "biological activity" includes, but is not limited to, the activity of a protein gene product, including enzyme activity.

[0416] The present invention provides oligonucleotides that are useful in these expression profiling methods. Each oligonucleotide is capable of hybridizing under a given set of conditions to a cell wall or wood polynucleotide or polynucleotide product. In one aspect of the invention, a plurality of oligonucleotides is provided, wherein each oligonucleotide hybridizes under a given set of conditions to a different cell cycle gene product. Examples of oligonucleotides of the present invention include SEQ ID NOs 461-690. Each of the oligos of SEQ ID Nos: 461-690 hybridizes under standard conditions to a different gene product of one of SEQ ID

NOs: 1-230. The oligonucleotides of the invention are useful in determining the expression of one or more cell cycle genes in any of the above-described methods.

1. Cell, Tissue, Nucleic Acid, and Protein Samples

[0417] Samples for use in methods of the present invention may be derived from plant tissue. Suitable plant tissues include, but are not limited to, somatic embryos, pollen, leaves, stems, calli, stolons, microtubers, shoots, xylem, male strolbili, pollen cones, vascular tissue, apical meristem, vascular cambium, xylem, root, flower, and seed.

[0418] According to the present invention "plant tissue" is used as described previously herein. Plant tissue can be obtained from any of the plants types or species described supra.

[0419] In accordance with one aspect of the invention, samples can be obtained from plant tissue at different developmental stages, from plant tissue at various times of the year (*e.g.* spring versus summer), from plant tissues subject to different environmental conditions (*e.g.* variations in light and temperature) and/or from different types of plant tissue and cells. In accordance with one embodiment, plant tissue is obtained during various stages of maturity and during different seasons of the year. For example, plant tissue can be collected from stem dividing cells, differentiating xylem, early developing wood cells, differentiated early wood cells, and differentiated late wood cells. As another example, polynucleotide expression in a sample obtained from a plant with developing wood can be compared to gene expression in a sample obtained from a plant which does not have developing wood.

[0420] Differentiating xylem includes samples obtained from compression wood, side-wood, and normal vertical xylem. Methods of obtaining samples for expression profiling from pine and eucalyptus are known. *See, e.g.*, Allona *et al.*, *Proc. Nat'l Acad. Sci.* 95:9693-8 (1998) and Whetton *et al.*, *Plant Mol. Biol.* 47:275-91, and Kirst *et al.*, INT'L UNION OF FORESTRY RESEARCH ORGANIZATIONS BIENNIAL CONFERENCE, S6.8 (June 2003, Umea, Sweden).

[0421] In one embodiment of the invention, polynucleotide expression in one type of tissue is compared to polynucleotide expression in a different type of tissue or to polynucleotide expression in the same type of tissue in a difference stage of development. Polynucleotide expression can also be compared in one type of tissue which is sampled at various times during the year (different seasons). For example, polynucleotide expression in juvenile secondary xylem can be compared to polynucleotide expression in mature secondary xylem. Similarly, polynucleotide expression in cambium can be compared to polynucleotide expression in xylem. Furthermore, gene expression in apical meristems can be compared to gene expression in cambium.

[0422] In another embodiment of the invention, a sample is obtained from a plant having a specific phenotype and polynucleotide expression in that sample is compared to a sample obtained from a plant of the same species that does not have that phenotype. For example, a sample can be obtained from a plant exhibiting a fast rate of growth and gene expression can be compared with that of a sample obtained from a plant exhibiting a normal or slow rate of growth. Differentially expressed polunucleotides identified from such a comparison can be correlated with growth rate and, therefore, useful for manipulating growth rate.

[0423] In a further embodiment, a sample is obtained from clonally propagated plants. In one embodiment the clonally propagated plants are of the species *Pinus* or *Eucalyptus*. Individual ramets from the same genotype can be sacrificed at different times of year. Thus, for any genotype there can be at least two genetically identical trees sacrificed, early in the season and late in the season. Each of these trees can be divided into juvenile (top) to mature (bottom) samples. Further, tissue samples can be divided into, for example, phloem to xylem, in at least 5 layers of peeling. Each of these samples can be evaluated for phenotype and polynucleotide expression.

[0424] Where cellular components may interfere with an analytical technique, such as a hybridization assay, enzyme assay, a ligand binding assay, or a biological activity assay, it may be desirable to isolate the polynucleotide expression products from such cellular components. Polynucleotide expression products, including nucleic acid and

amino acid gene products, can be isolated from cell fragments or lysates by any method known in the art.

[0425] Nucleic acids used in accordance with the invention can be prepared by any available method or process, or by other processes as they become known in the art. Conventional techniques for isolating nucleic acids are detailed, for example, in Tijssen, LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY: HYBRIDIZATION WITH NUCLEIC ACID PROBES, chapter 3 (Elsevier Press, 1993), Berger and Kimmel, *Methods Enzymol.* 152:1 (1987), and GIBCO BRL & LIFE TECHNOLOGIES TRIZOL RNA ISOLATION PROTOCOL, Form No. 3786 (2000). Techniques for preparing nucleic acid samples, and sequencing polynucleotides from pine and eucalyptus are known. *See, e.g.,* Allona *et al., supra* and Whetton *et al., supra*, and U.S. Application No. 60/476,222.

[0426] A suitable nucleic acid sample can contain any type of nucleic acid derived from the transcript of a cell wall or wood gene or polypeptide, *i.e.*, RNA or a subsequence thereof or a nucleic acid for which an mRNA transcribed from a cell wall or wood gene served as a template. Suitable nucleic acids include cDNA reverse-transcribed from a transcript, RNA transcribed from that cDNA, DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. Detection of such products or derived products is indicative of the presence and/or abundance of the transcript in the sample. Thus, suitable samples include, but are not limited to, transcripts of a gene or a polynucleotide, cDNA reverse-transcribed from the transcript, cRNA transcribed from the cDNA, DNA amplified from the genes, and RNA transcribed from amplified DNA. As used herein, the category of "transcripts" includes but is not limited to pre-mRNA nascent transcripts, transcript processing intermediates, and mature mRNAs and degradation products thereof.

[0427] It is not necessary to monitor all types of transcripts to practice the invention. For example, the expression profiling methods of the invention can be conducted by detecting only one type of transcript, such as mature mRNA levels only.

[0428] In one aspect of the invention, a chromosomal DNA or cDNA library (comprising, for example, fluorescently labeled cDNA synthesized from total cell mRNA) is prepared for use in hybridization methods according to recognized methods in the art. See Sambrook *et al., supra.*

[0429] In another aspect of the invention, mRNA is amplified using, *e.g.*, the MessageAmp kit (Ambion). In a further aspect, the mRNA is labeled with a detectable label. For example, mRNA can be labeled with a fluorescent chromophore, such as CyDye (Amersham Biosciences).

[0430] In some applications, it may be desirable to inhibit or destroy RNase that often is present in homogenates or lysates, before use in hybridization techniques. Methods of inhibiting or destroying nucleases are well known. In one embodiment of the invention, cells or tissues are homogenized in the presence of chaotropic agents to inhibit nuclease. In another embodiment, RNase is inhibited or destroyed by heat treatment, followed by proteinase treatment.

[0431] Protein samples can be obtained by any means known in the art. Protein samples useful in the methods of the invention include crude cell lysates and crude tissue homogenates. Alternatively, protein samples can be purified. Various methods of protein purification well known in the art can be found in Marshak *et al.*, STRATEGIES FOR PROTEIN PURIFICATION AND CHARACTERIZATION: A LABORATORY COURSE MANUAL (Cold Spring Harbor Laboratory Press 1996).

2. Detecting Level of Polynucleotide Expression

[0432] For methods of the invention that comprise detecting a level of polynucleotide expression, any method for observing polynucleotide expression can be used, without limitation. Such methods include traditional nucleic acid hybridization techniques, polymerase chain reaction (PCR) based methods, and protein determination. The invention includes detection methods that use solid support-based assay formats as well as those that use solution-based assay formats.

[0433] Absolute measurements of the expression levels need not be made, although they can be made. The invention includes methods comprising comparisons of differences in expression levels between samples. Comparison of expression levels can be done visually or manually, or can be automated and done by a machine, using for example optical detection means. Subrahmanyam *et al.*, *Blood.* 97: 2457 (2001); Prashar *et al.*, *Methods Enzymol.* 303: 258 (1999). Hardware and software for analyzing differential expression of genes are available, and can be used in practicing the present invention. *See, e.g.*, GenStat Software and *GeneExpress*® GX Explorer™ Training Manual, *supra*; Baxevanis & Francis-Ouellette, *supra*.

[0434] In accordance with one embodiment of the invention, nucleic acid hybridization techniques are used to observe polynucleotide expression. Exemplary hybridization techniques include Northern blotting, Southern blotting, solution hybridization, and S1 nuclease protection assays.

[0435] Nucleic acid hybridization typically involves contacting an oligonucleotide probe and a sample comprising nucleic acids under conditions where the probe can form stable hybrid duplexes with its complementary nucleic acid through complementary base pairing. For example, see PCT application WO 99/32660; Berger & Kimmel, *Methods Enzymol.* 152: 1 (1987). The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. The detectable label can be present on the probe, or on the nucleic acid sample. In one embodiment, the nucleic acids of the sample are detectably labeled polynucleotides representing the mRNA transcripts present in a plant tissue (*e.g.*, a cDNA library). Detectable labels are commonly radioactive or fluorescent labels, but any label capable of detection can be used. Labels can be incorporated by several approached described, for instance, in WO 99/32660, *supra*. In one aspect RNA can be amplified using the MessageAmp kit (Ambion) with the addition of aminoallyl-UTP as well as free UTP. The aminoallyl groups incorporated into the amplified RNA can be reacted with a fluorescent chromophore, such as CyDye (Amersham Biosciences)

[0436] Duplexes of nucleic acids are destabilized by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature and/or lower salt and/or in the presence of destabilizing reagents) hybridization tolerates fewer mismatches.

[0437] Typically, stringent conditions for short probes (*e.g.*, 10 to 50 nucleotide bases) will be those in which the salt concentration is at least about 0.01 to 1.0 M at pH 7.0 to 8.3 and the temperature is at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide.

[0438] Under some circumstances, it can be desirable to perform hybridization at conditions of low stringency, *e.g.*, 6 × SSPE-T (0.9 M NaCl, 60 mM NaH_2PO_4, pH 7.6, 6 mM EDTA, 0.005% Triton) at 37°C, to ensure hybridization. Subsequent washes can then be performed at higher stringency (*e.g.*, 1× SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes can be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25× SSPE-T at 37°C to 50°C) until a desired level of hybridization specificity is obtained.

[0439] In general, standard conditions for hybridization are a compromise between stringency (hybridization specificity) and signal intensity. Thus, in one embodiment of the invention, the hybridized nucleic acids are washed at successively higher stringency conditions and read between each wash. Analysis of the data sets produced in this manner will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest. For example, the final wash may be selected as that of the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity.

a. Oligonucleotide Probes

[0440] Oligonucleotide probes useful in nucleic acid hybridization techniques employed in the present invention are capable of binding to a nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. A probe can include natural bases (*i.e.*, A, G, U, C or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the nucleotide bases in the probes can be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes can be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

[0441] Oligonucleotide probes can be prepared by any means known in the art. Probes useful in the present invention are capable of hybridizing to a nucleotide product of cell wall biosynthesis genes, such as one of SEQ ID NOs: 1-230. Probes useful in the invention can be generated using the nucleotide sequences disclosed in SEQ ID NOs: 1-230. The invention includes oligonucleotide probes having at least a 2, 10, 15, 20, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, or 100 nucleotide fragment of a corresponding contiguous sequence of any one of SEQ ID NOs: 1-230. The invention includes oligonucleotides of less than 2, 1, 0.5, 0.1, or 0.05 kb in length. In one embodiment, the oligonucleotide is 60 nucleotides in length.

[0442] Oligonucleotide probes can be designed by any means known in the art. *See, e.g.,* Li and Stormo, *Bioinformatics* 17: 1067-76 (2001). Oligonucleotide probe design can be affected using software. Exemplary software includes ArrayDesigner, GeneScan, and ProbeSelect. Probes complementary to a defined nucleic acid sequence can be synthesized chemically, generated from longer nucleotides using restriction enzymes, or can be obtained using techniques such as polymerase chain reaction (PCR). PCR methods are well known and are described, for example, in Innis *et al. eds.*, PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS, Academic Press Inc. San Diego, Calif. (1990). The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Optimally, the nucleic acids in the sample are labeled and the probes are not labeled. Oligonucleotide probes

generated by the above methods can be used in solution or solid support-based methods.

[0443] The invention includes oligonucleotide probes that hybridize to a product of the coding region or a 3' untranslated region (3' UTR) of a wood or cell wall polynucleotide. In one embodiment, the oligonucleotide probe hybridizes to the 3'UTR of any one of SEQ ID NOs: 1-230. The 3' UTR is generally a unique region of the gene, even among members of the same family. Therefore, the probes capable of hybridizing to a product of the 3' UTR can be useful for differentiating the expression of individual genes within a family where the coding region of the genes likely are highly homologous. This allows for the design of oligonucleotide probes to be used as members of a plurality of oligonucleotides, each capable of uniquely binding to a single gene. In another embodiment, the oligonucleotide probe comprises any one of SEQ ID NOs: 461-591. In another embodiment, the oligonucleotide probe consists of any one of SEQ ID NOs: 592-690.

b. Oligonucleotide Array Methods

[0444] One embodiment of the invention employs two or more oligonucleotide probes in combination to detect a level of expression of one or more wood or cell wall polynucleotides, such as the genes of SEQ ID NOs: 1-230. In one aspect of this embodiment, the level of expression of two or more different polynucleotide is detected. The two or more polynucleotide may be from the same or different wood or cell wall gene families discussed above. Each of the two or more oligonucleotides may hybridize to a different one of the polynucleotides.

[0445] One embodiment of the invention employs two or more oligonucleotide probes, each of which specifically hybridize to a polynucleotide derived from the transcript of a polynucleotide provided by SEQ ID NOs: 1-230. Another embodiment employs two or more oligonucleotide probes, at least one of which comprises a nucleic acid sequence of SEQ ID NOs: 461-690. Another embodiment employs two or more oligonucleotide probes, at least one of which consists of of SEQ ID NOs: 461-690.

[0446] The oligonucleotide probes may comprise from about 5 to about 60, or from about 5 to about 500, nucleotide bases, such as from about 60 to about 100 nucleotide bases, including from about 15 to about 60 nucleotide bases.

[0447] One embodiment of the invention uses solid support-based oligonucleotide hybridization methods to detect gene expression. Solid support-based methods suitable for practicing the present invention are widely known and are described, for example, in PCT application WO 95/11755; Huber *et al.*, *Anal. Biochem.* 299: 24 (2001); Meiyanto *et al.*, *Biotechniques*. 31: 406 (2001); Relogio *et al.*, *Nucleic Acids Res.* 30:e51 (2002). Any solid surface to which oligonucleotides can be bound, covalently or non-covalently, can be used. Such solid supports include filters, polyvinyl chloride dishes, silicon or glass based chips, etc.

[0448] One embodiment uses oligonucleotide arrays, *i.e.* microarrays, which can be used to simultaneously observe the expression of a number of polynucleotides, genes or gene products. Oligonucleotide arrays comprise two or more oligonucleotide probes provided on a solid support, wherein each probe occupies a unique location on the support. The location of each probe may be predetermined, such that detection of a detectable signal at a given location is indicative of hybridization to an oligonucleotide probe of a known identity. Each predetermined location can contain more than one molecule of a probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There can be, for example, from 2, 10, 100, 1,000, 2,000 or 5,000 or more of such features on a single solid support. In one embodiment, each oligonucleotide is located at a unique position on an array at least 2, at least 3, at least 4, at least 5, at least 6, or at least 10 times.

[0449] Oligonucleotide probe arrays for detecting gene expression can be made and used according to conventional techniques described, for example, in Lockhart *et al.*, *Nat'l Biotech.* 14: 1675 (1996), McGall *et al.*, *Proc. Nat'l Acad. Sci. USA* 93: 13555 (1996), and Hughes *et al.*, *Nature Biotechnol.* 19:342 (2001). A variety of oligonucleotide array designs is suitable for the practice of this invention.

[0450] In one embodiment the one or more oligonucleotides include a plurality of oligonucleotides that each hybridizes to a different polynucleotide expressed in a particular tissue type. For example, the tissue can be developing wood.

[0451] In one embodiment, a nucleic acid sample obtained from a plant can be amplified and, optionally labeled with a detectable label. Any method of nucleic acid amplification and any detectable label suitable for such purpose can be used. For example, amplification reactions can be performed using, *e.g.* Ambion's MessageAmp, which creates "antisense" RNA or "aRNA" (complementary in nucleic acid sequence to the RNA extracted from the sample tissue). The RNA can optionally be labeled using CyDye fluorescent labels. During the amplification step, aaUTP is incorporated into the resulting aRNA. The CyDye fluorescent labels are coupled to the aaUTPs in a non-enzymatic reaction. Subsequent to the amplification and labeling steps, labeled amplified antisense RNAs are precipitated and washed with appropriate buffer, and then assayed for purity. For example, purity can be assay using a NanoDrop spectrophotometer. The nucleic acid sample is then contacted with an oligonucleotide array having, attached to a solid substrate (a "microarray slide"), oligonucleotide sample probes capable of hybridizing to nucleic acids of interest which may be present in the sample. The step of contacting is performed under conditions where hybridization can occur between the nucleic acids of interest and the oligonucleotide probes present on the array. The array is then washed to remove non-specifically bound nucleic acids and the signals from the labeled molecules that remain hybridized to oligonucleotide probes on the solid substrate are detected. The step of detection can be accomplished using any method appropriate to the type of label used. For example, the step of detecting can accomplished using a laser scanner and detector. For example, on can use and Axon scanner which optionally uses GenePix Pro software to analyze the position of the signal on the microarray slide.

[0452] Data from one or more microarray slides can be analyzed by any appropriate method known in the art.

[0453] Oligonucleotide probes used in the methods of the present invention, including microarray techniques, can be generated using PCR. PCR primers used in

generating the probes are chosen, for example, based on the sequences of SEQ ID NOs: 1-230, to result in amplification of unique fragments of the wood or cell wall polynucleotides (*i.e.*, fragments that hybridize to only one polynucleotide of any one of SEQ ID NOs: 1-230 under standard hybridization conditions). Computer programs are useful in the design of primers with the required specificity and optimal hybridization properties. For example, Li and Stormo, *supra* at 1075, discuss a method of probe selection using ProbeSelect which selects an optimum oligonucleotide probe based on the entire gene sequence as well as other gene sequences to be probed at the same time.

[0454] In one embodiment, oligonucleotide control probes also are used. Exemplary control probes can fall into at least one of three categories referred to herein as (1) normalization controls, (2) expression level controls and (3) negative controls. In microarray methods, one or more of these control probes may be provided on the array with the inventive wood or cell wall-related oligonucleotides.

[0455] Normalization controls correct for dye biases, tissue biases, dust, slide irregularities, malformed slide spots, *etc.* Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls, after hybridization, provide a control for variations in hybridization conditions, label intensity, reading efficiency and other factors that can cause the signal of a perfect hybridization to vary between arrays. In one embodiment, signals (*e.g.*, fluorescence intensity or radioactivity) read from all other probes used in the method are divided by the signal from the control probes, thereby normalizing the measurements.

[0456] Virtually any probe can serve as a normalization control. Hybridization efficiency varies, however, with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes being used, but they also can be selected to cover a range of lengths. Further, the normalization control(s) can be selected to reflect the average base composition of the other probes being used. In one embodiment, only one or a few normalization probes

are used, and they are selected such that they hybridize well (*i.e.*, without forming secondary structures) and do not match any test probes. In one embodiment, the normalization controls are mammalian genes.

[0457] Expression level controls probes hybridize specifically with constitutively expressed genes present in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level control probes. Typically, expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to certain photosynthesis genes.

[0458] "Negative control" probes are not complementary to any of the test oligonucleotides (*i.e.*, the inventive wood or cell wall-related oligonucleotides), normalization controls, or expression controls. In one embodiment, the negative control is a mammalian gene which is not complementary to any other sequence in the sample.

[0459] The terms "background" and "background signal intensity" refer to hybridization signals resulting from non-specific binding or other interactions between the labeled target nucleic acids (*i.e.*, mRNA present in the biological sample) and components of the oligonucleotide array. Background signals also can be produced by intrinsic fluorescence of the array components themselves.

[0460] A single background signal can be calculated for the entire array, or a different background signal can be calculated for each target nucleic acid. In a one embodiment, background is calculated as the average hybridization signal intensity for the lowest 5 to 10 percent of the oligonucleotide probes being used, or, where a different background signal is calculated for each target gene, for the lowest 5 to 10 percent of the probes for each gene. Where the oligonucleotide probes corresponding to a particular cell wall biosynthesis or wood development gene hybridize well and, hence, appear to bind specifically to a target sequence, they should not be used in a background signal calculation. Alternatively, background can be calculated as the average hybridization signal intensity produced by hybridization to probes that are not

complementary to any sequence found in the sample (*e.g.*, probes directed to nucleic acids of the opposite sense or to genes not found in the sample). In microarray methods, background can be calculated as the average signal intensity produced by regions of the array that lack any oligonucleotides probes at all.

c. PCR-Based Methods

[0461] In another embodiment, PCR-based methods are used to detect polynucleotide expression. These methods include reverse-transcriptase-mediated polymerase chain reaction (RT-PCR) including real-time and endpoint quantitative reverse-transcriptase-mediated polymerase chain reaction (Q-RTPCR). These methods are well known in the art. For example, methods of quantitative PCR can be carried out using kits and methods that are commercially available from, for example, Applied BioSystems and Stratagene®. See also Kochanowski, QUANTITATIVE PCR PROTOCOLS (Humana Press, 1999); Innis *et al., supra.*; Vandesompele *et al., Genome Biol.* 3: RESEARCH0034 (2002); Stein, *Cell Mol. Life Sci.* 59: 1235 (2002).

[0462] Polynucleotide expression can also be observed in solution using Q-RTPCR. Q-RTPCR relies on detection of a fluorescent signal produced proportionally during amplification of a PCR product. See Innis *et al., supra.* Like the traditional PCR method, this technique employs PCR oligonucleotide primers, typically 15-30 bases long, that hybridize to opposite strands and regions flanking the DNA region of interest. Additionally, a probe (*e.g.*, TaqMan®, Applied Biosystems) is designed to hybridize to the target sequence between the forward and reverse primers traditionally used in the PCR technique. The probe is labeled at the 5' end with a reporter fluorophore, such as 6-carboxyfluorescein (6-FAM) and a quencher fluorophore like 6-carboxy-tetramethyl-rhodamine (TAMRA). As long as the probe is intact, fluorescent energy transfer occurs which results in the absorbance of the fluorescence emission of the reporter fluorophore by the quenching fluorophore. As Taq polymerase extends the primer, however, the intrinsic 5' to 3' nuclease activity of Taq degrades the probe, releasing the reporter fluorophore. The increase in the fluorescence signal detected during the amplification cycle is proportional to the amount of product generated in each cycle.

[0463] The forward and reverse amplification primers and internal hybridization probe is designed to hybridize specifically and uniquely with one nucleotide derived from the transcript of a target gene. In one embodiment, the selection criteria for primer and probe sequences incorporates constraints regarding nucleotide content and size to accommodate TaqMan® requirements.

[0464] SYBR Green® can be used as a probe-less Q-RTPCR alternative to the Taqman®-type assay, discussed above. ABI PRISM® 7900 SEQUENCE DETECTION SYSTEM USER GUIDE APPLIED BIOSYSTEMS, chap. 1-8, App. A-F. (2002).

[0465] A device measures changes in fluorescence emission intensity during PCR amplification. The measurement is done in "real time," that is, as the amplification product accumulates in the reaction. Other methods can be used to measure changes in fluorescence resulting from probe digestion. For example, fluorescence polarization can distinguish between large and small molecules based on molecular tumbling (see U.S. patent No. 5,593,867).

d. Protein Detection Methods

[0466] Proteins can be observed by any means known in the art, including immunological methods, enzyme assays and protein array/proteomics techniques.

[0467] Measurement of the translational state can be performed according to several protein methods. For example, whole genome monitoring of protein -- the "proteome" -- can be carried out by constructing a microarray in which binding sites comprise immobilized, preferably monoclonal, antibodies specific to a plurality of proteins having an amino acid sequence of any of SEQ ID NOs: 231-460, or proteins encoded by the polynucleotides of SEQ ID NOs: 1-230 or conservative variants thereof. See Wildt *et al.*, *Nature Biotechnol.* 18: 989 (2000). Methods for making polyclonal and monoclonal antibodies are well known, as described, for instance, in Harlow & Lane, ANTIBODIES: A LABORATORY MANUAL (Cold Spring Harbor Laboratory Press, 1988).

[0468] Alternatively, proteins can be separated by two-dimensional gel electrophoresis systems. Two-dimensional gel electrophoresis is well-known in the art and typically involves isoelectric focusing along a first dimension followed by SDS-PAGE electrophoresis along a second dimension. See, *e.g.*, Hames *et al.*, GEL ELECTROPHORESIS OF PROTEINS: A PRACTICAL APPROACH (IRL Press, 1990). The resulting electropherograms can be analyzed by numerous techniques, including mass spectrometric techniques, western blotting and immunoblot analysis using polyclonal and monoclonal antibodies, and internal and N-terminal micro-sequencing.

3. Correlating Gene Expression to Phenotype and Tissue Development

[0469] As discussed above, the invention provides methods and tools to correlate cell wall polynucleotide expression to plant phenotype. Polynucleotide expression may be be examined in a plant having a phenotype of interest and compared to a plant that does not have the phenotype or has a different phenotype. Such a phenotype includes, but is not limited to, increased drought tolerance, herbicide resistance, reduced or increased height, reduced or increased branching, enhanced cold and frost tolerance, improved vigor, enhanced color, enhanced health and nutritional characteristics, improved storage, enhanced yield, enhanced salt tolerance, enhanced resistance of the wood to decay, enhanced resistance to fungal diseases, altered attractiveness to insect pests, enhanced heavy metal tolerance, increased disease tolerance, increased insect tolerance, increased water-stress tolerance, enhanced sweetness, improved texture, decreased phosphate content, increased germination, increased micronutrient uptake, improved starch composition, improved flower longevity, production of novel resins, and production of novel proteins or peptides.

[0470] In another embodiment, the phenotype includes one or more of the following traits: propensity to form reaction wood, a reduced period of juvenility, an increased period of juvenility, self-abscising branches, accelerated reproductive development or delayed reproductive development.

[0471] In a further embodiment, the phenotype that is differs in the plants compares includes one or more of the following: lignin quality, lignin structure, wood

composition, wood appearance, wood density, wood strength, wood stiffness, cellulose polymerization, fiber dimensions, lumen size, other plant components, plant cell division, plant cell development, number of cells per unit area, cell size, cell shape, cell wall composition, rate of wood formation, aesthetic appearance of wood, formation of stem defects, average microfibril angle, width of the S2 cell wall layer, rate of growth, rate of root formation ratio of root to branch vegetative development, leaf area index, and leaf shape.

[0472] Phenotype can be assessed by any suitable means as discussed above.

[0473] In a further embodiment, polynucleotide expression can be correlated to a given point in the cell cycle, a given point in plant development, and in a given tissue sample. Plant tissue can be examined at different stages of the cell cycle, from plant tissue at different developmental stages, from plant tissue at various times of the year (*e.g.* spring versus summer), from plant tissues subject to different environmental conditions (*e.g.* variations in light and temperature) and/or from different types of plant tissue and cells. In accordance with one embodiment, plant tissue is obtained during various stages of maturity and during different seasons of the year. For example, plant tissue can be collected from stem dividing cells, differentiating xylem, early developing wood cells, differentiated spring wood cells, differentiated summer wood cells.

[0474] It will be apparent to those skilled in the art that various modifications and variations can be made in the methods and compositions of the present invention without departing from the spirit or scope of the invention. Thus, it is intended that the present invention cover the modifications and variations of this invention provided they come within the scope of the appended claims and their equivalents.

[0475] The following examples are given to illustrate the present invention. It should be understood, however, that the invention is not to be limited to the specific conditions or details described in these examples. Throughout the specification, any and all references to a publicly available document, including a U.S. patent, are specifically incorporated by reference in their entirety.

EXAMPLE 1

Isolation and Characterization of cDNA Clones from *Eucalyptus grandis*

[0476] *Eucalyptus grandis* cDNA expression libraries were prepared from mature shoot buds, early wood phloem, floral tissue, leaf tissue (two independent libraries), feeder roots, structural roots, xylem or early wood xylem and were constructed and screened as follows.

[0477] Total RNA was extracted from the plant tissue using the protocol of Chang et al. (*Plant Molecular Biology Reporter* 11:113-116 (1993). mRNA was isolated from the total RNA preparation using either a Poly(A) Quik mRNA Isolation Kit (Stratagene, La Jolla, CA) or Dynal Beads Oligo $(dT)_{25}$ (Dynal, Skogen, Norway). A cDNA expression library was constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA clones in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNAs were packaged using a Gigapack II Packaging Extract (Stratagene) using an aliquot (1 – 5 αl) from the 5 μl ligation reaction dependent upon the library. Mass excision of the library was done using XL1-Blue MRF' cells and XLOLR cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing X-gal and isopropylthio-beta-galactoside (IPTG).

[0478] Of the colonies plated and selected for DNA miniprep, 99% contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and cDNA was purified by means of alkaline lysis and polyethylene glycol (PEG) precipitation. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye primer sequences were prepared using a Turbo Catalyst 800 machine (Perkin Elmer/Applied Biosystems Division, Foster City, CA) according to the manufacturer's protocol.

[0479] DNA sequence for positive clones was obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced first from the 5' end and, in some cases, also from the 3' end. For some clones, internal sequence was obtained using either Exonuclease III deletion analysis, yielding a library of differentially sized subclones in pBK-CMV, or by direct sequencing using gene-specific primers designed to identified regions of the gene of interest.

[0480] The determined cDNA sequences were compared with known sequences in the EMBL database using the computer algorithms FASTA and/or BLASTN. Multiple alignments of redundant sequences were used to build reliable consensus sequences. The determined cDNA sequences are provided in SEQ ID NOS: 1-230. Based on similarity to known sequences from other plant species, the isolated polynucleotide sequences were identified as encoding wood and cell wall proteins, as detailed in Tables 1 and 2. The predicted polypeptide sequences corresponding to the polynucleotide sequences of SEQ ID NOS: 132-230 are provided in SEQ ID NOS: 362-460.

EXAMPLE 2

Isolation and Characterization of cDNA Clones from *Pinus radiata*

[0481] *Pinus radiata* cDNA expression libraries (prepared from either shoot bud tissue, suspension cultured cells, early wood phloem (two independent libraries), fascicle meristem tissue, male strobilus, root (unknown lineage), feeder roots, structural roots, female strobilus, cone primordia, female receptive cones and xylem (two independent libraries) were constructed and screened as described above in Example 1.

[0482] DNA sequence for positive clones was obtained using forward and reverse primers on a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer and the determined sequences were compared to known sequences in the database as described above.

[0483] Based on similarity to known sequences from other plant species, the isolated polynucleotide sequences were identified as encoding wood and cell wall proteins, as displayed above in Table 1. The predicted polypeptide sequences corresponding to the polynucleotide sequences of SEQ ID NOS: 1-131 are provided in SEQ ID NOS: 231-361.

EXAMPLE 3
5' RACE Isolation

[0484] To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed. Using the SMART RACE cDNA amplification kit (Clontech Laboratories, Palo Alto, Calif.). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, and then ligating of the SMART RACE. Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA. Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced, and cloned. The process may be repeated until 5' and 3' ends of the full-length gene were identified. A full-length cDNA may generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

[0485] For example, to amplify the missing 5' region of a gene from first-strand cDNA, a primer was designed 5'→3' from the opposite strand of the template sequence, and from the region between ~100-200 bp of the template sequence. A successful amplification should give an overlap of ~100 bp of DNA sequence between the 5' end of the template and PCR product.

[0486] RNA was extracted from four pine tissues, namely seedling, xylem, phloem and structural root using the Concert Reagent Protocol (Invitrogen, Carlsbad, CA) and standard isolation and extraction procedures. The resulting RNA was then treated with DNase, using 10U/ul DNase I (Roche Diagnostics, Basel, Switzerland). For 100 µg of RNA, 9 µl 10x DNase buffer (Invitrogen, Carlsbad, CA), 10 µl of Roche DNase

I and 90 µl of Rnase-free water was used. The RNA was then incubated at room temperature for 15 minutes and 1/10 volume 25mM EDTA is added. A RNeasy mini kit (Qiagen, Venlo, The Netherlands) was used for RNA clean up according to manufacturer's protocol.

[0487] To synthesize cDNA, the extracted RNA from xylem, phloem, seedling and root was used and the SMART RACE cDNA amplification kit (Clontech Laboratories Inc, Palo Alto, CA) was followed according to manufacturer's protocol. For the RACE PCR, the cDNA from the four tissue types was combined. The master mix for PCR was created by combining equal volumes of cDNA from xylem, phloem, root and seedling tissues. PCR reactions were performed in 96 well PCR plates, with 1µl of primer from primer dilution plate (10mM) to corresponding well positions. 49 µl of master mix is aliquoted into the PCR plate with primers. Thermal cycling commenced on a GeneAmp 9700 (Applied Biosystems, Foster City, CA) at the following parameters:

94^0C (5 sec),
72^0C (3 min), 5 cycles;
94^0C (5 sec),
70^0C (10 sec),
72^0C (3 min), 5 cycles;
94^0C (5 sec),
68^0C (10 sec),
72^0C (3min), 25 cycles.

[0488] cDNA was separated on an agarose gel following standard procedures. Gel fragments were excised and eluted from the gel by using the Qiagen 96-well Gel Elution kit, following the manufacturer's instructions.

[0489] PCR products were ligated into pGEMTeasy (Promega, Madison, WI) in a 96 well plate overnight according to the following specifications: 60-80 ng of DNA, 5 µl 2X rapid ligation buffer, 0.5 µl pGEMT easy vector, 0.1 µl DNA ligase, filled to 10 µl with water, and incubated overnight.

[0490] Each clone was transformed into *E.coli* following standard procedures and DNA was extracted from 12 clones picked by following standard protocols. DNA extraction and the DNA quality was verified on an 1% agarose gel. The presence of the correct size insert in each of the clones was determined by restriction digests, using the restriction endonuclease *Eco*RI, and gel electrophoresis, following standard laboratory procedures.

EXAMPLE 4

Curation of an EST sequence.

[0491] During the production of cDNA libraries, the original transcripts or their DNA counterparts may have features that prevent them from coding for functional proteins. There may be insertions, deletions, base substitutions, or unspliced or improperly spliced introns. If such features exist, it is often possible to identify them so that they can be changed. Similar curation was performed on any sequence that has homology to sequences in the public databases.

[0492] The following is a general example of how a sequence was curated. After determination of the DNA sequence, BLAST analysis showed that it is related to an *Arabidopsis* gene on the publicly available *Arabidopsis* genome sequence. However, instead of coding for an approximately 240 amino acid polypeptide, the sequence being curated was predicted to code for a product of only 157 amino acid residues, suggesting an error in the DNA sequence. To identify where the genuine coding region might be, the DNA sequence to the end of each EST was translated in each of the three reading frames and the predicted sequences were aligned with the Arabidopsis gene's amino acid sequence. It was found that the DNA segment in one portion of the EST coded for a sequence with similarity to the carboxyl terminus of the Arabidopsis gene. Therefore, it appears that an unspliced intron was present in the EST.

[0493] Unspliced introns are a relatively minor issue with regard to use of a cloned sequence for overexpression of the gene of interest. The RNA resulting from transcription of the cDNA can be expected to undergo normal processing to remove

the intron. Antisense and RNAi constructs are also expected to function to suppress the gene of interest. On other occasions, it may be desirable to identify the precise limits of the intron so that it can be removed. When the sequence in question has a published sequence that is highly similar, it may be possible to find the intron by aligning the two sequences and identifying the locations where the sequence identity falls off, aided by the knowledge that introns start with the sequence GT and end with the sequence AG.

[0494] When there was some doubt about the site of the intron because highly similar sequences were not available, the intron location was verified experimentally. For example, DNA oligomers were synthesized flanking the region where the suspected intron was located. RNA from the source species, either Pinus or Eucalyptus, was isolated and used as a template to make cDNA using reverse transcriptase. The selected primers were then used in a PCR reaction to amplify the correctly spliced DNA segment (predicted size of approximately 350 bp smaller than the corresponding segment of the original consensus) from the population of cDNAs. The amplified segment was then subjected to sequence analysis and compared to the consensus sequence to identify the differences.

[0495] The same procedure was used when an alternate splicing event (partial intron remaining, or partial loss of an exon) was suspected. When an EST has a small change, such as insertion or deletion of a small number of bases, computer analysis of the EST sequence could still indicate its location when a translation product of the wrong size was predicted or if there was an obvious frameshift. Verification of the true sequence was done by synthesis of primers, production of new cDNA, and PCR amplification as described above.

EXAMPLE 5

Eucalyptus in silico data

[0496] In silico gene expression was used to determine the membership of the consensi EST libraries. For each library, a consensus was determined from the number of ESTs in any tissue class divided by the total number of ESTs in a class

multiplied by 1000. These values provide a normalized value that is not biased by the extent of sequencing from a library. Several libraries were sampled for a consensus value, including reproductive, bud reproductive, bud vegetative, fruit, leaf, phloem, cambium, xylem, root, stem, sap vegetative, whole plant libraries.

[0497] As shown below, a number of the inventive sequences exhibit vascular-preferred expression (more than 50% of the hits by these sequences if the databases were searched at random would be in libraries made from developing vascular tissue) and thus are likely to be involved in wood-related developmental processes. Many of the remaining wood and cell proteins exhibit vegetative-preferred expression, suggesting expression in leaf developmental processes and photosynthesis-related processes, or root-preferred expression, suggesting expression in root developmental processes and water and nutrient uptake. The data is shown in the Table 5.

TABLE 5: *Eucalyptus* In Silico Expression Profiles

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
132	eucalyptusSpp_002590	Calnexin	0.48	0.08	2.08	0.15	3.76	3.52	3.01					5.63
133	eucalyptusSpp_003495	Calnexin	0.72	0.17	0.71	0.38		0.22	1.06	0.31		0.47		4.01
134	eucalyptusSpp_013577	Calnexin							0.04	0.08				0.12
135	eucalyptusSpp_033927	Calnexin								0.04				
136	eucalyptusSpp_039632	Calnexin				0.08								
137	eucalyptusSpp_006372	Sucrose synthase		0.08	1.56	0.31	0.85	0.50	0.15	0.82		1.19		2.91
138	eucalyptusSpp_006373	Sucrose synthase				0.23	0.84	0.17	0.04	0.43		1.19		3.81
139	eucalyptusSpp_006549	Sucrose synthase		0.08	2.02	0.23	4.19	0.28	0.15	0.28		1.90		10.95

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
140	eucalyptusSpp_019813	Sucrose synthase								0.23				
141	eucalyptusSpp_033523	Sucrose synthase								0.55				
142	eucalyptusSpp_001430	Beta-glucosidase												0.74
143	eucalyptusSpp_001556	Beta-glucosidase	3.38	0.08	0.60		0.35	0.17	0.30	0.16			0.25	1.44
144	eucalyptusSpp_003619	Beta-glucosidase		0.17	0.18	0.15	0.17	0.17		0.04				2.29
145	eucalyptusSpp_006486	Beta-glucosidase	0.48	0.34	0.19									
146	eucalyptusSpp_006939	Beta-glucosidase		0.93				0.06	0.15	0.08				3.13
147	eucalyptusSpp_006955	Beta-glucosidase		0.08	1.53		3.32	0.17	0.04	0.28				0.70
148	eucalyptusSpp_007432	Beta-glucosidase			1.70			0.11	0.91	0.04				0.33

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
149	eucalyptusSpp_007745	Beta-glucosidase			0.19			0.06						6.23
150	eucalyptusSpp_007776	Beta-glucosidase			1.12		0.50	0.11	0.15					0.68
151	eucalyptusSpp_008889	Beta-glucosidase			1.08		1.49	0.39		0.04				0.21
152	eucalyptusSpp_009271	Beta-glucosidase		0.51	2.34									
153	eucalyptusSpp_010369	Beta-glucosidase	0.48					0.72						
154	eucalyptusSpp_010420	Beta-glucosidase						0.06		0.04				
155	eucalyptusSpp_010726	Beta-glucosidase				0.08		0.17	0.76	0.59				
156	eucalyptusSpp_011679	Beta-glucosidase					0.52	0.06						
157	eucalyptusSpp_036289	Beta-glucosidase						0.17		0.12				

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
158	eucalyptusSpp_037751	Beta-glucosidase								0.24				
159	eucalyptusSpp_011491	Beta-glucosidase			0.49	0.08	0.17			0.24				6.01
160	eucalyptusSpp_016710	Beta-glucosidase												0.33
161	eucalyptusSpp_017035	Beta-glucosidase					0.50							0.36
162	eucalyptusSpp_000843	Beta-glucosidase			1.08			0.61	0.15	0.04				1.13
163	eucalyptusSpp_005983	Beta-glucosidase				0.08		0.22	0.41					2.07
164	eucalyptusSpp_008977	Beta-glucosidase			0.09		0.17	0.39						1.59
165	eucalyptusSpp_023461	Beta-glucosidase					0.83	0.06	4.45					0.17
166	eucalyptusSpp_009517	Beta-glucosidase			0.90			0.11		0.04				0.13

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
167	eucalyptusSpp_019373	Beta-glucosidase								0.24				
168	eucalyptusSpp_021302	Beta-glucosidase		0.59		0.92		0.17	0.04					
169	eucalyptusSpp_021738	Beta-glucosidase		0.59		0.92		0.17	0.04					
170	eucalyptusSpp_024123	Beta-glucosidase		0.59		0.92		0.17	0.04					
171	eucalyptusSpp_033744	Beta-glucosidase								0.12				
172	eucalyptusSpp_041352	Beta-glucosidase					0.52							
173	eucalyptusSpp_006312	Beta-glucosidase		0.08	2.98	0.23	0.17	0.50	0.04	0.04				2.30
174	eucalyptusSpp_006494	Beta-glucosidase		0.08		0.15		0.17						
175	eucalyptusSpp_008515	Beta-glucosidase			1.04					0.08				0.61

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
176	eucalyptusSpp_011678	Beta-glucosidase					1.40	0.61						
177	eucalyptusSpp_016980	Beta-glucosidase		0.68		0.38	1.16		0.04	0.20				
178	eucalyptusSpp_020029	Beta-glucosidase								0.60				
179	eucalyptusSpp_021882	Beta-glucosidase										0.71		0.13
180	eucalyptusSpp_000640	Hexose pyrophosphorylase		0.34			1.57	0.73		0.08				0.26
181	eucalyptusSpp_012471	Hexose pyrophosphorylase					0.70	0.06						0.25
182	eucalyptusSpp_028949	Hexose pyrophosphorylase							0.22					
183	eucalyptusSpp_010858	Mannose isomerase			0.98			0.06		0.08				0.26
184	eucalyptusSpp_001308	Sucrose phosphate synthase		1.35		0.08	0.17	0.61	0.74	2.01				

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
185	eucalyptusSpp_034568	Sucrose phosphate synthase								0.39				
186	eucalyptusSpp_038142	Sucrose phosphate synthase								0.52				
187	eucalyptusSpp_002364	Xyloglucan endotransglycosylase					0.50							
188	eucalyptusSpp_003103	Xyloglucan endotransglycosylase		0.76		0.15	0.17							
189	eucalyptusSpp_003487	Xyloglucan endotransglycosylase								0.28				
190	eucalyptusSpp_003488	Xyloglucan endotransglycosylase	0.24			0.31				0.43				
191	eucalyptusSpp_003492	Xyloglucan endotransglycosylase	0.48						0.11	0.20				0.68
192	eucalyptusSpp_003494	Xyloglucan endotransglycosylase								0.04				0.50
193	eucalyptusSpp_004062	Xyloglucan endotransglycosylase			0.27			0.11		0.04				1.35

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
194	eucalyptusSpp_004063	Xyloglucan endotransglycosylase				0.08			0.37					0.74
195	eucalyptusSpp_005148	Xyloglucan endotransglycosylase			0.54									0.37
196	eucalyptusSpp_007619	Xyloglucan endotransglycosylase			2.46									1.00
197	eucalyptusSpp_010673	Xyloglucan endotransglycosylase					0.17	0.06	1.06	0.04				
198	eucalyptusSpp_010807	Xyloglucan endotransglycosylase					0.17	0.44		0.28				3.62
199	eucalyptusSpp_011549	Xyloglucan endotransglycosylase						0.06						0.23
200	eucalyptusSpp_012168	Xyloglucan endotransglycosylase						0.77		0.04				0.49
201	eucalyptusSpp_012541	Xyloglucan endotransglycosylase					1.05	0.06						0.38
202	eucalyptusSpp_012905	Xyloglucan endotransglycosylase												0.68

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
203	eucalyptusSpp_017386	Xyloglucan endotransglycosylase			0.16	1.15				0.24				6.20
204	eucalyptusSpp_022385	Xyloglucan endotransglycosylase						0.06						5.11
205	eucalyptusSpp_033851	Xyloglucan endotransglycosylase								0.35				
206	eucalyptusSpp_034061	Xyloglucan endotransglycosylase							0.30	0.20				
207	eucalyptusSpp_036012	Xyloglucan endotransglycosylase								0.16				
208	eucalyptusSpp_002298	Dirigent						0.06						6.38
209	eucalyptusSpp_002439	Dirigent				0.54		0.11						3.54
210	eucalyptusSpp_008836	Dirigent			0.09		0.17	2.28						0.84
211	eucalyptusSpp_009914	Dirigent			0.18			0.39						0.45

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
212	eucalyptusSpp_009915	Dirigent			0.16			0.50		0.20				1.23
213	eucalyptusSpp_010326	Dirigent						0.50						
214	eucalyptusSpp_017008	Dirigent				0.46	0.83							
215	eucalyptusSpp_017185	Dirigent				0.77	0.33		0.30					
216	eucalyptusSpp_019645	Dirigent								0.43				0.28
217	eucalyptusSpp_002197	Expansin						0.44		0.04				0.78
218	eucalyptusSpp_002399	Expansin			1.49			0.61	0.15					3.60
219	eucalyptusSpp_002532	Expansin		0.08	1.04		0.52	2.44	0.91	0.12				3.53
220	eucalyptusSpp_006932	Expansin		0.08			0.17			0.12				

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
221	eucalyptusSpp_013492	Expansin							0.56					
222	eucalyptusSpp_014985	Expansin				0.62	0.17		0.37					0.13
223	eucalyptusSpp_014986	Expansin							0.07					
224	eucalyptusSpp_015104	Expansin					0.17		0.04					
225	eucalyptusSpp_018610	Expansin								0.36				
226	eucalyptusSpp_020260	Expansin				0.08				0.44				
227	eucalyptusSpp_028458	Expansin						0.55						
228	eucalyptusSpp_031108	Expansin	1.69	0.08						0.08				
229	eucalyptusSpp_010481	Yieldin					2.62			0.08				0.12

SEQ ID	ConsID	Family	1	2	3	4	5	6	7	8	9	10	11	12
230	eucalyptusSpp_ 019062	Yieldin				0.46				0.43				

In the Table, the following numbers 1-12 represent the following tissues: 1 is bud reproductive; 2 is bud vegetative; 3 is cambium; 4 is fruit; 5 is leaf; 6 is phloem; 7 is reproductive; 8 is root; 9 is sap vegetative; 10 is stem; 11 is whole; and 12 is xylem.

EXAMPLE 6

Pine In Silico Data

[0498] In silico gene expression was used to determine the membership of the consensi EST libraries. For each library, a consensus was determined from the number of ESTs in any tissue class divided by the total number of ESTs in a class multiplied by 1000. These values provide a normalized value that is not biased by the extent of sequencing from a library. Several libraries were sampled for a consensus value, including reproductive, bud reproductive, bud vegetative, fruit, leaf, phloem, cambium, xylem, root, stem, sap vegetative, whole plant libraries.

[0499] As shown below, a number of the inventive sequences exhibit vascular-preferred expression (more than 50% of the hits by these sequences if the databases were searched at random would be in libraries made from developing vascular tissue) and thus are likely to be involved in wood-related developmental processes. Many of the remaining wood and cell wall proteins exhibit vegetative-preferred expression, suggesting expression in leaf developmental processes and photosynthesis-related processes, or root-preferred expression, suggesting expression in root developmental processes and water and nutrient uptake. The data is shown in the Table 6.

Table 6: Pine In Silico Expression Profiles

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
1	000420	Calnexin	0.16	0.42	0.22	1.16	0.27	2.20	0.96	0.93	0.60	0.90	7.03	6.88
2	009128	Calnexin			0.22	1.38	0.16	0.13		0.15	0.22		1.52	0.95
3	000082	Beta-glucosidase		0.14	0.33	0.24		0.56	0.34	0.07	0.36	0.18	1.23	0.93
4	000808	Beta-glucosidase	0.31		0.11	0.59	0.16	0.53	0.97	0.55	0.76		2.15	2.66
5	002641	Beta-glucosidase			0.22	0.29		0.45	0.15			0.36	0.20	
6	003151	Beta-glucosidase				10.45		0.34					0.10	0.85
7	003170	Beta-glucosidase								0.14	0.07		0.43	0.70
8	003171	Beta-glucosidase	0.16			0.46	0.16	0.17		0.15	0.07	0.18	1.46	1.25
9	005830	Beta-glucosidase		0.14						0.27			0.05	
10	006138	Beta-glucosidase			0.33									
11	006141	Beta-glucosidase			0.22	0.05	0.05	0.96	0.39	0.14	0.15		0.41	11.87
12	008153	Beta-glucosidase			0.33			0.46			0.18		0.39	2.75
13	008677	Beta-glucosidase			0.11	5.03		1.28	0.80		0.22		0.43	2.72
14	008688	Beta-glucosidase											0.05	
15	008701	Beta-glucosidase						0.44						0.14
16	010276	Beta-glucosidase				0.63		0.13		0.14			0.42	0.32

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
17	012343	Beta-glucosidase						0.28						
18	013199	Beta-glucosidase						0.48			0.39		0.23	0.17
19	014339	Beta-glucosidase	0.47			0.19		0.56						0.15
20	014357	Beta-glucosidase	0.16			0.25							0.10	1.28
21	014389	Beta-glucosidase	0.16						0.19					
22	015733	Beta-glucosidase								0.36			4.77	
23	015734	Beta-glucosidase											0.10	
24	019348	Beta-glucosidase											0.14	
25	020304	Beta-glucosidase											0.35	0.87
26	020305	Beta-glucosidase						0.13						
27	021499	Beta-glucosidase				0.60		0.15	0.26					0.72
28	021803	Beta-glucosidase					0.11	0.27	1.95					
29	024199	Beta-glucosidase									0.31			0.82
30	024166	Beta-glucosidase									0.08			
31	000560	Beta-glucosidase				0.63		0.13			0.25	0.36		2.85
32	008324	Beta-glucosidase			0.44			0.13					0.24	1.07
33	008526	Beta-glucosidase											0.15	0.57

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
34	013209	Beta-glucosidase											0.18	0.56
35	013210	Beta-glucosidase				0.30			0.58		0.04		0.67	0.57
36	018923	Beta-glucosidase				0.41							0.05	
37	022167	Beta-glucosidase					0.05	0.56	0.11					0.46
38	005555	Beta-glucosidase											0.55	
39	006798	Beta-glucosidase								0.14			0.05	7.44
40	006799	Beta-glucosidase				0.43	0.11	0.43			0.20		0.14	0.88
41	006802	Beta-glucosidase				0.21				0.14	0.04		2.72	
42	006803	Beta-glucosidase	0.16	0.28	0.11	0.40		0.47	0.41	0.14	0.04		0.75	3.68
43	013555	Beta-glucosidase						1.25			0.65			
44	014884	Beta-glucosidase								0.73			21.39	
45	001975	Beta-glucosidase	0.16		0.11	0.14		0.19	0.11					1.80
46	003684	Beta-glucosidase					0.05	0.33		0.15		0.18	0.05	
47	008566	Beta-glucosidase			0.22				0.15				2.41	
48	013146	Beta-glucosidase								0.58	0.04		2.53	
49	014358	Beta-glucosidase	0.16			0.05		0.13	0.29				0.16	1.19
50	014570	Beta-glucosidase	0.16							0.07				

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
51	014985	Beta-glucosidase								1.45			31.72	0.17
52	023047	Beta-glucosidase						0.41						0.46
53	006216	Hexose pyrophosphorylase	0.47	0.14		0.43		0.36	0.22	0.55			1.35	2.27
54	013260	Hexose pyrophosphorylase	0.16				0.11	0.31	0.11	0.07			0.67	1.45
55	014596	Hexose pyrophosphorylase	0.16			0.65				0.14			0.21	0.17
56	021340	Hexose pyrophosphorylase				0.64								1.73
57	022975	Hexose pyrophosphorylase						0.69	0.15		0.36			0.34
58	007714	Mannose isomerase			0.11			0.19		0.07	0.07		0.67	0.83
59	013469	Sucrose phosphate synthase						0.06					0.05	
60	016491	Sucrose phosphate synthase									0.07		0.23	0.16

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
61	001007	Xyloglucan endotransglycosylase		0.28		3.54		0.17	0.29		0.80	1.79	0.44	4.35
62	001008	Xyloglucan endotransglycosylase				0.97					0.20		0.17	2.09
63	001184	Xyloglucan endotransglycosylase								0.07			0.47	
64	001186	Xyloglucan endotransglycosylase		0.14		0.97						0.18	0.29	0.19
65	001187	Xyloglucan endotransglycosylase				0.39				0.15			1.80	
66	001191	Xyloglucan endotransglycosylase				0.19								
67	001197	Xyloglucan endotransglycosylase											0.05	
68	001603	Xyloglucan endotransglycosylase				0.24		0.19	0.11	0.07		0.36	0.63	1.00
69	001604	Xyloglucan endotransglycosylase	0.16											

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
70	002148	Xyloglucan endotransglycosylase									0.04	0.54	0.33	
71	005260	Xyloglucan endotransglycosylase				0.05	0.05				0.04		0.82	2.02
72	005658	Xyloglucan endotransglycosylase			0.11					0.07			4.05	
73	005659	Xyloglucan endotransglycosylase	0.16			0.59	0.44	0.27	0.15	0.07	0.26		2.32	0.31
74	005715	Xyloglucan endotransglycosylase												0.16
75	005718	Xyloglucan endotransglycosylase			0.11			0.15			0.04			1.72
76	006166	Xyloglucan endotransglycosylase		0.14			0.05		0.11	0.14				
77	008291	Xyloglucan endotransglycosylase			0.44	0.39					0.04		0.25	
78	008343	Xyloglucan endotransglycosylase			0.33	0.43								

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
79	010682	Xyloglucan endotransglycosylase				0.69		0.11						1.56
80	011081	Xyloglucan endotransglycosylase				0.24		39.12					1.28	
81	011726	Xyloglucan endotransglycosylase						0.62			0.04			
82	013444	Xyloglucan endotransglycosylase					0.11	0.19	0.19	0.42	0.07		1.27	0.51
83	014144	Xyloglucan endotransglycosylase	0.16										0.19	
84	014539	Xyloglucan endotransglycosylase	0.16											0.20
85	015716	Xyloglucan endotransglycosylase					0.33						0.09	
86	016453	Xyloglucan endotransglycosylase								0.22			0.04	
87	017884	Xyloglucan endotransglycosylase						0.13					0.19	

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
88	023707	Xyloglucan endotransglycosylase				0.21		0.14						
89	023708	Xyloglucan endotransglycosylase											0.18	
90	027337	Xyloglucan endotransglycosylase				0.10							0.18	0.15
91	001609	Dirigent				0.19					0.08	0.18		3.96
92	004488	Dirigent							0.19		0.04		0.19	
93	004489	Dirigent		0.14		1.04		0.61	0.63					3.36
94	005049	Dirigent	0.47	0.28					0.31				0.92	
95	005790	Dirigent	0.16	0.14			0.16		0.15					
96	005791	Dirigent			0.11			0.33			0.23		0.29	0.41
97	006230	Dirigent							0.11	0.14			1.81	
98	006231	Dirigent								0.29			4.39	
99	009358	Dirigent			0.11			0.06					1.14	
100	011003	Dirigent				0.43								0.75
101	014809	Dirigent								0.29			0.65	

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
102	014810	Dirigent											2.18	
103	018046	Dirigent											0.10	
104	018129	Dirigent											0.14	0.14
105	019464	Dirigent					0.27				0.07		0.05	
106	019641	Dirigent											0.32	
107	020854	Dirigent											0.11	
108	022079	Dirigent					0.16			0.22				
109	026378	Dirigent									0.07			
110	027112	Dirigent												1.62
111	000134	Expansin		0.42		0.43		0.11	0.11	0.27	0.04		0.19	0.75
112	003894	Expansin		0.56				0.98	0.31	0.27	0.32	0.36	0.41	3.90
113	005134	Expansin						0.82						
114	005738	Expansin	0.16	0.28			0.16		0.26				0.05	
115	006938	Expansin	0.16	0.14		0.35		0.41	1.04		0.62		1.92	3.63
116	007527	Expansin		0.14							0.68		0.50	
117	008477	Expansin				0.05								
118	008478	Expansin											0.24	

DNA Seq ID	Consensus ID PinusRadiata	Family	1	2	3	4	5	6	7	8	9	10	11	12
119	008479	Expansin											0.77	
120	008480	Expansin			0.11								0.19	0.33
121	008481	Expansin											0.05	
122	009863	Expansin												2.86
123	009864	Expansin	0.16			0.05		0.14					0.99	0.75
124	011105	Expansin				0.59		0.13			0.04			
125	012207	Expansin						0.40						
126	015481	Expansin								0.15	0.69		2.46	1.13
127	015617	Expansin					0.05						1.37	
128	015619	Expansin								0.29			1.93	
129	016977	Expansin											0.39	
130	021768	Expansin					0.11				0.07			
131	026140	Yieldin									0.07			

In the Table, the following numbers 1-12 represent the following tissues: 1 is bud reproductive; 2 is bud vegetative; 3 is callus; 4 is cambium; 5 is meristem vegetative; 6 is phloem; 7 is reproductive female; 8 is reproductive male; 9 is root; 10 is vascular; 11 is whole; and 12 is xylem.

EXAMPLE 7

[0500] This example illustrates how polynucleotides important for wood development in *P. radiata* was determined and how oligonucleotides which uniquely bind to those genes were designed and synthesized for use on a microarray.

[0501] Open pollinated trees of approximately 16 years of age were selected from plantation-grown sites, in the United States for loblolly pine, and in New Zealand for radiata pine. Trees were felled during the spring and summer seasons to compare the expression of genes associated with these different developmental stages of wood formation. Trees were felled individually and trunk sections were removed from the bottom area approximately one to two meters from the base and within one to two meters below the live crown. The section removed from the basal end of the trunk contained mature wood. The section removed from below the live crown contained juvenile wood. Samples collected during the spring season were termed earlywood or springwood, while samples collected during the summer season are considered latewood or summerwood (Larson et al., Gen. Tech. Rep. FPL-GTR-129. Madison, WI: U.S. Department of Agriculture, Forest Service, Forest Products Laboratory. 42p.).

[0502] Tissues were isolated from the trunk sections such that phloem, cambium, developing xylem, and maturing xylem are removed. These tissues were collected only from the current year's growth ring. Upon tissue removal in each case, the material was immediately plunged into liquid nitrogen to preserve the nucleic acids and other components. The bark was peeled from the section and phloem tissue removed from the inner face of the bark by scraping with a razor blade. Cambium tissue was isolated from the outer face of the peeled section by gentle scraping of the surface. Developing xylem and lignifying xylem were isolated by sequentially performing more vigorous scraping of the remaining tissue. Tissues were transferred from liquid nitrogen into containers for long term storage at -70 °C until RNA extraction and subsequent analysis was performed.

EXAMPLE 8

[0503] This example illustrates a procedure for RNA extraction and purification, which was particularly useful for RNA obtained from conifer needle, xylem, cambium, and phloem.

[0504] Tissue was obtained from conifer needle, xylem, cambium or phloem. The tissue was frozen in liquid nitrogen and ground. The total RNA was extracted using Concert Plant RNA reagent (Invitrogen). The resulting RNA sample was extracted into phenol:chloroform and treated with DNase. The RNA was then incubated at 65 °C for 2 minutes followed by centrifugation at 4 °C for 30 minutes. Following centrifugation, the RNA was extracted into phenol at least 10 times to remove contaminants.

[0505] The RNA was further cleaned using RNeasy columns (Qiagen). The purified RNA was quantified using RiboGreen reagent (Molecular Probes) and purity assessed by gel electrophoresis.

[0506] RNA was then amplified using MessageAmp (Ambion). Aminoallyl-UTP and free UTP were added to the in vitro transcription of the purified RNA at a ratio of 4:1 aminoallyl-UTP-to-UTP. The aminoallyl-UTP was incorporated into the new RNA strand as it was transcribed. The amino-allyl group was then reacted with Cy dyes to attach the colorimetric label to the resulting amplified RNA using the Amersham procedure modified for use with RNA. Unincorporated dye was removed by ethanol precipitation. The labeled RNA was quantified spectrophotometrically (NanoDrop). The labeled RNA was fragmented by heating to 95 °C as described in Hughes et al., *Nature Biotechnol.* 19:342 (2001).

EXAMPLE 9

[0507] This Example illustrates how genes important for wood development in *P. radiata* were determined and how oligonucleotides which uniquely bind to those genes were designed and synthesized for use on a microarray.

[0508] Pine trees of the species *P. radiata* were grown under natural light conditions. Tissue samples were prepared as described in, *e.g.*, Sterky *et al.*, *Proc. Nat'l Acad. Sci.* 95:13330 (1998). Specifically, tissue samples were collected from woody trees having a height of 5 meters. Tissue samples of the woody trees were prepared by taking tangential sections through the cambial region of the stem. The stems were sectioned horizontally into sections ranging from juvenile (top) to mature (bottom). The stem sections separated by stage of development were further separated into 5 layers by peeling into sections of phloem, differentiating phloem, cambium, differentiating xylem, developing xylem, and mature xylem. Tissue samples, including leaves, buds, shoots, and roots were also prepared from seedlings of the species *P. radiata*.

[0509] RNA was isolated and ESTs generated as described in Example 1 or Sterky *et al.*, *supra*. The nucleic acid sequences of ESTs derived from samples containing developing wood were compared with nucleic acid sequences of genes known to be involved in polysaccharide synthesis. ESTs from samples that did not contain developing wood were also compared with sequences of genes known to be involved in the plant cell cycle. An *in silico* hybridization analysis was performed using BLAST (NCBI) as follows.

EXAMPLE 10

[0510] Sequences that showed hybridization *in silico* to ESTs made from samples containing developing wood, but that did not hybridize to ESTs from samples not containing developing wood were selected for further examination.

[0511] cDNA clones containing sequences that hybridized to the genes showing wood-preferred expression were selected from cDNA libraries using techniques well known in the art of molecular biology. Using the sequence information, oligonucleotides were designed such that each oligonucleotide is specific for only one cDNA sequence in the library. The oligonucleotide sequences are provided in Table 5. 60-mer oligonucleotide probes were designed using the method of Li and Stormo, supra or using software such as ArrayDesigner, GeneScan, and ProbeSelect.

[0512] The oligonucleotides were then synthesized *in situ* as described in Hughes *et al., Nature Biotechnol.* 19:324 (2002) or as described in Kane *et al., Nucleic Acids Res.* 28:4552 (2000) and affixed to an activated glass slide (Sigma-Genosis, The Woodlands, TX) using a 5' amino linker. The position of each oligonucleotide on the slide was known.

EXAMPLE 11

[0513] This example illustrates how to detect expression of *Pinus radiata* genes of the instant application which are important in wood formation using an oligonucleotide microarray prepared as described above. This is an example of a balanced incomplete block designed experiment carried out using RNA samples prepared from mature-phase phloem (P), cambium (C), expanding xylem found in a layer below the cambium (X1) and differentiating, lignifying xylem cells found deeper in the same growth ring (X2). In this example, cell cycle gene expression was compared among the four samples, namely P, C, X1, and X2.

[0514] In the summer, plants of the species *Pinus radiata* were felled and the bark of the main stem was immediately pulled gently away to reveal the phloem and xylem. The phloem and xylem were then peeled with a scalpel into separate containers of liquid nitrogen. Needles (leaves) and buds from the trees were also harvested with a scalpel into separate containers of liquid nitrogen. RNA was subsequently isolated from the frozen tissue samples as described in Example 1. Equal microgram quantities of total RNA were purified from each sample using RNeasy Mini columns (Qiagen, Valencia, CA) according to the manufacturer's instructions.

[0515] Amplification reactions were carried out for each of the P, C, X1, and X2 tissue samples. Amplification reactions were performed using Ambion's MessageAmp kit, a T7-based amplification procedure, following the manufacturer's instructions, except that a labeled aaUTP was added to the reagent mix during the amplification step. aaUTP was incorporated into the resulting antisense RNA formed during this step. CyDye fluorescent labels were coupled to the aaUTPs in a non-

enzymatic reaction as described in Example 8. Labeled amplified antisense RNAs were precipitated and washed, and then assayed for purity using a NanoDrop spectrophotometer. These labeled antisense RNAs, corresponding to the RNA isolated from the P, C, X1, and X2 tissue samples, constituted the sample nucleic acids, which were referred to as the P, C, X1, and X2 samples.

[0516] Normalization control samples of known nucleic acids were added to each sample in a dilution series of 500, 200, 100, 50, 25 and 10 pg/μl for quantitation of the signals. Positive controls corresponding to specific genes showing expression in all tissues of pine, such as housekeeping genes, were also added to the plant sample.

[0517] Each of four microarray slides were incubated with 125 μL of a P, C, X1 or X2 sample under a coverslip at 42 °C for 16-18 hours. The arrays were washed in 1x SSC, 0.1% SDS for 10 minutes and then in 0.1 x SSC, 0.1% SDS for 10 minutes and the allowed to dry.

[0518] The array slides were scanned using an Axon laser scanner and analyzed using GenePix Pro software. Data from the microarray slides were subjected to microarray data analysis using GenStat SAS or Spotfire software. Outliers were removed and ratiometric data for each of the datasets were normalized using a global normalization which employed a cubic spline fit applied to correct for differential dye bias and spatial effects. A second transformation was performed to fit control signal ratios to a mean $\log^2 = 0$ (*i.e.* 1:1 ratio). Normalized data were then subjected to a variance analysis.

[0519] Mean signal intensity for each signal at any given position on the microarray slide was determined for each of three of P, C, X1, and X2 sample microarray slides. This mean signal/probe position was compared to the signal at the same position on sample slide which was not used for calculating the mean. For example, a mean signal at a given position was determined for P, C, and X1 and the signal at that position in the X2 microarray slide was compared to the P, C, and X1 mean signal value.

[0520] Signal data were then verified with RT-PCR to confirm gene expression in the target tissue of the genes corresponding to the unique oligonucleotides in the probe.

EXAMPLE 12

[0521] This example illustrates how RNAs of tissues from multiple pine species, in this case both *P. radiata* and loblolly pine *P. taeda* trees, were selected for analysis of the pattern of gene expression associated with wood development in the juvenile wood and mature wood forming sections of the trees, using the microarrays derived from *P. radiata* cDNA sequences described in Example 4.

[0522] Open pollinated trees of approximately 16 years of age were selected from plantation-grown sites, in the United States for loblolly pine, and in New Zealand for radiata pine. Trees were felled during the spring and summer seasons to compare the expression of genes associated with these different developmental stages of wood formation. Trees were felled individually and trunk sections were removed from the bottom area approximately one to two meters from the base and within one to two meters below the live crown. The section removed from the basal end of the trunk contains mature wood. The section removed from below the live crown contains juvenile wood. Samples collected during the spring season were termed early wood or springwood, while samples collected during the summer season were considered late wood or summerwood. Larson *et al., Gen. Tech. Rep.* FPL-GTR-129. Madison, WI: U.S. Department of Agriculture, Forest Service, Forest Products Laboratory. p.42.

[0523] Tissues were isolated from the trunk sections such that phloem, cambium, developing xylem, and maturing xylem were removed. These tissues were collected only from the current year's growth ring. Upon tissue removal in each case, the material was immediately plunged into liquid nitrogen to preserve the nucleic acids and other components. The bark was peeled from the section and phloem tissue removed from the inner face of the bark by scraping with a razor blade. Cambium tissue was isolated from the outer face of the peeled section by gentle scraping of the

surface. Developing xylem and lignifying xylem were isolated by sequentially performing more vigorous scraping of the remaining tissue. Tissues were transferred from liquid nitrogen into containers for long term storage at -70°C until RNA extraction and subsequent analysis was performed.

EXAMPLE 13

[0524] This example illustrates procedures alternative to those used in the example above for RNA extraction and purification, particularly useful for RNA obtained from a variety of tissues of woody plants, and an alternative procedure for hybridization and data analysis using the arrays described in Example 7 and 9.

[0525] RNA was isolated according to the protocol of Chang et al., Plant Mol. Biol. Rep. 11:113. DNA was removed using DNase I (Invitrogen, Carlsbad, CA) according to the manufacturer's recommendations. The integrity of the RNA samples was determined using the Agilent 2100 Bioanalyzer (Agilent Technologies, USA).

[0526] 10μg of total RNA from each tissue was reverse transcribed into cDNA using known methods.

[0527] In the case of *Pinus radiata* phloem tissue, it can be difficult to extract sufficient amounts of total RNA for normal labelling procedures. Total RNA was extracted and treated as previously described and 100ng of total RNA was amplified using the Ovation™ Nanosample RNA Amplification system from NuGEN™ (NuGEN, CA, USA). Similar amplification kits such as those manufactured by Ambion may alternatively be used. The amplified RNA was reverse transcribed into cDNA and labelled as described above.

[0528] Hybridization and stringency washes were performed using the protocol as described in the US Patent Application for "Methods and Kits for Labeling and Hybridizing cDNA for Microarray Analysis" (supra) at 42°C. The arrays (slides) were scanned using a ScanArray 4000 Microarray Analysis System (GSI Lumonics, Ottawa, ON, Canada). Raw, non-normalized intensity values were generated using QUANTARRAY software (GSI Lumonics, Ottawa, ON, Canada).

[0529] A fully balanced, incomplete block experimental design (Kerr and Churchill, *Gen. Res.* 123:123, 2001) was used in order to design an array experiment that would allow maximum statistical inferences from analyzed data.

[0530] Gene expression data was analyzed using the SAS® Microarray Solution software package (The SAS Institute, Cary, NC, USA). Resulting data was then visualized using JMP® (The SAS Institute, Cary, NC, USA).

[0531] Analysis done for this experiment was an ANOVA approach with mixed model specification (Wolfinger *et al., J. Comp. Biol.* 8:625-637). Two steps of linear mixed models were applied. The first one, normalization model, was applied for global normalization at slide-level. The second one, gene model, was applied for doing rigorous statistical inference on each gene. Both models are stated in Models (1) and (2).

$$\log_2(Y_{ijkls}) = \theta_{ij} + D_k + S_l + DS_{kl} + \omega_{ijkls} \quad (1)$$

$$R^{(g)}_{ijkls} = \mu^{(g)}_{ij} + D^{(g)}_k + S^{(g)}_l + DS^{(g)}_{kl} + SS^{(g)}_{ls} + \varepsilon^{(g)}_{ijkls} \quad (2)$$

[0532] Y_{ijkls} represents the intensity of the s^{th} spot in the l^{th} slide with the k^{th} dye applying the j^{th} treatment for the i^{th} cell line. θ_{ij}, D_k, S_l, and D_{Skl} represent the mean effect of the jth treatment in the ith cell line, the kth dye effect, the l^{th} slide random effect, and the random interaction effect of the k^{th} dye in the l^{th} slide. ω_{ijkls} is the stochastic error term. $R^{(g)}_{ijkls}$ represents the residual of the g^{th} gene from model (1). $\mu^{(g)}_{ij}, D^{(g)}_k, S^{(g)}_l$, and $DS^{(g)}_{kl}$ represent the similar roles as θ_{ij}, D_k, S_l, and DS_{kl} except they are specific for the g^{th} gene. $SS^{(g)}_{ls}$ represent the spot by slide random effect for the g^{th} gene. $\varepsilon^{(g)}_{ijkls}$ represent the stochastic error term. All random terms are assumed to be normally distributed and mutually independent within each model.

[0533] According to the analysis described above, certain cDNAs, some of which are shown in Table 7, were found to correspond to different steady state levels of RNA which may correspond to differences in gene expression or transcript stability.

Table 7: Pinus cDNAs corresponding to different Steady State RNA.

SEQ ID	Oligo ID	Gene_Family	Steady State RNA
8	Pra_003171_O_1	1,3-beta-D-glucanase	transcripts significantly higher in late developing xylem relative to cambium
56	Pra_021340_O_1	Mannose-1-phosphate guanylyltransferase (GDP)	transcripts significantly higher in early developing xylem relative to cambium
61	Pra_001007_O_1	Xyloglucan:xyloglucosyl transferase	transcripts significantly higher in early developing xylem relative to late developing xylem
69	Pra_001604_O_1	Xyloglucan:xyloglucosyl transferase	transcripts significantly higher in cambium relative to phloem
68	Pra_001603_O_1	Xyloglucan:xyloglucosyl transferase	and developing xylem
15	Pra_008701_O_1	1,3-beta-D-glucanase	
13	Pra_008677_O_1	1,3-beta-D-glucanase	transcripts significantly higher in cambium relative to
96	Pra_005791_O_1	Dirigent	developing xylem (in order of increasing magnitude of the
74	Pra_005715_O_2	Xyloglucan:xyloglucosyl transferase	difference)
93	Pra_004489_O_1	Dirigent	
17	Pra_012343_O_2	1,3-beta-D-glucanase	transcripts significantly higher in phloem relative to cambium
65	Pra_001187_O_1	Xyloglucan:xyloglucosyl transferase	transcripts significantly lower in phloem relative to cambium

SEQ ID	Oligo ID	Gene_Family	Steady State RNA
69	Pra_001604_O_1	Xyloglucan:xyloglucosyl transferase	(in order of increasing magnitude of the difference)
35	Pra_013210_O_2	Exo-1,4-beta-xylanase	
68	Pra_001603_O_1	Xyloglucan:xyloglucosyl transferase	

[0534] The involvement of these specific genes in wood development is inferred through the association of the up-regulation or down-regulation of genes to the particular stages of wood development. Both the spatial continuum of wood development across a section (phloem, cambium, developing xylem, maturing xylem) at a particular season and tree trunk position and the relationships of season and tree trunk position are considered when making associations of gene expression to the relevance in wood development.

EXAMPLE 14

[0535] This example demonstrates how one can correlate polysaccharide gene expression with agronomically important wood phenotypes such as density, stiffness, strength, distance between branches, and spiral grain.

[0536] Mature clonally propagated pine trees were selected from among the progeny of known parent trees for superior growth characteristics and resistance to important fungal diseases. The bark was removed from a tangential section and the trees were examined for average wood density in the fifth annual ring at breast height, stiffness and strength of the wood, and spiral grain. The trees were also characterized by their height, mean distance between major branches, crown size, and forking.

[0537] To obtain seedling families that are segregating for major genes that affect density, stiffness, strength, distance between branches, spiral grain and other characteristics that may be linked to any of the genes affecting these characteristics, trees lacking common parents were chosen for specific crosses on the criterion that they exhibit the widest variation from each other with respect to the density, stiffness, strength, distance between branches, and spiral grain criteria. Thus, pollen from a tree exhibiting high density, low mean distance between major branches, and high spiral grain was used to pollinate cones from the unrelated plus tree among the selections exhibiting the lowest density, highest mean distance between major branches, and lowest spiral grain. It is useful to note that "plus trees" were crossed such that pollen from a plus tree exhibiting high density was used to pollinate developing cones from another plus tree exhibiting high density, for example, and pollen from a tree

exhibiting low mean distance between major branches was used to pollinate developing cones from another plus tree exhibiting low mean distance between major branches.

[0538] Seeds were collected from these controlled pollinations and grown such that the parental identity was maintained for each seed and used for vegetative propagation such that each genotype was represented by multiple ramets. Vegetative propagation was accomplished using micropropagation, hedging, or fascicle cuttings. Some ramets of each genotype were stored while vegetative propagules of each genotype were grown to sufficient size for establishment of a field planting. The genotypes were arrayed in a replicated design and grown under field conditions where the daily temperature and rainfall was measured and recorded.

[0539] The trees were measured at various ages to determine the expression and segregation of density, stiffness, strength, distance between branches, spiral grain, and any other observable characteristics that may be linked to any of the genes affecting these characteristics. Samples were harvested for characterization of cellulose content, lignin content, cellulose microfibril angle, density, strength, stiffness, tracheid morphology, ring width, and the like. RNA was then collected from replicated samples of trees showing divergent stiffness and density, or other characteristics, from genotypes that were otherwise as similar as possible in growth habit, in spring and fall so that early and late wood development was assayed. These samples were examined for gene expression similarly as shown in Table 8 below.

Table 8: Pinus Genes Confer Wood Phenotypes

SEQ ID	Gene Family	Consensus_ID	Expression
61	Xyloglucan:xyloglucosyl transferase	pinusRadiata_001007	up in juvenile vs mature Xylem*
62	Xyloglucan:xyloglucosyl transferase	pinusRadiata_001008	up in juvenile vs mature Xylem *
control	Ribonucleoside-diphosphate reductase	pinusRadiata_000218	up in early vs late developing Xylem
control	Nitrite transporter	pinusRadiata_016801	up in mature vs juvenile Cambium

[0540] Ramets of each genotype were compared to ramets of the same genotype at different ages to establish age:age correlations for these characteristics.

EXAMPLE 15

[0541] This example demonstrates how responses to environmental conditions such as light and season alter plant phenotype and can be correlated to polysaccharide synthesis gene expression using microarrays. In particular, the changes in gene expression associated with wood density are examined.

[0542] Trees of three different clonally propagated *E. grandis* hybrid genotypes are grown on a site with a weather station that measures daily temperatures and rainfall. During the spring and subsequent summer, genetically identical ramets of the three different genotypes are first photographed with north-south orientation marks, using photography at sufficient resolution to show bark characteristics of juvenile and mature portions of the plant, and then felled. The age of the trees is determined by planting records and confirmed by a count of the annual rings. In each of these trees, mature wood is defined as the outermost rings of the tree below breast height, and juvenile wood as the innermost rings of the tree above breast height. Each tree is accordingly sectored as follows:

NM - NORTHSIDE MATURE
SM - SOUTHSIDE MATURE

NT - NORTHSIDE TRANSITION
ST - SOUTHSIDE TRANSITION

NJ - NORTHSIDE JUVENILE
SJ - SOUTHSIDE JUVENILE

[0543] Tissue is harvested from the plant trunk as well as from juvenile and mature form leaves. Samples are prepared simultaneously for phenotype analysis, including plant morphology and biochemical characteristics, and gene expression analysis. The height and diameter of the tree at the point from which each sector was taken is recorded, and a soil sample from the base of the tree is taken for chemical assay. Samples prepared for gene expression analysis are weighed and placed into liquid nitrogen for subsequent preparation of RNA samples for use in the microarray experiment. The tissues are denoted as follows:

P - phloem
C - cambium
X1 - expanding xylem
X2 - differentiating and lignifying xylem

[0544] Thin slices in tangential and radial sections from each of the sectors of the trunk are fixed as described in Ruzin, PLANT MICROTECHNIQUE AND MICROSCOPY, Oxford University Press, Inc., New York, NY (1999) for anatomical examination and confirmation of wood developmental stage. Microfibril angle is examined at the different developmental stages of the wood, for example juvenile, transition and mature phases of Eucalyptus grandis wood. Other characteristics examined are the ratio of fibers to vessel elements and ray tissue in each sector. Additionally, the samples are examined for characteristics that change between juvenile and mature

wood and between spring wood and summer wood, such as fiber morphology, lumen size, and width of the S2 (thickest) cell wall layer. Samples are further examined for measurements of density in the fifth ring and determination of modulus of elasticity using techniques well known to those skilled in the art of wood assays. *See, e.g., Wang, et al., Non-destructive Evaluations of Trees,* EXPERIMENTAL TECHNIQUES, pp. *28*-30 (2000).

[0545] For biochemical analysis, 50 grams from each of the harvest samples are freeze-dried and analyzed, using biochemical assays well known to those skilled in the art of plant biochemistry for quantities of simple sugars, amino acids, lipids, other extractives, lignin, and cellulose. *See, e.g.,* Pettersen & Schwandt, *J. Wood Chem. & Technol.* 11:495 (1991).

[0546] In the present example, the phenotypes chosen for comparison are high density wood, average density wood, and low density wood. Nucleic acid samples are prepared as described in Examples 1-2, from trees harvested in the spring and summer. Gene expression profiling by hybridization and data analysis is performed as described above.

[0547] Using similar techniques and clonally propagated individuals one can examine polysaccharide gene expression as it is related to other complex wood characteristics such as strength, stiffness and spirality.

EXAMPLE 16

[0548] This example demonstrates how a gene of the instant application can be linked to a tissue-preferred promoter and expressed in pine resulting in a plant with increased wood density.

[0549] A gene of the instant application, which is found by the methods of the previous examples to be more highly expressed during the early spring, is cloned into a DNA construct having the density-related polypeptide operably linked to a promoter is placed into an appropriate binary vector and transformed into pine using the methods described herein. Pine plants are transformed as described in herein and the

transgenic pine plants are used to establish a forest planting. Increased density even in the spring wood (early wood) is observed in the transgenic pine plants relative to control pine plants which are not transformed with the density related DNA construct.

EXAMPLE 17

[0550] This example demonstrates how gene expression analysis can be used to find gene variants which are present in mature plants having a desirable phenotype. The presence or absence of such a variant can be used to predict the phenotype of a mature plant, allowing screening of the plants at the seedling stage. Although this example employs eucalyptus, the method used herein is also useful in breeding programs for pine and other tree species.

[0551] The sequence of a putative density-related gene is used to probe genomic DNA isolated from *Eucalyptus* that vary in density as described in wood phenotypes are examined. One hybrid exhibits high wood density and another hybrid exhibits lower wood density. A molecular marker in the 3' portion of the coding region is found which distinguishes a high-density gene variant from a lower density gene variant.

[0552] This molecular marker enables tree breeders to assay non-transgenic *Eucalyptus* hybrids for likely density profiles while the trees are still at seedling stage, whereas in the absence of the marker, tree breeders must wait until the trees have grown for multiple years before density at harvest age can be reliably predicted. This enables selective outplanting of the best trees at seedling stage rather than an expensive culling operation and resultant erosion at thinning age. This molecular marker is further useful in the breeding program to determine which parents will give rise to high density outcross progeny.

[0553] Molecular markers found in the 3' portion of the coding region of the gene that do not correspond to variants seen more frequently in higher or lower wood density non-transgenic Eucalyptus hybrid trees are also useful. These markers are found to be useful for fingerprinting different genotypes of Eucalyptus, for use in identity-tracking in the breeding program and in plantations.

EXAMPLE 18

[0554] This example demonstrates the use of a vascular-preferred promoter functionally linked to one of the genes of the instant application.

[0555] A vascular-preferred promoter, such as any of those in U.S. Application No. 10/703,091, filed November 7, 2003, is then linked to one of the genes in the instant application and used to transform tree species. Boosted transcript levels of the candidate gene in the xylem of the transformants results in an increased xylem biomass phenotype.

[0556] In another example, a vascular-preferred promoter such as any of those disclosed in U.S. Application Serial No. 10/717,897, filed November 21, 2003, or U.S. Application Serial No. 10/703,091, filed November 7, 2003, both of which are incorporated by reference. For instance, a vascular-preferred promoter is linked to an RNAi construct containing sequences from one of the genes in the instant application and used to transform a tree of the genus from which the gene was isolated. Reduced transcript levels of the candidate gene in the xylem of the transformants results in an increased xylem biomass phenotype.

EXAMPLE 19

[0557] This example demonstrates the use of a vascular preferred promoter functionally linked to one of the genes of the instant application.

[0558] The plasmid pOX16 was cloned using the following steps. The plasmid pWVK223 (Figure 225, SEQ ID NO: 691) a plasmid derived from pBI121 (Clontech laboratories, Palo Alto CA) that had the 35S promoter GUS sequence replaced with the 4CL promoter from *P. taeda* (U.S. Patent 6,252,135) and the NOS promoter that drives the NPTII gene replaced with the UBQ10 promoter from Arabidopsis (Sun, C. W & Callis, J (1997) *Plant J.,* 11:101-111) was first made. A multicloning site was added at the HindIII and ClaI sites by using the synthesized complimentary oligonucletides MCSI and MCSII .

MCSI AGCTCTACAATTGGCTAGCAAAGTACTTAAAGCTTCCAT

MCSII GATGTTAACCGATCGTTTCATGAATTTCGAAGGTAGC

pWVK223 was then used as a backbone to created the intermediate plasmid pOX1 (Figure 226 and SEQ ID NO: 692) by replacing the NOS terminator with the AGAMOUS terminator from Liquidambar styraciflua (LSAGter) (US Patent 6,444,877). The NheI and ScaI restriction sites in the pOX1 plasmid were then used to add the gene of SEQ ID 8, isolated from the appropriate cDNA clone from Example 2 to create the plasmid pOX16 (Figure 227 and SEQ ID NO: 693).

[0559] The control DNA construct pOX2 was engineered by using the plamid pOX1 as the backbone. The GUS INT gene (Vancanneyt et. al. *Mol. Gen. Genet.* 220:245-250, 1990) was added at the HindIII and SmaI sites of the pOX1 plasmid to create the plasmid pOX2 (Figure 228 and SEQ ID NO: 694).

EXAMPLE 20

[0560] This example demonstrates the transformation and propagation of Cottonwood (*Populus deltoides*). The constructs pOX16 and pOX2 were made as described in the preceding example and were inoculated into *Agrobacterium* cultures by standard techniques.

[0561] *Populus deltoides* stock plant cultures were maintained on hormone-free BTM (Chalupa, Communicationes Instituti Forestalis Checosloveniae 13:7-39, 1983, available commercially from Sigma/Aldrich) or WPM medium (Woody Plant Medium - Lloyd, G., and McCown, B., 1981. Woody plant medium. Proc. Intern. Plant Prop. Soc. 30:421, available commercially from Sigma/Aldrich) in a growth room with a 16h photoperiod. For transformation, petioles were excised aseptically using a sharp scalpel blade from the stock plants, cut into 4-6mm lengths and placed on DKW medium (Driver and Kuniyuki, 1984, McGranahan et al. 1987, available commercially from Sigma/Aldrich) with 1 mg/ml BAP and 1 mg/ml NAA immediately after harvest, and incubated in a dark growth chamber (28 degrees C) for 24 hours.

[0562] *Agrobacterium* cultures containing the pOX16 construct were grown to log phase, indicated by an OD600 between 0.8-1.0 A, then pelleted and resuspended in an equal volume of Agrobacterium Induction Medium (AIM) (WPM salts with glucose at 5 g/l, 250 μM acetosyringone, 2 mM phosphate buffer, and 0.05 M MES, pH 5.8) The pellet was resuspended by vortexing. The bacterial cells were incubated for an hour in this medium at 28 degrees C in an environmental chamber, shaking at 100 rpm.

[0563] After the induction period, *Populus deltoides* explants were exposed to the Agrobacterium mixture for 15 minutes. The explants were then lightly blotted on sterile paper towels, replaced onto the same plant medium and cultured in the dark at 18-20 degrees C. After a three-day co-cultivation period, the explants were transferred to DKW medium in which the NAA concentration was reduced to 0.1 ug/ml and to which was added 400mg/L timentin to eradicate the Agrobacterium.

[0564] After 4 days on eradication medium, explants were transferred to small magenta boxes containing the same medium supplemented with timentin (400mg/L) as well as the selection agent geneticin (50 mg/L). Explants were transferred every two weeks to fresh selection medium. Calli that grew in the presence of selection were isolated and sub-cultured to fresh selection medium every three weeks. Calli were observed for the production of adventitious shoots.

[0565] Adventitious shoots were normally observed within two months from the initiation of transformation. These shoot clusters were transferred to DKW medium to which no NAA was added, and in which the BAP concentration was reduced to 0.5 mg/ml, for shoot elongation, typically for about 14 weeks. Elongated shoots were excised and transferred to hormone-free WPM or BTM medium at pH5.8, containing20 g/l sucrose and 5 g/l activated charcoal. See Table 9 below.

Table 9. Rooting medium for *Populus deltoids*.

BTM-1 Media Components		mg/L	
[0566]	NH_4NO_3	[0567]	412
[0568]	KNO_3	[0569]	475
[0570]	$Ca(NO_3)_2.4H_2O$	[0571]	640
[0572]	$CaCl_2.2H_2O$	[0573]	440*
[0574]	$MgSO_4.7H_2O$	[0575]	370
[0576]	KH_2PO_4	[0577]	170
[0578]	$MnSO_4.H_2O$	[0579]	2.3
[0580]	$ZnSO_4.7H_2O$	[0581]	8.6
[0582]	$CuSO_4.5H_2O$	[0583]	0.25
[0584]	$CoCl_2.6H_2O$	[0585]	0.02
[0586]	KI	[0587]	0.15
[0588]	H_3BO_3	[0589]	6.2
[0590]	$Na_2MoO_4.2H_2O$	[0591]	0.25
[0592]	$FeSO_4.7H_2O$	[0593]	27.8
[0594]	$Na_2EDTA.2H_2O$	[0595]	37.3
[0596]	Myo-inositol	[0597]	100
[0598]	Nicotinic acid	[0599]	0.5
[0600]	Pyridoxine HCl	[0601]	0.5
[0602]	Thiamine HCl	[0603]	1
[0604]	Glycine	[0605]	2
		[0607]	
[0606]	Sucrose	20000	
[0608]	Activated Carbon	[0609]	5000

[0610] After development of roots, typically four weeks, transgenic plants were propagated in the greenhouse by rooted cutting methods, or in vitro through axillary shoot induction for four weeks on DKW medium containing 11.4 uM zeatin, after

which the multiplied shoots were separated and transferred to root induction medium. Rooted plants were transferred to soil for evaluation of growth in glasshouse and field conditions.

EXAMPLE 21

[0611] This example demonstrates the effect of transforming a tree with the constructs from Example 19.

[0612] *Populus deltoids* plants transformed with the plasmids pOX16 and pOX2 as described in Example 20 were grown in Ray Leach supercells C10 "Cone-tainers"™ in a greenhouse. After 5 months plants were measured for height, caliper and volume. Height measurements were taken to the nearest cm by measuring from the neck of the supercell collar to the apical meristem of each plant. Caliper of the plants were measured using a digital caliper (Mitutoyo - Aurora, Illinois) to the nearest 0.01mm. Caiper measurements were taken at the clearest region of trunk (i.e. no branches, knots, or bulges) just above the neck of the supercell collar. Volume index was calculated using the following formula: Volume = $(\text{radius})^2 * 3.1415926 * \text{height}$.

[0613] pOX16 plants transformed with the gene of SEQ ID 8 when compared to the GUS control plants of pOX2 had a greater height, caliper and volume. When comparing all 65 ramets produced from all 5 translines of pOX16 to all 26 ramets produced from all 3 translines of the pOX2 control it was observed that the mean height was 126% greater than the control, the mean caliper was 134% greater than the control and the mean volume index was 227% greater than the control.

Table 10: Transgenic plant measurements for each plasmid

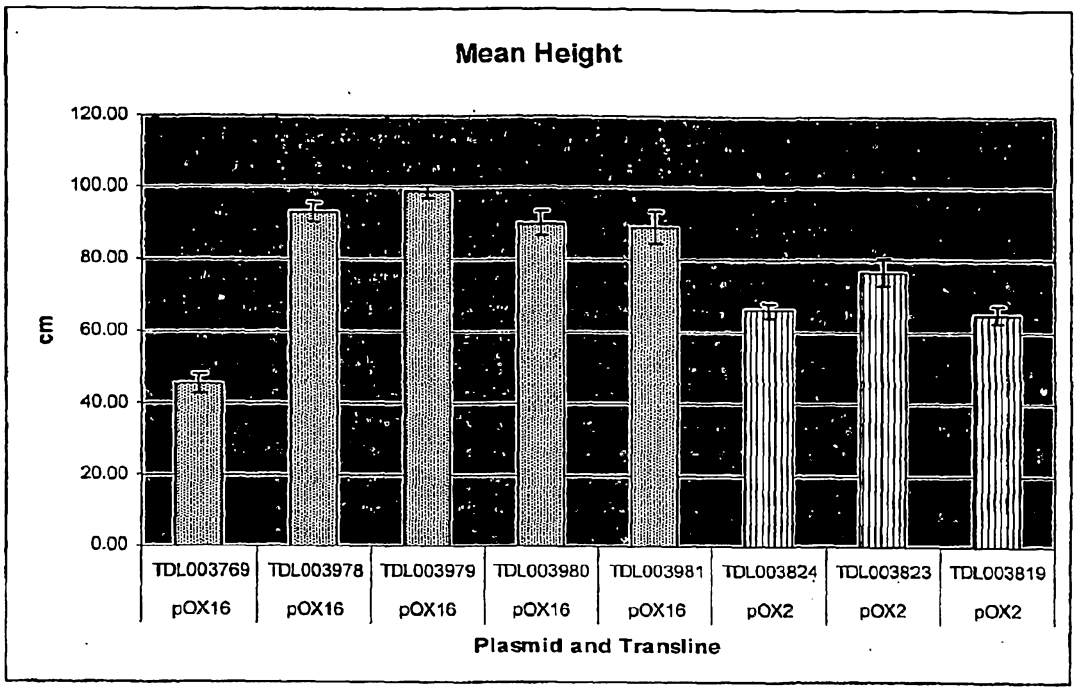
Plasmid	Number of ramets (n)	Mean Volume index	Mean Height	Mean Caliper
pOX16	65	32.40	88.19	6.84
pOX2	26	14.28	69.85	5.10

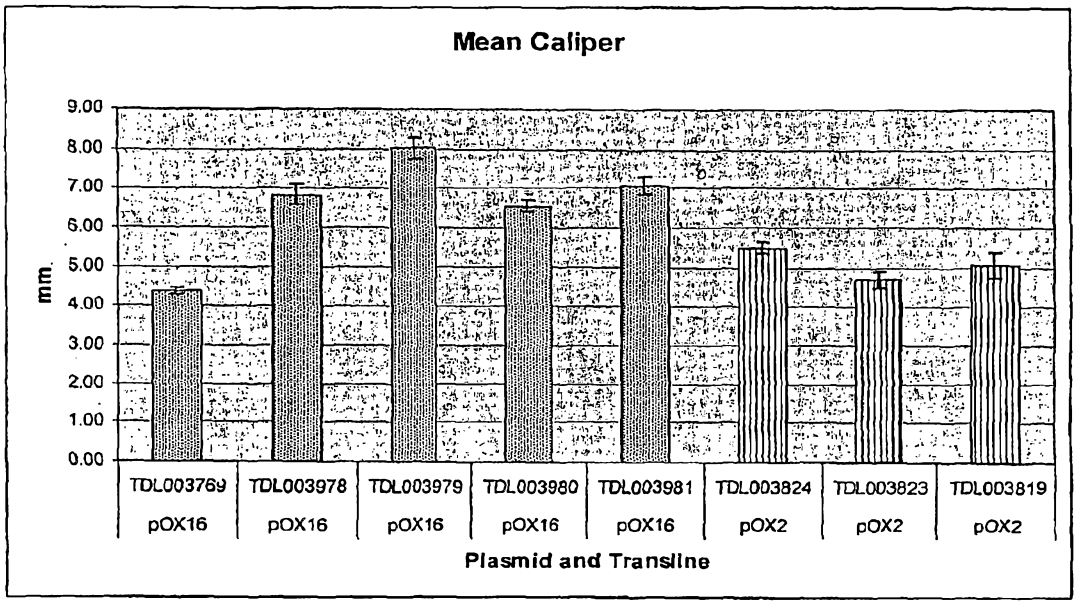
[0614] When comparing individual translines the increases in height, caliper and volume can be even higher, for example transline TDL003979 of pOX16 transformed plants showed the greatest increases in height, caliper and volume when compared to the pOX2 controls (see table 11).

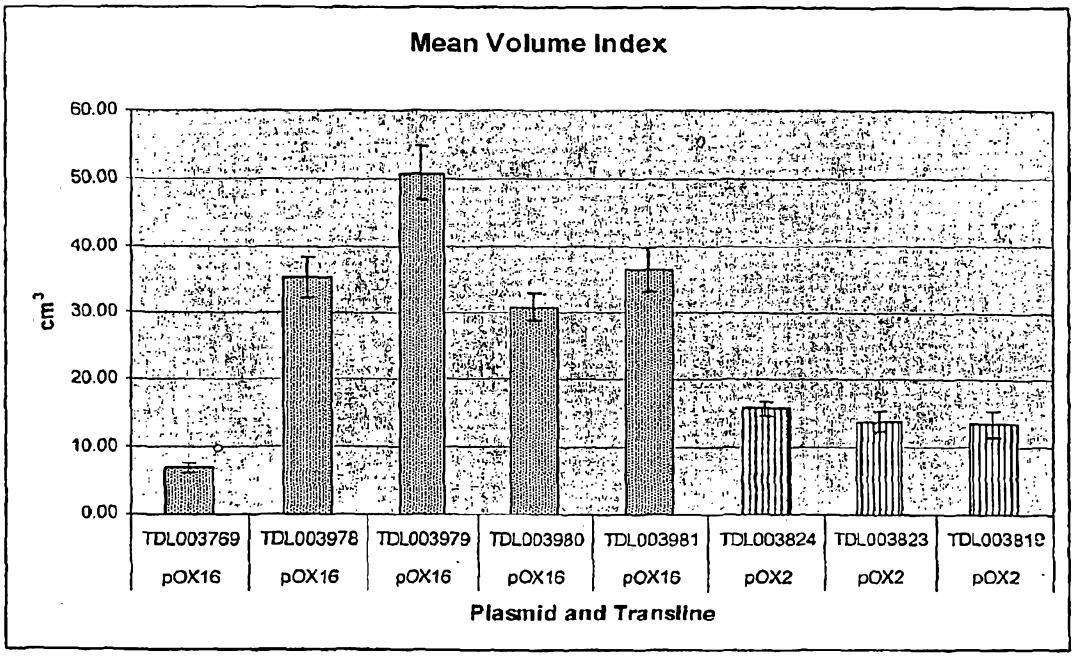
Table 11: Transgenic plant measurements for each transline

Plasmid	Transline	Number of ramets (n)	Mean Volume index (cm^3)	Mean Height (cm)	Mean Caliper (mm)
pOX16	TDL003769	6	6.82	45.00	4.37
pOX16	TDL003978	15	35.15	92.97	6.81
pOX16	TDL003979	14	50.89	98.61	8.02
pOX16	TDL003980	15	30.82	90.07	6.54
pOX16	TDL003981	15	36.45	89.14	7.07
pOX2	TDL003824	11	15.73	65.91	5.49
pOX2	TDL003823	10	13.81	76.70	4.69
pOX2	TDL003819	5	13.38	64.80	5.07

[0615] When analyzing each transline separately it was observed that 4 of the 5 pOX16 translines had significant increases in height, caliper and volume when compared to the controls. This can be easily observed in the graphs below.


Mean Height
120.00
100.00
80.00
60.00
40.00
20.00
0.00
cm
TDL003769 pOX16
TDL003978 pOX16
TDL003979 pOX16
TDL003980 pOX16
TDL003981 pOX16
TDL003824 pOX2
TDL003823 pOX2
TDL003819 pOX2
Plasmid and Transline


Mean Caliper
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
mm
TDL003769 pOX16
TDL003978 pOX16
TDL003979 pOX16
TDL003980 pOX16
TDL003981 pOX16
TDL003824 pOX2
TDL003823 pOX2
TDL003819 pOX2
Plasmid and Transline


Mean Volume Index
60.00
50.00
40.00
30.00
20.00
10.00
0.00
cm3
TDL003769 pOX16
TDL003978 pOX16
TDL003979 pOX16
TDL003980 pOX16
TDL003981 pOX16
TDL003824 pOX2
TDL003823 pOX2
TDL003819 pOX2
Plasmid and Transline

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Interpretation of this specification

It will therefore be understood that the invention could take many forms and be put to many different uses. All such forms and uses are embodied within the spirit and scope of the invention, which is to be understood as not being limited to the particular details of the embodiments or the examples discussed previously, but which extends to each novel feature and combination of features disclosed in or evident from this specification (including in the accompanying claims and drawings). All of these different combinations constitute various alternative aspects of the invention.

Throughout this specification, unless the context requires otherwise, the word "comprise" is (and variants, variations or other forms of that word, such as "comprises" or "comprising" are) to be understood as implying the inclusion of a stated element, feature or integer or group of elements, features or integers, but not the exclusion of any other element, feature or integer or group of elements, features or integers. Further, wherever used in this specification, the term "includes" is not a term of limitation, and is not be taken as excluding the presence of other any element, feature or integer or group of elements, features or integers.

It is further to be understood that any discussion in this specification of background or prior art documents, devices, acts, information, knowledge or use ('**Background Information**') is included solely to explain the context of the invention. Any discussions of such Background Information is not be taken as an admission in any jurisdiction that any such Background Information constitutes prior art, part of the prior art base or the common general knowledge in the field of the invention on or before the priority date of the appended claims or any amended claims later introduced into this specification.

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated polynucleotide comprising a nucleic acid sequence comprising SEQ ID NO: 93 or a nucleic acid sequence at least 90% identical to SEQ ID NO: 93.

2. An isolated polynucleotide as claimed in claim 1, in which the polynucleotide encodes a polypeptide that regulates cell wall development in a monocotyledenous plant.

3. An isolated polynucleotide as claimed in claim 2, in which the monocotyledenous plant is selected from the group consisting of turfgrass, wheat, maize, rice, oat, barley, orchid, iris, lily, onion, sugarcane, and sorghum.

4. An isolated polynucleotide as claimed in claim 3, in which the turfgrass is selected from the group consisting of Agrostis spp., Poapratensis, Lolium spp., Kentucky Bluegrass And Perennial Ryegrass Mix; Festuca arundinacea, Festuca rubra commutata, Cynodon dactylon, Pennisetum clandestinum, Stenotaphrum secundcttum, Zoysiajaponica, and Dichondra micrantha.

5. An isolated polynucleotide as claimed in claim 1, in which the polynucleotide encodes a polypeptide that regulates cell wall synthesis in a dicotyledenous plant.

6. An isolated polynucleotide as claimed in claim 5, in which the dicotyledenous plant is selected from the group consisting of cotton, tobacco, Arabidopsis, tomato, potato, aspen, eucalyptus, Sweetgum, acacia, poplar, willow, teak, mahogany, chestnut, elm, sugar beet, broccoli, cassava, sweet potato, pepper, poinsettia, legumes, alfalfa, soybean, carrot, strawberry, lettuce, oak, maple, walnut, rose, mint, squash, daisy, geranium and cactus.

7. A DNA construct comprising the isolated polynucleotide as claimed in claim 1 operably linked to a promoter.

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8. A DNA construct as claimed in claim 7, in which the isolated polynucleotide encodes an RNA transcript.

9. A DNA construct as claimed in claim 8, in which the isolated polynucleotide is in a sense or antisense orientation relative to the promoter.

10. A DNA construct as claimed in claim 8, in which the RNA transcript induces RNA interference of SEQ ID NO: 93 or a nucleic acid sequence at least 90% identical to SEQ ID NO: 93.

11. A DNA construct as claimed in claim 8, in which the RNA transcript is a small interfering RNA.

12. A plant cell transformed with a DNA construct as claimed in any one of claims 7 to 11.

13. A transgenic plant comprising at least one plant cell as claimed in claim 12.

14. A transgenic plant as claimed in claim 13, in which the transgenic plant has a difference in phenotype from a plant of the same species that has not been transformed with the DNA construct.

15. A transgenic plant as claimed in claim 14, in which the difference in phenotype is a difference in lignin quality, lignin structure, wood composition, fiber yield, cell division or cell development.

16. A transgenic plant as claimed in claim 14, in which the transgenic plant is a woody plant.

17. A transgenic plant as claimed in claim 16, in which the woody plant is a tree.

18. Wood obtained from a transgenic plant as claimed in claim 17.

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19. Wood pulp obtained from a transgenic plant as claimed in claim 17.

20. A method for producing a transgenic plant, comprising the steps of (a) transforming at least one plant cell with a DNA construct as claimed in any one of claims 7 to 11; (b) culturing the transformed at least one plant cell under conditions that promote growth of a plant; and (c) selecting a transgenic plant that exhibits a phenotype that is different from a plant of the same species that has not been transformed with the DNA construct.

21. An isolated polynucleotide as claimed in any one of claims 1 to 6, the isolated polynucleotide being substantially as described in this specification and with reference to the examples of the invention provided in the specification, including in the accompanying sequence listings and drawings.

22. A DNA construct as claimed in any one of claims 7 to 11, the DNA construct being substantially as described in this specification and with reference to the examples of the invention provided in the specification, including in the accompanying sequence listings and drawings.

23. A plant cell as claimed in claim 12, the plant cell being substantially as described in this specification and with reference to the examples of the invention provided in the specification, including in the accompanying sequence listings and drawings.

24. A transgenic plant as claimed in any one of claims 13 to 17, the transgenic plant being substantially as described in this specification and with reference to the examples of the invention provided in the specification, including in the accompanying sequence listings and drawings.

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25. A method as claimed in claim 20 for producing a transgenic plant, the method being substantially as described in this specification and with reference to the examples of the invention provided in the specification, including in the accompanying sequence listings and drawings.

Dated: 8 February 2012

ARBORGEN INC.

By its Patent Attorneys

KNIGHTSBRIDGE PATENT ATTORNEYS

Figure 1: Amino Acid sequence of 231. The conserved calreticulin domain is underlined, The Calreticulin family signatures 1 and 2 are in italics and the Calreticulin family repeated motif signatures are in bold.

MVSMDRRWIPLLLALLCLMSPLNALVSASESTFYESFDESFEGRWIVSQKEDYKGVWKYEK
SKGHEDYGLLVSEVAKKYAIVRELPETIDPKDGSLVLQYEV*RLQNGLECGGAYLKYL*RPQEA
GWKPAEFDNESPYS*IMFGPDKCG*ATNKVHFIYKHKNPKSGEYVEHHLKYPPSIPSDKKTHVY
SAILTPDNQVRILIDGEEKKKANLLSADDFEPALIPPKT**IPDPEDKKPEDWD**ERAKI**PDPDAEK**
PEDWDEDAPMEIEDLEAVKPEGWLDDEPEEV**DDPEATKPDDWD**DEEDGEWEAPKVSNPK
CDEAPGCGEWTRPMKSNPDYKGKWYAPMIDNPNYKGIWKPQQIPNPEYFELEKPDLEPIAAI
GIEIWTMQDGILFDNILITHDEKVAEEYRKNTWKAKFSNEKEEEDVDSPLPGELSGFQKKIFDV
LYKIANIPFLEAYKLKIIDLIEQGEKKPNLTIGILVAVLVVLLTTIYKLLFGGKKQPVQKVELKSQP
EQDASASENNKEDSDIAAENEKSDAAEKEKSGDENEIEGEDAAPRQRRVRRET

Figure 2: Amino Acid sequence of 232. The conserved calreticulin domain is underlined,The Calreticulin family signatures 1 and 2 are in italics and the Calreticulin family repeated motif signatures are in bold.

MAGRRSLLYAVFLLLFATLVSAEVFFEERFDDSWESRWVQSDWKKDESLAGDWVHTAGKW
NGDPNDKGIQTHTDYRFFAISAAYPEFSNKDKTLVLQFS*VKHEQKLDCGGGYVKLL*SGEIDQ
KNFSGETPYS*IMFGPDICG*YSTKKVHTILSYKGKNHPIKKDVPCETDQLTHVYTFILRPDATYSI
LIDNTDKQSGSLYKDWDLLPPKT**IKDPNAKKPEDWD**DKEYIPDPEDKKPEGYDDIPKEI**PDPD**
ATKPEDWNDEEDGEWTAPTIANPEYKGPWKPKKIKNPNYKGKWKAPMIDNPDFKDDPELY
VFPNLKYLGIELWQVKSGTLFDNILISDDPEYAKKLAEETWAKHKDAEKEAFDEAEKKKEEEE
KEKESDDEEDTDEKEEKSDDEDADELDDEHKEADKKEHELDSEHKEEDKKEHDEL

Figure 3: Amino Acid sequence of 234. The conserved Glycoside hydrolase, family 17, domain is underlined.

MGRAGLRTSLLCILIFLSGLALSNAQSKISSSTTGINYGQVADDLPSPELVVGLLQTNSINKVKL
YSVNETVLKAFANTGIELIVGMGNENVGNMTDPTKATEWVNENIRAYLPATKITGIAVGNEVY
TGTDTQLMANLVPAMKNIHSALVSIGADMNIKVTTPHSLAVLGNSFPPSAGSFASNVKSLMKP
LLDLLSQIGSPFFINAYPYFAYKGDPSQISLAYVLFEPNTGVIDPNNNVHYNNMLYAQIDAVYS
ALSALGYANIEVTVSETGWPSKGDANEAGATLQNAQTYNGNLLQLLAQNQGTPLRPKLVLQ
AYLFALFNEDMKPGPASERNYGLFKPDGTAVYNLGLSGTLSTGSPSTGSTSTGSFTTGTPPP
AAYPSTTDSSYSYYSSAKETYSVISFYNHLLLLGLSTFFVVPLFLP

Figure 4: Amino Acid sequence of 235. The conserved glycosyl hydrolases domain of family 17 is underlined.

MGASVMGSGDLRMFCLLALVLLSGLVLSNSASSTSSSATGINYGQVADNLPSPEVVVGLLQT
RNINKVKIFSANETVLKAFANTGIELIVAIGNENVGNMTDPTKATEWVNENIQAYLPATKITCIA
VGNEVYTGTDTQLMENLVPAMKNIHSALVSIGADTDIKISTPHSLGVLGNSYPPSAGSFTSDL
TSLMKPLLDFLSQIDSPFFVNVYPFFAYKANPSQISLDYVLFRPNAGVVDPNNNISYNNMLYA
QVDAVYSALSALGYPNLEVTVSETGWPSMGDADEAGATLQNAQTYNGNLLQLLAQNQGTP
LRPKVVLQAYLFALFNEDMKTGPTSERNYGLYKPDGTAVYSLGSTGTLSTGSTRTVATASYP
TAADGPSSSAKETYSVVSFYNHLQLLGLSTFFVFLLFRP

Figure 5: Amino Acid sequence of 236. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MVFGISCRMAMVFIVWALMAFLSVGLEDSKALAITGSTVGINYGQIADNLPPPAKVAELLKALK
VTKVKLYDWNPAILKAFANSDVELVVGIGNGFVAGLMDTQAALSWVTQNIQPYLSSTKVTGF
SVGNEVYTGDDAALKANLVPAMRSIHTALVSLGLDSAIKISTAHSLSVLTSSYPPSAGAFDPAI
MQLLREHLDFLAVTGAPFWINAYPFFAYKDNAGKISLDYALLKPNPGTDDPNTHLHYDNMLY
AMVDAVYSALGAMGYGNLEVRISETGWPSKGDADELGASIQNAATYNRNLLQRLLKNQGTP
MKPNSALQAYIFALFNEDLKNGPTSERNYGLFKPDESMVYNIGLEGGLTVEFSAYASSAQI

Figure 6: Amino Acid sequence of 237. The conserved Glycoside hydrolase, family 17, domain is underlined.

MEIIVRVSAITILLPLFIHCIRCGESIGRSRTLVEHSPALGVNYGQMADNLPSPSGVAKLVQSTT
ISKLRIYGADPAILQAFANTGIGLLVGISNDQIPSLNQLAVAQNWVKSNIVPFVPATDIIGISVGN
EVLFSGDRVLISQLLPALQNLHTALVEVSLDQQIKVSTPHSMAILSASAPPSAGRFSGSFDMK
ALLDFLQKIGAPFMINPYPYFAYKSDPTDRTLAYALFEPNQGSYDTNTGLKYTNMFDAQLDAV
YSAMKYLGYTDIDIVVAETGWPSAGDPSETGASLQNAIAYNGNLIKHVTSMAGTPMMPNRSI
EIYIFGLFNEDLKPGPTSERNFGLFKTDMTMAYDVGLLRSQSASPSPAAPRTGGPVVAPPTA
KVWCIAKPGVDEKSLKQNLDYACGQGIDCKPIQQGGPCYLPNTMASHAAYAMNAYYQSAG
RNSLNCDFAQTGTVTSKDPSYGGCVYSTVNS

Figure 7: Amino Acid sequence of 238. The conserved Glycoside hydrolase, family 17, domain is underlined.

MEMIVKATTITILLPVILCCIPCGESGSGGRSLAQRLPALGVDYGQTADNLPPPSAVAKLVQST
SISKLRLYGADPAILQAFANTGIGLVVGIGNDQIPSLNQLAVAQNWIKNNIVPFVPATDIIGISVG
NEVLFSGDGSLISQLLPALQNLHTALVEVSLDQQIKVSTPHSLAILSTSVPPSAGRFNESFDMK
SLLDFLQKIGAPLMINPYPYFAYKSNPTDQTLAYALFEPNPGFYDTNSGLTYTNMFDAQLDAV
YSAMKYLGYPGVDIVVAETGWPAVGDPTETGVSLQNAIAYNGNLIKHVTSMTGTPLRPNRYI
QTYIFALFNEDLKPGPTSERNYGLFKVDMTMAYDVGLLQSPSAAPSPPAPRTGGPVTTPPTG
KVWCIAKPGAEEQTLEANLNYVCGQGIDCRPIQPGGPCYSPNTVAGHAAYAMNAYYQTAGR
NNWNCDFAQTGTLTSTDPSYGACVYPTV

Figure 8: Amino Acid sequence of 239. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASKDQMKILLLGCVAIYCYSIIAGGDKIGVNNGMVGDNLPPADQVVALMKQNNIGKYRIFQ
GSPEVLPAFANSGIDVIVGIETNRLQEMSSSQDAADSWVKTNIVPFYPATNIKYIAVGNEVVKV
KENVSYLLPAMKNIQTALQNANPQNKIKVSTTHASESVIGNALIPPSKGVFLDDVKDTMSSVL
KFLSDNEAPFMANVYPFFSYVNENWRNISLEYALFKSTSPVMQDGDHSYINLFDAIVDTIISA
MENLGYQDFPLIITESGWPSAGLNVATVDNAQAYNNNLIKHVLSNAGTPKRPGRSIETYIFAIF
NENQKPGAETERHFGLFNPDKTPVYSVNFSPY

Figure 9: Amino Acid sequence of 240. The conserved Glycoside hydrolase, family 17, domain is underlined.

MEAKTRPTAELDLRRGMGFRWAFILLLSVASIQSTEGFSVTGTVGINYGQIANNLPPPSQVVE
LLQASNLTNVRIYDANPQILNALRNTSVEIVVSLGNEYVATMSARPDKARQWVKKNVAAYIPA
GTNITGVLVGNEVYAGNDTVLKNNLMGALKNIHSALVSLGLDNTVKVSTAHSFDVFVSSFPPS
SCAFSDKSVTYMKQLLDFLSATHAPFLVNVYPYFAYKGDPSNVPLDYALFRPSNGVVDSKTN
LHYDNLFYAQIDAAYSALAALGYGKVEVRVSETGWPSKGDDDELGATPENAKTYNGNLLER
LHKKEGTPLKPNVSVQAFIFALFNENLKSGPTSERNYGLFKPDGTETYDLGLKGLKRIVSSLP
PPPTVATGNSSNSTPTTAITSLTAPSPSVSTGDGTNSSSDSSSAKGMHSLVFISFYLQILALSS
FISVLILEH

Figure 10: Amino Acid sequence of 241. The conserved Glycoside hydrolase, family 17, domain is underlined.

MEAKTRPTAELDLRRGMGFRWAFILLLSVASIQSTEGFSVTGTVGINYGQIANNLPPPSQVVE
LLQASNLTNVRIYDANPQILNALRNTSVEIVVSLGNEYVATMSARPDKARQWVKKNVAAYIPA
GTNITGVLVGNEVYAGNDTVLKNNLMGALKNIHSALVSLGLDNTVKVSTAHSFDVFVSSFPPS
SCAFSDKSVTYMKQLLDFLSATHAPFLVNVYPYFAYKGDPSNVPLDYALFRPSNGVVDSKTN
LHYDNLFYAQIDAAYSALAALGYGKVEVRVSETGWPSKGDDDELGATPENAKTYNGNLLER
LHKKEGTPLKPNVSVQAFIFALFNENLKSGPTSERNYGLFKPDGTETYDLGLKGLKRIVSSLP
PPPTVATGNSSNSTPTTAITSLTAPSPSVSTGDGTNSSSDSSSAKVVL

Figure 11: Amino Acid sequence of 242. The conserved Glycoside hydrolase, family 17, domain is underlined.

MPTPKPKIFWLLLLILGLTIHAYAEDYTIGVAYGQYGDNLPSVQESIDLIQRLKVGRVKIYSTNP
VILKALSNTGIKVSVMVRNEDIAGLSASQSVADKWVNDNIVPFYPATEINIILVGNEILTDYSNK
QTWYQLVPAMQSIWQALVNYNLDHINVGTPLAMDMLGSSVPISAFPPSAGTFRDDIAETVMK
PMLEFLHRTNSYFFMDVYSYFPYLFDPEDISLEYANFGENDKKYTDPNGLVYTNMLDQQLDA
VVAAMSKMGYDDIKLAIAETGWPNAGDISQLGANINYAALYNRRVIRRMVADPPLGTPRRPN
QFIPTYIFLLYDEDKKSGPGTERHWGFVYPNGTLMYEIDLTGKLQDSDYGPLPPPPPPYKGK
LWCVADPTADVYALPSAIDSACSQGDSTCDAIQPGEPCYEPNTVIDHASYAFNSNWQRSKN
FYSGCDFNKTAKLVTEDPSHGNCIYEFVDCVQKSVLC

Figure 12: Amino Acid sequence of 243. The conserved Glycoside hydrolase, family 17, domain is underlined.

MGEKLGSRGLLILLAFVLCISFTAEAIGVNYGRMGDDLPPPSEVAKFLQTTIIDKVKLFDADPG
VLQAFANTNIGVVVAVANDQIAALNKLPAAQDWVKKNVAPFVPATNIIAISVGNEILSTGDKVLI
SQLVPAMQNLHTALVGASLDKQIKVSTPHSLGILSASEPPSIGRFRRGYDRVILKPLLNFLRTT
GAPFMINPYPYFGYTDKTLNYALFKPNQGVFDNNTGITYTNMFQAQLDAVYSAMKLLGFSDV
DIVVAETGWPSVGDPDQTAVNVENALSYNGNLIKLVNTNAGTPLMPNKTFDTYIFSLFNEDLK
PGPTAERNFGLFKPDMTMVYDVGLMKSESATPAPISTAPVTPATPAPISTAPVTPTTPAPIST
APVTPTTPAPVTGTDKSWCVAKPDADPNVLQDNIDYACGQGVDCSAIQAGGQCFTPNTVVA
HATYAMNSYYQLTGRHSYDCDFAQTGFLTQEDPSYGTCVYPTI

Figure 13: Amino Acid sequence of 244. The conserved Glycoside hydrolase, family 17, domain is underlined.

MDGMHGSKVCRYSRMQRTVPMLCTLLVAALGHLVILSAAANSGVFPPFYTRALGINYGRVA
DNLPSPSSAVALIKNLQAGYVKIYDADPQVLSALSNTALQVTITVRNQDISNISSSPTVAEQWV
QANVLPHYPATLITAIMVGNEVLSDYQNQATWLLLLPAMANIHASLLNHGLADSIKVTTSLAM
DVLSSSYPPSEGTFRSDVASPVLQPLLDFANRTGSFLFLDIYPFFAWSANPANVSLDYATLSL
DRNTAEFQDAGLSYSNMLDAQLDAVLAAMDRLGFPSVNVVIGETGWPTKGDDNQPGTNVP
NATLYNQQLVQKALADPPRGTPRRPGAFIPTYIFSLFNEDQKPGPTTERNWGLFYPNGTPVY
PIVLSNDAPVLSHISVPSQNNAPFPSTPPGPVAAVQWCVVSPVAVAQVDETSLQAALDYACG
AGADCSLIEPGEPCYLPNTLVSHASYAFNSYWQKNKAAGATCDFNGSAVLSSSDPSVGDCV
FDHM

Figure 14: Amino Acid sequence of 245. The conserved Glycoside hydrolase, family 17, domain is underlined.

MGLMWVMFVCSLVLHIAGANEPEASPQPNPGIGVNYGTEGNNLPSPKQVAKMLGKTIVNRV
KIYNSEPSILQAFANTGIAVVVGLENEKVQRISESPTAGQAWVAQRIAPYYPSTLIILITVGNEV
LTNSDGSLDSALVPAIQNIHSGLVALGLDDKIKVSTPHSMAILSSSFPPSASTFATSLLPIMKPL
LKFLDDTGAPFMVNAYPYFAYRDNPKEVSLDYVLFGQSPGVSDPKGFTYNNMLDAQIDSIYS
AMAALGHNDTIPVTVSETGWPSKGDPDDIGVNPDNARNYNTRVIKHVTSNAGTPMRPNRVIE
TFIFALFNENHKPGPTTERNFGLLNPDGSKVYDVDLSCGWCASPPPPYSPPASPPPSPISLF
SGPPKGSRGGLGFAVYCIAKPSSDPSVLQESLDFSCGLGGADCASIRQGGPCYNPNTVHAH
ASYAMNSYYQIHGRNYWNCDFKSTGLVTFTDPSYGSCHYPQE

Figure 15: Amino Acid sequence of 246. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAMEGPRSGLALIISNFIFFLLSGSARTGTASNATIGINYGQIADNLPSPQRVAGLLRSINIIKKV
KLYDANREVLEAFANTGIEFVVGLSNEYVGNMTDQAAAVDWVKENVQGYLPGTNITCIAVGN
EVFTSNNTLWMSNLVPAMQNIHSALVSLGLQDSVNVTTAHSSFVLATSYPPSAGAFKPELTA
FLRPLLDFLSQTTSPFLINAYPYFAYKDNADQIPLDYVLFQPNAGTVDPGTNLHYSNMLHAQI
DAVYSALSALGYSAMEIKVSETGWPSKGDSDEVGATPENARIYNGNLLQLLAQNQGTPMRP
SVRLESYVFALFNEDQKPGKTSERNYGLFKSDGSPAYDVGLHGSLSGASANPILYSKVVVSS
LCSLFLLFFLGL

Figure 16: Amino Acid sequence of 248. The conserved Glycoside hydrolase, family 17, domain is underlined.

MGVSLMGRGSLGMSCLWALVLLSGLALSNALSSTSATTTGINYGQVADDLPPPELVVGLLQT
SNIGRIKLYTVNATVLKAFANTGIELIVGVANDIIGNLTDSNSATEWVNENIQTYLPATKIIGIAVG
NEVYTGTDTQLMANLVPAMQNIHSALVSIGADTDIIISTPHSLGVLATSYPPSAGSFQPGLESL
LEQLLALLSQIGSPFFINAYPYFPYEAQPSQIPLDYVLLEPNASAVVDQNNNVVYKNMLYAQV
DAVYSALSALGYPNIEVIVTETGWPSNGDADEAGATLQNAQTYNGNLLQLLAQNKGTPLRPN
VVLQAYLFALFNEDMKPGPTSERNYGLFGPNGVEVYNVGLTGSLSIGNKKAVSVGSPTGSA
DTPYYNTASAKETCTDISFYNHLQVLALSSFLVLLLFLP

Figure 17: Amino Acid sequence of 249. The conserved glycosyl hydrolases, family 17, domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MGMLYWTMDKLLLLFWVLLLMLAQSPGLTRGSTVGVCYGREGDDLPTPDKVAQLVKSIALK
NIIIYDSNVQVLQAFAHTGIELIIGIPNSDLLGFSQYQSTADTWVTNNLLPYYPATMIKYIAVGTE
VTESTINVTSLVVPAMRNLQTALKKAGLDQKIKVSSTHALSILSRSFPPSAGAFDSKYAFFLSP
LLQFLAQTQSPFMINVYPYYAYRDSPRKVSLDYALFRPNDGVIDQNTGLVYTNMFDAQLDAL
FFALEALNFRS**LRVMVTETGWPSKG**GSKEPAATPDNAATYNGNLVRHVINNTGTPSRPGQE
IDTYVFALFNENRKPGLESERNWGLFYPDETKVYNVDISGTGLPYVATGGNLTSVDGTSWCV
ASPSAKESDLQKALDWACGSGNVDCSPIQPGQPCYEPDNLASHASYAFNSYYQKNGASSV
ACNFGGTGNITTINPSYESCVYTTSRNGLANTTSTLSSSGVDSIASFSWLIGWVTTLFLVHLLT
ILKWL

Figure 18: Amino Acid sequence of 250. The conserved Glycoside hydrolase, family 17, domain is underlined.

MTFLFWVLVIFVLVGWVQGLGVNWGTQASHPLPPDAVVEMLKDNGITKVKLFDADEHTMKA
LANSGIQVMVGIPNDQLQVMATSTKDAANWVETNVTEFNLDGGVDIGYVAVGNEPFLKAYN
GTFIQYTFPALQNIQNALNKAGLKNIKATVPLNADVYQGDTPSEGQFRPDINDLMIQICQFLAS
NGAPFTVNIYPFLSLYTNENFPVDFAFFDGTGQPVIDGNIQYTNVFDAALDTLFWALKRAGFP
DLPVLVGEVGWPTDGDKHANINFAQRFNQGLLKHIMNGRGTPLRPQNIETYLFSLVDEDAKS
IAPGNFERHWGIFQYDGTPKYALDLSGQTQNTALVSAKGVKYLPRRWCVFNPSASPSVLTQ
LPDSITYACTHGDCTSLGFGSSCNSLDYQGNASYAFNSYYQVNNQQNGACGFSSLAIVTES
DPSQGTCKFEIQIAVSAASNTMNSYLYSLISVAGAVAVVLLSVL

Figure 19: Amino Acid sequence of 251. The conserved glycosyl hydrolases family 17 domain is underlined.

MNDKMPLYLLYVFYCLAIFVIPTEAGREWNSIGINYVRAGKNLLSPAEAVSLMKALKIGRVKLY
DSDPEVLTALANSGLSVVIAVKNEEIPTVASSILNADEWVKQSVLAHYPATRINAITVGNEILTD
YNNQDRWSKLVPAMQNIHSSLVRWNLNKRIKVTTTVAMDALNSSSAPSLARIRDDIAESVMK
PLLRFMSNSKSFYFVNAYPYFAWAANANKVPVDYAIFGAAKEAVQDGGLKYTDMLSAQLDA
NLAAMEKLGYPHVKIAISETGWPASGGPGANVDLAATYNRRVVVRMLANPPLGTPRRPRTF
VPTYLFALFDADNNKHGTTRNWGMLYPNGSQVYPVDMTDKLTDLEFESLKSIRPFPARPTPI
RSSISRSSPLTGSYPSPVPSYYSGPPTLVNPPAASPSTDNIPFSSPIPSVHPNPHPTINVPPYS
PSPISTSPPTFSPPIVNYPPHCMPYPPTTPITTPPFAPYPPSNPTVPYTPNPPSTTPYSPYPPS
TPSTPSSQSLWCVAKPTVPNSVLQQAMNYACGAGADCKSIQPNGLCFSPDTMVAHASFAF
NSYWQKNKGIGGTCDFGGTAMLITMDPSYEGCHFGLI

Figure 20: Amino Acid sequence of 252. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASNEQMKRIVIGLIAVFCCAIVTDGDKIGVNYGMQGDNLPPADQVVTLLNGHNIGKMKLFN
PDGGALNAFANSGIDVIVGVSNNDLQAISSSQDSANGWVNDNIVRYSSTSIKYIAVGNEVLPS
TQYVSYLVPAMNNIQTAIQNANLQNIKVSTPHAFNVIGVSSPPSHGAFSDDVKDTMSSILKFLS
DNGAPFMANVYPYFSYAGDTTDIHLDYALFQPTATPVTDGDHSYKNLFDAMVDSIFSAMEAL
GYSNVPLIVTESGWPSAGADAATTENAQAYNNNLIQHVLSNSGTPKRPGTNIETYIFALFNED
QKTGDEIERHFGLFNPDQSPAYSVNFSP

Figure 21: Amino Acid sequence of 253. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASNEQMKRILIGFIAIFCCSIVTDGDKIGVNYGMLGDNLPPADQVVTLLNGNNIGKVKLFDP
DGGALNAFANSGIDVIVGVSNSDLQAISSSQDSANGWVNDNIVPYSSTSIKYIAVGNEVLPST
QYVSYLVPAMNNIQTAIQNANLQNIKVSTPHAFSVIGNSYPPSKGAFSDDVKDTISSILKFLSD
NGAPFMVNVYPYFSYVGDSNDIHLDYALFQPTATAVTDQDHSYSNLFDAMVDSVFSAMEAL
GYSNIPLIVTESGWPSAGADAATTENAQAYNNNLIQHVLSNAGTPKRPGTNIETYIFALFNED
QKTGDEIERHFGLFNPDQSPAYSVNFYPN

Figure 22: Amino Acid sequence of 254. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAAMKITLIGCIAILCSILADAAQIGVNNGMVGNNLPHADEVVTLLKEHNIGKYRIFQGSPGVLK
AFENSGIEVIVGIETNRLQQISSSQEAANGWVKDNIVPFYPATNIKYIAVGNEVFKSNENVQYL
VPAMKNIQTALNMANLQNKIKVSTTHASESVIGNSYPPSKGAFTDEVKDTMRSVLQFLSDNE
APFMANVYPFFSYVNNWKNIKLDYALFQSKSPVVESYTNLFDAIVDTIISAMENLGYDNIPLIVT
ESGWPSGGNINVATIEYARTYNNNLIRHVLSNAGTPKRPGRSIETYIFALFNEDKPSQDDTER
HYGLFYPNKSPVYAVNFSP

Figure 23: Amino Acid sequence of 255. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASKEQAKIILVGFIAIFWGSILTDGDKIGINYGIQGSDLPPADEAVSLMKKNNIGKARIFKAQ
KDALKALADSGIDVIVGVATEDLQGISSSQHSADAWVNDNIVAFYPATNIKYIAVGNLILCSPQ
YISYLLPAMTNIQIALQNANLQNSIKVSTTHNMSVIAGIDFPVSNGANGDNVKDTTRSLLNFLIA
HNSAPSQGTFSDDVKDSMRSILEFLSYHGSPYMANVYPYFIFTGGSSGSMSLDYALFKPTSP
LVDGVRRYTNLFDAMVDTIISAMENLGYPDVPLIVTESGWPSFGEDVATVENAQTYNNNLIKH
VLSNAGTPKRPGTSIETYIFALFRENLKSGPTTEHDFGLFNRDQTPAYTVNFSPLL

Figure 24: Amino Acid sequence of 256. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASTEQAKIILVGFIAIFWGSILTDGDKIGVNYGIQGSNLPPADEAVSLMKKNNIGKCRILKAN
RDELKALANSGIDVIVGVGTEELQAISSSQDSADAWVNDNIVAFYPATNIKYIAVGNLILCSPQ
YISYLLPAMTNIQTALQNANLQNSIKVSTTHNMSVIAGIDFPVSNGANGDNVKGTTRSLLNFLI
AHNSAHSQGTFSDDVKDSMRSILEFLSYHGSPYMANVYPYFIFTGSSGSISLDYALFKPTSPL
VDGVRRYTNLFDAMVDTIISAMENLGYPDVPLIVTESGWPSFGEDVATVENAQTYNNNLIKH
VLSNEGTPKRPGTSIETYIFALFRENLKSGPTTEQDFGLFNRDQTPAYTLNFSP

Figure 25: Amino Acid sequence of 257. The conserved Glycoside hydrolase, family 17, domain is underlined.

MERQWFAILIICALGSMVCAVEGLGVNWGTMALHQLPPDIVVQMLKDNGIKKVKLFDADSNT
LQALANTDIEVMVAIPNNMLQRFSDSYKAAEKWVDKNVTRYNFSGGVNIKYVAVGNEPFLSA
YNGSYLNNTFPALQNIHKALVKAGLADQIKVTVPLNADVYNSPTDNAVPSAGDFRADIHDLMS
EIVTFLNDNGSPFTVNIYPFLSLYADENFPTDFAYFDGDSQPLVDGNIQYTNVFDANLDTLVW
SLKKAGVPNMTIIVGEVGWPTDGDKHATAAAAQRFNQGLLKHITSNQGTPMRPGNIEAYLFG
LLDEDAKSVAPGNFERHWGIFGYDGQPKYELDLSGPLQNGGLVPAKNVQYLPPKWCVFKT
NATDQSKILDSIKYACTYSDCTAMGYGSSCNNLDLYGNASYAFNMYFQVMNQYEINCDFTGL
AMITEQNASQGTCKFPIGIAYGAAERSIKIHSILAAVLLGVVTFILSFL

Figure 26: Amino Acid sequence of 259. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MEIIVRVSAITILLPLFIHCIRCGESIGRSRTLVEHSPALGVNYGQMADNLPSPSGVAKLVQSTT
ISKLRIYGADPAILQAFANTGIGLLVGISNDQIPSLNQLAVAQNWVKSNIVPFVPATDIIGISVGN
EVLFSGDRVLISQLLPALQNLHTALVEVSLDQQIKVSTPHSMAILSASAPPSAGRFSGSFDMK
ALVDFLQKTGAPFMINPYPYFAYKSDPTDRTLAYALFEPNQGSYDTNTGLKYTNMFDAQLDA
VYSAMKYLGYTDIDIVVAETGWPSAGDPSETGASLQNAIAYNGNLIKHVTSMAGTPMMPNRS
IEIYIFGLFNEDLKPGPTSERNFGLFKTDMTMAYDVGLLRSQSASPSPAAPRTGGPVVAPPTA
KVWCIAKPGVDEKSLKQNLDYACGQGIDCKPIQQGGPCYLPNTMASHAAYAMNAYYQSAG
RNSLNCDFAQTGTVTSKDPSYGGCVYSTVNS

Figure 27: Amino Acid sequence of 260. The conserved family 10 glycoside hydrolase domain is underlined.

MHFTTAALVSALAATPVVYGQLDSKFKAKGKKYFGTCSDSGLLSVSQNANIIKSDFGALTPEN
SAKWDSIEPSRNGFNFGGFDTLVNFAQSNGKLVRGHTFVWHSQLPSWVSSIGDAATLTTVI
QNHITTIATRYKGKIYGWDVVNEIFNEDGSLRSSIFSQRLGENFVSIAFKAARAADSNAKLYIN
DYNLDSVNSKVNGLVALVNRQKSAGTPIDGIGSQTHLSAGGSGGVQAAIQKLATTGCDVAIT
ELDIASAPTSDYVAVVKACLNTPKCVGITVWGISDKDSWRTGANPLLFDSNYQKKAAYNSIIS
ALA

Figure 28: Amino Acid sequence of 261. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MENFVLVLFCIGIGVFFNGGSLVQSAGSFPCDPSTGLSSFPFCNTSLPIGDRVKDLVGRLTLQ
EKVEQLVDQTTAIPRLGIPVYLWWSEALHGVSNVGHGTKFGGSIPGATSFPQVILTAASFNTS
LWKEIGQVVSTEARAMYNAGQAGLTFWSPNVNIFRDPRWGRGQETPGEDPLVASLYATNY
VQGLQETNGADTNRLKVAACCKHYTAYDVDNWNGFQRYTFDAIVSQQDLEDTYDVPFKSC
VLNGNVASVMCSYNKVNGVPTCADKNLLAGTIRGNWSLNGYIVSDCDSVSVYYNQQHYGAT
PEDAAADAINAGLDLDCGSFLGQHTEAAVNESKVTESAVDQALINTFTVLMRLGRFDGDPAQ
QPYGNLGPNDVCTNENQQLALEAAREGIVLLKNDGSLPLAAKNISSLAVIGPNANVTKTMIGN
YAGIPCKYTTPFQGLSAYTQTLYAPGCANVACISNDSLIAEAVQTASSADATVLIVGGDLSLEA
ESLDRTSLLLPGQQQQLVTQVADASKGPVILVIMSGGPFDISFAKNSDKISGILWVGYPGQAG
GAAIADVIFGEYNPGGRLPVTWYPEEFSINVNMTNMTMRADPATGYPGRTYRFYTGQTVFE
FGYGMSYTSFNITVVHAPELISVPLDEKYTCSPTQSESCETISLTNTKCDNMSLQVDVDVNNI
GNRDGSHVLFLFSTAPSNNVDAPNKQLIDFKKVYVEAGATERVIFTPDVCKDLSIVDKTGTRM
LPVGSRLLYIGDLEHSVSLQISS

Figure 29: Amino Acid sequence of 262. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MGLMENLVFVFVFCIVVFLKEGSLAQSVGNFPCSGQSSFPFCSTSLPIGDRVKDLVGRLTLP
EKVQQLVNTASAIPRLGIPKYEWWSEALHGVSNLGPGTRFGGSVPGATSFPQVIGTAASFNT
SLWQAIGQVVSTEARAMYNAGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPVLASKYASN
YVRGLQDTDGGDPNRLKVAACCKHYTAYDVDNWSGVQRYTFNAIVTQQDLEDTYNPPFQS
CVADGNVASVMCSYNKVNGIPTCADKNLLAGTIRGKWNLNGYIVSDCDSVKVLFESQHYTPT
PEDAAADAILAGLDLNCGDFLGLHTEAAVKAGKLPESAVDAALVNIFTVLMRLGWFDGDPTK
QPYGNLGPKDVCTAEHQQLALEAARQGIVLLKNDGPLPLAANKVHSLAVIGPNANVTKTMIG
NYAGIPCKYTTPLQGLSAYTRTLYAAGCADVLCSGNNLLGAAVQTAGNADATVLIVGGDQTL
EKESLDRMDLLLPGQQQQLISQVAAASKGPVILVIMSGGPFDISFAKDNNKISGILWVGYPGQ
AGGAAIADVIFGAYNPGGRLPVTWYPQDFAAKIPMTNMNMRPDPATGYPGRTYRFYTGKTV
YMFGDGLSYTNFKHTLVHAPKLISLPMDGKHSCSHKSSNSCEAIRVTHTKCQNLFLEVHVEV
SNVGRREGGHVLFLFSSPPSKHHAPKKQLLGFRKLHLQAGAMEKVHFTLNVCKDLSIVDKTG
TRKLPVGSHLLHIGDVQHSVSLQISS

Figure 30: Amino Acid sequence of 263. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MKSLWWLVNIVMMMVLGAIAEEPPFACDSRNPATRSYAFCDSSKPITVRVEDLISRLSLVEKV
EQLTNNASAVQRLGIPKYEWWSEALHGVSQWGRGIHFNGPIHTATSFPQVILTAASFDVKLW
YHIAQAIGIEARAIYNAGQASGLTFWTPNINIFRDPRWGRGQETPGEDPLLSSRYSVAYVRGL
QGDPLSSSSKTNVRSSTHLRASACCKHFTAYDMDNWEGHTRFSFDAMVTKQDLLDTYQPP
FKSCVELGRASGIMCSYNSVNGVPTCGDFNLLTSTARRDWGFQGYITADCDAVATIYTSHRY
TPTAEDAVADVLKAGMDVDCGNYLGKYTMSAIAKRKVNESDIDRALRNLFSVRMRLGLFDG
DLNHQLEGKLKMRVVCSAEHQRLALQAARQGIVLLKNSRKHLPLSKTRTKSLAVIGPNANNA
TTLLGNYYGLPCHTITPLQGLQRYVRDTLYYSGCEDLACISNNLFGEAVEIAKKVDEVVVVVG
LDQTQEKEERDRIKLTLPGQQEKLVYQVSHAAKRPVVLVILSGGPVDVSFAVNDPQISSIIWA
GYPGQAGGQALAEIIFGDYNPGGRLPVTWYPQDFVKIPMTDMNMRPNHHTGYPGRTYRFY
TGKKVFDFGQGLSYSAYSYEFSSTTIKKIDLNVTMEHVETLGDTGKAHVRVENSPCRKLKFR
CSILVRNHDNMDGRHAVLLYSKSPATHKGAPQKQLIGFRSVHVPGKQTTNITFVVKPCDHFS
TVEENGQRLLAIGSHSLIVGDTQYSVSLVTKHSNRNP

Figure 31: Amino Acid sequence of 264. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MGPLAIAIADLLLWMLFLCCGIHGQPMFPCDSRIPNAANYPFCRTTLPIKDRVNDLIGRLTLKE
KAQHLVSRSGAVSRLGIPVYEWWSEALHGVSNVGPGTHFDPRSVPAATSFPQVILTAASFN
TALWEVIGQAVSTEARAMYNAGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPLLSSKYATY
YVRGLQSPDGRNPNRLKVAACCKHYTAYDLDNWNGVDRFHFDAKVSQQDLEDTYNPPFKS
CVIDGHVASVMCSYNKINGVPSCADPKLLNGVIRGEWGLNGYIASDCDSVDVLYNTQHWTS
TPERAVADVINAGLDIDCGTFLGDHAEAAVRVGKLRESLIDEALSHSLTVQMRLGLFDGNPA
MQHYGNLGPRDICTNQHQQLALEAARQGIVLLKNNNRVLPLSATRIRSLAVIGPNADATNAMI
GNYAGIPCRYSTPLHALGKYTATIYKPGCENVACNRNLPLIHAAAQAASRADATVIIVGADQSI
EAEALDRVNLLLPGEQQQMVIETAAFSRGPVILVVMSGGPMDISFAKYNSKISSILWVGYPGE
AGGDALADIIYGHHNPGGRLPVTWYPQDFVAKAPMTNMNMRPDRATGYPGRTYRFYTGRT
VYPFGYGLSYTTFSHTLVNAPELVSLSLHDSPLMPYNGTNNSCTSVHVENTKCQGLLFDIHM
DVHNTGNRDGGHAVLLFFSPPTIHRSPQKSLMDFRKVHVGAGATERVQFSIDVCKDLSIVDEI
GVKKLALGSHILHVGDVQHSLNLQIE

Figure 32: Amino Acid sequence of 265. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MGPKAISNIAGLILWMLFLCCGIHGQPNFPCDSRIPNAASYPFCKTSLPIRARVSDLIGRLTLKE
KVQQLVSKSAGVPRLGIPSYEWWSEALHGVSNIGPGTQFAAGSVPAATSFPQVILTAASFNT
SLWEAIGQAVSTEARAMYNAGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPLVVGRYGTY
YVRGLQSTGGKNRNRLKVAACCKHYTAYDLDNWNGFDRFHFDAKVTQQDLEDTYNPPFKS
CVMDGHVASVMCSYNKVNGVPTCADPKLLNGIIRGQWKLNGYIASDCDSADVLYNTQHWTT
TPERAVADVLGAGLDVNCGTFLGDHAEAAVKVGKVKEALINRALINSFTVRMRLGVFDGNPA
TQPFGNLGPRDVCSEQHQQLALEAAREGIVLLKNNNRVLPLFKTRTRTLAVIGPNADVTNVMI
GNYAGIPCRYTTPRQGLGKYATTIYKPGCQNVACQRNPTLIHDASQAASQADATVIIVGADQ
SVEREGLDRGSLLLPGQQEQMVLEVTAASRGPVILVVMSGGPMDISFARDSNKISSILWVGY
PGQAGGDALADIIFGHHNPGGRLPVTWYPQDFVTRVPMTNMNMRPDRATGYPGRTYRFYT
GKAVYPFGYGLSYTTFSHSLVHAPEMVSLSLHENQLLSCHGTNNSCNSVNVENTKCEGLLL
DVHLDVQNTGSRDGGHAVLLFSSPPAVHGAPQKNMVGFRKVHVGAGTTERVHFSIDVCKD
LSIADESGAKKLLLGSHLLHAGDVQHSLNLQIE

Figure 33: Amino Acid sequence of 266. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MRLLTVMSRQIQALCISIVLSLSIVIVISDSTDYACKEHDVNSVSYGFCNTSLPIKERVEDLIRR
MTLEEKVGQLSNGASDVQRLGIPRYEWWSESLHGIATNGPGVNFDGPITAATVFPQIILSAAS
FNSTLWFRTAQAIAVEARAMYNVGQAGLTFWAPNINIFRDPRWGRGQETPGEDPLLTSEFA
VAFVRGFQGENESHDTMEKSQRSRARRELKMEGLNSLQTEPSRLMLSACCKHFTAYDLDS
WQGHARYTFNAVVSEQDLKDTFQPPFQRCVQDGHASCMMCSYNQLNGVPVCANYDLLTQ
MTRNDWGLEGYITSDCDAVAIISEDQHYATCAEDAVTDVLKAGMDINCGTYLLRNTMSAIKQ
GKLHESVIDQSLFNLFSIRMRLGLFDGDPKQQEYGHLGPDHVCTNEHWQLALEGSRQGIVLL
KNIGNALPVSKNKINSIAVIGPNANATEEMLGDYIGIPCNPVTPFVALQNYIGNVSFSKGCENV
ACSSNAKFGEAVDIAAKADAVVIVVGLDLTQETEDHDRVNLTLPGQQQRLVSEVAVASKGPV
VLVLMCGGPVDVSFAKDDPRISSILWVGYPGEAGGQALAEIIFGDYNPGGRLPMTWYPQKFI
NVPMTDMNMRPNSSTGYPGRTYRFYTGETVFQFGEGLSYSNYSYKFSSKDGHIILPFSSPS
YGEWVSDYIDIDDIPCESFKFTTKLTVQNHGSMDGSHVVLLFSRYGGNFRGAPHEQLIDFKR
VHIVAGKTTDVSFLVNPCKHFGMVMEDGRRVLAIGNHELMVGDTRLSVSLKTSFLSRK

Figure 34: Amino Acid sequence of 267. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MGASAVPIAGLILWILFFRCGIHGELMFACDSRIPNAANYPFCSTALPIKDRVNDLIGRLTLEEK
IQQLVSKAAGVPRLGIPGYDWWSEALHGVSNVGPGTQFAAGSVPAATSFPQVILTAASFNIS
LWDAIGQAVSTEARAMYNTGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPLLVSQYAANY
VRGLQLTDSLDTNRLKVAACCKHYTAYDLDNWNGADRFHFDAQVTQQDLEDTYNPPFKNC
VIDGQAASVMCSYNKVNGVPTCADPKLLNGVIRGEWGLNGYIVSDCDSAEVMYNTQHWTST
PERAVADIMESGLDVNCGNFLADHGEAAVKVGKLKETFIDTALFNSFTVQMRLGLFDGNPAF
QPYGNLGPGDVCSEQHQQLALEAARQGIVLLKNNNGALPLSPTQIRSLAVVGPNADVTNVMI
GNYAGIPCRYTTPLQGLGKYTATIHKLGCENVACQSNSILLSEASEAATQADATVIIVGADQTV
EAEMLDRVSLSLPGQQEQLVLDTADAARGTVILVVMSGGPMDISFARDNPKICGILWVGYPG
QAGGDALADILFGQHNPGGRLPVTWYPEEFAIKVPMTNMNMRPDPATGYPGRTYRFYTGN
SVYPFGYGLSYTTFSHSLVRAPKLVSLSLHESLLKSCRGMNNSCASVEVENTKCQGLLFDLH
AEVHNTGSRDGDHVLLLFASPPAIQGIPQKRLMGFRKVHVGAGGTERVHFSIDVCKDMSIVD
GNGVKQLLLGSHLLHVGDTKHTLRVEIE

Figure 35: Amino Acid sequence of 268. The conserved Glycoside hydrolase, family 5, domain is underlined.

MGHICSCKWQFLILLCFVFFPFAAPTEGRRLAQTPKVRGVNLGGWLVVEGWIKPSLFDDIKD
NDLLDGTKVQFKSAKLNTYVSAENGGGQNAVVNRDNASTWETFKMWRVSDGMYQLRVFS
GQFLTAENGGGGNMSAEADSPADWETFHIIRHHKHPNRVHIRVFNGMYMQAQSQEQLTAD
YQGDPGWHDNSATFQMIIVANDLHGDYQLANGYGRDKAKKVYHRHRSSFITDKDFKFLSRN
GINTVRIPVGWWIAYDPNPPAPFVGGSLQSLDNAFKWADHYGLQVIVDLHAAPGSQNGMEH
SASRDGSADWSNSSDHISQSLTVIDFLASRYSNNSMLLGIELLNEPLATTVPVDVLASYYSNG
YQTVRKYSATTYVIMCQRIGNADPHELYQINDAFSNIVVDVHYYNLFDDYFDNKTAQDNIDFIS
KNREPQVEALNSTNGPLIFVGEWTNEWKVQGASRSEYQQFGDAQLQAYEKASFGWSYWT
LKNEEKHWDFEWNIKHNYLRLGNSRATSNKSISWRIYAFLLIFGCIYV

Figure 36: Amino Acid sequence of 269. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MVSRMNSGWYVFLCVVILCKCAGAIGYARYKDPSQPIDARVKDLLSRMTLEEKIGQMTQIER
TDATADVMKHYYIGSVLSGGGSVPAPKASPATWINMVDELQKGAMSTRLQIPMIYGIDAVHG
HNNVYGATIFPHNIGLGATRDPDLARRIGAATALEVRATGIQYTFAPCVAVCRDPRWGRCYE
SYSEDPKIVKAMTEIIVGLQGNPPANSTKGGPFIAGQSNVAACAKHFVGDGGTTKGIDENNTV
INYQGLFNIHMTPYFDAIAKGVSTIMVSYSSWNGQKMHANHFLVSQVLKKQLGFKGFVISDW
QGIDRITSPPDANYSLSVLDGVGAGIDMVMVPDNFTDFISDLTSQVKGGFISMSRINDAVQRIL
RVKFTMGLFEHPMADPSLANQLGSKEHRELAREAVRKSLVLLKNGKSASKPLLPLDKNAPKI
LVAGTHPDNLGYQCGGWTIEWQGLSGNSTIGTTILEAIKFAVSPSTDVVYQQNPDANYVKGQ
GFSYAIVVVGEAPYAEMKGDNFNLTIPLGGGDTIKNVCGSLKCLVILISGRPLVIEPYLPLVDAF
VAAWLPGTEGQGVTDVIFGDHGFQGKLPRTWFKSVDQLPMNVGDKHYDPLFPLGFGLT

Figure 37: Amino Acid sequence of 270. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MDSIWCLFLFLVAFGKCADAAQYTLYKDPSQPVSARVDDLLARMSLEEKIGQMTQTERSVAT
PDVMTNYYIGSVLSGGGSAPAPQASPATWMNMVDGLQKGAMATRLQIPMIYGIDAVHGHNN
VYGATIFPHNVGLGATRDPDLVKRIGAATALEIRSTGIQYTFAPCVAVCRDPRWGRCYESYS
EDPTIVKAMTEIIYGLQGQPPANSTKGVPYVAGQSNVAACAKHFVGDGGTTQGVDESNTVT
DYKQLVNIHMTPYFDAIAKGVSTIMVSYSSWNGHKMHANRFLISHVLKKQLSFKGFVISDWQ
GIDRITSPPNANYSLSVLESVGAGIDMVMVPFNFADFINDLTSQVKGGFIPMSRINDAVQRILT
VKFTMGLFEHPMGDPSLANQLGSKEHRDLAREAVRKSLVLLKNGKSASQPLLPLNKNAPKIL
VAGTHPDNIGYQCGGWTIEWQGLSGNITIGTTILSAIQSAVSSSTEVVYQQNPDANYVKEQG
FSYAIVVVGEPPYTEMFGDNLNLTIPLGGGDTINNVCGSLKCLVILISGRPLVIEPYLPLVDAFV
AAWLPGTEGQGVTDVIFGDYSSQGKLSRTWFKSADQLPMNAGDQHYDPQFPLGFGLTTTV
AENISSSFGVL

Figure 38: Amino Acid sequence of 271. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MANRMDSGWCLLLFVVVLCRCAEAVEYAKYKDSSQPIDARVDDLLARMTLEEKIGQMTQIER
TVATADVMKNYYIGSVLSGGGSEPAPQASPATWINMVDGLQKSALSTRLQIPMIYGIDAVHG
HNNVYGATIFPHNIGLGATRDPDLVRRIGAATALEVRATGIPYTFAPCVAVCRDPRWGRCYE
SYSEDPTVVKSMTQIILGLQGQPPAKYKRGIPFVAGESNTVACAKHFVGDGGTTDGINENNT
VISYDGLVNIHMAPYFDAIAKGVSTIMISYSSWNGVKMHANRFLVSQVLKKQLGFKGFVISDW
QGIDRITSPAGANYSLSVFDGVSAGIDMVMVPYNFMDFIGDLTSQVKSGLISMTRINDAVRRIL
RVKFTMGLFEHPMANPSLANQLGSKAHRELAREAVRKSLVLLKNGKSDSKPLVPLDKNATKI
LVAGTHPDNLGYQCGGWTITWQGLSGNTTKGTTILEAIQSAVSPSTEVVYQENPDANYVKG
QGFSYAIVVVGEAPYAETAGDNLNLTIPLGGGDTINNVCGSVKCLVILVSGRPLVITPYLPLVE
AFVAAWLPGSEGQGVTDVIFGDYGFQGKLSRTWFKSVDQLPMNVGDKHYDPLFPFGFGLT
TTVAKNL

Figure 39: Amino Acid sequence of 272. The conserved N-terminal and C-terminal domains of glycoside hydrolases family 3 are underlined.

MDSGWYLLLFVVVLCRCAEATEYAKYKDPSQSITARVDDLLARMTLEEKIGQMTQIERTVAT
ADVMKNYYIGSVLSGGGSAPAPKASPATWMNMVDELQKGAMSTRLQIPMIYGIDAVHGHNN
VYGATIFPHNVGLGATRDPDLARRIGVATALEVRATGIQYAFAPCIAVCRDPRWGRCYESYS
EDPKIVKTMTEIIFGLQGQPPANSTKGVPFLAGQSNVAACAKHFVGDGGTTEGINENNTVISY
KGLVHIHMAAYFDAIAKGVSTVMVSYSSWNGGKMHANRFLVSRVLKKQLGFKGFVISDWQG
IDRITSPAGANYSLSVFDGVSAGIDMVMIPYNFKDFINDLSSQVKSGLIPMTRINDAVRRILRVK
FTMGLFEHPLGNPSLANQLGSKEHRELAREAVRKSLVLLKNGKSANKPLLPLEKNASKVLVA
GTHPDNLGYQCGGWTMEWQGLSGNITVGTTILEAIKLAVSPSTEVVYEQNPDANYVKGQGF
SYAIVVVGEAPYAETFGDNLNLTIPLGGGDTIKTVCGSLKCLVILISGRPLVIEPYLPLVDAFVA
AWLPGTEGQGVTDVIFGDYRFQGKLARTWFKSVDQLPMNIGDQHYDPLFPLGFGLV

Figure 40: Amino Acid sequence of 273. The conserved Glycoside hydrolase, family 5, domain is underlined.

MAACINIHARNCPQGCFKFVILVLITSCLAYGSEASEVRRLTIGTQKYHSVALGGWLVIEGWIK
PSLFDGIPDNDLLDGTQIQLKSMKLGTYIVAENGGGQKVAVNRTNPLKWETFRIWRVRDGYY
QLRVFNKQFLGADNGGGGVVKAVATTPRSWETFQIIRNNADRNRVHLKALNGMYLQANSKD
QLTADFKGEPAWDGNNAATFEMSFTGHMQGEFQISNGYGPERAAQVLKEHRSTFIREDDFV
FLSKQGISAVRIPVGWWIASDPKPPAPFVGGSLECLDKAFSWAQNHGIKVIIDLHAAPGSQNG
DEHGGGRDGYIEWADSQKNIDTTLSTIDFLASRYAAHPALLGIELLNEPRSSGISLNNLTAYYT
QGYNIVRKYSSSAYVIMCNRIGPVDPKELFQINNGLFRTVVDVHYYNLFDDSTFKHMTVQQNI
DYIKNTRAQTLQSLVSANGPLIFVGEWVAEWEVQNATQSDYERYGDAQFQVYGTASFGWT
YWTLRNIGNRHWDFQWMVNNQYLRLPSIQI

Figure 41: Amino Acid sequence of 274. The conserved Glycoside hydrolase, family 5, domain is underlined.

MAAYIDVHAKKLSQRCFGFVITLLVFTSSLAYGRKILEARRLTNDTQKYHSVNLGGWLVIEGW
IKPSLFDGIPDKDLLDGTQIQLKSMKLGTYVVAEDGGGTIMAVNRTNPSGWETFSLWRARDG
YYQFRVFNKQFVGADNGGGGIVEAVATTPNSSETFQIIRNPANSNSVHIKVFNGMYMQAQSK
DQLTADFEGEPGWDDNNAATFEMTIVRTLQGEFQISNGYGPEKATQVLNEHRSTFITEDDFV
FMSKNGISAVRIPVGWWIASDPYPPAPFVGGSLACLDKAFSWAQNHDIKVIIDLHAAPGSQN
GDEHSGTRDGFIEWPESQENIDKSLSVIDFLAARYAAHPALLGIELLNEPRSPAVSLNNVTDY
YSRGYDIVRKYSSSAYVIMCNRIGPADPKELFQMNNGLSRTVVDVHYYNLYDDATFKNMTVQ
QNIDYIKTTRAQTLQSLVSANGPLIFVGEWVDEWELNSATQSDYQRYGDAQLQVYGEASFG
WAYWTLRNIGSRHWDLEWMVQNQYLLLPASNQS

Figure 42: Amino Acid sequence of 275. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MGFIHTMAIPESKVFWLLLAIVGGVIHAYAEDYTIGIDYGQLGDNLPSTEEAIHLIQRMKVGRV
KIYDTNPEILKALAHTGIKVSVMVKNEVIANVSANQSFADKWVKNNVVYFYPATKINIVLVGNEI
LSDYSNNQTWYQLVPAMLRIRRALVRYKLHHIKVGTPSAMDVLNTSFPPSSGAFRDDVAETV
MKPMLEFLTRTRSYFFIDVYPYFAWSSDPTNISLEYASFGDHDKNYTDPNGLVYTNLLDQQL
DAVVAAMSKLGYEDIRLIIAETGWPNAGDLNQLGANIFNSAHYNRRLIRRMLADPPLGTPRRP
NQFIPTYIFSLFNEDQKSGPGTERHWGLLYPNGTRVYEIDLTGELQDSEYKPLPPPPPPYTGK
LWCVVDANANVSSLPSAINYACSQGNNTCASIQPGKPCYQPNTVIDHASYAFNSYWQQFKN
SGGTCYFNGAATLVTQDPSRGSCTYPFT

Figure 43: Amino Acid sequence of 276. The conserved glycosyl hydrolases family 17 domain is underlined.

MRRRMGLLFSVLVMFVWVGWVRGLGVNWGTQASHPLPPDILVGLLKDNGIKKVKLFDAEER
AMRALAKSGIEVMAGIPNDQLQRMANSQKAAANWVEANATEFSLDGGVDIRYVAVGNEPFL
KAYNGTFIQYTFPALQNIQNALNKAGLKNIKATVPLNADVYQGDTPSEGQFRPDINDLMIQICQ
FLASNGAPFTVNIYPFLSLYTNENFPVDFAFFDGTGQPVIDGNIQYTNVFDAALDTLFWALKR
AGFPDLPVLVGEVGWPTDGDKHANINFAQRFNQGLLKHIMNGRGTPLRPQNIETYLFSLVDE
DAKSIAPGNFERHWGIFQYDGTPKYALDLSGQTQNTALVSAKGVKYLPRRWCVFNPSASPS
VLTQLPDSITYACTHGDCTSLGFGSSCNSLDYQGNASYAFNSYYQVNNQQNGACGFSSLAI
VTESDPSQGTCKFEIQIAVSAASNTMNSYL

Figure 44: Amino Acid sequence of 277. The conserved Glycoside hydrolase, family 17, domain is underlined.

MATNIILIVCIAIFCCSILAESAQIGVNYGMLGTSLPPAGQVVTLMKSNNIGKMKIFQADKDALK
AFANSGIEVIVGVGNNELQLISSSQDAANGWVNDNIRPFYPATNIKYIAVGNEVLIKTTYGSYL
VPAMRNIQTALQNANLQNNIKVSTTHSSDVSEGYPPSNGVFKDEVKDTMKSVLQFLLDHGSP
FMGNIYPYFSYINNRAQITLDYALFKSTSTVVPDKGRSYKYLFDALVDTLVSAMEALGYPNIPLI
VTESGWPSAEADVATVDNARTYNNNLIRHVLSNEGTPKRPGKSIETYIFALFNENKKNPGTE
QHFGLFYPNQQHVYPVNFSP

Figure 45: Amino Acid sequence of 278. The conserved Glycoside hydrolase, family 17, domain is underlined.

MATFKDQSRIFLIGCVAIFCCSVLADGDKIGVDYGMTADNLPSPDEVVTLMKSNNIGKTRIYQ
ENDVVLQAFANSGIDVIVGVANEELKNISSSQDSANRWVNEHIVPFYPATNVKYIAVGNEVLIT
LDNVQYVPYLVPAMNNIQTAIQNAKLQDSIKVSTTHRPDVSSGYPPSKGVFVDAVKDTMSQIL
NFLSQNGGPFMADVYPYFSYIGNTKDISLDYALFKSTSTVVQDGDHSYTNLFDAMVDTLLSA
MEASGYPNIPIVITESGWPSAGAEVATIENAQTYNNNLIKHVLSNAGTPKRPGMSIDTYVFALF
NEDLKPGDETEKHFGLFDPNTKQPVYSVNFSP

Figure 46: Amino Acid sequence of 279. The conserved Glycoside hydrolase, family 17, domain is underlined.

MKILSRFLLLLLLIASFSEVALGGPFVGVNIGTDVSNMPSASAVVALLKNQQITHVRLYDADRQ
MLTALANTGIEVVVSVPNNQLLGVGQSRSTAANWVNKNVAAYLPNTNITAIAVGSEVLTTIPN
AALVLVPAMRFLHSALVAANLDGQVKVSTPHPAELILDSFPPSQAFFNSSWNSVMIPLLAFLR
DTKSYLMLNVYPYYVYMQGNGVVPLDYALFRPLPPNKEAVDPNTLLHYTNVFDAVVDAAYY
AMASLNFTNIPVVVTETGWPSMGDANEPDATVDNADTYNSNLVRHVLNSTGTPKLPGVAVN
TFIYELFNEDLRPGGTSEENWGLFSANSTPVYVLHLNGAGSPLGNDTSAQTFCVALSGADN
QLLQAALDWACGPGQADCSAIQAGQSCYTPDTVADHASYAFDSYYHKMNMAPGSCDFNG
VGTITNTDPSHGSCIFQGSVSANGTSSVNGTVLGNETFPLTGTNITSLNSSAPHLQSQIHPILF
PLVALPILFWNLPIL

Figure 47: Amino Acid sequence of 280. The conserved Glycoside hydrolase, family 17, domain is underlined.

MGSLNRSMVCSMLISVFFCFVFGALHMVSADFANKQALGINYGQVANNLPSPAIAVQLMKSI
NVGYVKIYDADSQVLTALANTSLPLVITVANEDIPNIASGSSNADQWVQKNVLPYYPATQIFMI
MVGNEVLSNPQIQSTWSQLVPAMENLQASLVKHNLDDSIKVTTSVAMDALASSYPPSNGSF
KADIAASIMQPMLSFLNRTDSYFFVDAYPYFAWSSNPVNISLNYVLFGVSTTEILDGQLQYSN
MLDAQLDAVVAAMADLGFPQVKLAVSETGWPTKGAADEPGANVANAAKYNRRLVSRFSAS
PPVGTPRRPGAFIPVFVFALFNEDQKTGPVTERNWGVFYPNGTPVYNIDLSGGNQGSAYTPI
IRSGTNNNTFSAPAGAPASAAAPIPTAAPITTAAAPIPTAAPITTAAPTPSTLQQWCVAKSGVN
NMTAVQQALDYACGAGADCSAIQAGNACYQPNTVEAHASYAFNSYWQSTKSNGGTCYFN
GVAALTTSDPSFQGCSFPFQ

Figure 48: Amino Acid sequence of 281. The conserved Glycoside hydrolase, family 17, domain is underlined.

MASSNKVGVCYGMVANNLPLPDQVANLIRSRNIGKVRLFQAHHEAQRALQNSGGIEVIVGVG
NDELQKIASDQAAANGWVNDNIRQFYPATNIKYIAVGNEVFSSENRQHLPYLVPAMRNIQTA
VQNANLQSSIKVSTTHATSVLGNSYPPSQGEFADELKSSMSDVLNFLAENGSPFMANVYPYF
SYIYNQAQISLDYALFKSADPVVSDEGRLYKSLFDALVDSLISAMEKSGHPDIPIVITESGWPS
AGNEAATVENAQTYNNNLIKHVLSNAGTPKRPGQHIDTYIFALFNENLKGGDEPERHFGLFY
PDQNLVYPVNFSP

Figure 49: Amino Acid sequence of 282. The conserved Glycoside hydrolase, family 17, domain is underlined.

MWVLPLLLLLLFLFCPFILGARVNGGAFVGVNIATDLSNMPSPSQVVSLLQTQQIKHVRLYDV
ERDMLLALANTSIQVVISIPNNQVLAIGESNSSAANWVKKNVADYLPNTNITGIVVGNEVLTTL
PNAALVLVSAMKFLQSALVAANLDQQVKISSSHSSDIILDAFPPSQAIFNQSFNDIIGPMLEFLQ
DTGSYFMMNLYPYYTFMEGKGKVPLDYALFEPLTPDKEAVDPNTLLHYTNVFDALVDAAYYS
MGNLNYTNIPVVVAETGWPSDGDATEPYATINNADTYNSNLVIHVLNITGTPKRPTIPVNTYIY
ELYNEDLRPGPLSEQNWGLFFANSSPVYVLHLTDAGEFLANDTTNQTFCIAKPGADLKLLQA
ALDWACGPGEANCTAIQGGEDCFNPDTVEAHSSYAFDSYYHNTGMAAGSCDFKGVAIITTT
DPSHGSCVYPGSGGANQTSASKNNTSVSGSMDMGHMDNSVLMMLHILLLFLWF

Figure 50: Amino Acid sequence of 283. The conserved Nucleotidyl transferase is underlined.

MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAIGVDEVVLAINYQPEVMLSFLK
AFETKLGIKITCSQETEPMGTAGPLALARDKLIDGSGDPFFVLNSDVISEYPLKQMIDFHTKHG
GEASIMVTKVDEPSKYGVVILDEETGKVERFVEKPKVFVGNKINAGIYLLNPSVLDRIELRPTSI
EKEVFPKIAQEKQLYAMVLPGFWMDIGQPRDYISGLRLYLDSLRRNTSDKLATGVNIVGNVIV
DSTAQIGEGCLIGPDVAIGPGCVIEAGVRLSRCTIMRGVRIKKHACVSGSIIGWHSTVGQWAR
VENMTILGEDVHVSDEVYSNGGVVLPHKEIKSSILKPEIVM

Figure 51: Amino Acid sequence of 284. The conserved Nucleotidyl transferase is underlined.

MSIGDRKSVAVIMVGGPTKGTRFRPLSLNLAKPLFPLAGQPMVHHPILACKKIPNLAHIYLIGF
YEEREFALYVSSISNELKIPVRYLREDKPHGSAGGLYHFKDLIMEDDPANIFLLNCDVCCSFPL
ADMLEAHCKYGGMGTILVIKVSAESANQFGELVADSVTGELLHYAEKPETFVSDRINCGVYV
FTPDIFLGIQDVSTQRKDRATMRRVSSFEALQSATKALPTDFVRLDQDILTPLAGKKKLYTYET
SDFWEQIKTPGMSLRCSSLYLSQYRLTSPELLAKSNGGRTATIVGDVYIHPSAKVHPTAKIGP
NVSISANARIGAGVRLIGCIILDDVELKENSIVMHSIVGWKSSIGRWSRVQGEANYTSKLGITIL
GEDVTVEDEVVVANCIVLPHKMLNMSVQEEIIL

Figure 52: Amino Acid sequence of 285. The conserved Nucleotidyl transferase is underlined.

MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAIGVDEVVLAINYQPEVMLSFLK
EFEAKVGIKITCSQETEPMGTAGPLALARDKLDDGSGEPFFVLNSDVICEYPLKQMLEFHKKH
GGEASIMVTKVDEPSKYGVVILDEETGRVDRFVEKPKIFVGNKINAGIYLLNPSVLNMIELRPT
SIEKEVFPKIASKKQLYAMILPGFWMDIGQPKDYISGLRLYLDSLRRNLPKKLSFGAHIIGNVIV
DETAQIGEGCLIGPDVAIGPGCVIEAGVRLSRCTVMRGVRIKKHACVSGSIIGWHCTVGQWA
RVENMTVLGEDVHVCDEVYSNGGVVLPHKEIKSSITKPEIVM

Figure 53: Amino Acid sequence of 286. The conserved nucleotidyl transferase family domain is underlined.

MAGEGKVIAVIMVGGPTKGTRFRPLSLNIAKPLFPLAGFPMVHHPILACKKIPNLAHIYLIGFYD
ERLFSLYLSNVSSELKIPVRYLCEDKPHGSAGALFKFHDLLMEDNPKEIFVMHCDICCSFPLV
DMQMAHRNYGGIGTMLVKKVSTEATGKFGELVADPLTKELLHFAEKPETHVSDYINCGVYIF
TPDIFVTMQTLTPTRKERGIFRRLSSFESLEFSSPSVQKDVIRLDEDLFTPLVGKKMIYTFETS
DFWEQIKTPGMSLRCSSLYLKQYHMKTPELLSSADAIMTVNIIGDVYIHPSSKIHPTAKIGPNV
SISANARIGPGVRLRDCIILDDVEVQDNAIVMHAIIGWKASIGKWARVQGERNYGAKNGISILG
EAVTVEDEVVVLSSTVLPHKALNQSVQGEIIL

Figure 54: Amino Acid sequence of 287. The conserved nucleotidyl transferase family domain is underlined.

MKALILVGGFGTRLRPLTLSLPKPLVDFANKPMILHQIEALKEAGVDDVILAVNYQPESMMKFL
TEFEAKLGIRIQCSREIEPLGTAGPLALAKDKLIDGSGQPIFVLNSDVICEFPLKEMLEFHKSCG
AEASVMVTRVDEPSKYGVVVLDEETGRVKRFVEKPQMFVGNKINAGIYLLNPSVLDRIELKPT
SIEKDIFPRIAEENQLYAMVLPGFWMDIGQPRDYLTGLRLYLDYLRTKSDVLASGSQFQGNVL
IDESVQIGEGCLIGPDVSIGPGCIIEAGVRLSNCAIMSGVRIKKHACVSWSIVGWHSTVGQWA
RAENMTILGEDVHISDEIYSNGGVVLPHKEIKSNILKPEIVM

Figure 55: Amino Acid sequence of 288. The conserved Eukaryotic phosphomannomutase domain is underlined.

MDCRKAGVLALFDVDGTLTPARKVVSQEMLEFMQELRKVVAVGVVGGSDLAKITEQLGKTVI
SDYDYVFSENGLVAHKGSKAIGNQSFKAFLGDEKLKELINFTLHYIADLDIPVKRGTFIEFRSG
MLNVSPIGRNCSQEERDEFERYDKVHGIRTKMVEVLREKFAPLNLTYSIGGQISFDVFPQGW
DKTYCLRYVENDFQEIHFFGDKTYKGGNDHEIFESSKTIGHTVTSPEDTRRQCTELFFQ

Figure 56: Amino Acid sequence of 289. The conserved group 1 glycosyl transferase domain is underlined.

MAGNEWMNGYLEAILDGGGVGDDNDYTRQKKESSVKSGVTVIPQLGAFNPARYFIDEVVHG
TDETDIHHFWVKVTATKNPEERNTRLENLCWRIWHISRRKKKGKLEQSKRLQKLRQERERG
RRDVTEDMSEDLSEGEKLGGDGQGLKFSESHYNLELLTEQSLKGKRLYVIMISLHGLVRGEN
MELGRDSDTGGQVKYVVEFAKALAKMPEVYRVDLLTRQICSPDLDSSYGEPTEMLTSDQDD
DILESGGAYIVRIPCGCKEKYIQKELLWPYIPEFVDGALGHILNISKALGDLIGEDTPVWPHVIH
GHYADAGDAACLLSGALNVPMVLTGHSLGRNKLEQLLKQGLHSKEDINATYKIMRRIEAEEL
CLDSAELVVTSTRQEIEEQWGLYDGFDLELNRKLRQRAKRGVHSYGRYMPRMSVIPPGMDF
SNVVVHDENSDNDLDNDSVQLPESPLWGEIPRFLNNPSKPIILALARPDPKKNMATLVKAFG
ECIKLRKLANLMLIMGNRDDIDQMPAASANVLTTVLKLIDKYDLYGEVAYPKHHKQSEVADIYR
IAAKTKGVFINPALVEPFGLTLIEAAAHGLPMVATKNGGPVDIQRTLNNGLLVDPHNDKEIAAA
LYRLVVDKNLWVECRQNGLQNIHLYSWPQHCRTYLSRISQCRMRHPQWQSENDQNENMD
SESDSGSFKDAPDTSLRLSLDADRPSRSSSVNSPFDLDKLLQNEENVGGISEHIRMIIEKTKD
NQSKLGDTNDVNSQEKQSIEHSNSLGSSGKHLLRRRKRLFVIAVDCYDASGEPLLSRQAIIIQ
EIMNAVCSAGNFSSPGFILSTALTVPETISMLQSIGIKVSAFDALICSSGSQLLYTAGDNPDSPI
YPDPDYDSHIDYRWGAEGLRKSMKKLRGPENSRFLAEDAEASNFHCLAYQVKNISTAPKAD
ELRRQLRMRGLRCHVIYTQNCSRLRVLPLHASRSQALRYLYVRWGLDIANMYVFLGEKGDT
GYEELIGGMHKTLILKGTVVDGSEKMLRS

Figure 57: Amino Acid sequence of 290. The conserved group 1 glycosyl transferase domain is underlined.

MAGNDWINGYLEAILDAGAGFTEAETRPALTVADGGGFNPTKYFVEEVVTGFDESDLHRTWI
KVVAMRNSLERNNRLENMCWRIWHLARRQKQIEWDDAQRLAKRRIEREQGRRDATEDMSE
DLSEGEKADVATPRATPKRAFSRNFSDLQVWSDDNKGKRLYIVLISLHGLVRGENMELGRD
SDTGGQVKYVVELARALSMMPGVYRVDLLTRQISSPDVDWSYGEPTEMLSSGSYDVDGHG
GGESSGAYIIRIPCGPRDKYIPKELLWPYIQEFVDGALGHILNMSKVLGDQAGKGDPVWPYVI
HGHYADAGDSAALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINATYKIMRRIEAEE
LSLDAAELVITSTKQEIVEQWGLYDGFDVRLEKILRARAKRQVSCHGRFMPRMVVIPPGMDF
SNVVVADQEPAEADGDLAALINGDVNLSPKALPPIWSEVMRFFTNRHKPMILALSRPDPKKN
LTTLVKAFGECRPLKELANLTLVMGNRDDIDEMSGGNAAVLTTVLKLIDKYDLYGQVAYPKHH
KQSDVPDIYRLAAKTKGVFINPALVEPFGLTLIEAAAYGLPMVATKNGGPVDIHSTLTNGLLVD
PHDQKAIANALLELVADKNLWNECRRNGLRNIHLFSWPEHCRKYLSRVAVCRMRHPQWQT
DTLMDTTMDEESMGDSLKDVQDMSLRLSVDGEKYSVNGSLDNSAEVDKLLAAKGDPETYN
QVKRILDKLKKGPPSSITQETEPKPDVNEPRAPANNVSVSNKYLALRKKRKLFVIAVDCYDDT
GNVSPRMLEIIQEIIKAVRSDATAARFAGLVLSTALTVDEILGMLNSGNILPHEFDALICSSGSE
LYYPTIPAYPDDGSNKKLCPDPDYDSHIDYRWGGEGLRKTMSLLTASERDGQEKQERVIFED
AKHSNAHCLAYVVKDSTRVRKVDEFRQRLRMRGLRCHPMFCRNSTQLHVIPLLASRSQALR
YLFVRWGLDVANMHVFVGETGDTDYEEMLAGLHK

Figure 58: Amino Acid sequence of 291. The conserved Glycoside hydrolase, family 16, domain is underlined.

MDTPLHLLFLLLASSAALASANFYNDVDITWGNDRAKILDNGQQLQLTLDRSSGCGIQSKQE
YLFAKIDIQMKLVPGNSAGTVTTFYLSSQGPKHDEIDFEFLGNLSGDPYILHTNVFAQGLGGR
EQQFYLWFDPTLDFHTYSVLWTSNQIIFSVDGSPVRVFKNRETELGKVDSNYHYPKTQAMR
VYSSLWNADDWATRGGLVKTDWTKAPFVASLRNFNAAATSSFDAAAEEVALESNQEQRQR
LQWVRKNYMIYDYCADTKRFPQGPPPECK

Figure 59: Amino Acid sequence of 292. The conserved Glycoside hydrolase, family 16, domain is underlined.

MDTPLHLLFLLLASSAALASANFYNDVDITWGNDRAKIIDNGQELQLTLDRSSGCGIQSKQEY
LFAKIDIQIKLVPGNSAGTVTTFYLSSQGPKHDEIDFEFLGNLSGDPYILHTNVFAQGLGGREQ
QFYLWFDPTLDFHTYSVLWTSNQIIFSVDGSPIRVFKNRETEMGKVDNNYHYPKSQAMSVYS
SLWNADDWATRGGLVKTDWTKAPFVASFRNFSAATASSFDAAAEEAALESNQEQRLEWVR
KNYMIYDYCGDTKRFPQGPPPECK

Figure 60: Amino Acid sequence of 293. The conserved Glycoside hydrolase, family 16, domain is underlined.

MEMGKPLLFLFLLISSSLLLIVSANFYNDVDVTWGNGRGQILDNGQQLQLTLDPTSGSGFQS
KKEYLFAKIDMQIKLVPGNSAGTVTAYYLSSQGPKHDEIDYEFLGNLSGDPYIMHTNIFAQGL
GNREQQFYLWFDPTLAFHTYSVLWTPNQITLSVDGIPVRVFKNRETELAKVDSNYHYPKSQA
MRVYSSLWNADDWATRGGLVKTDWTKAPFVASFSDFNAATSSSNFAGEGALDSNQGQKL
QWVRNKYMIYDYCADTNRFPQGLPAECK

Figure 61: Amino Acid sequence of 294. The conserved Glycoside hydrolase, family 16, domain is underlined.

MDTPLLFLLLLISSTLLLTVSANFYNDVDITWGNDRAKILDNGQQLQLTLDRTSGCGFQSKEE
HLFAKIDMQIKLVPGNSAGTVTAYYLSSQGPKHDEIDFEFLGNLSGDPYIMHTNVFAQGLGNR
EQQFYLWFDPTLDFHTYSVLWTSNQIIFSVDETPVRVFKNRETELGKVDSNYHYPNSQAMR
VYSSLWNADDWATRGGLVKTDWTKAPFVASFSDFNAATSSSNFDGEDVLDSNEEQKLQWV
RKNYMIYDYCADTKRFPQGLPAECK

Figure 62: Amino Acid sequence of 295. The conserved glycoside hydrolase, family 16, domain is underlined.

MDTGTPLLFLFLLITSSSLLVIVSANFYNDVDITWGDGRGKILDNGQQLQLTLDRTSGSGFQS
KNEYLFAKVDMQIKLVPGNSAGTVTAYYLSSQGPKHDEIDYEFLGNLSGDPYIMHTNIFAQGL
GNREQQFYLWFDPTLAFHTYSVLWTPNQITFSVDETPVRVFKNRETELGKVDSNYHYPKSQ
AMRVYSSLWNADDWATRGGLVKTDWTKAPFVASFRNFSAATSSSNFAAEEALDSNQEQKL
QWVRNNYMIYDYCADTKRFPQGLPAECK

Figure 63: Amino Acid sequence of 296. The conserved Glycoside hydrolase, family 16, domain is underlined.

MQTHHSESSLLLLVLAFEIALFFLIFNRLLSIIITDMDTPLLFISLLSLASLVVTVSANFYNDFDIT
WGNDHAQILDNGNQLQLTLDHTSGCGCQSKEEYLFAKIDMQIKLVPGNSAGTVTTYYLSSQ
GPKHDEIDFEFLGNLSGDPYVMHTNIFAQGLGNREQQFYLWFDPTLDFHTYSVLWTPNQIIF
SVDGTPVRVFKNREKELGNNFHFPNSQAMRIYSSLWNADDWATRGGLIKSDWSKAPFVAYF
SNFSAVISSSNFVIEEDLDSNQEQKLQWVRNNYMIYDYCADTKRFPQGLPPECK

Figure 64: Amino Acid sequence of 297. The conserved Glycoside hydrolase, family 16, domain is underlined.

MDMGMPLLFLFLLITSSSLLVTVSANFYNDVDITWGNGRGKILDNGQQLQLTLDRTSGCGFQ
SKNEYLFAKIDMQIKLVPGNSAGTVTAYYLSSQGSEHDEIDYEFLGNLSGDPYIMHTNIFAQG
LGNREQQFYLWFDPTLDFHTYSVLWTPNQIFSVDGIPVRVFKNRETELGKIDSNYHYPKSQA
MRIYSSLWNADDWATRGGLVKTDWTKAPFVASFSNFSAATSSSNFAGEEALDSNQEQKLQ
WVRKNYMVYDYCADTKRFPHGLPAECK

Figure 65: Amino Acid sequence of 298. The conserved Glycoside hydrolase, family 16, domain is underlined.

MMLAVALVCIWVCGLFSQPGSAVGSSRPRLAGKLVTENFAGLQFEEAYTSLFGDENVKVAE
DGKTVMLSLDKRTGSGLLSQDMYLYGLFSASMKLPDDYTAGVVAAFYTSNGDMFPGTHDEL
DFEFLGNIRGKEWRIQTNVYGNGSTAYGREERYTLWFDPTEDFHQYTILWTEKSTVFFVDDV
PIREIPRTDAMGAHYPGKPMSVYATVWDGSDWATKGGRYRVNYKYSPFVVTLANLILEGCA
VDPLEQFPAVSCSADTTSSASLSKLAELSEDQKALMEWFRGKYISYSYCDDAVRYPSNPSD
CPPRDPHKKIATAHVKFGHHQRHHKKNRKSRRSSSSSAASAAVSL

Figure 66: Amino Acid sequence of 299. The conserved glycoside hydrolase, family 16, domain is underlined.

MMLAVALVCIWVCGLFSQPGSAVGSSRPRLAGKLVTENFAGLQFEEAYTSLFGDENVKVAE
DGKTVMLSLDKRTGSGLLSQDMYLYGLFSASMKLPDDYTAGVVAAFYVSNGDMFPGTHDEL
DFEFLGNIRGKEWRIQTNVYGNGSTAYGREERYTLWFDPTEDFHQYTILWTEKSTVFFVDDV
PIREIPRTDAMGAHYPGKPMSVYATVWDGSDWATKGGRYRVNYKYSPFVVTLANLILEGCA
VDPLEQFPAVSCSADTTSSASLSKLAELSEDQKALMEWFRGKYISYSYCDDAVRYPSNPSD
CPPRDPHKKIATAHVKFGHHQRHHKKNRKSRRSSSSSAASAAVSL

Figure 67: Amino Acid sequence of 300. The conserved Glycoside hydrolase, family 16, domain is underlined.

MARIIPIVLASAILLVASLQSEVNAANQIFNADFQILFASDHVKTSDDGQIWELMLDKKSGSGF
QTKNSYRFGFFTMKLKLVAGDSAGVVTTYYMASKDFETRDELDFEFLGNVSGQPYALQTNIY
VNGVGGREQRNELWFDPTADFHTYSFLWNDHQLIFFVDLVPLRVHRHTNVTDNVYPKNRP
MSLLSSIWNADNWATRGGLDKTNWSYAPFISSYQNFNADACMWEDPFPACVSTTGENWW
DKPPAWTLTDAQKLDYAWARRNFLIYDYCQDTKRFNGTLPVECSVGPW

Figure 68: Amino Acid sequence of 301. The conserved Glycoside hydrolase, family 16, domain is underlined.

MGLVGRMMHWPCVLGSIVVLCSLIVGSQCAAFNDFFYPSWALDHVMYEGELLKLKLDNTSG
AGFASKSTYIFGKVNVQIKLVPEDSAGTVTAFYMSSQGDQHDEFDFEFLGNTSGEPYAVQTN
VFSKGVGKREQRIFLWFDPTTDFHSYSFLWNRQQVVFFVDDVPVRVFGNNEKVGVPYPQS
QPMGVYSSIWNADDWATQGGLVKTDWSHAPFVSTYTNFSIDACDYSLKTTCSSWWDEPAY
ASLDAKQRLKLKWVQEKYMTYDYCKDSARFPTPPPECSA

Figure 69: Amino Acid sequence of 302. The conserved Glycoside hydrolase, family 16, domain is underlined.

MCLQRICWVRAMLIKMVPKLLLVLLVAAMAAMAASPPKPVDVPFPKNYVPTWAADHIKYING
GNEVQLSLDKWTGTGFQSKGTYLFGHFSMQIKMVPGDSAGTVTAFYLSSQNAEHDEIDFEF
LGNRSGQPYILQTNVFSGGKGNREQRIYLWFDPTKDYHAYSVLWNMHQIVFFVDDVPIRVFK
NSRDLGVRYPFNQPMKIYSSLWNADDWATRGGLEKTDWSKAPFVASYRGFHVDGCEASVT
ESTCATQGRRWWDQKAFDDLDGMQWRKLKGVRNSYTIYNYCADKVRSPAMPPECTRDRD
I

Figure 70: Amino Acid sequence of 303. The conserved Glycoside hydrolase, family 16, domain is underlined.

MLINMVPNVLLFLLVAAMAATATPPPKPVDVPFQKNYVPTWASDHIKYINGGNEAQLSLDKW
TGTGFQSKGSYLFGHFSMQIKMVPGDSAGVVTAFYLSSQNSEHDEIDFEFLGNRSGQPYILQ
TNVFSGGKGDREQRVYLWFDPTKDYHSYTVLWNMHQIVFFVDDVPIRVFKNSKDLGVRYPF
NQPMKIYSSLWNADDWATRGGLEKTDWSKAPFVASYKGFHVDGCEASMPHSACPTLGRR
WWDQKAFDDLDGQQWRKLKWVRDRYTIYNYCTDRVRYPKMSPECTRDRDI

Figure 71: Amino Acid sequence of 304. The conserved Glycoside hydrolase, family 16, domain is underlined.

MGGTWRTVGLSFLFLVFSSLIASVCSQSQGDDSSAKVFDDNFQIMWAEDHFRTSENGQVW
HLVLDQNSGSGFKSKYKYRFGWFSMKLKLVPGDSAGVVTAYYMSSNTDMNRDELDFEFLG
NRSGEPYALQTNIYAKGVGGREQRHILWFDPTTQFHTYSILWNSHQIVFFVDQVPLRVHRHT
EATSDVFPKEQGMYMFSSIWNADNWATRGGLEKTNWTAAPFVSSYKKFHGLGCKWGDDN
TTLLPCANDKNASASHWWDEAVAWTLTKKQRENYRWVNSKYLLYDYCNDQSRYSIKPVEC
SVAPWD

Figure 72: Amino Acid sequence of 305. The conserved glycoside hydrolase, family 16, domain is underlined.

MGRTWRAMGMSFLVLVLIGLIACVSCQSDGDDSSPKVFDDNFQILWAQDHFRTSENGQVW
HLVLDQNSGSGFKSKNKYRFGWFSMKLKLVPGDSAGVVTAYYMSSDTDMNRDELDFEFLG
NRSGQPYGLQTNIYSNGVGGREQRHILWFDPTTEFHTYSILWNAHQIVFFVDQVPLRVHRHT
KATRHVFPRKQGMYMFSSIWNGDNWATRGGLEKTNWAAAPFVSSYKKFHGLGCKWEDQN
TTQSSCAHSNNASARHWWDKPEARTLTKKQREYYRWVNSKYLTYDYCHDQPRYPIKPVEC
SVAPWD

Figure 73: Amino Acid sequence of 306. The conserved Glycoside hydrolase, family 16, domain is underlined.

MAGQRNWFKRIEFIVIFVVCLNSVSARPASFAEDFKVTWADDHVKTRSDNNSIDLILDQNSGA
GFASKNQYMFGLVSMNIKLVAGDSAGTVTAFYMSSDKEEVRDELDFEFLGNRSGQPYTVQT
NVFALGKGGREQRVNLWFDPSLEFHRYSILWNHYHIVFSVDDIPIRVYKNNEARGVPFPKNQ
SMGIFSTLWEADNWATRGGLEKIDWSKAPFVASYRGFEIESCQYPGNASCVVNTSNWWEG
LSYSGLRPNQARLYKWVRTNYMIYDYCKDTPRYPVLPTECNAGI

Figure 74: Amino Acid sequence of 307. The conserved glycoside hydrolase, family 16, domain is underlined.

MEVSSASCLRGYVHFLLTAIICTAISPTVYADIYSDIDVTWGENNAWVLNNGQGLQLSLTNYS
GSGFQSYKEFLFGSVDISMKLVPGNSAGTVTTYYLSSTGEGHDEIDMEFLGNVSGEPYILHT
NIYVNCSADKEQQFYLWFDPTADFHNYSILWNPQQIAIFVDGLPIRVFANNENIGVPYPNEQA
MRVFSSIWNGDQWATQGGRVKIDWSSSPFVASYMNFNTDVCEWNGNGSTSQCWATNWW
NQNNLNYGQQGQLQWVRSNYLIYDYCKDYARFNYQLPAECAQQPQ

Figure 75: Amino Acid sequence of 308. The conserved Glycoside hydrolase, family 16, domain is underlined.

MCSEAMKTAQFLGLFLILLLHSAAMAATPKPVSVPFGKNYGASWGSDHIKEFHGGRKVELLL
NKQYGAGFESKGTYLFGHFSMQIKLVPGDSAGTVTAFYLSSQTAEHDEIDFEFLGNRSGQPY
ILQTNVFTGGKGEREHRIYLWFDPTKDYHSYAVLWNMYQIVFFVDSVPIRVFKNCKNLGIRFP
FNQPMKIYSSLWNADNWATRGGLEKTDWSKAPFTASYKQFHVDACEASVSESVCATQGRR
WWDQVEFRDLDGRQWRFLKWVRKHYTIYNYCTDAARNKKMPPECVRDRDNI

Figure 76: Amino Acid sequence of 309. The conserved glycoside hydrolase, family 16, domain is underlined.

MYDCKRQNTIKPFTGHFHALLVLAFVLIVSVCPNADHVRVSEAARRGHKGRYPRASQFPTVA
FNRGFHVLWGPQHQTIWNDQSGITIWLDRNSGSGFKSLRPYKSGYFSAAIKLQAGYTAGVN
TAFYLSNNEAHPDYHDEIDIEFLGNIPGRPYTLQTNIYVRAGNAGRGRIITGREQQIHLWFDPT
KDFHRYSILWTPLKIIFFVDDIPIRKYRRTNPYTFPARPMWLYGSIWDASPWATDNGKYKVDY
SYQPFVAQYRGFVLA

Figure 77: Amino Acid sequence of 310. The conserved glycoside hydrolase, family 16, domain is underlined.

MAGYEGRRICIYWWVITVMLCRLVVGSQCAAFNDLFYASWAADHVMSQGDLLQLKLDHTSG
AGFASKSTYLFGKVNVQIKLVPGDSAGTVTAFYMSSQGDQHDEFDFEFLGNTSGEPYVVQT
NVYSNGVGNREQRIYLWFDPTANFHSYSFLWNRHQSVFFVDDVPIRVFSNNEKRGVPFPQT
RPMGVYSSIWNADDWATQGGRVKTDWSHAPFISTYTSFNIDACKYSPGSSCTSWWDQPAY
ASLTAKQRMQLKWVHEKYMIYDYCKDPVRFGTPPAECTA

Figure 78: Amino Acid sequence of 311. The conserved Glycoside hydrolase, family 16, domain is underlined.

MSTNGAYLWALVWASVISAGLGLGNGNFDDDFYIMWAPDHVTRLYNGHGVQISMDRQSGS
GFATKKQYLFGKFEMQIKLPPGNSAGTVVAVYLYSNQPNRDEIDIEFLGNVDGKDIIMQTNVF
ANGYDDREQRIKLWFDPTADFHTYTIFWNRYHIVFLVDGFPIRVHQNNAVRGIPFPRMQPMS
LYTTIWNGESWATNGGKTKITWEPYPFVAQFRNFYIDGCEWNGNPRFCKGGSTQNWWNK
RTYAYFNAGDRLKLHWVRKHYLVYDYCNDKVRFKVAPEECRYHI

Figure 79: Amino Acid sequence of 312. The conserved glycoside hydrolase domain of family 16 is underlined.

MAFIRKLPLLVLAFMLVLSVAHIQVSEAAGRPQSSHGTAYPLRSQLSAVKFNQAFDVLWGPQ
HEQVSNDESGITIWLDRNSGSGFKSQRAYDSGYFSAAIKLQAGYTAGVNTAFYLSNNEVHPD
SHDEIDIEFLGTIPGQPYTLQTNIYVRAANGGTERIITGREQQIHLPFDPTSDFHRYSILWTPSKI
VFSVDNVPIRKYSRTGSAFPTRPMWLYGSIWDASSWATDNGKYKVDYNYQPFVARYTDFIL
TDCTQSRAAECS

Figure 80: Amino Acid sequence of 313. The conserved Glycoside hydrolase, family 16, domain is underlined.

MEAPNLSGYLHLVLMIVIIWSTGIYPTVHANFYNDIDIAWGYNNVNIFDNGEELQLSLNNASGS
AFQSKAQFLFGSVDMFMKLVPKNSAGTVTTFYLSSTGDRHDEIDLEFLGNVSGQPYILHTNIY
TNGSGNREQEFYLWFDPTSEFHNYSILWNPQQIVLFVDGLPIRVFGNNEDIGVPYANGQAM
RAYSSIWDGDSWATQGGRVKIDWSYSPFVASYRNFTADVCEWTGSGSSSQCWANIPSNW
WNQAAYESLTYAQQGQLQWVRNNFLVYDYCKDPARFNNQLPAECYRQP

Figure 81: Amino Acid sequence of 314. The conserved Glycoside hydrolase, family 16, domain is underlined.

MGTSGTSSQYSSSAFLQPRSCMNIIAVLIIFTLLNSIIPVHGESEKHIPVTSRFQTINFYNGYSNL
WGPQHQQVSEDESSTTIWLDSSSGSGFKSLEAYKSGFFSAAIKLQAGYTAGVIAALYLSNNQ
EYPGHHDEIDIEFLGTTPGKPYTLQTNVYINGTGDGQVLTGRELKFHLWFDPTEDFHNYSLL
WTPSYIIFYVDDIAIRKYPRRISSTYPLRPLWVYGSIWDASSWATENGKYRADYRYQPFVAKF
SKFILSGCPVSDSTCSATFSNSLISTGTGGLTSQERSRMKSIQTNNLVYNYCKDRERYPTRLP
ECGKRYAPSLINGND

Figure 82: Amino Acid sequence of 315. The conserved glycoside hydrolase, family 16, domain is underlined.

MAFVGCQEGGRVMHCALLCIFVTLCNLLVSSQCASFDDFFYPSWAVDHVMSQGELLQLKLD
NISGAGFASKSTYIFGKANVQIKLVPGDSAGTVTAFYMSSQGDQHDEFDFEFLGNTSGEPYA
VQTNVYSKGVGNREQRIFLWFDPTADFHSYSFLWNRQQVVFFVDDVPVRIFSNNEKRGVPY
PQTQPMGVYSSIWNADDWATQGGLVKTNWSHAPFISTYKNFSIDACQYSSKTNCSSWWDQ
PGYASLDAKQRLKLKWVHEKYMTYDYCKDSARFPTPPAECE

Figure 83: Amino Acid sequence of 316. The conserved Glycoside hydrolase, family 16, domain is underlined.

MASTGSQDDSAYRYTTIIRKQGHYQKHGSRHHLSASTGIQVVMVMAFFLVSSSSAARISSRP
LLRDQNRTATTVDFDQNYDITWGNQLVKFLDNRRSVELRMDQSSGSGFASKNKYLFGYFST
RIKLVPGDSSGTVTAFYLSTQQTSKHDEMDFEFLGNKPGKPHYLSTNVFVNGVGNRESRIRL
WFDPTADFHTYSLLWNRHQILFMVSGVVVRVFKNSETSLGVPYPSSKPMQVIASLWNGENW
ATDGGKSKINWKQSPFIATFEGFDIEGHKCEGDSESSPFCPSSPSSEWWEDLGSKGLSAEQ
MRQLRWVRRNYMDYDYCTDKTRFPKPPPECALNTI

Figure 84: Amino Acid sequence of 317. The conserved Glycoside hydrolase, family 16, domain is underlined.

MLREAMKTAQFLGLFLILLLHSAAMAATPRTPVSVPFGNNYVASWGADHIKEFHGGRKVELL
LNKQYGAGFESKGTYLFGHFSMQIKLVPGDSAGTVTAYYLSSQTAEHDEIDFEFLGNRSGKP
YILQTNVFTGGKGEREHRIYLWFDPTKDYHSYAVLWNMYQIVFFVDSVPIRVFKNCKDLGVR
YPFNQPMKLYSSLWNADDWATRGGLEKTDWSKAPFLASYEQFHVDACEASAPQSACATQ
GRRWWDQEEFRDLDGRQWRYLKWVRKQYTIYNYCTDISRNAKMPPECVRDRDNE

Figure 85: Amino Acid sequence of 318. The conserved Glycoside hydrolase, family 16, domain is underlined.

MKRRAKLLGFGINWRKIVYISSVVNLILSSVESSSFNDNFDISWGTVQLLNNGQTAQLTMDKA
SGSGFQSKDEYLFGSLSMSIKLVSGNSAGTVTSYYMSSDAASHDELDYEFLGNLPGNPYTL
QTNVFANGVGNREQRLNLWFDPTADFHNYSILWNHNQIVFWVDSIPIRVFKNNEETAGIPYP
NSRPMRILSTLWNGENWATDGGRVKIDWSKAPFVASYQSFEVNACSAPSNSSLPCANNWW
EQPEFQSLDESQLGKLDWVRKNYMTYDYCHDTSGRFSTTPAECAFNA

Figure 86: Amino Acid sequence of 319. The conserved Glycoside hydrolase, family 16, domain is underlined.

MKSHISLLGSRRSSPELVYLSLLIILNLCTVKATFSDNFEISWGNVRLLNNGQTVQLTMDKASG
SGFQSKMDYLFGSLSMRIKLISGDSAGTVTSYYMSSEASQHDELDYEFLGNLPGQPYTMQT
NVFASGIGNREQRLKLWFDPTADFHNYSILWNQKQIVFWIDSIPIRVFKNNEAAGVPYPDQRP
MKIISTLWNGEDWATDGGRVKIDWNDAPFIASYQSFEVDACSSSPCVNDWWDQSTFQSLN
QQQLTQLDWVRKNYMTYDYCNDASRYPTPPRECALNP

Figure 87: Amino Acid sequence of 320. The conserved Glycoside hydrolase, family 16, domain is underlined.

MATSFSFYKLVLVVALLLTNGANVVVMLVSADQSLQPPLPSQPVTRYFKTMAFDEGFSNIWS
PDHQNVSQDRNSVTLKIDRYSGAGFKSKKTYLYGFFNAALKLQAGYTAGIVTTFYLSNSDVY
PDLHDELDFEFLGTIPGEPYTLHTNIYGNGSGDGNITSRIGREQRFHLWFDPTQEFHNYTILW
TPHQIMFFVDSIPIRQFRKLKSVRKQYPGKPMSIYATVWDGSDWATDGGKHRANYSYEPFLS
TYTNFIISGCTAGQPDCKPGRLDHRFPPILSKAQKEDLHFVRKNYMIYDYCHDTSRYPKGLPE
CPRSFPRRSPVFRPRHV

Figure 88: Amino Acid sequence of 321. The conserved Plant disease resistance response protein domain is underlined.

MAAPKSSNLSLLALIILLMGGTHHAVGMDLKKTEIEFYMHDVVTASKNFTTMKVAHSPEFGMI
RVIDNALTEDLQQNSKELGRARGMYVQDSFSGVNLLMVLTVIFQAGEHSGSTLCLQGQDGR
KQREISVVGGTGHFRHATGHAILEKQLSMGENAILNFNVTVLHRSELAE

Figure 89: Amino Acid sequence of 322. The conserved Plant disease resistance response protein domain is underlined.

MATKGFLETTIAVSAVLLLVCLHIAEAEVKTKLGREKISHLHFYFHDVVTGKNATAVQVASAPT
TKYSPTGFGAVVVMDDCLTAGPEATSKLVGRAQGIYVSSGQEDFHLLMATTFVFESGMYNG
STLAMIGKNAPLEEVREMPIVGGSGLFRFARGYALAHTHSIDGTTAVVKYNVTVLHY

Figure 90: Amino Acid sequence of 323. The conserved Plant disease resistance response protein domain is underlined.

MANKGYSAATITVAAVLLLSLFYLEAEAEAEAKLKLGREKISHLHFYFHDLVAGKNVTAVKVAS
APTTNSSATLFGAVMVMDDWLTEGPEATSKMVGRAQGIYVSSSQEDFHLLMATTFVFESGK
YNGSTLAMIGKNAALEQVREMPIVGGSGLFRFARGYALARTHAFELNTGNAVVEYNVTVLHY

Figure 91: Amino Acid sequence of 324. The conserved plant disease resistance response protein family domain is underlined.

MGPRFLFLAIIANVLLMFAAGEGEVNMVFYLHDNLTGTNVTAVPVAGLNGSSSNAGKFGTVV
TISDVITRRPEISESDSDNIIGRAQGMYVDTNPVTGLDFLMVFTLIFEDKKYRGSTLEFQGTDR
FAQPRREFAVVGGTGKFRFARGYAVANTESLSGVNAIIKFNGTIRTD

Figure 92: Amino Acid sequence of 325. The conserved Plant disease resistance response protein domain is underlined.

MKGFSAVNTAMAAVVLLVCLYLAVAEAKVKLGPEKISHLHFYFHDLVDGTNVTAVEVASAPTT
DSYFTQFGLVRVMDDPLTEEPKATSKMVGRAQGIYVSSCQHRVQLLMATTFIFESGKYNGS
TLAMVGKNAVFDDVREMPILGGSGLFRLARGYALARTHSLDLKTGNAVVEYDVTVVHY

Figure 93: Amino Acid sequence of 326. The conserved Plant disease resistance response protein domain is underlined.

MAIKGYSSVNITVAVYCYWFVLYLAAAEAEEKIGHGKISHLHFYFHDLVGGKNVTAVEVASAP
TTDSYFTQFGLVRVMDDRLTKGPKVTSKMVGRAQGIYVSSCQHRLQLLMATTFVFESGKYN
GSTLAMVGKNAVFDEVREMPIVGGSGFFRLARGYALARTHSFDLNTGNAIVEYNVTVLHY

Figure 94: Amino Acid sequence of 327. The conserved plant disease resistance response protein family domain is underlined.

MAIKKYNRDVHLCFVCLVLFTVMLQTSNGHRWKKHSLPKPCRNLVLYFHDVIYNGSNAKNAT
STLVGAPQGANLTLLAGKDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSSW
LGFTFVLNSTDYRGTITFSGADPILTKHRDISVVGGTGDFLMTRGIATISTDAYEGDVYFRLCV
NITLYECY

Figure 95: Amino Acid sequence of 328. The conserved plant disease resistance response protein family domain is underlined.

MAIKNHNTAVHLGFIWLVVFSAMLLQSSDAHSYMKRPLPKPCRNLVLYFHDVIYNGLNAMNA
TSTLVGAPQGANLTLLAGRDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSS
WLGLTFVLNSTDYKGTITFSGADPILKKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLC
VNITLYECY

Figure 96: Amino Acid sequence of 329. The conserved Plant disease resistance response protein domain is underlined.

MGSRVLLPAMATATIVIFLLHAAAGERETNLVFYMHDNVSGNNVTAFTVAGLNGTSSDPGKF
GTIVVNWDAATKGAQATGTADPDNIVGRIQGMYVNTNLVTGLDFLMLFTVIFEDMEYKGSTL
EFHGTDKFFAPHRELAVVGGTGKFRFARGYAILTTEVLSGPNAVVKFNTTLRY

Figure 97: Amino Acid sequence of 330. The conserved Plant disease resistance response protein domain is underlined.

MRKFNDNARSNINNIAVAAAATTFLFWVALTIFERHEMKEKTSYLQFYFHDIVSGKNVTAVEV
ASSPTTGSSFTEFGLVRVMDDWLTEGPEPTSKMLGRAQGIYVSSCQEKVHLLMTLTFVFDS
GKYNGSTLAVVGKNAVFDEVREMPIVGGSGFFRFARGYALARTHSLDLTTGNAIVKYNVTVF
HY

Figure 98: Amino Acid sequence of 331. The conserved Plant disease resistance response protein domain is underlined.

MAIENNNRAVYLCFVWLLLFTVLLQASDGHGWNKDPFRRPSRNLVLYFHDVIYDGTNAKNAT
ATLVGAPHGANLTHLTAKDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYNMKNTFNAW
LGFTFVLNSTHYKGTITFAGADPILTKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLRV
NITLYEWY

Figure 99: Amino Acid sequence of 332. The conserved plant disease resistance response protein family domain is underlined.

MAIKNNNRAVYLCFLIWLLVFTLSLRSSDGHGWNKYPFRRPSRNLVFYFHDVIYDGTNAKNA
TSTLVGAPHGAKLTHLAAKDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSA
WLGFTFVLNSTDYKGTITFAGADPILTKYRDTSVVGGTGDFLMARGIATISTDAYEGDVYFRL
RVNITLYEWY

Figure 100: Amino Acid sequence of 333. The conserved Plant disease resistance response protein domain is underlined.

MAKLSAGVASNVNSIAVAATLLLLLLALTAEAKEGYDSKVEEKTSDLHFYFHDTVSGKNVTTM
QVARASGTNSSPTLFGLAVVLDDIVTKGPEPASQLLGRMQGLYTLSGLEERAMQMVVTLVFS
SGQYNGSTLSLVGINRIYHPVREIPIVGGSGLFRLARGYVLARTHSLVQNGNAVVECNVTVLH
Y

Figure 101: Amino Acid sequence of 334. The conserved plant disease resistance response protein family domain is underlined.

MAGKNYSTATIAVAVVLLFVCLHIAAVQAKVKLGNEKISHLHFYFHDLLVGKNVTAVQVASAP
TTNNYFTQFGMVRVMDDWLTEGPEGTSKMLGRAQGIYVSACQEKFQLLMATTFVFESGRY
NGSTLAMVGKNAVLEQVREMPIVGGSGFFRFARGYALAHTHSIDFKTGNAVVEYNVTVLHY

Figure 102: Amino Acid sequence of 335. The conserved Plant disease resistance response protein domain is underlined.

MASRCLFATLATATLVMAAAGEGVLNMAFYMHDHLNRNKDQTAFPVAGVNGSSSEASKFG
TLVVISDMVTKRPQITEYDTENILGRAQGTYVNTNPVTGLDFLMVFSLIFQNAEYNGSTLEIQG
TERFDQPHREYAVVGGTGKLRFARGYAVGTTVSTSGENAVLKINATFCTV

Figure 103: Amino Acid sequence of 336. The conserved Plant disease resistance response protein domain is underlined.

MASGILFPVMAIIVIVSLQPAAGESEMNMVFYLHDNLSGTNVTSFPVAGLNGSSSDAGKFGTL
VVTSDVKTKGPNSGSDNIAGRAQGTYVNTNMVNGLDFSMVFTLIFEDMEYGGSTLVIRGTDR
FDQPQCEYALVGGTGKFRFARGYAVVTTESVSAPNAVLKFNTTFLIPS

Figure 104: Amino Acid sequence of 337. The conserved plant disease resistance response protein family domain is underlined.

MAGFKFLFPAMAVTILVVFLKKAAAAAIEGEMNMVFYMHDNVKGNNVTAIPVAGTNGSSSPP
GHFGTVVVISDVITKFPDVAESESQNIVGRAQGMYINTNLDTRRDFLMVFTVIFNNMEYNGST
LEVQGTDRFDQTQREYAVIGGTGKFRFARGYAVVTTESLSGQNSVLKFNTTLSTL

Figure 105: Amino Acid sequence of 338. The conserved plant disease resistance response protein family domain is underlined.

MAIKSGRALHLSFVWLVLSTALLQTSDVYSWKKKPLRKPYRNLVLYFHDVIYDGTNADNATS
TLVGAPHWANLTHLTAKDHQFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSAWL
GFTFVLNSTDHRGTITFAGADPILTKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLCVN
ISLYE

Figure 106: Amino Acid sequence of 339. The conserved Plant disease resistance response protein domain is underlined.

MGSGVLFSAVAKTTLVLVFVQAAAGISETNMVLYMHDNLTGRNVTSFPVAGLNGSSSDPGK
FGTVVIMSDPITKQPEVTDSDGNNYLGRAQGAYINTNPHTGMEFLMVFAITFESMEYNGSTL
QIQGIERFDQPQREYFVVGGTGQFRYARGYVVCTMEYVSGENAVLRLNTTFRTD

Figure 107: Amino Acid sequence of 340. The conserved plant disease resistance response protein family domain is underlined.

MPVKPSSRELVHLCILWLLVSTVLLQVTDGFVWKKREYEKPNWNKVFYFHDVLYNGNNAEN
ATSAIVAAPQGANLTSLTDNNHFGDLVVFDDPITLDNDMHSPPVGRAQGFYFYDMKNTFSA
WLGFTFVLNSTEHRGTITFAGADPILTKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLR
VNTTLYECYNCLLSASASHDNQ

Figure 108: Amino Acid sequence of 341. The conserved expansin/Lol pl family domain is underlined.

MKIFNNPLLFAVWALSMVSAALSCDRCLRKSKVASFARANINGACGYGNSATSLTARGGLV
MASASAKIYRDGVGCGACYQIRCTDPGVCTKSGVKVLVTDFTKSTQTDFVLSARSFSKLAVA
SKAAQFLKMGTVDIDYKRIPCDYGSQNMTVKVDKSSKYPDYLAVQFLYQGGQTDITAVDIDR
VGSSGWQYMTHKNGAIWGIQNPPIGSLSFRLLVTGGYDGSWVWPTRNLLPAIWRPGSVYD
SGVQITEIAQEGCSPCETGNWTDTRTP

Figure 109: Amino Acid sequence of 342. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MAFLWLVSLGLLSMLRAAHGSGWTSAHATFYGGGDATGTMGGACGYGNLYSQGYGTNTA
ALSTALFNNGFSCGACYEIQCNDDLQWCLPGSIVVTATNFCPPNNALPNDNGGWCNPPLEH
FDLSEPVFQHIAKFRAGIVPVQYRRVPCQRKGGIRFTINGHSYFNLVLITNVGGAGDVEAVSV
KGAKTGWQPMSRNWGQNWQSNSYLDGQSLSFKVTTSDGKTVTSYNVASSNWQFGQTFA
GEQMN

Figure 110: Amino Acid sequence of 343. The conserved expansin/Lol pl family domain is underlined.

MRRTVGLQWPLVPNVCVNVTAFCFVLLLLFSCKEAALGLEHTELNRDDLEWRPATATWYGS
PDGDGSDGGACGYGGLVDQKPLRARVGAVSPVLFKGGEGCGACYKVKCMEKGLCSEKPV
TVVITDECPGGYCAFGRTHFDLSGAAFGRMATNGKTPALLNTGELPVLYRRTLCEYPGKNIT
FHVTEGSTAYWFSILIEYEDGDGDVGAMHLKQADSDAWMEMNHVWGANWCLLGGTPLKAP
FSVRVTTLTSKRTLSARNVIPDHWYPNATYKARLNFED

Figure 111: Amino Acid sequence of 344. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MGALGFLVVGLLLVTTRATMASSWISAHATFYGGSDASGTMSGACGYGNLYSQGYGANTA
ALSTALFNNGLSCGACFQVMCNDDPQWCLRGSVVVTATNFCPPGGWCNPPLRHFDLSRPV
FLKIAKYKAGVVPILYRRVPCHKKGGIRFTINGHSYFNLVLISNVGGAGDVHGVWIKGSRTGW
QPMSRNWGQNWQSNSYLNGQSLSFKVTTSDGRSVTSYNVASVNWQFGQTFSGAQFH

Figure 112: Amino Acid sequence of 345. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MGFLAFIGLFVFNFLSMARFAHGWTNAHATFYGGGDASGTMGGACGYGNLYSQGYGTSTA
ALSTALFNNGLSCGACFAIRCNDDPQWCLPGAIVVTATNFCPPNNALPNNAGGWCNPPLQH
FDLSEPVFQHIAKFRAGIVPVMYQRVPCHRSGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSI
KGSRTGWQPMSRNWGQNWQSNSYLNGQSLSFKVTTSDGRTVTSYNAAPSNWQFGQTFA
GAQIR

Figure 113: Amino Acid sequence of 346. The conserved expansin/Lol pl family domain is underlined.

MATRTPNFFLFCSLGFMLIVTVPSPVLSCSSCVYQSKLAYYAYSGAVNVGACGYGSFAAKLY
GGNVGAASSDLYRNGVGCSACYQIRCTDPKLCNKSGTTIVVADFTQNNQTYFVVSRSTFSS
LAIADKGSQLIKGGIIDIEYKRVPCQYKDQNLVVRVDGSSQYPHYLAVQFLYQGGQTDIVSVD
VAQVGTSGWHYMTRNHGAVWEIQKPPGGALQFRFVVTSGYDGKWLWAKKAVLPSDWKSE
GLYDSGIQISDVALENCNPCNENNSGWADSSWIYV

Figure 114: Amino Acid sequence of 347. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MATVKLATIFGLWWIASTAYALDYGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGTN
TAALSTALFNNGATCGACYQMKCNQQSDPQWCLPGTVTVTATNLCPPNSALPNDNGGWC
NPPLQHFDMAQPAFQQIAIYRSGIVPIMFRRVPCVRKGGVRFAINGHSYFNLVLITNVGGAG
DVEAVSIKGSNTGWQAMSRNWGQNWQSNSYLNGQTLSFQVTTSDGRTITSYNVASANWQ
FGQTFEGLQF

Figure 115: Amino Acid sequence of 348. The conserved expansin domain is underlined and the Expansin/Lol pl domain is in bold.

MAPVKLATIFGLLWIVGTAYALDYGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGTN
TAALSTALFNNGATCGACYQMKCNQQSDPQWCLPGTVTVTATNLCPPNCWNVNSNCRLR
GQRRTWATMDSNSLPARISSQRPPRNHRSKPQNQPVSYRTTLQRKVVSVQRAPMQLGAD
NCPPSDAGMTSATDTHRKVSLG

Figure 116: Amino Acid sequence of 349. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MNSGRSLHSDHLFGCKMAPVKLVTMFSFLWVAGAAYALDSGWQSAHATFYGGSDASGTM
GGACGYGNLYSQGYGTNTAALSTALFNNGATCGACYQMKCNHHSDPQWCLPGTVTVTAT
NLCPPNSALPNDNGGWCNPPLQHFDMAQPAFQHIAIYRSGIVPIIFRRVPCVRKGGVRFTING
HSYFNLVLITNVGGAGDVEAVSIKGSNTGWQAMSRNWGQNWQSNSYLNGQALSFQVTTS
DGRTITSYNVAPANWQFGQTFEGLQF

Figure 117: Amino Acid sequence of 350. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MAPLKLATMFSFLWIAGTAYAQDSGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGT
NTAALSTALFNNGATCGACYEMKCNDQSDSQWCLPGTVTVTATNLCPPNSALPNDNGGWC
NPPLQHFDMAQPAFQQIAIYRSGIVPIMFRRIPCVREGGVRFTINGHSYFNLVLITNVGGAGD
VEAVSIKGSNTGWQTMSRNWGQNWQSNSYLNGQTLSFQVTTSDGRIITSYNVAPANWQF
GHTFEGLQF

Figure 118: Amino Acid sequence of 351. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MAPLKLATMFSFLWIAGTAYAQDSGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGT
NTAALSTALFNNGATCGACYEMKCNDQSDSQWCLPGTVTVTATNLCPPNSALPNDNGGWC
NPPLQHFDMAQPAFQQIAIYRSGIVPIMFRRIPCVREGGVRFTINGHSYFNLVLITNVGGAGD
VEAVSIKGSNTGWQTMSRNWGQNWQSNSYLNGQTLSFQVSTSDGRIITSYNVAPANWQF
GQTFEGVQF

Figure 119: Amino Acid sequence of 352. The conserved expansin/Lol pl family domain is underlined.

MKRFRCMSPCKFSAWLVIGAVSVFLCVKASWALEEEELEWHPATATWYGSPDGDGSDGGA
CGYGNLVDVKPYRKRVGAVSPVLFKGGEGCGACYKVKCTDERMCAKRAVTFVVTDECPGG
PCAFGKTHFDLSGSAFGRMAIADKTTTILNSGEIPVLYRRTLCEFPRKNVTFHVNEGSTAYWF
SILIEYEDGDGDVGAVHLREADSDEWMAMQHSWGANWCLLGGPMKAPFSLRVTTLSSNRT
LSARNIIPQNWYPTASYRSRLNFDR

Figure 120: Amino Acid sequence of 353. The conserved expansin/Lol pl family domain is underlined.

MKRFRCMSPCKFSAWLVIGAVSVFLCVKASWALEEEELEWHPATATWYGSPDGDGSDGGA
CGYGNLVDVKPYRKRVGAVSPVLFKGGEGCGACYKVKCTDERMCAKRAVTFVVTDECPGG
PCAFGKTHFDLSGSAFGRMAIADKTTTILNSGEIPVLYRRTLCEFPRKNVTFHVNEGSTAYWF
SILIEYEDGDGDVGAVHLREADSDEWMAMQHSWGANWCLLGGPMKAPFSLRVTTLSSNRT
LSARNIIPQNWYPTASYRSRLNFDR

Figure 121: Amino Acid sequence of 354. The conserved expansin domain is underlined and the Expansin/Lol pl family domain is in bold.

MQTRRGSWVAYLLLLLLLNLGWWKQLIIMPTSAAYANDGWKYAFATFYSESDALGTMAGAC
GFGDLYRQGYGVNTAALSSVLYNGGQACGACFELRCVEDPLYCHPGTSIVVTATNFCPPNY
GLPGEDGGWCNPPRQHFVLPVTAFEKIAMWKIGTMNVQYRRVRCAKVGGMRFAINGKDFF
LTVLISNVAGDGAVSGVKVKGSKTGWLSMGTNWGQNWHVNADYRGQALSFEVTTSDGKT
VTSYNVAPSDWQFGHTYKGKQFS

Figure 122: Amino Acid sequence of 355. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MLTSGFVLVAVAIIFANKFVSAHDYNGGWYYAHATFYGGADASGTMQGACGYGNLYSQGY
GTNTAALSTVLFNSGASCGSCFEIKCVDDPQWCLPGSPSIVVTATNFCPPNYALPNDNGGW
CNPPREHFDMAMPAFEQIGIWKAGIVPVQYRRVACVKEGGMRFTINGNYYFYLILVTNVGGD
GVVADVKVKGSNTGWLPLSRNWGQNWQCNTILKGQALSFRVTSSGGRTVTSYNVAPSH
WQFGQTFEGNQF

Figure 123: Amino Acid sequence of 356. The conserved pollen allergen/expansin family C-terminal domain is underlined.

MATQTPVVFVLYCILGVNLLIVFPSLALGCTSCVHQSKLAYYAYPGAVDVGACGYGSFAETLY
GGNVGGSSRDLYRNGVACGACYQMRCTDSKLCTKSGTTIVVTDFTESSQTDFVVTRSTFSS
MALPDHGDQLLKAGIIDIEYKRVPCQYKNQNMSVKVDKLSRYPNYLAVQFLYQGGQTDIVSV
DVEQVGSSEKHDLKRNYGAVWDIENPPEGALQFGFVIVSGYNGKRVWPTKSVLPSDWKVG
GVYDSGLQTNDVSLEKCSPCDHNDRGWGDSRIP

Figure 124: Amino Acid sequence of 357. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MISMTSMVRVKSVALVSMSTIIWLITRAHGYGDWESAHATFYGGSDASGTMGGACGYGNLN
SQGYGTNTAALSTALFNDGLSCGACYEMQCNDDAQWCLPGTVTVTATNFCPPNNALPNDN
GGWCNPPLQHFDMAEPAFQQIAKYKGGIVPILYRRVPCVRKGGIRFTVNGHSYFNLVLITNV
GGPGDVHAVSIKGSRTGWQPMSRNWGQNWQSNSYLNGQSLSFQVTTSDGKTFVSYNAA
PSSWQFGQTFEGCQV

Figure 125: Amino Acid sequence of 358. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MRSMELVKSIALASLLTFIWLLTGAHGYGGWESAHATFYGGSDASGTMGGACGYGNLYSQ
GYGTNTAALSTALFNDGLSCGACYEMRCNDDPQWCLPGTVTVTATNFCPPNNALPNDNGG
WCNPPLQHFDMAEPAFLKIAKYRGGIVPILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGA
GDVHAVSIKGSRSGWQPMSRNWGQNWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSN
WQFGQTFEGSQV

Figure 126: Amino Acid sequence of 359. The conserved pollen allergen/expansin family C-terminal domain is underlined.

MAIGIIERQAASLVKGFVIALVFSISVAEGSGYTSSGWTSGHATFYGGSDASGTMGGACGYG
DLYSTGYGTKTAALSTALFNSGATCGACFQIQCDISKDPQWCLPGPKSITITATNFCPPNYAL
PSNDGGWCNPPLMHFDMAQPAWEQIAIYSGGIVPVQFRRVPCTPVGGVRFTINGRSYFELV
LLSNVGGAGDISAVSIKGSNTGWQPMSRNWGVNWQSNSYLSGQSLSFQVTTSDGNSITFY
NVAPSNWQFGQTFATSQQFN

Figure 127: Amino Acid sequence of 360. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MQSPLKSRVRYVLMVLAIIFAQTLAAADDCDGDWNSAHATLYGGGDAAGIMAGACGYGNLY
SQGYGTNTAALSAILFDSGAACGACFEIKCVDDSQWCLPGSPSVVITATNFCPPNYALSNDN
GGWCNPPREHFDMAMPAFEQIAIWKAGIVPVQYRRVRCAKGGGIRFTIHGNRYFYLILITNV
GGDGDVAEVMVKGSNTDWLPLTRNWGQNWQSNTNLQGQALSFQVSSSSGHTITSYNVA
PSDWQFGQTFQGNQF

Figure 128: Amino Acid sequence of 361. The conserved Glycoside hydrolase, family 16, domain is underlined and the Carbohydrate-binding WSC domain is in bold.

MFSTKFFAAAAATFSLIRFSTAVYDPSSQRNLAMYWGSGSDQLDLAHFCDETNVDIIPIGFINF
FPPQANGLVAETFGDQCWDGNYTGPGYDGTNNPNDNFLYEQCPNLQRDLYYCQQNTNKKI
LLSLGGAVGNYYLNGPSDGEYLAEFLWGAYGPYNESWTGVRPLDRGYYNTNLTEHIDFDGF
DFDIEQTTPDQQAGYIACIKRLRQLFIEHKAVNPCSKDYIISGAPQCPLDEPYMSTAIAGAQFD
VLWIQFYNNGANGCTARNYTDSKALGKTSGFNYDSWVTKVNGGASAGAKLYIGLLAGQAAS
EFSPNDYIDGPAIQTLVSQYHSHPQFGGIMLYEATVAENNAQFYNTVKGILNDTALAGTVTSS
AKVCSSTTSTSSKTSSTSTSTTSTSSKVTTTSSSTSSKASTTSSSSSTSSSSSTSSTSSSKTS
SSSSSSSSTKTSTSSSVSSTSTTSSSSSSSSSSLSSSSSSSSTSAYPTTSSSSVISSTTSAS
STSSSSSSSSEISSSTSVSSTSSETPTSTPTPTTVPSVG**SCTYLGCYTEATTTRALSGAVYDN**
YTLMSVEICAGFCTGFTYFGVEYGGECYCGNEFGEGSVVSPPIDCSMTCAGTPTELCGAGD
RLDVYSCAGSATTTSSSVSGSSTSSIESSTSSSVSISSSSSVVSTSSSSVVSSTSSEVTPTTS
STSSSVSSTSSLSSTSVYSDSSSSVTSTSTSSLSSSSSVSETLTSTSSSSIYSPTITSTAYTNS
SSAIVTPTSSLYTNSSSVITTSSSSSSSKSVCTRKTHTSSGSVSITSSYSVSGTATSISSYSVSS
GSSSSSASGIISTPSSSLSGSATSSAQGTATSASTTQYTTSTVYTTSVHTITSCAATVTNCPAR
STVLTTETIALYTTVCPVTATETGKGVPTTSSPVKPTSSGSGSGETTSYTTSTVYATSVYTITS
CAPTVTNCPARIGSVTTETIALYTTVCPVTATETGKVAPSSTPSASSPVLPGKGGKSSSSAAG
YPVSGTESVKHTTISSTT

Figure 129: Amino Acid sequence of 362. The conserved calreticulin domain is underlined, the Calreticulin family signatures 1 and 2 are in italics and the Calreticulin family repeated motif signatures are in bold.

MAMAGSTGRRQQQLLLLALALSSLAAIASAAVLFEERFEDGWETRWVKSDWKKDENMAGE
WNYTSGKWNGDSDDKGIQTSEDYRFYAISAEYPEFSNKDKTLVFQFSV*KHEQKLDCGGGY*
*MKLL*SGDVDQKKFGGDTPYS*IMFGPDICGYSTKKVHAILTYNGTNQLDQKGCSLTDQLTHVY*
TFVLRPDATYTILIDNVEKQTGSLYSDWDLLPPKQ**IKDPEAKKPEDWD**DKEYIPDPEDKKPEG
YDDIPKE**IPDSDAKKPEDWD**DEEDGEWTAPTIANPEYKGPWNPKKIKNPNYQGKWKAPMID
NPDFKDDPELYVFPKLKYVGIELWQVKSGTLFDNVLICDDPEYAKKVAEETWGKNKDAEKAA
FDEAEKKREEEEAKDEPVDSDIEDEDDDADADDAEDDSDSVIKAEADESAESADSKDEVKD
EL

Figure 130: Amino Acid sequence of 363. The conserved calreticulin domain is underlined, the Calreticulin family signatures 1 and 2 are in italics and the Calreticulin family repeated motif signatures are in bold.

MMEGRRIRLLARALTVLLLSFQICASDVIFHESFDESFEGRWVVSEKEEYQGVWKHSKSEGH
DDYGLLVSEKARKYAIVKELDDVVSLKDGTVVLQYEV*RLQDGLECGGAYLKYL*RPQDAGWK
VKEFDNESPYTIMFGPDKCGATNKVHFIFKHKNPKTGEYVEHHLKHPASVPYDKLSHVYTAV
LKPDNELRILIDGEEKKKANFLSAEDFEPALIPPKT**IPDPDDKKPEDWD**ERAK**IPDSDAVKPDD**
WDEDAPMEIVDEDAVKPEGWLDDEPEEI**DDPEATKPEDWD**DEEDGEWEAPKIDNPKCETA
PGCGEWKRPTKSNPAYKGKWHAPLIDNPNYKGIWKPQEIPNPDYFELERPNFEPIAAIGIEIW
TMQDGILFDNVLIASDEKVAESYRETAWKPKFEVEKEKQKEEDKATGSDGLSAIHKKVFDVL
YKVADVSFLEPYKPKILELIEKAEEKPNIAIGVLGSIVVVILTVFFKILFGGKKPVANVPEPRREA
AAETSNNQGSQGDKEDEDEKEDAGDAAAAAAPRKRPNRREI

Figure 131: Amino Acid sequence of 364. The conserved calreticulin domain is underlined,The Calreticulin family signatures 1 and 2 are in italics and the Calreticulin family repeated motif signatures are in bold.

MEGSRIPRLVPALALVLISFAFLQIRASDVIFYDSFDQPFVGRWVVSVKDDYTGEWKHSKSEG
HDDYGLLVSEKARKYAIVKELDEIVSLKDGTIALQYEV*RLQNGLECGGAYLKYL*RPQDAGWK
VKEFDNDSPYT*IMFGPDKCG*STNKVHFIFKHKNPKTGEYVEHHLKFPPSVPYDKLSHVYTAV
LKPDNELRILIDGEEKKKANFLSAEDFEPPLIPPKT**IPDPDDKKPEDWD**EQEK**IPDPDAVKPD**
DWDEDAPMEIVDEDAVKPEGWLDDEPEEI**DDPEATKPEDWD**DEEDGEWEAPKIDNPKCEL
APGCGEWKRPMKRNPAYKGKWHAPLIDNPNYKGI**WKPQE**IPNPDYFELERPQFDPIAAIGIEI
WTMQDGILFDNILIASDEKVAETYRETTWKPKFEVEKEKQKEEDKDSDSPGLSAVHKKAFDV
LYMIADVPFLDPYKPKILDLIEKAEKQPNITIGVLVSIVVIILTLFFKILFGGKKPAVNVPEPRSEA
APETSDGPGSSGDKEDEDEDEDEDEKEETAAAPRRRSIRREA

Figure 132: Amino Acid sequence of 365. The conserved calreticulin domain is underlined.

MKALLFLSFVLFVAVATATVHFQEEFDAGWEKRWVYSTADDASGSAGKFTATPGQYYGDA
QKDSGVQTSTDARFYKASAQFPKFSNKDKPLVLQYSVKNEQELDCGGAYLKLSPPGVDQKS
LTGETPYNIMFGPDVCGYSTRRVHFIFNYKGTNHLIKKTVAPSSDKLTHLYTAIINPDQTYEIRI
DNEKKESGKLVDDWDFLPPKEINDPSISKPADWVEEKEIPDPEDKKPEGYDDIPKEIPDPDAK
KPEDWDSELDGEWEPPTIPNPEYKGEWHPKLIPNPAYKGPWVHPQIPNPDYHYDDSIYAFE
HEFVAFEIWQVKSGTIFDHILVTDSLEEAEAFATGHFAAQQKAEKAMYDKQEEEKQEKEKAE
REAEKQKLEEEGKKEDDDEDEDEEEEEDEGKGHSHDEL

Figure 133: Amino Acid sequence of 366. The conserved calreticulin domain is underlined,The Calreticulin family signatures 1 and 2 are in bold.

MAGTERRQQLLFLLPTSPLCLALLLLLSSLARLALSEVIFEERFLDGWKRRWVVSDWKKSEG
KAGTFKYTAGKWPGDPDDKGIQTIKDAAHSAISAKLPEFSNKNRTLVLQYSI**KFEQEIECGGG**
YIKLLSGFVNQKKFGGDTPYSLMFGPDICGTQTKKLHVILSYQGQNYPIKKELECETGKLTHF
YTFILRPDATYSILVDNRERDSGSMYTDWDILPPRRIKDVNAKKPADWDDREYIEDPNEVKPE
GYDSIPSEIPDPKAKEPDNWDEEADGVWKPPKVPNPAFKGPWKRKKIKNPNYKGKWKIPWI
NNPEFEDDPDLYVMKPIQYVGIEVWQVKAGAIFDNVLICDDPEYAKQVVEEVFANREAEKEA
FEEAEKVRKAQEEEEARRAREEGERRRRERGYDRRYRDRYRDKYRRHDRRDYMDDYHDE
L

Figure 134: Amino Acid sequence of 367. The conserved sucrose synthase domain is underlined.The conserved group 1 glycosyl transferase domain is in bold

MAAPKLGRIPSIRDRVEDTLAAHRNELVSLLSRYVAQGKGILQPHHLLDELENIISEDEGKSSL
SDGPFSEVLKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVHELSVEQLTVSEYLGFKEELVD
GKSEDSFVLELDFEPFNASFPRPNRSSSIGNGVQFLNRHLSSIMFRNKDCLEPLLNFLRAHKY
KGHTLMLNDRIPSISRLQSALAKAEEYLSKLPTDTPYSEFEYMLQGLGFERGWGDTAERVLE
MIHLLLDILQAPDPSTLETFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRAL
ENEMLLRIQKQGLDIAPKILIVTRLIPDSKGTTCNQRLERVSGTEHSHILRVPFRSDQGILRKWI
SRFDVWPYLETFALDAAHEITAELQGFPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTK
YPDSDIYWKKFDEKYHFSCQFTADLLAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGL
YRVVHGIDVFDPKFNIVSPGADMCIYFPYSEKQKRLTALHGSIEKLLYDPEQNDEHIGSLSDR
SKPMIFSMARLDKVKNMTGLVECYAKNSKLRELANLVVVAGYIDVKKSKDREEIAEIEKMH
ELMKEYNLDGQFRWMAAQTNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGL
PTFATCHGGPAEIIEHGVSGYHIDPYHPDQAATLLADFFEQSKRDPNHWTKISAAGLQRIYE
RYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRELVKTVPVAADEPH

Figure 135: Amino Acid sequence of 368. The conserved sucrose synthase family domain is underlined and the group 1 glycosyl transferase domain is in bold.

MAAPKLGRIPSIRDRVEDTLAAHRNELVSLLSRYVAQGKGILQPHHLLDELENIISEDEGKSSL
SDGPFSEVLKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVHELSVEQLTVSEYLGFKEELVD
GKSEDSFVLELDFEPFNASFPRPNRSSSIGNGVQFLNRHLSSIMFRNKDCLEPLLNFLRAHKY
KGHTLMLNDRIPSISRLQSALAKAEEYLSKLPTDTPYSEFEYMLQGLGFERGWGDTAERVLE
MIHLLLDILQAPDPSTLETFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRAL
ENEMLLRIQKQGLDIAPKILIVTRLIPDSKGTTCNQRLERVSGTEHSHILRVPFRSDQGILRKWI
SRFDVWPYLETFALDAAHEITAELQGFPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTK
YPDSDIYWKKFDEKYHFSCQFTADLLAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGL
YRVVHGIDVFDPKFNIVSPGADMCIYFPYSEKQKRLTALHGSIEKLLYDPEQNDEHIGSLSDR
SKPMIFSMARLDKVKNMTGLVECYAKNSKLRELANLVVVAGYIDVKKSKDREEIAEIEKMH
ELMKEYNLDGQFRWMAAQTNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGL
PTFATCHGGPAEIIEHGVSGYHIDPYHPDQAATLLADFFEQSKRDPNHWTKISAAGLQRIYE
RYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRELVKTVPVAADEPH

Figure 136: Amino Acid sequence of 369. The conserved sucrose synthase domain is underlined.The conserved group 1 glycosyl transferase domain is in bold

MAERLLTRVHSLRERLDETLLAHRNDILAFLTRIEAKGKGILQHHQLIAEFEAISEEHRKKLSEG
AFGEILRSSQEAIILPPWIALAVRPRPGVWEYIRVNIHALVVEELQVTEFLHFKEELVNGNLNG
NFVLELDFEPFTAQFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLEFLQVHCYKGKNM
MVNTRIQNVFSLQHVLRKAEEYLSALKPETPYSQFEHKFQEIGLERGWGDTAERVLEMIRLLL
DLLEAPDPCTLENFLGRIPMVFNVVIMSPHGYFAQDDVLGYPDTGGQVVYILDQVRALESEM
LHRIKQQGLDITPRILIVTRLLPDAVGTTCNQRLEKVFGTEYSHILRVPFRTEKGMVRKWISRF
EVWPYLETYTEDVANEIAGELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPE
SDIYWKKFEEKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVV
HGIDVFDPKFNIVSPGADMSIYFSYTEEKLRLKSFHAEIEELLFSDVENKEHLCVLKDRNKPIL
FTMARLDRVKNLTGLVEWYGKNTRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYGLIET
YNLNGQFRWISSQMNRVRNGELYRYICDMRGAFVQPALYEAFGLTVVEAMTCGLPTFATC
KGGPAEIIVHGKSGFHIDPYHGDQAAETLANFFEKCKVDPSHWDKISQGAMQRIKDKYTWQ
IYSERLLNLTAVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVE

Figure 137: Amino Acid sequence of 370. The conserved sucrose synthase domain is underlined and the Glycosyl transferase, group 1, domain is in bold.

MDSSPALKTTEPVPDSMPEAPSQSRYHMKRCFAKYMEKGRRIMKFHHLMDELESAIDAKTE
RELVLGSDLGYILCYTQEALVVPPHMAFAVRRSPGNWEYVKVSSDSLSVEGMSAADYLKFK
AMIYDEEWAKDENALEVDFGALDFSVPHLTLSSSIGNGVDFISKYLSSKLSGTPDSAQPLVDF
LASINYQGENLMINETLDTAPKLQMALIVAEASLASVPKDTPFQDFEMRFKEWGLEKGWGDT
AEKVKDTIRWLSEVLQAPDPTNMEKFFSRLPMIFNVVIFSPHGYFGQSDVLGLPDTGGQVVYI
LDQVRALEEELLLRIKEQGINAKPQILVVTRLIPDARGTKCNQELEPIIGTKHSNILRVPFRTEK
GVLRQWVSRFDIYPYLERFTQDATIKILDQLEGKPDLIIGNYSDGNLVASLMASKLGTTQGTIA
HALEKTKYEHSDVKWKELDPKYHFSCQFIADTIAMNATDFIITSTFQEIAGSHDRPGQYESHA
AFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYSEKQKRLTQLNRAIEELLYSRVDNDEH
IGYLADKKKPIIFSMARLDTVKNITGLVEWYGKNARLRSLVNLVIVGGFFDSSKSKDREEMA
EIRKMHDLIAKYKLKDQIRWIAAQTDRYRNGELYRWIADTRGAFVQPALYEAFGLTVIEAMN
CGLPTIATNQGGPAEIIVDGVSGFHIDPNHGEESSNKIADFFEKCKVDNEYWNKISAGGLKRI
NECYTWKIYANKMLNMGCIYTFWRQLNKEQKQAKQRYIQMFYSLQLRNSMKTVPIKTDEPE
QAAPKPPPKVQPTMSTRRTQSRIHK

Figure 138: Amino Acid sequence of 371. The conserved sucrose synthase family domain is underlined and the group 1 glycosyl transferase domain is in bold.

MADRVLNRSHSPRERLDEALFADRNDCLVFLSRLKAKGKGILQRHQILAVFEAIPEESRARLL
DGAFGKVLKSTQEAIVSSPWVALAVRARPGVWEHIRVNVHALLLEHFQVDEYLHFKEALVDG
SLNPDSEPLTATFGRPTLSTSIGNGVECIRRSLSDKLFPDKESLHPLLEFLQVHSYKGKNMMV
NARVQNVSSLQPVLRQAEEYLNTLKPETPFPKFEHKLQEIGLEQGWGDTAEWVLDMIQDLL
DLLMVPNPGALEKFLGRIPMVFDVVIVSPHGYFAQDNVLGYPDTGGQVIYILDQVRALETEML
HRIKQQGLDITPRILIITRLLPDAVGTTCGQRLEKVFRTKHSRILRIPFRDKKGIVSEWISRFKV
WPYLERFAEDVAKELRGELQRNPDLIIGNYSDGNIVAYSLAKKLGVTQCTIAHALEKGKYPGS
DIYWKKFDNEYHLSCQFTADLLTMNYTDFIIASTSEEIAGSKDTVGQYESYTNSTLPGLYRVV
HGINVFDPKFNIVSPGADMSIYFPYTEQKRRLKSFHPEIKELLFSDVENKEHLCVLKDKNKPII
FTMARLDRVKNLTGLVEWYGKNPKLREVANLVVVGGDRRKDSKDLEEQSEMKTMYDLIE
KYKLNGQFRWISSQTNQVRNGELYRYICDTKGVFVQPAIYEAFGLTVVEAMTCGLPTFATC
NGGPAEIIVHGKSGYHIDPYHGDQAAELLVEFFEKCKVDKSHWDKISKGAMQRIEEKYTWKI
YSERLLNLTAVYGFWKHVTSLDRRESRRYLEMFHALVYRPLAQSVPPAVE

Figure 139: Amino Acid sequence of 372. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASFLSNPSSLSFLLLLLLLHASRLAFSQSFVGVNYGQVADNLPPPESTAKLLQSTTIGKVR
LYGADPAIIKALANTGIGIVIGAANGDIPSLAADPNAAGQWVGANILPFYPASKITLVTVGNEVF
MSNDENLMSQLLPAMQNMQRAITAAGLGGKVKVSSVHAMSLLSQSDPPSSGRFHPSFEAR
MRDVLQFQRENGSPLPINPYPFFAYQSDPRPETLAFCLFQPNAGRVDSGTGIKYMNMFDAQ
VDAVYSALKALGYKDIEIMVAETGWPYNGDSNEVGTSVENAKAYNGNLIAHLRSLVGTPLMP
GKSVDTYIFALYDEDLKPGPTSERSFGMYKPDLTMTYDIGLAKSSQTPASPKAPVTPTPVTPT
PKPTGPGWCVPKSGVSDAQLQASLDYACSNNIDCSPIQPGGACFDPNTIASHAAFAMNLYY
QTLGRNPWNCDFSQTATLTTNNPSYNGCVYPGGST

Figure 140: Amino Acid sequence of 373. The conserved glycoside hydrolase, family 16, domain is underlined.

MASSSSLLRALFLLLSLSDSATQILGLEFGINYGQIADDLPSPSRVATLLGSLNVSRVKLYDAD
PNVLQAFSNSNVDFIIGIGNDNLQNMTILANAQDWIQQHVQPYIGQTQISCIVVGNEVLNSSN
NQWMPYLVPAMKTVYSALSNLGLNKQVAVTTAHSLNILATSYPPSAGSFWPNLAQYLQPLLN
FQAQINTPFLINAYPYFAYKGSPSEVSLNYVLFQPNEGLTDPVTNLHYDNMLYAQIDAVYSAIK
AMGHTDITVRISETGWPSKGDDDEAGATLENAHIYNENLLQRIEQKQGTPAKPSVPIDIYVFA
LFNENLKPGPTSERNYGLYYPDGTPVYSLGLQGYLPELYSATGTRPGLYSATGTRVLPFSVV
LVSIMTFLMNI

Figure 141: Amino Acid sequence of 374. The conserved glycosyl hydrolases domain of family 17 is underlined.

MASSALPPSNLLLLLLLLLISGLACVAAMAAPIGVNYGQIANNLPSPDHAVTLVKSIGATRVKLY
DADSRVLCAFAHTGVEFTVGLGNEFLVQMKDPKNALSWVKSNVQSFLPDTNITTIAVGNEVF
TSNDTSLRDLLMPAMKNVHDALASLGLDKQVTVTTAHSLAILETSYPPSTGRFRRDVASRVS
QVLDFQCQTGSSFLINAYPYFAYKANPKQVPLDFVLFQASQGITDPSTGLNYENMLFAQIDAV
HSALAAVGYANMTVHVSETGWPSRGDDDEVGATPENAKKYNGNLIKIVKQKKGTPMKPNSD
LNIYVFALFNENMKPGPMSERNYGLFKPDGTPSYTLSSGGGGGGGGGGTSNGTSSGGFGG
GGGGGGSASDGTPPAPIGYLSVSSGANELRSLGAACLMLALFLIKLVF

Figure 142: Amino Acid sequence of 375. The conserved glycosyl hydrolases domain of family 17 is underlined and the glycosyl hydrolases family 17 signature is in bold.

MAKSSPFAADSLSIPSMLLFALMVFTILHRTAAQTGVCYGMLGNNLPSAQEVVALYKQNNIPT
MRIYDPNPQALQALGGSNIELVLGLANPDLQSIASSQANASAWVQNNIKNHGNVRFKYVAVG
NEVKPSDSFAQFLVPAMRNIRTALAGAGLEQIKVSTSVDTGVLSESFPPSKGVFRSDYMPLL
GPIIGLLVETQAPLLVNVYPYFSYIGDPQGIRLDYALFTAPSVVVTDGALGYQNLFDASLDAVY
SALEKADGGSLKIVVSETGWPSAGGGEATTLDNARTYNTNLAKHVKGGTPRRPRGPIETYV
FAMFDENQKSPETEKYWGLFLPNKQPKYSIDLN

Figure 143: Amino Acid sequence of 376. The conserved glycosyl hydrolases domain of family 17 is underlined.

MANPHLPPLSLLLLLLLLGSAHGVSAVGVNYGTIGNNLLPPKKVAQLLQSTLIDRVKIYDSNPD
ILDAFSNTGIDLVVAVENPLVANLSKDPSAAAEWLASRVAPFLPATSVVSVAVGNEYLTSGDD
KLEPNDVVQAMQNLHAALVARGLDRKIKVSTPHSMAVLAASFPPSSSTFAMTLLPTMTSIVQ
FLADTGAPFMINAYPYFAYRDNPSSVDLEYALLGNKTTVRDPKGYVYTNMLDAQIDAVRSAIG
ALGFGNRSIEITVSESGWPSKGEDGDKAATPENARTYNTRLIERAQANRGTPMRKEERVEIF
VFALFNENKKEGGVAERNFGLFAGDGSKAYDVDLSCQFCSGGVSGFGEKAAGSSGVALRG
PSVWCVAKPHAEEGVLQAVVDFCCGAGGVDCREVYEGGDCYAPEKVHAHASYAMNAYYQ
MHGRNYWNCDFKGTGLVTFGDPSYGRCRYSQQ

Figure 144: Amino Acid sequence of 377. The conserved glycosyl hydrolases domain of family 17 is underlined.

MQMGLLHLLVFSSLLLALCSAEILSKVGVNYGQLGNNLPSPTRSVWLIKHQLKAQRVKIYDAN
PSILRALKHTGIQVSVMVPNELINAIAVNQTLADSWVGSNVVPFHPATKIRYLLVGNEILSSAD
NTTWFNLVPAMRKVKKALKRHKVHHKVKVGTPLAMDVLATSYPPSSGSFRPDVSDRVMKP
MLQFLNRTKSFFFIDVYPYFAWSSDPKTIDLNYALFESKNVTVKDPGTGLVYTNLFDQMVDA
VTFAMKKLGYPNIPIWIAETGWPNAGDYDQIGANIYNAATYNRNVVKKLSARPAIGTPARPG
WVLPSFMFALYNENQKTGPGTERHFGLLYPNDSFVYDIDLSGETPDTEYGKLPAPTNNEPYE
GKIWCVVAKRANRSALASALSYACSQGNATCGPIQPGKACHRKGSLVRQASYAFSSYWAQ
FRKTGGSCYFNGLATQTIEDPSYGSCEFPAVTL

Figure 145: Amino Acid sequence of 378. The conserved glycoside hydrolase, family 17, domain is underlined.

MMGERGLGRILLLLLPFLPIALGAFVGINIGTDVTNLPEASDIVAVLKSNEITHVRLYNADAHML
KALANSGINVMVGVTNEEVLGIGEYPATAAAWINKNVAAYLPATNITAIAVGSEVLTAIPHAAP
VLVPAMNNLHKALVASNLNFVVKVSTPQSTDVIPKPFPPSAAAFNSSWNSTLYQLLQFLKNT
NSSYMLNAYPYYGYTQGNGIFPLDYALFRSLPSVKQIVDPNTLFHYSSMFDAMVDATYYSIEA
MNFSGIPVMVTETGWPWFGGSNEPDATAENAQTFNNNLIKRVLNGSGPPSQSDVPINTYIYE
LFNEDKRPGPVSEKNWGVFFTNGTSVYPLSLGTSGRITGNSSGIFCVAKQDADSDKLQDGL
NWACGQGHANCAAIQEGQPCYSPNTVANHASYAYNDYYQKMQGVGGTCDFQGTAMTTTV
DPSYGSCKFTGSSNSSSTVTTPVASAPFSPIGGGSPTSAVLASKLKYVICTISVVLTLL

Figure 146: Amino Acid sequence of 380. The conserved glycosyl hydrolases domain of family 17 is underlined and the glycosyl hydrolases family 17 signature is in bold.

MAISKLAPLLFLALVFLSIAEPGEPSLFADIKQGQDPDKEPYVGVNVGTDVSHLLSPPNLVSFL
QVQKITHVRVYDADPDLLKALAKTKIRVIIGVPNNQLLAIGSSNATAASWVGRNVVAYYPETSII
GIAVGDEVLTTVPSSAPLLVPAIESLYSALVAANLHTQIKVSTPHAASIILDSFPPSQAYFNQSL
VSVMLPLLQFLSRTGSPLMMNLYPYYVFMQNKGVVPLDNALFKPLTPAKEMVDPNTLLHYTN
VLDAMIDATYVSMKNLNVTDVVVLVSESGWPSKGDSKEPYATVDNADTYNSNLIKHVLDRT
GTPLHPELTSSVYIYELFNEDLRSPPMSEANWGLFYGNSTAVYLLHVSGSGGFLANDTTNQT
YCIAMDNVDSRTLQTALDWACGQGQANCSEIQPGEDCYQPSNVKNHASYAFDSYYQKEGK
AAGSCDFKGVAMITTTDPSHGSCIFPGSKKVSNATKQVVNSTVSSGATESSRFFIFSSNRRT
AIDKALGSVFSVLFSFFLAVALWTPI

Figure 147: Amino Acid sequence of 381. The conserved Glycoside hydrolase, family 17, domain is underlined

MEHLPLAFFFLLLSVLSLADGGSIGVNYGRVADNLPPATKVVQLLKSQGVQKVKIYDADPAVL
HAFAGTGIRLTVDLPNEKLFAAARSLSFSLDWVQQNVADYPTTQIEAIAVGNEVFVDTHNTTR
FLVPAMKNIHTALVKHNLHNAIKISSPIALSALQASYPSSAGSFRPELIEPVFKPMLEFLRQTGS
YLMVNAYPFFAYESNSDVISLDYALFRENPGVVDAGNGLRYFNLFDAQIDAVFAAMSALKYD
DIKMVVTETGWPSKGDENEVGASKDNAAAYNGNLVRRILTGGGTPLRRQADLTVYLFALFN
ENKKPGPSSEQNYGLFYPNQDKVYDVPLTVEGLKNYHDTGKSAPAGGGQRGVAAPVKGGR
GGVSKSSSANTWCVAKGEAGKEKLQAALDFACGEGGADCRPIQRGSTCYDPNTLEAHASY
AFNSYYQMKGRAFWTCDFGGAASIVSQPPKYGKCDFPTGY

Figure 148: Amino Acid sequence of 382. The conserved glycoside hydrolase, family 17, domain is underlined.

MITEMSKIIPRMLSDSVFDIVFLLLSSSFFMQGARAGIGVNYGTVADNLPPPAQVAHFLLESTTI
DRIRLFDADPDILKAFANTGIAVTVTVPNDLIPQLAKLSNAQDWVRTNVEPYVPATDIVRILVG
NEVLATANRLLLGNLVMSMRMLHAALANASLDGRIKVSTPHSLGILSSSSPPSSGKFRLGYD
VHILRPLLNFLRETGSPFLVNPYPFFGFSKDTLDYALFRPNAGVMDENSKLVYTNMLDGQLD
AVYSAMKVLGFTDIEVVIAETGWPSLCDSTQVGVDAKTAAEYNSNLIRHVSSGAGTPLMPKR
TFETYIFALFNENLKPGPTCERNFGLFRPDMTPVYDAGILRPTARSSVPIDPIPAPSSMTPPTS
PASMSPPKGTQWCLPKTGADPDALQRNIDYVCGLGLECRPIEEGGACFLPNTVRAHAAYAM
NAYYQAMGGNNYDCDFKGTGAVTAIDPSYGKCTYHG

Figure 149: Amino Acid sequence of 383. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MANLFPLATAVFFLSVACPHLSRAAYTIGVNYGTVADNLPPPSQVATFLKTKTAIDRVKLFDA
NPDILRAFAGTGIAVTVTVGNGDIISLSKLPAAQAWVSANILPFHPKTLINRIAVGNEILATSDKN
LIARLLPAMKALHSALQLVNVTNVQVTTPHSLGILSSSEPPSTGRFRRGYDRAIFAPILDFHRQ
TKSAFMVNPYPFFGFTAKTLNYALFKPNAGIFDAATGKNYTNMFDAQMDAVYSAMKKVGYE
DVEIVVGETGWPSVGDANQPDVNMANAVSYNGNLVRHVNAGKGTPLMPNRKFETYVFALF
NEDLKPSTSERNYGLFKPDLTPVYDVGILRNEPAGGPAPASPSPTAQPSPTAPPTSSGKKW
CVPRSDASDQALQANIDYVCSAQVDCKPIQTGGACFDPNTVRSHAAYAMNAYYQSMGGQHD
YDCDFDKTGVVTAVDPSTSSSIPCF

Figure 150: Amino Acid sequence of 384. The conserved Glycoside hydrolase, family 17, domain is underlined.

MLQPRTKVATFSLLLVLSSSFPAAEPAIGVNWGTISFHRLRPSTVVDLLQQNKIQKVKLFDAD
PGALKALEGSGIEVMVGIPNEMLTVLGSSSVASDLWVRQNVSSFVGKGGVAIRYVAVGNEPF
LSSYAGQFQNYVMPALLNLQQSLAKANLAGYVKLVVPCNADAYEADLPSQGAFRPELTQIVT
QLVSFLNSNGSPFVVNIYPFLSLYGSTDFPQDYAFFGGTTHAVTDGANVYTNAFDGNFDTLV
AALTKLGYGQMPIVIGEVGWPTDGALNANLTAARAFNQGLINHVLSNRGTPLRPGVPPMDVY
LFSLLDEGAKSVLPGNFERHWGIFSFDGQAKYALNLGLGNRLLKDARNVQYLPSRWCVADP
SKDLSAVMNHMKLACSVADCTTLNYGGSCNGIGAKGNISYAFNSYYQLQMQNSQSCDFDG
LGMVTFLDPSVGECRFLVGVTESTSAAVETYWRGVIVWVLVMWSVWVFEV

Figure 151: Amino Acid sequence of 385. The conserved family 17 glycoside hydrolase domain is underlined

MAIPPLATLVLLVVLSQASCFANSQSFIGVNYGQVADNLPQPSATAKLLQSTSIEKVRLYGTD
PAIIGVLANTGIGIVIGAANGDIPALANDPNFAKNWVNANVVPFYPSSKIILITVGNEVMTSGDH
NLMTQLLPAMQNMQNALNAVSLGGKIKVSSVHSMAVLKSSEPPSSGSFDPSDEMKGILGFN
NATGSPFAINPYPYFAYRSDPRPETLAFCLFQPNAGRLDTKTQIKYTNMFDAQVDAVRSALN
SFGYKNVEIVVAETGWPYKGDSNEVGPSIENAKAYNGNLIAHLRSLVGTPLMPGISVDTYLFA
LYDEDLKPGPTSERAFGLFKSDLSMNYDIGLSKSSQTPAAPKMPAAPSPNATVTPSPNATVT
PSPKPDKANWCIPKSGVSDAQLQANLDYACGQGIDCRPIQPGGACFEPNTLAAHAAYAMNL
YYQNSNRSPTNCDFSQSATFSSNNPSYNGCVYPSGKS

Figure 152: Amino Acid sequence of 386. The conserved glycoside hydrolase, family 17, domain is underlined

MAESISHYPFPTLGLIVLCFMTMFSIGSSVGVNWGTQSNHQLPPEKVVKMLKENGIKKLKLFE
YDEKILGALAGSKIEVMLAVPNYMLEIMSVDPSFAASWVDTNVTSYRYTGGVNIKYIAVGNEP
FLQSYNHKYVRQVLPALRNIHEALHRARLSSKVKVTVPFNADVYYSPPPNEYPSSGDFRPEV
RDAAIEIIHFLYINDSPFTVNIYPFLSLYQNQNFPVDFAFFDGTTEPVKDGDRVYTNVFDANFDI
LVSALTKAGYSDMEIIVGEIGWPTDGDKFANIKNAQRFNQGLLKHALSGDGTPARKGVINVYL
FSLIDEDTKNIDPGNFERHWGLFEYDGKPKYELDLSGSEKDTRLVPVMGVSYMPRRWCILNP
ELNDLTDLGENIDYACKSSDCTALGYGSSCNNLSSQGNASYAFNRYYQMNDQRIMACDFQG
LAVVTENDPSTEGCQFPLMIASGDSMSWNQGLLHTSFRFYLWFLVFWVIL

Figure 153: Amino Acid sequence of 387. The conserved Glycoside hydrolase, family 17, domain is underlined.

MEKFDLFKWVLCGSIVLFGVGCGRVDGLGVNWGTLATRKLPPKTVVQMLKDNGIQKVKLFD
ADRKTMSALAGSGIEVMVAIPNDQLAVMGSYDRAQEWVKKNVTAYNFTGGVNVKYVAVGN
EPFLKSYNGSFVNTTLPALQNIQKALNEAGLGDTVKATVPLNADVYESPEDNPLPSAGTFRS
DISDVMTQIVKFMAENNAPFTVNIYPFLSLYGNNDFPFNYAFFDGATPIVDKGIEYTNVFDANF
DTLVSALKAVGHGNMTIIIGEVGWPTEGDINANNGNAYRFYNGLFTKLGANRGTPLRPGYIEV
YLFGLIDEDAKSVAPGNFERHWGLFRYDGQPKFLIDLTGRGQNKLLIPAQNVEYQPQKWCTF
NAGAKDVSKLVDNINFACTYADCTTLGYGSSCNSLDANGNASYAFNAYFQTQNQDPDSCNF
QGLATVTTKNISQGSCNFTIQLVASSTSILRPLIVLTVISMAYTFLLQ

Figure 154: Amino Acid sequence of 388. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MASLFPLTAAVVFLSVACPHLSRAAYTIGINYGTIADNLPPPSKVATFLKTKTTIDRVKIFHASP
DILRAFAGTGIAVTVSVGNEDIVSLSKLPAAKSWVSANILPFYPKTLINRIAMGNEILATSDKTLI
ANLLPAMKALHSALQLANVTNVQVTTPNSLGILASSYPPSNGSFRSGFDRTIFAPILKFHRQT
NSSFMVNPYPFFAITPENVNSLLNYSLFKPIPSSTFDAATGKNYTNMFDAQMDAVYSAMKKV
GYED**VEIVVGETGWPSVG**DPNQPGVSMANAESYNSNLVRHVNSGKGTPLMPNRKFETYIFA
LFNENKKPSTSERNYGLFKPDLTPVYDVGILRNSVNAVPLHLLG

Figure 155: Amino Acid sequence of 389. The conserved Glycoside hydrolase, family 10, domain is underlined and the Carbohydrate-binding CenC-like domains are in bold

MRRVCACFLTSPAKTPPKHGTQRVSKQTAGNQKSESASNNSEVMANSSGSQG**TNIIQNHNF**
SGGLHSWHPNCCESWVVSAESGDCYAMVTNRKECWQGLEQDITSRVTPGSTYSVSACVG
VSGSLQGSADVLATLRLEHQDSAATYKRIGITSVSKERWDKVEGSFSLSSMPNRVVFYLEG
PSSGIDLLIKSVVITCQSANGKERVDREHIAAGD**ENIILNPIFDDGLKNWAGRGCKIVLHDSM**
ADGKIVPQSGKYFVSATERTQTWNGIQQEVTGRLQRKLAYEVTALVRIFGNNVSSTDVRITL
WTQTPDLREQYIGVANVQATDKDWTQMQGKFLLNGSPSKVIIYIEGPPAGTDILVNSLTVKH
AAKAAPSPPPVIQNPAFG**VNIIGNSDLDNGTNEWFPLGNCTLSVRAGSPHILPSSARDSLGP**
HEPLSGSYILVTNRTQTWMGPAQMITDKLKLFLTYQVSAWVRIGSGASGPQNINVALGVDN
QWVNGGQVEANDDRWHELSGSFRIEKQPSKVMVYIQGPAPGVDLMVAGVQIFPVDRQAR
FNHLKHLTDKLRKRDVVLKFSGADSSSLVGATVIVKQTQNSFPFGSCISRTNIDNEDFVDFFV
KNFNWTVFGNELKWYWTEPQQGNFNYRDADEMLDLCKSHGIETRGHCIFWEVESTVQAW
VQSLNNNDLMSAVQNRLNGLLSRYKGKFSHYDVNNEMLHGSFYQGRLGKDIRANMFKTAN
QLDPSATLFVNDYHVEDGCDTKSCPEGYIEHILGLQEQGAPVGGIGIQGHIDNPVGPIINSALD
KLGILGLPIWFTELDVSSVNEYVRADDLEVMLREAFAHPAVDGIMLWGFWELFMSRDNAHLV
NAEGDVNEAGKRYLALRKEWSSHAHGHVNEQGEYTFRGFHGTYDVLIVTSSKRTTKSIVVD
KGESPLVVPISL

Figure 156: Amino Acid sequence of 390. The conserved glycoside hydrolase, family 10, domain is underlined.

MTMILPGFSRTAPIAGAMRTSPGFNMFLFLSLAFALLSLGSAISGQIMQTVFDDYYDSSATTQ
CLAEPGSLMYGGGVILNPEFIHGTSGWTVLGEGATEVRISHTNNRFMVARDRKRPTDSFSQ
KVQLEKGMFYAFSAWVQASQGSETVAVVFRTRDGKFVRGGSVVAKQGCWSLLKGGIAANS
SSPADVLFESKNTSTEIWVDNVALQSFSKKQWRTHQEESIEKVTRKRKSTVRFQITSANERG
LGVGGANVLIKQIKPGFPFGCGMNFHILESADYQNWFASRFRYATFTNAMKWYSTEKEQGQ
EDYSVADAMLKFVQDNNISIRGHNVFWDDPKYQPDWVRTLSPDDLRKAAEKRINSVVSRYA
GELIAWDVVNENLHFSFFEDNLGENASSMYYSMAYKLDPTPRMFLNEYNTIEYSGDEKVSP
GNYKKRFQEIFTYPGNEDIPAGIGVQGHFGAGQPNSAYMRSGLDILATTGLPIWLTEVSVAP
GANQQYLEEVLREAYSHPGVEGIIMFAGPAYAGFNSTALADMNFDNTPTGDVVDQLIQEWR
FKDLAARADDEGFFSTKLLHGEYEITITDPISNSSSTSRFQVTKDSFKIIYHFHM

Figure 157: Amino Acid sequence of 391. The conserved Glycoside hydrolase, family 10, domain is underlined.

MKDASAFISFLVFFLLLCSPWIAASLDDPQYDHTAYTKCKEEPEKPLYNGGILEPHQLPQFAS
SSPALLLHNLTASTKYSFSSWVKIESSDSDSALVTASLRTNHETYDCIGTVAAKSGCWSFLKG
GFTLDLPSNSATLSFESSDGRYIAIAISSTSLQPFTDQQWRRNQQDMINKVRKRAVMIHVSNH
NGDRLQGVEINVKQVYKDFPFGSAIAKTILGNEAYQNWFVERFNAAVFENELKWYATEPYPG
QINYTIADEMLEFIRANRIVTRGHNIFWEDPKYNPEWVQNLSGPQLESAVDTRIQSLMSRYRE
EFVHWDVSNEMLHFDFYERRLGPNATLHFFQTAHESDPLATLFMNEFNVLETCSDANSTVD
SYISRMRDLKRGGVSMDGIGLEGHFTVPNLPLMRAILDKLGTLRLPMWLTEVDISSTLSKESQ
ALHLEEVLREGFSHPSLNGIMLWTALHPNGCYQMCLTDADFRNLPAGDVADSLLGEWRTKE
VNGKTNEHGSYSFEGFLGEYEVSVMHGDQTANSTFALSQGVETRHVTILL

Figure 158: Amino Acid sequence of 392. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MMTPAQNRAPKVSSVLLCLCCIHAFFSCAVRLVAGQTPKPVFACDVDGNPSLAAFGFCNTS
WGVEARVADLVQRLTLQEKVGFLVSGAGNVDRLGIPKYEWWSEALHGVSYVGPGTKFSSL
VPGATSFPQVILTAASFNATLFETIGKVVSTEARAMHNVGLAGLTFWSPNVNIFRDPRWGRG
QETPGEDPLLSSKYASGYVRGLQKSDDGNADRLKVAACCKHYTAYDVDNWKGVNRLTFNA
VVTQQDLDDTFQPPFKSCVLDGNVASVMCSYNQVNGKPTCADPDLLAGTIRGKWKLNGYIV
SDCDSVEVLYDKQHYTKTPEEAAAKAILAGLDLNCGSFLGQHTEAAVKGGLLNESAVDKAIS
NNFATLMRLGFFDGDPRKQLYGKLGPDDVCTPSNQELAREAARQGIVLLKNTAGSLPLSSTA
IKSLAVIGPNANVTKTMIGNYEGTPCKYVTPLQGLAAIVSTMYVAGCADVGCSTAQTDDAKKA
AASADATVLVMGADQSIEREDFDRVNLNLPGQQSLLVSEVANVSKGPVVLVIMSGGGMDVS
FAKDNAKITSILWVGYPGEAGGAAMADVIFGDHNPSGRLPMTWYPQSYVDAVPMTNMNMR
PDPATGYPGRTYRFYTGPTVYSFGDGLSYSSFSHGQVQVPQLVSVPLDEGHICHSSACESL
EAKSETCSNLVFDVHLNVKNVGRFSGSHTVFLFSSPPSVHRSPQKHLLGFEKVFLASQSEAQ
VQFKVDVCKDLSVVDELGGRKVALGTHVLHVGDLKHALSVQIGSSGLSLSPPRHF

Figure 159: Amino Acid sequence of 393. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MMTPAQNRAPKVSSVLLCLCCIHAFFSCAVRLVAGQTPKPVFACDVDGNPSLAAFGFCNTS
WGVEARVADLVQRLTLQEKVGFLVSGAGNVDRLGIPKYEWWSEALHGVSYVGPGTKFSSL
VPGATSFPQVILTAASFNATLFETIGKVVSTEARAMHNVGLAGLTFWSPNVNIFRDPRWGRG
QETPGEDPLLSSKYAAGYVRGLQKSDDGNADRLKVAACCKHYTAYDVDNWKGVNRLTFNA
VVTQQDLDDTFQPPFKSCVLDGNVASVMCSYNQVNGKPTCADPDLLAGTIRGKWKLNGYIV
SDCDSVEVLYDKQHYTKTPEEAAAKAILAGLDLNCGSFLGQHTEAAVKGGLLNESAVDKAIS
NNFATLMRLGFFDGDPRKQLYGKLGPDDVCTPSNQELAREAARQGIVLLKNTAGSLPLSSTA
IKSLAVIGPNANVTKTMIGNYEGTPCKYVTPLQGLAAIVSTMYVAGCADVGCSTAQTDDAKKA
AASADATVLVMGADQSIEREDFDRVNLNLPGQQSLLVSEVANVSKGPVVLVIMSGGGMDVS
FAKDNAKITSILWVGYPGEAGGAAMADVIFGDHNPSGRLPMTWYPQSYVDAVPMTNMNMR
PDPATGYPGRTYRFYTGPTVYSFGDGLSYSSVSHGQVQAPQLVSVPLDEGHICHSSACESL
EAKSETCSNLVFDVHLNVKNVGRFSGSHTVFLFSSPPSVHRSPQKHLLGFEKVFLASQSEAQ
VQFKVDVCKDLSVVDELGGRKVALGTHVLHVGDLKHALSVQIGSSGLSLSPPRHF

Figure 160: Amino Acid sequence of 394. The conserved N-terminal and C-terminal domains of glycoside hydrolases family 3 are underlined.

MXGTALPAAAAGTATLLLLLLISGGIGRLAVGAREPFACDPKDERTRGFPFCQASSPVPERA
RDLVGRLTLQEKAKLLGNDAAAVPRLGIKGYEWWSEALHGVSNVGPGTRFGGDFPGATSFP
QVITTAASFNASLWEAIGQVVSDEARAMYNGGMGGLTYWSPNINILRDPRWGRGQETPGED
PVVVGQYAASYVRGLQGADGNGGGRLKVAACCKHFTAYDLDNWNGVDRYHFNARVSKQD
MEDTFSVPFRMCVMEGKVASVMCSYNQVNGIPTCADPNLLRKTVRGAWRLDGYVVSDCDS
VGVFYGNQHYTSTPQQAVADAIKAGLDLDCGPFLGKHTEEAVRGGLMNEADIDGALLNTLAV
QMRLGMFDGEPSAQPYGTLGPKDVCTPAHQELALEAARQGIVLLKNQGPALPLSPRRHRAV
AIIGPNSDVTVTMIGNYAGVACGYTTPLQGIGKYTKTIHQQGCADVACSDDKLFEGAIKAARG
ADATVLVMGLDQSIEAEFKDRDSLLLPGRQQELVSKVAMASKGPTVLVLMSGGPVDISFAKN
DPRVAAILWAGYPGQAGGTAIADILFGATNPGGKLPMTWYPQDYLASVPMTVMDMRPTRSN
LYPGRTYRFYGGPVVYPFGHGLSYTHFVHTLASAPSTVVVPLAGRRPANATMGPGKAVRVT
HARCARLSLRVQLDVQNAGARDGAHTVLVFSTPPEDGGARWAPPRSQLVGFQRVHVAAGA
RERVGINIHVCKSLSVVDGAGVRRIPMGEHRLQIGDVVHSVSLQAEPLRVI

Figure 161: Amino Acid sequence of 395. The conserved glycoside hydrolase, family 3, N-terminal domain is underlined, and the conserved glycoside hydrolase, family 3, C-terminal domain is in bold.

MRNRQVQILSLLITFASAATLLSTPAAAQPPPFSCDPSSPSTKSFPFCKASLPISKRAQDLVSR
LTLDEKISQLVSSTPAIPRLGVPAYEWWSESLHGVSNAGRGIHFDGTIKSATSFPQVILTAASF
DADLWYRIGQVIGTEARAVYNAGQATGMTFWAPNINIFRDPRWGRGQETPGEDPLVTGKYA
VSYVRGVQGDRPQGGGKSRGGLQASACCKHFTAYDLDRWKGVDRYDFDAQVTAQDMAD
TFQPPFQKCIQDGKASGIMCAYNRVNGVPSCADYNLLSNIARRQWSFHGYITSDCDAVSIMY
DNQKYAKTPEDAVADALKAGMDVNCGTYLQNHTKSAVEQRKVSVSEIDRALHNLFSVRMRL
GLFNGDPKKQPFGNIGPDQVCSQKHQDLALEAARSGIVLLKNKEKHLPLQRSKSASLAVIG
PNANKASNLLGNYAGPPCKSVTLLQALQSYVKDTRYQPGCDDVVCSSPQIAQAVEVAKAA
DHVVLIMGLDQTQEREDFDRVDLVLPGRQQEFITTVAQAAKKPVILVILCGGPVDIRFARDD
QNIGSILWAGYPGEAGGMALSEIIFGEHNPGGRLPVTWYPQEFTRVPMTDMRMRPEPSTG
YPGRTYRFYQGQSIFEYGHGLSYTEYSYKFISVTRELFYLSQSAKSQPDEASDASPRYRLVS
DLGADFCKKSNFVATVKVKNHGDMVGKHPVLLFVRHAKPSSGSPMKQLVAFQSVELKGGE
TMKVQLALNPCDHLSRANENGVMILEEGWRFLEVGDQEYPINVMA

Figure 162: Amino Acid sequence of 396. The conserved N-terminal and C-terminal domains of glycoside hydrolases family 3 are underlined.

MSVMGRYSVPIKAFLLICCLAAVTTEAEYVKYRDAKQPMGARVRDLMRRMTLAEKIGQMTQI
ERSVATPDVMKNYFIGSVLSGGGSVPAPKASPETWVNAVNEIQKAALSTRLGIPMIYGIDAVH
GHNNVYNATIFPHNVGLGVTRDPVLLKKIGDATALEVRATGIPYAFAPCIAVCRDPRWGRCY
ESYSEDHRIVRMLTEIIPGLQGDLPANSPKGVPFVAGKNKVAACAKHFVGDGGTTKGINENN
TVVDYNGLLSIHMPAYLDAIRKGVATVMVSYSSWNGKKMHANGDLVTGFLKNKLKFKGFVIS
DWEGIDRITSPPHANYSYSVQAGVGAGIDMVMVPYKVTEFLDDLTKQVQNNVIPMSRIDDAV
KRILRVKFVMGLFDNPLADNSLANQVGSPEHRELAREAVRKSLVLLKNGKSSGKPLIPLPKKA
QKILVAGSHADNLGNQCGGWTIAWQGLNGNDLTTGTTILNAVKSTVHPDTQVVYNENPDAN
FVKSNNFAYAIVVVGEPPYAETFGDSLNLTIPEPGPSTIRNVCGSVKCVVVVISGRPVVIEPYV
SNIDALVAAWLPGTEGQGVADLLFGDYGFTGKLARTWFRSVDQLPMNVGDPHYDPLYPFGF
GLTTKGTKESDPTYS

Figure 163: Amino Acid sequence of 397. The conserved Glycoside hydrolase, family 5, domain is underlined.

MAHCRHHPLVLLCSLFVFLPSILAQTADFNLPLRAINLGNWLVTEGWMMPSRFDGLIGQLLD
GAQVQFKSTQLKKFLCAEGANIVINRDRAAGWETFRLWRISDTKFNIRAFNKNFVGLKDKKIVI
AEVYGTPSASETFEIIRNPNRPNRVRLRASNELFLQAKTLTSVTADYNGDTNWNDNDPSIFDI
NIVGGLQGEYQITNGYGPSTAPQLLRDHWNNYITEQDFRFMATNNVTAVRIPVGWWIAYDPT
PPKPFVGGSLYALDRAFTWAENYRMKVIVDLHAAPGSQNAESHSATRDGFVEWGDSYIQET
VKVIEFLAARYCNRSALVAIELMNEPRAPDVKLNDLIDYYRLGYEAVRRYTMDAYVILSNRLG
PADPLELFQFVRGLSRVVIDVHYYNLYDPKFKQWNLQQNIGYIYVDRENDLSKITQKRGPLSF
VGEWTSALDFDGATKEDSGRFAKAQQDVYRQATFGWAYRSYKCHYDTWSLEQMIEDGLIKI
VA

Figure 164: Amino Acid sequence of 398. The conserved glycoside hydrolase, family 3, N-terminal domain is underlined, and the Glycoside hydrolase, family 3, C-terminal is in bold

MGSAEDARCVYKDPNAAIEDRVNDLLSRMTLQEKVGQMTQIERRVATPSVLSGLSIGSILSA
GGSGPFGVIGSESSKQALSSDWADMVDGFQKAALESRLGIPLIYGIDAVHGNNSIYGATIFPH
NIGLGATRDAELVRRIGVATALEVRASGIPYTFAPCVAVLKDPRWGRSYESYSEDTDIVRKMT
PIVAGLQGQPPQGHPKGYPFVAGRNNVIACAKHFVGDGGTERGVNEGNTVTSYEDLERIHM
APYLDCISQGVCTVMASYSSWNGRRLHSDYFLLTEVLKDKLGFKGFVISDWEGLDRLSQPH
GSNYRQSISLAVNAGIDMIMVPFRHEQFAEDLTALAESGEVPMSRIDDAVQRILRVKFVSGLF
EHPFSDRSLLQIVGCKSHRELAREAVRKSLVLLKNGKDPMKPFLPLDKNAKKILVAGSHAD
**DLGYQCGGWTATWHGSSGRITIGTTILDAIKEAVGGNTEVIYEQNPSPSTLASHDYTFAIVA
VGEGPYAETLGDNPELAIPFNGTDVIKSVAERIPTLVLVVSGRPLVIEPHVLEKIDALVAAWL
PGSEGTGITDVVFGDYDFEGQLPISWFRTVEQVPMDHKANSYDPLFPLGFGLKCKKEA**

Figure 165: Amino Acid sequence of 399. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MGSAEDARCVYKDPNAAIEDRVNDLLSRMTLQEKVGQMTQIERRVATPSVLSGLSIGSVLSG
GGSGPLGLAESASSERALLSDWTDMVDGFQKAALESRLGIPLIYGIDAVHGNNNIYGATIFPH
NIGLGATRDAELVRRIGVATALEVRASGIPYTFAPCVAVLKDPRWGRSYESYSEDTDIVKKMT
AIVTGLQGQPPQGHPKGYPFVAGRNNVIACAKHFVGDGGTERGVNEGNTVTSYEDLERIHM
APYLDCISQGVCTVMASYSSCNGRRLHTDYFLLTEVLKNKLGFKGFVISDWEGLDRLSQPHG
SNYRQSISLAVNAGIDMIMVPFRHEQFAEDLIALAESGEVPISRIDDAVQRILRVKFVSGLFEH
PFSDRSLLQIVGCKSHRELAREAVRKSLVLLKNGKEPTKPFLPLDKNAKKILVAGSHADDLGY
QCGGWTVAWHGSSGRITIGTTILDAIKEAVGGNTEVIYEQNPSPSTLASHDYTFAIVAVGEGP
YAETLGDNAELAIPFNGTDVIKSVAERIPTLVLVVSGRPLVIEPHVLEKIDALVAAWLPGSEGT
GITDVVFGDYDFEGQLPVSWFRTVEQLPMDHKANSYDPLFPLGFGLKCKKEA

Figure 166: Amino Acid sequence of 400. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MGSAEDARCVYKDPNAAIEDRVNDLLSRMTLQEKVGQMTQIERRVATPSVLSGLSIGSVLSG
GGSGPLGLAESASSERALLSDWTDMVDGFQKAALESRLGIPLIYGIDAVHGNNNIYGATIFPH
NIGLGATRDAELVRRIGVATALEVRASGIPYTFAPCVAVLKDPRWGRSYESYSEDTDIVKKMT
AIVTGLQGQPPQGHPKGYPFVAGRNNVIACAKHFVGDGGTERGVNEGNTVTSYEDLERIHM
APYLDCISQGVCTVMASYSSWNGRRLHTDYFLLTEVLKNKLGFKGFVISDWEGLDRLSQPH
GSNCRQSISLAVNAGIDMIMVPFRHEQFAEDLIALAESGEVPISRIDDAVQRILRVKFVSGLFE
HPFSDRSLLQIVGCKSHRELAREAVRKSLVLLKNGKEPMKPFLPLDKNAKKILVAGSHADDLG
YQCGGWTVAWHGSSGRITIGTTILDAIKEAVGGNTEVIYEQNPSPSTLASHDYTFAIVAVGEG
PYAETLGDNPELAIPFNGTDVIKSVAERIPTLVLVVSGRPLVIEPHVLEKIDALVAAWLPGSEGT
GITDVVFGDYDFEGQLPISWFRTVEQVPMDHKANSYDPLFPLGFGLKCKKEAR

Figure 167: Amino Acid sequence of 401. The conserved N and C terminal domains of family 3 ofThe Glycoside hydrolases are underlined.

MKKNGESSHLYGGILVLCCFSGVTRAEYLKYKDPKQPLNTRINDLLSRMSLEEKIGQMTQIER
SVASFEVMKKYYIGSVLSGGGSVPAPQASAETWIDMVNDFQNGSLSTRLGIPMIYGIDAVHG
HNNVYRATIFPHNVGLGATRDPALVKRIGAATALEVRATGIPYVFAPCIAVCRDPRWGRCYE
SYSEDPKIVQAMTEIIPGLQGDLPAGSRKGVPYVAGKKNVAACSKHYVGDGGTTNGVNENN
TVTDWHGLLGIHMPGYYTSIIKGVSTVMVSYSSWNGVKMHANGNLVTGFLKNKLRFRGFVIS
DWEGIDRITSPPHANYSYSIQAGISAGIDMVMVPSNFTEFIDGLTFQVKNKIIPMSRIDDAVRRI
LRVKFTMGLFEDPLADTSLVNQLGSQEHRELAREAVRRSLVLLKNGEGADAPLLPLPKKAPKI
LVAGSHADNLGYQCGGWTIQWQGLSGNNLTSGTTILSAIKNTVDPKTKVVYEENPDTDTVKS
GKFSYAIVVVGEHPYAETFGDSSNLTIADPGTSTIGNVCGAVKCVVVIISGRPVVIQPYVAVMD
AIVAAWLPGTEGQGVADVLFGDYGFTGKLPRTWFKTVDQLPLNVGDPHYDPLFPFGFGLTT
APVKRN

Figure 168: Amino Acid sequence of 402. The conserved N and C terminal domains of family 3 of the Glycoside hydrolases are underlined.

MGGAFLRTLGVLTLWWFVASVMAQSADYVAYKDPKQPVAARVKDLLSRMTLEEKIGQMTQI
DRMVATDDFMKTYSIGSVLSGGGSTPLPEASAEDWVNMINGYQKGALSSRLGIPMIYGIDAV
HGHNNVYNATIFPHNIGLGATRDPKLVKKIGAATALEVRATGIPYVFAPCIAVCRDPRWGRCY
ESYSENEDIVRQMTEIIPGLQGDIPSGSRKGVPYVDGKNKVAACAKHFVGDGGTSKGINEDN
TVVDMHGLLSIHMPAYTDAIIKGVSTVMVSYSSWNGEKMHANRDLVTGFLKNTLKFKGFVIS
DWQGIDRITSPPHANYTYSVEAGILAGIDMVMVPFNFTEFINDLTYLVKEKVIPMDRIDDAVGR
ILFVKFTMGLFENPLADLSLVNELGSQAHRELAREAVRNSLVLLKNGKNETDPLLPLPKKPKKI
LVAGSHADNLGYQCGGWTITWQGFSGNNYTRGTTILSAINSTVDLSTEVVYQENPDKDFVK
STDFDYAIVVVGEHPYAETAGDSTTLTMADPGPTTITNVCEAMKCVVIVVSGRPLVIEPYISSI
DALVAAWLPGTEGQGVADVLFGDYGFSGKLPRTWFKSVDQLPMNFGDLHYDPLFPFDFGL
KTESVPGLVARATSHGADGGPRLLMVTACLAISLYVTGYRWRASKF

Figure 169: Amino Acid sequence of 403. The conserved glycosyl hydrolases domain of family 17 is underlined and the glycosyl hydrolases family 17 signature is in bold.

MASPAFSCLLLLVSIFALAESGSVGLNWGRVANDLPPPAKVVELLKSQGITLVKLYDTYDGAL
TALAGSGISVVVALPNEQLSSAASAQSFTDSWVQSNISKYYPSTKIVAIAVGNEVFVDPNNTT
DFLVPAMNNVHASLVKYNLSDISVSSPIALSALQTSYPTSSGSFKSDLVEPVIKPMLEFLRKTG
SYLMVNVYPFFAYTANSDQISLDYALLKQNPGVVDSGNGLKYNSLFDAQVDAVYAAMSALQ
YNDLKLVVTETGWPSKGDANEVGAGTQNAAAYNGNLVRRALTGTGTPLRPNNTVDVYLFA
LFNENQKTGPTSERNYGLFYPDEQKVYSIPLTLEQLASDPNNASKAQVPTAPVGQTWCVAN
GKAGEKKLQAALDYACGKGGADCQPIQQGSACYNPNTLEAHASYAFNSYYQKNARGAGTC
NFGGAAFVVTQVPEYGECDFPTGY

Figure 170: Amino Acid sequence of 404. The conserved Glycoside hydrolase, family 17, domain is underlined.

MAASFLSNPSSLSFLLLLLLLHASRLAFSQSFVGVNYGQVADNLPPPESTAKLLQSTTIGKVR
LYGADPAIIKALANTGIGIVIGAANGDIPSLAADPNAAGQWVGANILPFYPASKITLVTVGNEVF
MSNDENLMSQLLPAMQNMQKAITAAGLGGKVKVSSVHAMSLLSQSDPPSSGRFHPSFEAR
MRDVLQFQRENGSPLPINPYPFFAYQSDPRPETLAFCLFQPNAGRVDSGTGIKYMNMFDAQ
VDAVYSALKALGYKDIEIVVAETGWPYNGDSNEVGPSVENAKAYNGNLIAHLRSLVGTPLMP
GKSVDTYIFALYDEDLKTGPTSERSFGMYKPDLTMSYDIGLAKSSQTPVTPTPKPTGPGWCV
PKSGVSDAQLQASLDYACSHNIDCGPIQPGGACFDPNTVASHAAFAMNLYYQTSGRNPWN
CDFSQTATLTTNNPSYNGCVYPGGST

Figure 171: Amino Acid sequence of 405. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MAVPPFVLLLLLVGCASTVKSDQEPFIGVNIGTDLSDMPHPTQVVALLKAQNIRHIRLYNTDR
GILAALANTGIQVIVSVPNEQLLGIGQSNSTAANWVSQNIIVHYPATNITGISVGSEVLTALPNA
APILVNALKFIHSALVASNLDRQIKVSTPLSSSVILDSFPPSQAFFNKSLNPVLVPMLNFLQSSG
SYLMLNVYPYYDYMQSNGVIPLDYALFKPLPSNKEAVDANTLLHYSNVFDATVDAAYFAMAF
LNFTN**IPVVVTETGWPSKG**DSNEPDATVDNANTYNSNLIRHVLNKTGTPKHPGITVSTYIYEL
YNEDTKAGPLSEKNWGLFDASGSPIYILHLTGSGSVLANDTTNQTYCTAKEGADPKMLQAAL
DWACGVGKVDCSPMLQGESCYEPDTLSAHATYAFDTYYHQMGKAPGTCDFNGVAAITTTD
PSHGTCIFSGSLGRNATSVNVTAPSMNSTTSGSPALNYYNQHVLLLVVDESSGLECLVLVEW
YISR

Figure 172: Amino Acid sequence of 406. The conserved glycoside hydrolase, family 17, domain is underlined

MAESISHYPFPTLGLIVLCFMTMFSIGSSVGVNWGTQSNHQLPPEKVVKMLKENGIKKLKLFE
YDEKILGALAGSKIEVMLAVPNYMLEIMSVDPSFAASWVDTNVTSYRYTGGVNIKYIAVGNEP
FLQSYNHKYVRQVLPALRNIHEALHRARLSSKVKVTVPFNADVYYSPPPNEYPSSGDFRPEV
RDAAIEIIHFLYINDSPFTVNIYPFLSLYQNQNFPVDFAFFDGTTEPVKDGDRVYTNVFDANFDI
LVSALTKAGYSDMEILVGEIGWPTDGDKFANIKNAQRFNQGLLKHALSGDGTPARKGVIDVY
LFSLIDEDTKNIDPGNFERHWGLFEYDGKPKYELDLSGSEKDTRLVPVMGVSYMPRRWCILN
PELNDLTDLGENIDYACKSSDCTALGYGSSCNNLSSQGNASYAFNRYYQMNDQRIMACDFQ
GLAEVTENDPSTEECQFPLMLASGDSMSWNQGSLHTSFRFYLWFLVFWVIL

Figure 173: Amino Acid sequence of 407. The conserved family 17 glycoside hydrolase domain is underlined and the glycosyl hydrolases family 17 signature is in bold.

MAKIISMASGCSSAPAVCLLGLLIASFCTAGVQSIGVCYGMLGNNLPSASEVVALYKSRGITQ
MRLYDPSQPALQALRGSNIELILGVPNSELQALASNPANANSWVQRNVKNYSPGVRFRYIAV
GNEVSPVNGGTAQFARFVLPAMRNIQAALRSSGLQNQIKVSTAIDMTLIGNSYPPSQGAFRG
DVRSYLDPIISFLVNNNSPLLANIYTYFSYVGNPKDISLPYALFTSPSVVVRDGAHEYRNLFDA
MLDALYSALERAGGASLR**VVVSESGWPSAG**AFAATVDNARTYNGNLIKHVKGGTPKRPNG
AIETYIFALFDENQKQPELEKHFGLFFPNKQPKYPLSFAQGRIWDVYDNVTGPLKSDM

Figure 174: Amino Acid sequence of 408. The conserved glycoside hydrolase, family 17, domain is underlined.

MGFFKFIAFSRLCVALLFLAELVTSVGGIGVNWGTQTTHPLPPATVVRMLKDNGFQKVKFFD
ANSSYLSALSKSGLQVMLGIPNDMLSSLASNVEAAENWVAQNLSTYVSSNGVDIRHIAVGNE
PFLSTYNGTYLNTTLPALQNVQAAVVKAGLSTQVKVTIPLNADVLESSTNLPSDGDFRSDIRD
LMLEIVKFLSDNGAPFTINIYPFISLYNDPNFPAEFAFFDSSSSPLNDKGTIYTNVLDANHDMLV
WALQKNGYGNMSITVGEIGWPTDGDKNANAKSAQRFNQGFMTQYSAGKGTPLRPGQMDA
YLFSLIDEDAKSIQPGNFERHWGLFSFDGQPKYQLNLGSTSSNGLVAARDVKYLAKKWCVM
SQSASLQDSQVAPSVSYACANADCTSLGYGNSCSNLTAQGNISYAFNSYYQQHDQLDTAC
QFPNLSVITDNDPSVGDCKFIIMIQSQSMSLVGSDGSRGRGIVPAILVSSLLYMILWMP

Figure 175: Amino Acid sequence of 409. The conserved glycoside hydrolase, family 17, domain is underlined.

MALLLLFLLLFPVSLASADEGPFIGVNIGTDLSNMPSPTQVVALLKAQNIRHVRLYDTDHAMLL
ALANSGIRVTVSVPNDQLLGIGQSNATAAYWVARNIVAHVPATNITVIAVGSEVLTTLQNAAPV
LVSAMKFIHSALVASNLDSRIKVSTPHSSSIIIDSFPPSQAFFNRTWDPVMVPLLKFLQSTGSY
LMLNVYPYYDYMQSNGAIPLDYALFRPLPPNKEAVDSNTLLHYNNVFDAVVDAAYFAMSYLN
FTNVPIVVTESGWPSKGDSSEADATLENANTYNSNLIKHVLNNTGTPKHPGVAVSTYIYELYN
EDQRPGSVSEKNWGLFDANGVPIYILHLTGAGTVLANDTTNQTFCVGKDGADKKMLQAALD
WACGPGKVDCSLLLQGQACYEPDNVVAHATYAFNAYYQKMGKALGTCDFKGVATVTTTNP
SHGSCIFPGSGGRNGTSVNGTILAPSSNSTTSGCPPQYFFDVGSITSSLIITILHLALVLL

Figure 176: Amino Acid sequence of 410. The conserved nucleotidyl transferase family domain is underlined.

MGSAEERVVAVIMVGGPTKGTRFRPLSLNIPKPLFPLAGQPMVHHPISACKRIPNLAQIYLVG
FYEEREFALYVSSISNELKVPVRYLKEDKPHGSAGGLYNFRDLIMEDSPSHIFLLNCDVCCSF
PLPEMLEAHISYGAMGTLLVIKVSAESASQFGELIADPSTKELLHYTEKPETFVSDLINCGVYIF
TPEIFSAIRNVSTQRKDRANLKRVSSFEALQPATRNLPTDFMRLDQDILSPLAGKRQLYTYET
MDFWEQIKTPGMSLKCSGLYLAQFRSTSPHLLASGDGTKGATIIGDVYIHPSAKVHPTAKIGP
NVSISANARVGAGARLMNCIILDDVEIKENAVVTHSIIGWKSSIGKWSRAQGGGDYNAKLGITI
LGEAVTVEDEVVVINSIVLPNKTMNISVQEEIIL

Figure 177: Amino Acid sequence of 411. The conserved Nucleotidyl transferase domain is underlined

MENSGEMEKVVAVIMVGGPTKGTRFRPLSFNTPKPLFPLAGQPMVHHPISACKRIPNLAQIFL
IGFYDEKEFALYVSSISNELRVPVRYLKEDKPHGSAGGLYHFRNLIMEDSPSHIFLLNCDVCC
NFPLPDMLEAHKRYGGMGTMLVVKVSAESANQFDVFSAIEDVSNDREDRANLRRLSSIDIST
STRTNIPTDFVRLDQDILSPLSGKKQLYTYETMDYWEQIKTPGISLKCSGLYLAQFRLTSPHLL
ASGDGTRSATVVGDVFVHPSAKVHPTAKIGPNVSISANVRVGPGVRLISCIILDDVELEDNAIVI
NSIVGWKSSLGRWSRVQADGDYNSKLGITILGESVVVEQEVVVVNSIVLPNKILNVSVQDEIIL

Figure 178: Amino Acid sequence of 412. The conserved Nucleotidyl transferase is underlined.

MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAIGVSEVVLAINYQPEIMLNFLK
GFEAKLGIKITCSQETEPLGTAGPLALARDKLLDDSGEPFFVLNSDVISEYPLKEMIQFHKAHG
GEASIMVTKVDEPSKYGVVIMEESTGQVEKFVEKPKIFVGNKINAGIYLLNPSVLDRIQLRPTSI
EKEVFPKIAAEKQLFAMVLPGFWMDIGQPRDYITGLRLYLDSIRKKSSEKLATGPHIVGNVLV
DETAKIGEGCLIGPDVAIGPGCVVESGVRLSRCTVMRGVRIKKHACISSSIIGWHSTVGQWAR
VENMTILGEDVHVGDEIYSNGGVVLPHKEIKSSILKPEIVM

Figure 179: Amino Acid sequence of 413. The conserved Mannose-6-phosphate isomerase family domain (type I) is underlined, the Phosphomannose isomerase signature 1 (type I) is in bold, and the Phosphomannose isomerase signature 2 (type I) is in italics.

METRSSPKLRRLRCSVQKYDWGRRGAESRVAKLFALNSGAEADPDRPYAEFWMGTHGSG
PSFLLPAGCGNGGHKVSPDVTLKAWISSNPDVLGDKVVAEWGCDLPFLFKVLSIAKPLSIQA
HPDKELARA**LHKARPDVYKDANHKPE**MALALTKFEAICGFISMEELKQVLCDVPEIAELVGST
DVEKFIKLGEQEVEKAKCLLQSIFTKLMSASADIVALAVSQINSRLELESQVRPLTDKEQLVLR
LEKQYPADVGVISAFFLNYVRLNPGEALYLGANEP***HAYVSGECIECMATSDNVVRAGLTPKT***
KDIQTLCSMLTYKQGFPDILKGVPLKTYITRYIPPFDEFEVDRCVLPKGSSAVFSAVLGPSIFLV
TDGEGTINVGSVKQDVVAEGYVLFVPANVEIHVTSVTELHVYRAGVNDRFLKSRELENGKKS
QI

Figure 180: Amino Acid sequence of 414. The conserved group 1 glycosyl transferase domain is underlined.

MAGNDWINSYLEAILDVGPALDDKKSSLLLRERGRFSPTRYFVEEVITGFDETDLYRSWVKA
QATRSPQERNTRLENMCWRIWNLARQKKQLEGEEAQRKSKRRLERERGRREATADMSED
LSEGEKGDAVSDISTHGDSNRGRLPRISSVDAMETWVGQQKGKKLYLVLISLHGLIRGENME
LGRDSDTGGQVKYVVELARALGSMPGVYRVDLLTRQISSPDVDWSYGEPTEMLSPRNSEG
LSDEMGESSGAYIVRIPFGPRDKYVPKELLWPHIREFVDGALSHVIQMSKVLGEQVGGGQPV
WPVAIHGHYADAGDSAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLSRDEINTTYKIMRRI
EAEELSLDSSEIVITSTRQEIDEQWRLYDAFDPILEKKLRARIKRNVSCYGRFMPRMAIIPPGM
EFHNIAPQDGDMDGEMEGNDDHPTTQDP**PIWTEIMRFFNNPRKPMILALARPDPKKNITTLV**
KAFGECRPLQELANLTLIMGNRDGIDEMSSTSSSVLLSVLKLIDKYDLYGQVAYPKHHKQSDV
PDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAHGLPMVATKNGGPVDIHRVLDNGLLIDPHDQR
SIADALLKLVADKHLWARCRQNGLKNIHLFSWPEHCKTYLSRIASCKPRHPQWQRSEDGLG
NSESDSPSDSLRDIQDLSLNLKFSLDGEKNDASGNENSVGSEENSADRKNKLENAVMTWSK
GVLKDKKTGLVEKSDPNANSSKFPPLRRRKHIFVLAVDCDSLTDLLEIIQKVFSSVENERNEG
SIGFILSTSLTMSEVHSFLVSGGLSPNDFDAFICNSGSDLYYPSLNSENRPFVIDFYYHSHIEY
RWGGEGLRKTLVRWATNINDKRAENEAQIVTLAEKLSTDYCYTFKVEKLGMVPPVKEVRKM
MRIQALRSHAVYCQNWTRLNVIPVLASRAQALRYLYVRWGVDLSKMVVFVGECGDTDYEGL
LGGLHKSVILKGVCGSASNQFHANRNYPLSDV

Figure 181: Amino Acid sequence of 415. The conserved group 1 glycosyl transferase domain is underlined.

MAGNEWINGYLEAILDAGRYNVKRRGDGKIGGGGKGGVVATEFDGNEREGSLFSPTRYFVE
EVVNSFDESDLHKTWIKVIATRNTRERNNRLENMCWRIWHLARKKKQIAWDDAQRLAKRRL
EREQGRSEAADDLSELSEGEKEKGDGSHSPEPAKDKIARINSDLQAWSDDEKPRQLYIVLIS
MHGLVRGENMELGRDSDTGGQVKYVVELARALASTKGVYRVDLLTRQITSHEVDSSYGEPI
EMLSCPADAGDGCGAYIIRMPCGPSNEYIPKESLWPHVPEFVDGALNHIVNMARVLGEQIDG
KPVWPYVIHGHYADAAEAAALLSGVLNVPMVLTGHSLGRNKFEQLLKQGRLSREDINTTYKI
MRRIEAEELGLDAAEMVVTSTRQEIEEQWGLYDGFDLKLERKLRVRRRRGVSCYGRYMPR
MVVIPPGMDFSNVKVEDSTESESDLKSLISSDKTPNKRHLPRI**WSEVMRFFSNPHKPMILALS**
RPDPKKNVTTLLKAFGECQHLRELANLTLILGNRDDIEEMPEGSSVVLTNVLKLIDKYNLYGQ
VAYPKHHKQSDVPEIYRLAAKTKGVFINPALVEPFGLTLIEAAAYGLPIVATRNGGPVDILKALN
NGLLIDPHDQKAIADALLKLVADKSLWAECRKNGLKNIHCFSWTEHCHNYLSQVDHCRNRHP
TSRFQIMPIPEEPLSESLRDVEDLSLKFSIDGELKANGELDLATRQKELIEALTRKVHPNGGSP
SISLSSRRQKIFAIALDPYDSGGLFTNIFRVTIKNIMKVARGYSGLNRVGFVLLTGATLQETLNA
FKGSDINVEEFEALSCNSGSSIYYPGRDFIADVDYEGHLEYRWPGDNVRSMVLRLAKAEDG
MEDDIEELKAGCNSRCFAFSIKPGGKVRRIDDLRQALRMRGFRCHIVYSCAGTRLSVMPLFA
SRIQALRYLSIRWGIDFADSVVFVGDKGDTDYEQLLGGLHKTIILNGTVECGSEKLLRSEENFK
RVDVVALNSPRIRIVEDGSEEDISRA

Figure 182: Amino Acid sequence of 416. The conserved group 1 glycosyl transferase domain is underlined.

MAGNEWVNSYLEAILDVGPALDDPKSSSLLLRERGRFSPTRYFVEQVITGFDETDLHRSWLR
AAATRSPQERNTRLENMCWRIWNLARKKKQLEGEEAQRIAKRRLEHERGRREATADMSED
LSSEGEKGDSATDISSQGGERMPRTGSVDIMDKWASRQKDCKLYLVLISLHGLVRGENLEL
GRDSDTGGQVKYVVELARALGTIPGVYRVDLLTRQISAPDVDWSYGEPTEMLRTRNSEFPL
QEIGESSGSYIIRIPCGPRNKYVQKELLWPHIPEFVDGALSHITQMSKVLGEQIGGGRPVWPA
AIHGHYADAGDAAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLAEEINTAYKIRRRIEAEE
LSLDTSEIIITSTRQEIEQQWRLYDGFDPVLERKLRARIKRGVSCHGRYMPRFVVIPPGMEFR
NIVPHDGDMNGEVEKNPPIWPEIMRFFSNPRKPMILALARPDPKKNITTLVKAYGECHQLREL
ANLTLIMGNRDDLDEMSTTNAAVLLSILKLIDKYNLYGQVSYPKHHKQSDVPDIYRLAAKTKG
VFINPALIEPFGLTLIEAAAYGLPVVATKNGGPVDILRVLDNGQLVDPHDQHAIANALLKLVSDK
QLWSRCRENGLKNIHLFSWPEHCRTYLSRIISCKPRGPQWQNNDDKLDKSESDSPGDSLRD
IQDISLNLKFTLDGEKSEGNATFLEENADDAKSNVENTVLTLAKGVLRGIAKGTSTEKANEDIG
AGDFSTFRRRKWIYVIAVDCDATADYIDIIKRIMEATRKENAAGFILSTALTILEVHSLLTSGGLN
LTDFDAFICSSGSDLLYPSSSSDDGPSGLPFVIDLDYRSHIEYRWGGEGLRKTLVRWAASIND
KKDGENIVAEDESGSSSYCFSFKVEDYDLIPPVKELRKLMRIQALRCHVVCCQNGRKLNVIPV
LASRVQALRYLFVRWGMDLSKFVVFVGECGDTDYEGLIGGVHKTVILKGLGCESRKLHAHR
GYPLEHVVPYDSPNVAEAEGSD

Figure 183: Amino Acid sequence of 417. The conserved Glycoside hydrolase, family 16, domain is underlined.

MASPAWALFLGLVLMASGAMGAAPRKPVAVPFGRNYMPTWAFDHIKYFNGGSEIQLSLDKY
TGTGFQSKGSYLFGHFSMDIKLVAGDSAGTVTAFYLSSQNSEHDEIDFEFLGNRSGQPYIVQ
TNVFTGGKGDREQRIYLWFDPTAAYHSYSVLWNMYQIVFFVDDVPIRVFKNSKDLGVKFPFN
QPMKLYSSLWNADDWATRGGLEKTDWSKAPFVASYRGFHIDGCEASVEAKFCATQGQRW
WDQKEFQDLDAFQYRRLRWVRSKYTIYNYCADRKRYPAMSPECRRDRDV

Figure 184: Amino Acid sequence of 418. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domains are in bold.

MAFQGVLSNKMAMALVALGLLVAAAAASGNFNKDFDITWGDGRAQIPSSGQLLTLSLDKTS
GSGFRSKKQYLFGKIDMQLKLVPGNSAGTVTAYYLSSLGSAHDEIDFEFLGNLSGDPYTLHT
NVFTQGKGNREQQFHLWFDPTKDFHTYSILWNPQSIIFSVDGTPIREFKNLESKGVAFPKSQ
AMWIYSSLWNADDWATRGGLVKTDWTQAPFTASYRGFNDEQACVGSSGSSSCSSSSGDK
SWLSQSLDATGQQRIKWVQKNYMIYNYCADTKRFSQGFPPECSLS

Figure 185: Amino Acid sequence of 419. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domains are in bold.

MASPSAPSLCITTLLLVVVSWATSASARNFYQDFDITWGDGRAQILNNGDLLTLSLDKASGS
GFQSKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSTWDEIDFEFLGNLSGDPYILHTNV
FSQGKGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESIGVPFPKAQPM
RIFSSLWNADDWATRGGLVKTDWTQAPFTASYRNFNADNTCIWSSGSSSCTSSSSSSDGN
AWLSEELDSTSQERLKWVQSNYMIYNYCTDAKRFPQGLPRECAMS

Figure 186: Amino Acid sequence of 420. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domains are in bold.

MASRSTSSLCRAALLLMVVSWATSASARNFYQDFDITWGDGRGQILNNGDLLTLSLDKASG
SGFQSKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSTWDEIDFEFLGNLSGDPYILHTN
VFSQGKGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESIGVPFPKAQP
MRIFSSLWNADDWATRGGLVKTDWTQAPFTASYSNFNADNACVWSSGSSSCTSSSSSSDG
NAWLSEELDSTSQESLKWVQSNYMIYNYCTDAKRFPQGFPPECSMS

Figure 187: Amino Acid sequence of 421. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domains are in bold.

MASRSTSSLCTTALLLLVVSWAASAFARNFYQDFDITWGDGRAQILNSGDLLTLSLDKASGS
GFQSKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSTWDEIDFEFLGNLSGDPYILHTNV
FSQGKGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESIGVPFPKAQPM
RIFSSLWNADDWATRGGLVKTDWTQAPFTASYRNFNADNACVSSSGSSSCTSSSSSSDGN
AWLSEELDSTSQERLKWVQSNYMIYNYCTDAKRFPQGVPPECTMS

Figure 188: Amino Acid sequence of 422. The conserved Glycoside hydrolase, family 16, domain is underlined.

MASLSTSSLCIATLLLVVVSWGTFASARNFYQDFDITWGDGRAQILNNGDLLTLSLDKASGSG
FQSKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSAWDEIDFEFLGNLSGDPYILHTNVFS
QGKGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESVGVPFPKAQPMRI
FSSLWNADDWATRGGLVKTDWTQAPFTASYRNFNADNACVWSSGSASCTSSSSSSDGNA

Figure 189: Amino Acid sequence of 423. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domain is in bold.

MAHEGGGPSASSMVVFVSLLLMAAASPAAGNFYQDFDLTWGGSDRAKIFSGGQLLSLSLDR
VSGSGFRSKKEYLFGRIDMQLKLVAGNSAGTVTAYYLSSQGPTHDEIDFEFLGNLSGDPYIL
HTNVFTQGKGNREQQFYLWFDPTRNFHTYSVIWKPQHIIFLVDNIPIRVFKNGESIGVPFPKN
QPMKIYSSLWNADDWATRGGLIKTDWSKAPFTAYYRKFQATACTWSTGSSSCEIGRPASYS
GSTWKINELDAYGRRRLRWVQKYFMIYDYCADGKRFPQGIPAECKRSRF

Figure 190: Amino Acid sequence of 424. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domain is in bold.

MAHEGGGPSASSMVVLVSLLLMAAASPAAGNFYQDFDLTWGGSDRAKIFSGGQLLSLSLDR
VSGSGFRSKKEYLFGRIDMQLKLVAGNSAGTVTAYYLSSQGPTHDEIDFEFLGNLSGDPYIL
HTNVFTQGKGNREQQFYLWFDPTRNFHTYSVIWKPQHIIFLVDNIPIRVFKNGESIGVPFPKN
QPMKIYSSLWNADDWATRGGLIKTDWSKAPFTAYYRKFQATACTWSTGSSSCEIGRPASYS
GSTWKINELDAYGRRRLRWVQKYFMIYDYCADGKRFPQGIPAECKRSRF

Figure 191: Amino Acid sequence of 425. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domain is in bold.

MAVPVFSKVSVSFGLFVGLALLVGLVAGARFEELYQPGWAMDHFVYEGEVLKLKLDNYSGA
GFGSKSKYMFGKVTIQIKLVEGDSAGTVTAFYMSSDGPNHNEFDFEFLGNTTGEPYLVQTN
VYVNGVGNREQRLGLWFDPTTDFHSYSVLWNQRQVVFLVDETPIRVHTNLEHRGIPYPKDQ
PMGVYSSIWNADDWATQGGRIKTDWTHAPFITSYRNFEIDACECPATMAAADNAKRCSSAG
RERRYWWDEPTVSELSLHQNHQLKWVQAHHMVYDYCKDTARFPVMPAECEHHRH

Figure 192: Amino Acid sequence of 426. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domain is in bold.

MASAALAMILFTSVLLKSLMVASAGNLNQEFDITWGDGRAQILNNGDLLTLSLDKASGSGFQ
SKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSKGSTWDEIDFEFLGNLSGDPYILHTNVFSQ
GKGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESSGVPFPKSQPMRIY
SSLWNADDWATRGGLVKTDWSRAPFTASYRNFNADACVWSSGSSSCGSGAASSDGSSWL
TQELDTTSQQRLKWVQQNYMIYNYCSDSKRFPQGPPPECNLS

Figure 193: Amino Acid sequence of 427. The conserved glycoside hydrolase, family 16, domain is underlined and the beta-glucanase domains are in bold.

MQDSRMEKMVSPLSILLCISLVLLAEPRSSDAAPQSKGSFVDNFDIMWSEEHFKTSADGQIW
YLSLDKETGCGFQTKQRYRFGWFSMKLKLVGGDSAGVVTAYYMCSENGAGPERDELDFEF
LGNRSGQPYLIQTNVYKNGTGSREMRHMLWFDPTEDFHSYSILWNSHQIVFFVDQVPVRVF
KNNGEANNFFPNEKPMYLFSSIWNADDWATRGGLEKTDWTKAPFVSTYKDFSFDGCQWED
PFPACVSTTTKNWWDQYSAWHLSEDQKKDYAWVQRNLVIYDYCKDTQRFPTLPWECSLSP
WD

Figure 194: Amino Acid sequence of 428. The conserved glycoside hydrolase, family 16, domain is underlined

MLHSHLGLLSLTCFAVLLVLASGSSPNLPIISFDEGYTQLFGDNNLALHGDGQSVHLALDERT
GSGFASQDLYLHGFFSASIKLPADYTAGVVVAFYMSNGDMYEKNHDEIDFEFLGNIREKNWR
IQTNIYGNGSTSVGREERYGLWFDPSDDFHQYGILWTDSQIIFYVDNVPIREFKRTEAMGGQ
FPSKPMSLYATIWDGSDWATNGGKYRVNYKYAPYVAKFSDLVLHGCAVDPIEHQLSCNDVP
SHKAIPQGISPRQRTKMEYFRKKHMTYSYCYDRARYKVPPPECVINPGEAEHLRVFDPVTFG
DGRHHRPKRHRQSRTSRADASI

Figure 195: Amino Acid sequence of 429. The conserved Glycoside hydrolase, family 16, domain is underlined.

MSASWSVTSCLFFASCALLVVLAVGSPENSNSELPVVSFDEGYAHLFGDDNLVIHGDGKSV
HLTLDERTGSGFVSQDLYLHGFFSASIKLPADYTAGVVVAFYMSNGDMFEKTHDEIDFEFLG
NIRGKEWRVQTNVYGNGSVGVGREERYNLWFDPSDDFHQYSILWTDSLIVFYVDNVPIREV
KRTKAMGGDFPSKPMTLYATIWDGSSWATNGGKYRVSYKYAPYIVEFSDLVLHGCAVDPME
HSSACDAVLPSGSIPTAITREQRVQMESFRKRHMTYSYCYDRARYKIPPPECILSVKEAKHLR
SFDPVTFGQGKRHFAKRRHRRVSATSM

Figure 196: Amino Acid sequence of 430. The conserved Glycoside hydrolase, family 16, domain is underlined

MALLYLSLLLVLLMLPICPGNAQWPPAPGYWPSSRFRSMSFYQGFKNLWGPQHQRVDQSA
LTIWLDSTSGSGFKSVKPFRSGYFGASIKLQPGYTAGVITSFYLSNGEAHPGFHDEVDIEFLG
TTFGKPYTLQTNVYIRGSGDGRIIGREMKFHLWFDPTQAFHHYAILWRPNELIFLVDDIPIRRY
PRKSAATFPMRPMWLYGSIWDASSWATEDGKYKADYRYQPFIARYTNFKASGCSAYSPAW
CRPVSASPYRSGGLTRQQYRVMRWVQAHHMVYNYCRDSRRDHSLTPECRI

Figure 197: Amino Acid sequence of 431. The conserved glycoside hydrolase, family 16, domain is underlined

MKYLRSFLVIVSVLNLVCVSFSSVVSTGNFNKDFFVMWSPDHVNTSADGRTRSMVLDQESG
AGFSSNDMFLFGQIDMKIKLISGHSAGTVVAFYLTSDQPNRDEIDFEFLGNVSGQPYILQTNV
YADGFDNREERIYLWFDPTQDFHNYSILWNLHQIVFFVDSIPIRTYRNHADKGVAFPRWQPM
GVKATLWNGDSWATRGGHDKIDWSKGPFVASFGDYKMDACVWKGNPRFCRAESPTNWW
NNEDFSSLTSTQRRWFKWVRRYHMIYDYCQDNARFQNNLPKECSLPKY

Figure 198: Amino Acid sequence of 432. The conserved glycoside hydrolase, family 16, domain is underlined.

MTSPSTRLCVCLFHLAAISALASAGNFYKDFDITWGDHRSQILNGGQELTLSLDQASGSGFK
SKNEYLFGRIDMEIKLVEGNSAGTVNAYYLSSQGPTHDEIDFEFLGNLSGNPYTLHTNVFSQ
GKGNREQQFHLWFDPTKAFHTYSIVWNTRRIIFLVDNSPIRVFNNLESIGVPFPSNQPMRIYS
SLWNADDWATMGGRVKTDWTKAPFTASFRNFNANACVVSSGSSSCGSKSTNNLQTSAWQ
EQSLNAAGRNRLRWVQQKYMIYNYCSDSKRFPQGLPPECKRSRFL

Figure 199: Amino Acid sequence of 433. The conserved glycoside hydrolase, family 16, domain is underlined.

MPTSISSYSFPRTTMLVVCAILIGSSVVALAGNFYQDFDVTFGDGRVKVLDNGQLVTLSLDKA
SGSGFKSKNQYLYGKFDMQIKLVPGNSAGTVTTLYLHSDGSTWDEIDLEFLGNLSGDPYILH
TNLYSQGKGNREQQFYLWFDPTADFHTYSVLWNPVHVVYYVDGIPIREFKNLNAAGVPYPK
SQPMTLYSTLWDAEDWATRGGLVKTDWSQAPFTASFSGFNASACVWSNGASTCLSSSAAS
AKYPWFSQQLDAASLQTMKSVQQKYMIYDYCKDTKRFPQGLPLECTLKTKS

Figure 200: Amino Acid sequence of 434. The conserved glycoside hydrolase, family 16, domain is underlined.

MALLQENTLFFSLLFLLCMAISVSSHNRPYSPPDVPRLTDLFPHVAVDQQGFSKFFGAQNVRLL
NNGSYANLALDKSSGSGLVSRSKYHYGFFSAAVKLPAGLSSGVVVAFYLSNADAFPHSHDEI
DIELLGHDKRNDWVLQTNIYSNGSVSTGREEKFYFWFDPTQEHHYYSIIWNSHHIVFFVDNIP
VREFPSSGVFSSTYPSKPMSVYATIWDGSQWATHGGKYPVNYKYAPFVVSLAETEMVGCV
SNPRQQPLSSCSNQSTSSGSDPVEGQDFAALSQQQITAMQWARSKLMFYSYCKDTSRFKV
MPPECK

Figure 201: Amino Acid sequence of 435. The conserved glycoside hydrolase, family 16, domain is underlined.

MDPLRRLVSLAVTTSSSSSSSSSLTLLLALLFYAASAAAAFDIVPITFDEAYAPLFGDSNVVRS
GDGKSVRLLLDRFSGSGFISSNLYKYGFFSARIKLPSDYTAGIVVAFYTSNGDVFEKTHDELDI
EFLGNIKGKKWRFQTNVYGNGSTSRGREERYTLWFDPTRAFHRYSILWTANNIIFYVDEVPIR
EIIRNDAMGGDFPAKPMALYATIWDASDWATSGGRYKVNYKYAPFVAEFKDLVLQGCPVDPI
DQYSSGHCYDKLALLEAQDFATVTAQRHAAMRRFRQNYMYYSYCYDTVRYAIPPPECVILQ
SEKERFKDTGRLKFGGSHKKRSRRRGHRIPLVSEEQPVM

Figure 202: Amino Acid sequence of 436. The conserved glycoside hydrolase, family 16, domain is underlined

MDRHPPPHSRRFSLYQPPSYFSLSLLSIFIFSCFLSTSDAAFDVTPISFDEGYRPLFGDGNVV
RSPAGDGVRILLDRFTGSGFISSDMYQHGFFSAKIKLPSDYTAGVVVAFYTSNGDVFEKTHD
ELDIEFLGNIRGKPWRFQTNVYGNGSTSRGREERYTLWFDPTKEYHRYSILWTANKIIFYVDE
VPIREIVKSEAMGGDFPSKPMSLYATIWDASDWATSGGRYKVNYKYAPFVAEFKDLVLEGC
MADPIRQLPASGCHAKDAQLEARDFATITSSQRRAMRRFRERYMYYSYCYDTLRYPVPPPE
CMIIPSEKARFKDTGRLKFGGSHKRRSRRRERIPAASVSDNQASM

Figure 203: Amino Acid sequence of 437. The conserved glycoside hydrolase, family 16, domain is underlined.

MSHPRTQMAISKRRSPSCSLIALTMMVWLWSSHVVPRVAGCDGFDELFQPNWAPEHFECE
GDQTKLTLDSSSGCGFGSRKAYLFGLTSVQIKLVQGDSAGTVTAFYMSSDGPNHDELDFEF
LGNLSGEPYLVQTNVYVNGTGDREQRHSLWFDPTTDFHTYSLFWNRRYITFLVDGIPIRVFA
NKEESHGVPYPKNQPMRVLGSVWNADDWATQGGRVKTNWSHAPFVSSFRAFDIDACELS
PETADVTTKCGQLGRYWWDRPSFNELGRRQSRQLKWVCKKYLVYDYCEDKPRFSELPKEC
VG

Figure 204: Amino Acid sequence of 438. The conserved plant disease resistance response protein family domain is underlined.

MAKPGLTAMVVAALALVVAMVATLAHAEADDPKKVDAWFNGLSHADRKTTRLHFYFHDTLS
GRNPTAVRVAEATMTEKSPTLFGVVNMIDDPLTEGPEPESPLVGRAQGFYGSVGLESMALH
MNMNLVFTTPEYNGSTLSILGHNPALETYREMPIVGGTGVFRLASGVVTAKTYFLNLTTGDA
VVEYKVIALHY

Figure 205: Amino Acid sequence of 439. The conserved plant disease resistance response protein family domain is underlined.

MAKPGLTAMVVAAVALVVAAVALVVAMVAKHAHAEADDPEKVDAWFNGLSHADRKTTRLHF
YFHDTLSGSNPTAVRIAEAKSPTGFGVVNMIDDPLTKGPEPESPLVGRAQGFYGSVGLESTA
LHMSMNLVFTTPEYHGSTLSILGRNPALETYREMPIVGGTGVFRLASGVVTAKTYFLNLTTGD
AVVEYKVIALHY

Figure 206: Amino Acid sequence of 440. The conserved plant disease resistance response protein family domain is underlined.

MGARVIVSLLFLFLIFGSNADAANKRIRNRRPCKRLVFFFHDVLYNGNNAKNATSAIIGAPAWA
NQTILAGQSHFGDLVVFDDPITLDNNLHSKPVGRAQGFYIYDKKDIFTAWLGFSFVFNSTQHT
GSLNFAGADPLMNKTRDISVIGGTGDFFMARGVATLMTDSFEGEVYFRLRTDIKLYECW

Figure 207: Amino Acid sequence of 441. The conserved plant disease resistance response protein family domain is underlined.

MATLSPISSLLLLLLLLLSSGSPTLASAFATALDPSLMGINLGKEKLSHFRFYWHDVQSGPHPS
SVTVVPPPSNSSATFFGLINMIDNPLTLRPDPGSELVGRAQGLYSSASQEEVGLLMIMNFAFV
AGKYNGSGITVLGRNPVLQKVREMPVISGCGLFRFARGYAQATTHTFDRKTGDAVVEYNVY
VLHY

Figure 208: Amino Acid sequence of 442. The conserved plant disease resistance response protein family domain is underlined.

MATLIPISSLLLLVLLSSAAPAPASAFATALDPSLMGVHLGKEKLSHFRFYWHDVLSGPNPSS
VRVTTPPSNASATGFGLVNVIDNPLTLLPDPASELVGRAQGLYSSASQEEVALLMIMNFAFVS
GKYNGSGITVMGRNPVFHKVREMPVISGCGVLRFARGYAQASTHTFDLKTGNAVVEYNVYV
LHY

Figure 209: Amino Acid sequence of 443. The conserved plant disease resistance response protein family domain is underlined.

MVKPGLTAMVVAALALALATAVALACAEVDDPEKVNAWFNRLSHAEHKTTHLHFYFHDTLSG
KNPTAVRIAEATMTEKSPTLFGVVNMIDDPLTEGPEPESPLIGRAQGFYGSVGLESLALHMNV
NLVFTTPEYNGSTLSILGRNPALETYREMPIVGGTGVFRLASGVATAKTYFFNLTTGDAVVEY
KVIAMHY

Figure 210: Amino Acid sequence of 444. The conserved plant disease resistance response protein family domain is underlined.

MALISAPKMLTATTFSQLLLLSTYSILMHSYSSKATVQHPHTTKLVLYFQDIIAGPNANDIPVVG
IPGKLWSFSQFGTVFVADEPITETPDPNSAMVGRAQGMYVISSLDGSNVKTVFSIVFTNQAY
NGSTLELQGAGKQLQRVLEFAVVGGTGKFRFARGYTTLETISFSQGHGVIQFNVTVRHD

Figure 211: Amino Acid sequence of 445. The conserved plant disease resistance response protein family domain is underlined.

MRNLVAHKSCFLVLFLLLLFTSQFSSATKKTFNRDQPCKRFVLYFHDILFGGNDVANATSAAV
ANETGLGNFKFGKLFVFDDPMTKDKNYLSPAVARAQGFYFYDMKNDYNAWFAYSLVFNSTE
HKGTLNIMGADIMAAQTRDLSIVGGTGDFFMARGIATFETDLFQGAKYFRIKMDIKLYECY

Figure 212: Amino Acid sequence of 446. The conserved plant disease resistance response protein family domain is underlined.

MAVHIAKLVAFSLLCMSTVFVAANSHTFARSLLPQELGLKKEKLSHLHFYFHDIVSGRNPTAV
RVAEAKMTNSSATGFGAVVMIDDPLTEGPEMSSKEVGRAQGIYALSSQNDVGLLMVQNYVF
TEGKYNGSTLSVLGRNAVFSGVREMSIVGGSGLFRFARGYAQAKTHTMDRKTGDTVVNYN
VYVFHY

Figure 213: Amino Acid sequence of 447. The conserved expansin/Lol pl family domain is underlined and the C-terminal of the pollen allergen/expansin domain is in bold.

MASVSRVVGLVSLILFSTLAEARIPGVYTGGPWQSAHATFYGGSDASGTMGGACGYGNLYS
QGYGVNTAALSTALFNNGFSCGACFEIKCANEPQWCHSGSPSILVTATNFCPPNYALPNDN
GGWCNPPRPHFDLAMPMFLKIAEYRAGIVPVSYRRVPCRKQGGIRFTINGFRYFNLVLVTNV
AGAGDINKLWVKGSKTGWMSMSRNWGQNWQSNSVLAGQSLSFRVTAGDRRTSTSWNIV
PSNWQFGQTFTGKNFRV

Figure 214: Amino Acid sequence of 448. The conserved expansin/Lol pl family domain is underlined and the C-terminal of the pollen allergen/expansin domain is in bold.

MAAARVMALALAFLGVALSATRMAEARIPGIYTGGPWQSAHATFYGGADASGTMGGACGY
GNLYSQGYGVNTAALSTALFNNGFSCGACFEIKCANDPQWCHSGSSSIFVTATNFCPPNYA
QPSDNGGWCNPPRPHFDLAMPMFLKIAEYRAGIVPVAYRRVPCRKRGGIRFTINGFRYFNLV
LISNVAGAGDIVRVSVKGSRTGWMSMSHNWGQNWQSNSVLVGQSLSFRVTGSDRRTSTS
WNIVPAGWQFGQTFTGKNFRV

Figure 215: Amino Acid sequence of 449. The conserved expansin/Lol pl family domain is underlined and the C-terminal of the pollen allergen/expansin domain is in bold.

MTRASVVFAASLISFSLMWLADARIPGVYSGGPWQTAHATFYGGSDASGTMGGACGYGNL
YSQGYGVNTAALSTALFNNGLSCGACFEIKCANDPTWCHSGSPSIFVTATNFCPPNFAQPSD
NGGWCNPPRPHFDLAMPMFLKIAEYRAGIVPVSFRRVPCRKRGG**MRFTINGFRYFNLVLISN**
VAGAGDIVRVSVKGARTGWMSMSRNWGQNWQSNAVLAGQALSFRVTASDRRSSTSWN
MVPAGWQFGQTFTGKNFRV

Figure 216: Amino Acid sequence of 450. The conserved expansin/Lol pl family domain is underlined and the pollen allergen/expansin family C-terminal domain is in bold.

MQQRRRGSPSSSSSAAALLLGRLWLLLVLGAATTSASAQVKKRVPNARWKPATATWYGSP
DGDGSDGGACGYGSMVDVRPLRARVGAVSPVLFKNGEGCGACYKVKCLDRGICSRRAVTII
VTDECPGGYCSGGNTHFDLSGAAFGRMAIAGEAGPLRNRGVLPVQYRRTPCKYPGKNIAFH
VNEGSTDYWLSLLVEFEDGDGDVGSMHIRPASSSEWIEMKHLWGANWCITGGPLQGPFSV
KLTSLSTNRTLSARDVIPGNWSPKATYTSRLNFF

Figure 217: Amino Acid sequence of 451. The conserved expansin domains are underlined and the Expansin/Lol pl family domain is in bold.

MANFAAISAVALVFLCLKSAFGDYGGWEGGHATFYGGGDASGTMGGACGYGNLYSQGYG
TNTAALSTALFNNGLSCGACYEMRCNDDPRWCLPGTIMVTATNFCPPNLALSNDNGGWCN
PPLQHFDMAEPAFLQIAQYKAGIVPVSFRRVPCVKKGG**VRFTINGHSYFNLVLITNVGGAGD**
VHSVSIKGSRTGWQAMSRNWGQNWQSNAYMNGQALSFQVTTSDGRTVTSYNAAPANWQ
FGQTFEGSQF

Figure 218: Amino Acid sequence of 452. The conserved pollen allergen/expansin family C-terminal domain is underlined.

MAVVGLLLVGCLAMWVCSVDGYGGGGWINAHATFYGGSDASGTMGGACGYGNLYSQGY
GTNTAALSTALFNNGLSCGSCYEIRCVNDRQWCLPASIVVTATNFCPPNNALPSNAGGWCN
PPLQHFDLSEPVFEHIARYRAGIVPVAYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDV
HAVSVKGSRTGWMSMSRNWGQNWQSNNYLNGQSLSFKVTTSDGRSVMSYNAAPAHWSF
GQTFSGVQFR

Figure 219: Amino Acid sequence of 453. The conserved pollen allergen/expansin C-terminal domain is underlined

MAVVGLLLVGCLAMWVCSVDGYGGGGWINAHATFYGGSDASGTMGGACGYGNLYSQGY
GTNTAALSTALFNNGLSCGSCYEIRCVNDRQWCLPASIVVTATNFCPPNNALPSNAGGWCN
PPLQHFDLSEPVFEHIARYRAGIVPVAYRRYVHCNARPSFFGRVKKLGACVKHMNSLVRLVN
LQCPVWGTFCRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHAVSVKGSRTGWMSMS
RNWGQNWQSNNYLNGQSLSFKVTTSDGRSVMSYNAAPAHWSFGQTFSGAQFR

Figure 220: Amino Acid sequence of 454. The conserved Expansin/Lol pl family domain is underlined.

MALLLCFLLSLFISSATACDRCVHQSKAAYFSKASALSSGACGYGSLAVGLNSGFLAAAIPSL
YKDGAGCGACFQIRCKNANLCTKGGTRVIVTDLNRNNNTDFVLSSRAFAAMARQGMSQDIL
RQGIVDVEYKRVPCDYKDRNLAVRVEESSRKPNYLAIKVLYQGGQTEIVAMDVAQVGSSYW
TYMSRNHGAVWNTSRVPDGALQFRFVVTPGYDGKWIWAKSVLPADWQNGVVYDSGVQIT
DIAQEGCSQCDDGSW

Figure 221: Amino Acid sequence of 455. The conserved pollen allergen/expansin C-terminal domain is underlined

MALLQSPSICFPLALLLALLINSSHCFNPKSLNISKVQSNGDWSPAGATWYGSPNGAGSDGG
ACGYGSGVDQAPFSSMVSAGGPSLFKSGKGCGACYQVKCTENAACSGNPVTVVITDECPG
GPCVAESAHFDLSGTAFGAMASSGKADELRNAGVLQIQYQKVKCNFPGAKVAFHVDSGSN
PNYFAALIEYEDGDGELGAVNLKQALDSDSWLPMQQSWGAVWKLDGAGQLRAPFSIKLTSL
DSGKTLVANNVIPAGWQPGQTYRSVVNFAV

Figure 222: Amino Acid sequence of 458. The conserved expansin domain region is in bold, and the conserved pollen allergen/expansin family C-terminal domain is underlined.

MVPLGFLVVGLLSQFVPVSRAYGYYGGWTNAHATFYGGSDASGTMGGACGYGNLYSQGY
GTNTAALSTALFNNGLSCGACFELRCVNDPQWCLPGAIVVTATNFCPPGGWCDPPQLHFD
LSQPVFQHIAQYRAGIVPVAYRRVRCRRSGGIRFTVNGHSYFNLVLITNVGGAGDVHSVAIK
GSRTRWQPMSRNWGQNWQSNSDLNGQSLSFLVTASDGRSVVSYNVAPSGWSFGQTYTG
GQFRY

Figure 223: Amino Acid sequence of 459. The conserved Glycoside hydrolase, family 18, domain is underlined.

MASKSSTSPAFLFSMILALVVGINGGGIAIYWGQNGNEGTLAEACASGNYKFVNLAFLNVFG
NGQTPMINVAGHCDPSSGGCTGLSSEIKSCQARGVKVMLSIGGGVGSYYLPSAEDARYVAT
YLWDNFLGGQSSSRPLGDAVLDGIDFVIATGTNQHWDDLARYLSAYSISGKKVYLAAAPQCP
YPDAWVGGALQTGLYDYVWVQFYGNPPCEYSSGNMGNLEDAWNQWTSIPAGEIFLGLPAS
ADASSGFIPASNLTSIVLPTIKGSAKYGGVMLWSRTVFPSSRASGHDSHVYARDGFPDSPIR
RFPIRRFSVSIQLGYVMIVDGSSSQLLLKRRRLAIPDPMEAEPAKVLSLSLSHSIFSMLMLGL

Figure 224: Amino Acid sequence of 460. The conserved glycoside hydrolase, family 18, domain is underlined and the chitinases family 18 active site is in bold.

MPSPPPSKPSLSLLLLLFSSSLIRASHGGGIAIYWGQNGNEGTLASTCATGKYAYVNLAFLYK
FGGGQTPQINLAGHCDPTSGGCTSTSNGIRSCQNQGIKVMLSLGGGVGSYSLASQADARNV
ANYLWNNFLGGTSSSRPLGDAVLDGIDFDIELGSTKYWDDLARYLSDYSKQGKKVYLTAAP
QCPYPDSHMGAALNTGLFDYVWVQFYNNPPCQYSSGDISKLTSSWSKWVASINAGKMFVG
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Figure 225

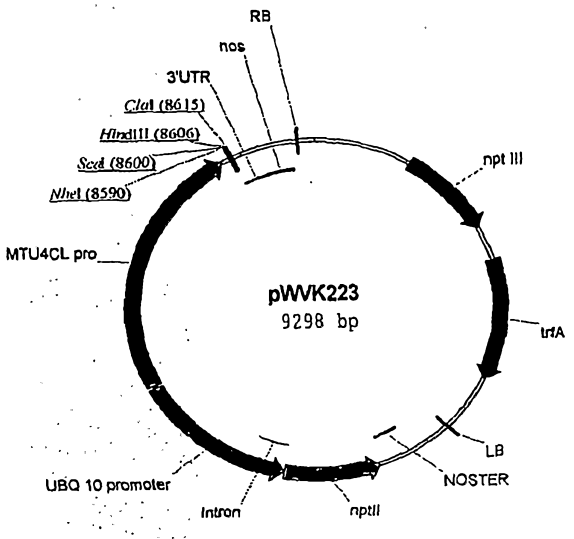


Figure 226

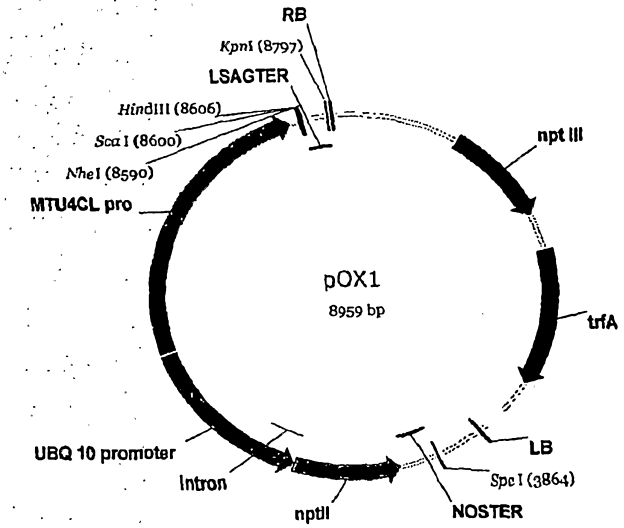


Figure 227

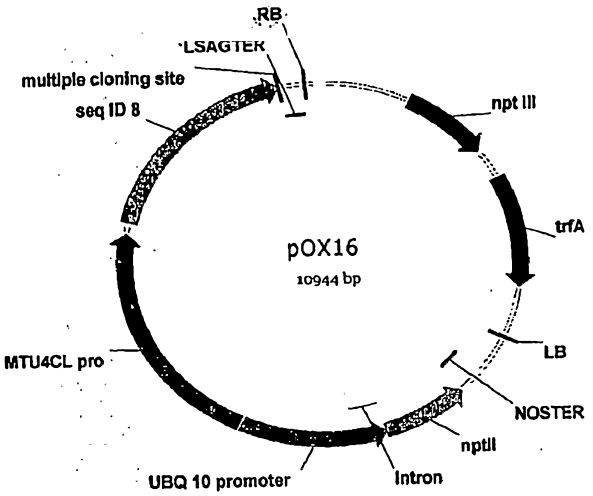
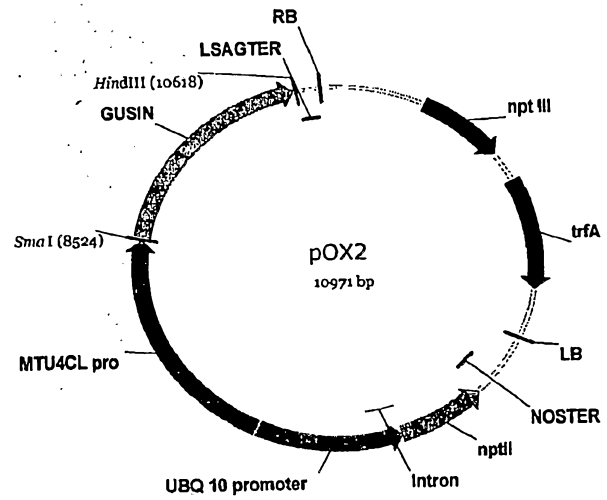


Figure 228



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SEQ ID NO: 61

pinusRadiata_001007
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AGAGGCAGAGGCTCCAGTGGGTACGAAAGAACTACATGATCTACGATTATTGTGCAGACAC
CAAGAGATTCCCCCAGGGACCGCCTCCCGAATGCAAATAAAACCTCAATCCTTTGAATTCAG
AGAATGAACTCTGAATTCTACCTTCCAAGTATTCTGATTCATTTCTATTACATTAATTCTTTCA
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ACAAAA

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pinusRadiata_001184
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CTTGACAATGGCCAACAACTACAGTTGACTCTGGATCGAACTTCAGGTTGTGGGTTTCAATC
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SEQ ID NO: 68
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SEQ ID NO: 69
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CTCCTCGGCCTCACTTTCTAAACTTGCCGAGCTCTCGGAAGACCAGAAGGCATTAATGGAAT
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SEQ ID NO: 70
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SEQ ID NO: 125 pinusRadiata_012207
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SEQ ID NO: 126
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SEQ ID NO: 219
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QKNFSGETPYSIMFGPDICGYSTKKVHTILSYKGKNHPIKKDVPCETDQLTHVYTFILRPDATYSIL
IDNTDKQSGSLYKDWDLLPPKTIKDPNAKKPEDWDDKEYIPDPEDKKPEGYDDIPKEIPDPDATK
PEDWNDEEDGEWTAPTIANPEYKGPWKPKKIKNPNYKGKWKAPMIDNPDFKDDPELYVFPNLK
YLGIELWQVKSGTLFDNILISDDPEYAKKLAEETWAKHKDAEKEAFDEAEKKKEEEEKEKESDDE
EDTDEKEEKSDDEDADELDDEHKEADKKEHELDSEHKEEDKKEHDEL

SEQ ID NO: 233
pinusRadiata_000082
MAPDLKLVFVLLLLSAMYCSGSLDVNGKSMDELSSSQGQLRLGLRKVLEKKATTVTNSDDVRPS
ELGNITPSTTPHSRYTYPITTPTPPTIITTPPAITTPTPVITTPTTPTTTPVLNPPTAPVTTTPTTPTTT
TPAVSGTQSWCVARTNVPENSLQVALDYACGIGGADCKAVQQGGQCYQPITVAAHASYAFNSY
YQKNSKAPGTCDFGGHAIITTTNPSYGSCTYASGSSTISTPPPATIITAPPPPATVGIVAAPPPPAT
IGIGAAPPPPFGTTPTTTTPGYNVSTPTGGITSPIGGGITSPTVGGITGGLGPSASTYNTTPSYGS
APSFFQDLPSSFILFLLSLVVAVILG

SEQ ID NO: 234
pinusRadiata_000808
MGRAGLRTSLLCILIFLSGLALSNAQSKISSSTTGINYGQVADDLPSPELVVGLLQTNSINKVKLYS
VNETVLKAFANTGIELIVGMGNENVGNMTDPTKATEWVNENIRAYLPATKITGIAVGNEVYTGTD
TQLMANLVPAMKNIHSALVSIGADMNIKVTTPHSLAVLGNSFPPSAGSFASNVKSLMKPLLDLLS
QIGSPFFINAYPYFAYKGDPSQISLAYVLFEPNTGVIDPNNNVHYNNMLYAQIDAVYSALSALGYA
NIEVTVSETGWPSKGDANEAGATLQNAQTYNGNLLQLLAQNQGTPLRPKLVLQAYLFALFNED
MKPGPASERNYGLFKPDGTAVYNLGLSGTLSTGSPSTGSTSTGSFTTGTPPPAAYPSTTDSSYS
YYSSAKETYSVISFYNHLLLLGLSTFFVVPLFLP

SEQ ID NO: 235
pinusRadiata_002641
MGASVMGSGDLRMFCLLALVLLSGLVLSNSASSTSSSATGINYGQVADNLPSPEVVVGLLQTRN
INKVKIFSANETVLKAFANTGIELIVAIGNENVGNMTDPTKATEWVNENIQAYLPATKITCIAVGNE
VYTGTDTQLMENLVPAMKNIHSALVSIGADTDIKISTPHSLGVLGNSYPPSAGSFTSDLTSLMKPL
LDFLSQIDSPFFVNVYPFFAYKANPSQISLDYVLFRPNAGVVDPNNNISYNNMLYAQVDAVYSAL
SALGYPNLEVTVSETGWPSMGDADEAGATLQNAQTYNGNLLQLLAQNQGTPLRPKVVLQAYLF
ALFNEDMKTGPTSERNYGLYKPDGTAVYSLGSTGTLSTGSTRTVATASYPTAADGPSSSAKETY
SVVSFYNHLQLLGLSTFFVFLLFRP

SEQ ID NO: 236
pinusRadiata_003151
MVFGISCRMAMVFIVWALMAFLSVGLEDSKALAITGSTVGINYGQIADNLPPPAKVAELLKALKVT
KVKLYDWNPAILKAFANSDVELVVGIGNGFVAGLMDTQAALSWVTQNIQPYLSSTKVTGFSVGN
EVYTGDDAALKANLVPAMRSIHTALVSLGLDSAIKISTAHSLSVLTSSYPPSAGAFDPAIMQLLRE
HLDFLAVTGAPFWINAYPFFAYKDNAGKISLDYALLKPNPGTDDPNTHLHYDNMLYAMVDAVYS
ALGAMGYGNLEVRISETGWPSKGDADELGASIQNAATYNRNLLQRLLKNQGTPMKPNSALQAYI
FALFNEDLKNGPTSERNYGLFKPDESMVYNIGLEGGLTVEFSAYASSAQI

SEQ ID NO: 237
pinusRadiata_003170
MEIIVRVSAITILLPLFIHCIRCGESIGRSRTLVEHSPALGVNYGQMADNLPSPSGVAKLVQSTTISK
LRIYGADPAILQAFANTGIGLLVGISNDQIPSLNQLAVAQNWVKSNIVPFVPATDIIGISVGNEVLFS
GDRVLISQLLPALQNLHTALVEVSLDQQIKVSTPHSMAILSASAPPSAGRFSGSFDMKALLDFLQ
KIGAPFMINPYPYFAYKSDPTDRTLAYALFEPNQGSYDTNTGLKYTNMFDAQLDAVYSAMKYLG

YTDIDIVVAETGWPSAGDPSETGASLQNAIAYNGNLIKHVTSMAGTPMMPNRSIEIYIFGLFNEDL
KPGPTSERNFGLFKTDMTMAYDVGLLRSQSASPSPAAPRTGGPVVAPPTAKVWCIAKPGVDEK
SLKQNLDYACGQGIDCKPIQQGGPCYLPNTMASHAAYAMNAYYQSAGRNSLNCDFAQTGTVTS
KDPSYGGCVYSTVNS

SEQ ID NO: 238
pinusRadiata_003171
MEMIVKATTITILLPVILCCIPCGESGSGGRSLAQRLPALGVDYGQTADNLPPPSAVAKLVQSTSIS
KLRLYGADPAILQAFANTGIGLVVGIGNDQIPSLNQLAVAQNWIKNNIVPFVPATDIIGISVGNEVLF
SGDGSLISQLLPALQNLHTALVEVSLDQQIKVSTPHSLAILSTSVPPSAGRFNESFDMKSLLDFLQ
KIGAPLMINPYPYFAYKSNPTDQTLAYALFEPNPGFYDTNSGLTYTNMFDAQLDAVYSAMKYLG
YPGVDIVVAETGWPAVGDPTETGVSLQNAIAYNGNLIKHVTSMTGTPLRPNRYIQTYIFALFNEDL
KPGPTSERNYGLFKVDMTMAYDVGLLQSPSAAPSPPAPRTGGPVTTPPTGKVWCIAKPGAEEQ
TLEANLNYVCGQGIDCRPIQPGGPCYSPNTVAGHAAYAMNAYYQTAGRNNWNCDFAQTGTLT
STDPSYGACVYPTV

SEQ ID NO: 239
pinusRadiata_005830
MAASKDQMKILLLGCVAIYCYSIIAGGDKIGVNNGMVGDNLPPADQVVALMKQNNIGKYRIFQGS
PEVLPAFANSGIDVIVGIETNRLQEMSSSQDAADSWVKTNIVPFYPATNIKYIAVGNEVVKVKENV
SYLLPAMKNIQTALQNANPQNKIKVSTTHASESVIGNALIPPSKGVFLDDVKDTMSSVLKFLSDNE
APFMANVYPFFSYVNENWRNISLEYALFKSTSPVMQDGDHSYINLFDAIVDTIISAMENLGYQDF
PLIITESGWPSAGLNVATVDNAQAYNNNLIKHVLSNAGTPKRPGRSIETYIFAIFNENQKPGAETE
RHFGLFNPDKTPVYSVNFSPY

SEQ ID NO: 240
pinusRadiata_006138
MEAKTRPTAELDLRRGMGFRWAFILLLSVASIQSTEGFSVTGTVGINYGQIANNLPPPSQVVELL
QASNLTNVRIYDANPQILNALRNTSVEIVVSLGNEYVATMSARPDKARQWVKKNVAAYIPAGTNI
TGVLVGNEVYAGNDTVLKNNLMGALKNIHSALVSLGLDNTVKVSTAHSFDVFVSSFPPSSCAFS
DKSVTYMKQLLDFLSATHAPFLVNVYPYFAYKGDPSNVPLDYALFRPSNGVVDSKTNLHYDNLF
YAQIDAAYSALAALGYGKVEVRVSETGWPSKGDDDELGATPENAKTYNGNLLERLHKKEGTPL
KPNVSVQAFIFALFNENLKSGPTSERNYGLFKPDGTETYDLGLKGLKRIVSSLPPPPTVATGNSS
NSTPTTAITSLTAPSPSVSTGDGTNSSSDSSSAKGMHSLVFISFYLQILALSSFISVLILEH

SEQ ID NO: 241
pinusRadiata_006141
MEAKTRPTAELDLRRGMGFRWAFILLLSVASIQSTEGFSVTGTVGINYGQIANNLPPPSQVVELL
QASNLTNVRIYDANPQILNALRNTSVEIVVSLGNEYVATMSARPDKARQWVKKNVAAYIPAGTNI
TGVLVGNEVYAGNDTVLKNNLMGALKNIHSALVSLGLDNTVKVSTAHSFDVFVSSFPPSSCAFS
DKSVTYMKQLLDFLSATHAPFLVNVYPYFAYKGDPSNVPLDYALFRPSNGVVDSKTNLHYDNLF
YAQIDAAYSALAALGYGKVEVRVSETGWPSKGDDDELGATPENAKTYNGNLLERLHKKEGTPL
KPNVSVQAFIFALFNENLKSGPTSERNYGLFKPDGTETYDLGLKGLKRIVSSLPPPPTVATGNSS
NSTPTTAITSLTAPSPSVSTGDGTNSSSDSSSAKVVL

SEQ ID NO: 242
pinusRadiata_008153
MPTPKPKIFWLLLLLILGLTIHAYAEDYTIGVAYGQYGDNLPSVQESIDLIQRLKVGRVKIYSTNPVIL
KALSNTGIKVSVMVRNEDIAGLSASQSVADKWVNDNIVPFYPATEINIILVGNEILTDYSNKQTWY
QLVPAMQSIWQALVNYNLDHINVGTPLAMDMLGSSVPISAFPPSAGTFRDDIAETVMKPMLEFL
HRTNSYFFMDVYSYFPYLFDPEDISLEYANFGENDKKYTDPNGLVYTNMLDQQLDAVVAAMSK
MGYDDIKLAIAETGWPNAGDISQLGANINYAALYNRRVIRRMVADPPLGTPRRPNQFIPTYIFLLY
DEDKKSGPGTERHWGFVYPNGTLMYEIDLTGKLQDSDYGPLPPPPPPYKGKLWCVADPTADV
YALPSAIDSACSQGDSTCDAIQPGEPCYEPNTVIDHASYAFNSNWQRSKNFYSGCDFNKTAKLV
TEDPSHGNCIYEFVDCVQKSVLC
SEQ ID NO: 243
pinusRadiata_008677

MGEKLGSRGLLILLAFVLCISFTAEAIGVNYGRMGDDLPPPSEVAKFLQTTIIDKVKLFDADPGVL
QAFANTNIGVVVAVANDQIAALNKLPAAQDWVKKNVAPFVPATNIIAISVGNEILSTGDKVLISQLV
PAMQNLHTALVGASLDKQIKVSTPHSLGILSASEPPSIGRFRRGYDRVILKPLLNFLRTTGAPFMI
NPYPYFGYTDKTLNYALFKPNQGVFDNNTGITYTNMFQAQLDAVYSAMKLLGFSDVDIVVAETG
WPSVGDPDQTAVNVENALSYNGNLIKLVNTNAGTPLMPNKTFDTYIFSLFNEDLKPGPTAERNF
GLFKPDMTMVYDVGLMKSESATPAPISTAPVTPATPAPISTAPVTPTTPAPISTAPVTPTTPAPVT
GTDKSWCVAKPDADPNVLQDNIDYACGQGVDCSAIQAGGQCFTPNTVVAHATYAMNSYYQLT
GRHSYDCDFAQTGFLTQEDPSYGTCVYPTI

SEQ ID NO: 244
pinusRadiata_008688
MDGMHGSKVCRYSRMQRTVPMLCTLLVAALGHLVILSAAANSGVFPPFYTRALGINYGRVADNL
PSPSSAVALIKNLQAGYVKIYDADPQVLSALSNTALQVTITVRNQDISNISSSPTVAEQWVQANVL
PHYPATLITAIMVGNEVLSDYQNQATWLLLLPAMANIHASLLNHGLADSIKVTTSLAMDVLSSSYP
PSEGTFRSDVASPVLQPLLDFANRTGSFLFLDIYPFFAWSANPANVSLDYATLSLDRNTAEFQDA
GLSYSNMLDAQLDAVLAAMDRLGFPSVNVVIGETGWPTKGDDNQPGTNVPNATLYNQQLVQK
ALADPPRGTPRRPGAFIPTYIFSLFNEDQKPGPTTERNWGLFYPNGTPVYPIVLSNDAPVLSHIS
VPSQNNAPFPSTPPGPVAAVQWCVVSPVAVAQVDETSLQAALDYACGAGADCSLIEPGEPCYL
PNTLVSHASYAFNSYWQKNKAAGATCDFNGSAVLSSSDPSVGDCVFDHM

SEQ ID NO: 245
pinusRadiata_008701
MGLMWVMFVCSLVLHIAGANEPEASPQPNPGIGVNYGTEGNNLPSPKQVAKMLGKTIVNRVKIY
NSEPSILQAFANTGIAVVVGLENEKVQRISESPTAGQAWVAQRIAPYYPSTLIILITVGNEVLTNSD
GSLDSALVPAIQNIHSGLVALGLDDKIKVSTPHSMAILSSSFPPSASTFATSLLPIMKPLLKFLDDT
GAPFMVNAYPYFAYRDNPKEVSLDYVLFGQSPGVSDPKGFTYNNMLDAQIDSIYSAMAALGHN
DTIPVTVSETGWPSKGDPDDIGVNPDNARNYNTRVIKHVTSNAGTPMRPNRVIETFIFALFNENH
KPGPTTERNFGLLNPDGSKVYDVDLSCGWCASPPPPYSPPASPPPSPISLFSGPPKGSRGGLG
FAVYCIAKPSSDPSVLQESLDFSCGLGGADCASIRQGGPCYNPNTVHAHASYAMNSYYQIHGR
NYWNCDFKSTGLVTFTDPSYGSCHYPQE

SEQ ID NO: 246
pinusRadiata_010276
MAMEGPRSGLALIISNFIFFLLSGSARTGTASNATIGINYGQIADNLPSPQRVAGLLRSINIIKKVKL
YDANREVLEAFANTGIEFVVGLSNEYVGNMTDQAAAVDWVKENVQGYLPGTNITCIAVGNEVFT
SNNTLWMSNLVPAMQNIHSALVSLGLQDSVNVTTAHSSFVLATSYPPSAGAFKPELTAFLRPLL
DFLSQTTSPFLINAYPYFAYKDNADQIPLDYVLFQPNAGTVDPGTNLHYSNMLHAQIDAVYSALS
ALGYSAMEIKVSETGWPSKGDSDEVGATPENARIYNGNLLQLLAQNQGTPMRPSVRLESYVFA
LFNEDQKPGKTSERNYGLFKSDGSPAYDVGLHGSLSGASANPILYSKVVVSSLCSLFLLFFLGL

SEQ ID NO: 247
pinusRadiata_012343
MARISFKLRLQALFLLWLFTSCPLFAAGARHARILESQRDNPGQRLWCIAKPSAYESDLLVNINY
ACSQSGVDCSVLQNGNPCYYPNTPVSHAAVAMNLYFQHYGRNYWNCYFNNTGLVVLTDPSYG
NCEYISQ

SEQ ID NO: 248
pinusRadiata_013199
MGVSLMGRGSLGMSCLWALVLLSGLALSNALSSTSATTTGINYGQVADDLPPPELVVGLLQTSN
IGRIKLYTVNATVLKAFANTGIELIVGVANDIIGNLTDSNSATEWVNENIQTYLPATKIIGIAVGNEVY
TGTDTQLMANLVPAMQNIHSALVSIGADTDIIISTPHSLGVLATSYPPSAGSFQPGLESLLEQLLAL
LSQIGSPFFINAYPYFPYEAQPSQIPLDYVLLEPNASAVVDQNNNVVYKNMLYAQVDAVYSALSA
LGYPNIEVIVTETGWPSNGDADEAGATLQNAQTYNGNLLQLLAQNKGTPLRPNVVLQAYLFALF
NEDMKPGPTSERNYGLFGPNGVEVYNVGLTGSLSIGNKKAVSVGSPTGSADTPYYYNTASAKET
CTDISFYNHLQVLALSSFLVLLLFLP
SEQ ID NO: 249
pinusRadiata_014339

MGMLYWTMDKLLLLFWVLLLMLAQSPGLTRGSTVGVCYGREGDDLPTPDKVAQLVKSIALKNIII
YDSNVQVLQAFAHTGIELIIGIPNSDLLGFSQYQSTADTWVTNNLLPYYPATMIKYIAVGTEVTEST
INVTSLVVPAMRNLQTALKKAGLDQKIKVSSTHALSILSRSFPPSAGAFDSKYAFFLSPLLQFLAQ
TQSPFMINVYPYYAYRDSPRKVSLDYALFRPNDGVIDQNTGLVYTNMFDAQLDALFFALEALNF
RSLRVMVTETGWPSKGGSKEPAATPDNAATYNGNLVRHVINNTGTPSRPGQEIDTYVFALFNE
NRKPGLESERNWGLFYPDETKVYNVDISGTGLPYVATGGNLTSVDGTSWCVASPSAKESDLQK
ALDWACGSGNVDCSPIQPGQPCYEPDNLASHASYAFNSYYQKNGASSVACNFGGTGNITTINP
SYESCVYTTSRNGLANTTSTLSSSGVDSIASFSWLIGWVTTLFLVHLLTILKWL

SEQ ID NO: 250
pinusRadiata_014357
MTFLFWVLVIFVLVGWVQGLGVNWGTQASHPLPPDAVVEMLKDNGITKVKLFDADEHTMKALA
NSGIQVMVGIPNDQLQVMATSTKDAANWVETNVTEFNLDGGVDIGYVAVGNEPFLKAYNGTFIQ
YTFPALQNIQNALNKAGLKNIKATVPLNADVYQGDTPSEGQFRPDINDLMIQICQFLASNGAPFTV
NIYPFLSLYTNENFPVDFAFFDGTGQPVIDGNIQYTNVFDAALDTLFWALKRAGFPDLPVLVGEV
GWPTDGDKHANINFAQRFNQGLLKHIMNGRGTPLRPQNIETYLFSLVDEDAKSIAPGNFERHWG
IFQYDGTPKYALDLSGQTQNTALVSAKGVKYLPRRWCVFNPSASPSVLTQLPDSITYACTHGDC
TSLGFGSSCNSLDYQGNASYAFNSYYQVNNQQNGACGFSSLAIVTESDPSQGTCKFEIQIAVSA
ASNTMNSYLYSLISVAGAVAVVLLSVL

SEQ ID NO: 251
pinusRadiata_014389
MNDKMPLYLLYVFYCLAIFVIPTEAGREWNSIGINYVRAGKNLLSPAEAVSLMKALKIGRVKLYDS
DPEVLTALANSGLSVVIAVKNEEIPTVASSILNADEWVKQSVLAHYPATRINAITVGNEILTDYNNQ
DRWSKLVPAMQNIHSSLVRWNLNKRIKVTTTVAMDALNSSSAPSLARIRDDIAESVMKPLLRFMS
NSKSFYFVNAYPYFAWAANANKVPVDYAIFGAAKEAVQDGGLKYTDMLSAQLDANLAAMEKLG
YPHVKIAISETGWPASGGPGANVDLAATYNRRVVVRMLANPPLGTPRRPRTFVPTYLFALFDAD
NNKHGTTRNWGMLYPNGSQVYPVDMTDKLTDLEFESLKSIRPFPARPTPIRSSISRSSPLTGSY
PSPVPSYYSGPPTLVNPPAASPSTDNIPFSSPIPSVHPNPHPTINVPPYSPSPISTSPPTFSPPIVN
YPPHCMPYPPTTPITTPPFAPYPPSNPTVPYTPNPPSTTPYSPYPPSTPSTPSSQSLWCVAKPT
VPNSVLQQAMNYACGAGADCKSIQPNGLCFSPDTMVAHASFAFNSYWQKNKGIGGTCDFGGT
AMLITMDPSYEGCHFGLI

SEQ ID NO: 252
pinusRadiata_015733
MAASNEQMKRIVIGLIAVFCCAIVTDGDKIGVNYGMQGDNLPPADQVVTLLNGHNIGKMKLFNPD
GGALNAFANSGIDVIVGVSNNDLQAISSSQDSANGWVNDNIVRYSSTSIKYIAVGNEVLPSTQYV
SYLVPAMNNIQTAIQNANLQNIKVSTPHAFNVIGVSSPPSHGAFSDDVKDTMSSILKFLSDNGAPF
MANVYPYFSYAGDTTDIHLDYALFQPTATPVTDGDHSYKNLFDAMVDSIFSAMEALGYSNVPLIV
TESGWPSAGADAATTENAQAYNNNLIQHVLSNSGTPKRPGTNIETYIFALFNEDQKTGDEIERHF
GLFNPDQSPAYSVNFSP

SEQ ID NO: 253
pinusRadiata_015734
MAASNEQMKRILIGFIAIFCCSIVTDGDKIGVNYGMLGDNLPPADQVVTLLNGNNIGKVKLFDPDG
GALNAFANSGIDVIVGVSNSDLQAISSSQDSANGWVNDNIVPYSSTSIKYIAVGNEVLPSTQYVSY
LVPAMNNIQTAIQNANLQNIKVSTPHAFSVIGNSYPPSKGAFSDDVKDTISSILKFLSDNGAPFMV
NVYPYFSYVGDSNDIHLDYALFQPTATAVTDQDHSYSNLFDAMVDSVFSAMEALGYSNIPLIVTE
SGWPSAGADAATTENAQAYNNNLIQHVLSNAGTPKRPGTNIETYIFALFNEDQKTGDEIERHFGL
FNPDQSPAYSVNFYPN

SEQ ID NO: 254
pinusRadiata_019348
MAAMKITLIGCIAILCSILADAAQIGVNNGMVGNNLPHADEVVTLLKEHNIGKYRIFQGSPGVLKAF
ENSGIEVIVGIETNRLQQISSSQEAANGWVKDNIVPFYPATNIKYIAVGNEVFKSNENVQYLVPAM
KNIQTALNMANLQNKIKVSTTHASESVIGNSYPPSKGAFTDEVKDTMRSVLQFLSDNEAPFMAN
VYPFFSYVNNWKNIKLDYALFQSKSPVVESYTNLFDAIVDTIISAMENLGYDNIPLIVTESGWPSG
GNINVATIEYARTYNNNLIRHVLSNAGTPKRPGRSIETYIFALFNEDKPSQDDTERHYGLFYPNKS
PVYAVNFSP

SEQ ID NO: 255
pinusRadiata_020304
MAASKEQAKIILVGFIAIFWGSILTDGDKIGINYGIQGSDLPPADEAVSLMKKNNIGKARIFKAQKD
ALKALADSGIDVIVGVATEDLQGISSSQHSADAWVNDNIVAFYPATNIKYIAVGNLILCSPQYISYLL
PAMTNIQIALQNANLQNSIKVSTTHNMSVIAGIDFPVSNGANGDNVKDTTRSLLNFLIAHNSAPSQ
GTFSDDVKDSMRSILEFLSYHGSPYMANVYPYFIFTGGSSGSMSLDYALFKPTSPLVDGVRRYT
NLFDAMVDTIISAMENLGYPDVPLIVTESGWPSFGEDVATVENAQTYNNNLIKHVLSNAGTPKRP
GTSIETYIFALFRENLKSGPTTEHDFGLFNRDQTPAYTVNFSPLL

SEQ ID NO: 256
pinusRadiata_020305
MAASTEQAKIILVGFIAIFWGSILTDGDKIGVNYGIQGSNLPPADEAVSLMKKNNIGKCRILKANRD
ELKALANSGIDVIVGVGTEELQAISSSQDSADAWVNDNIVAFYPATNIKYIAVGNLILCSPQYISYLL
PAMTNIQTALQNANLQNSIKVSTTHNMSVIAGIDFPVSNGANGDNVKGTTRSLLNFLIAHNSAHS
QGTFSDDVKDSMRSILEFLSYHGSPYMANVYPYFIFTGSSGSISLDYALFKPTSPLVDGVRRYTN
LFDAMVDTIISAMENLGYPDVPLIVTESGWPSFGEDVATVENAQTYNNNLIKHVLSNEGTPKRPG
TSIETYIFALFRENLKSGPTTEQDFGLFNRDQTPAYTLNFSP

SEQ ID NO: 257
pinusRadiata_021499
MERQWFAILIICALGSMVCAVEGLGVNWGTMALHQLPPDIVVQMLKDNGIKKVKLFDADSNTLQ
ALANTDIEVMVAIPNNMLQRFSDSYKAAEKWVDKNVTRYNFSGGVNIKYVAVGNEPFLSAYNGS
YLNNTFPALQNIHKALVKAGLADQIKVTVPLNADVYNSPTDNAVPSAGDFRADIHDLMSEIVTFLN
DNGSPFTVNIYPFLSLYADENFPTDFAYFDGDSQPLVDGNIQYTNVFDANLDTLVWSLKKAGVP
NMTIIVGEVGWPTDGDKHATAAAAQRFNQGLLKHITSNQGTPMRPGNIEAYLFGLLDEDAKSVA
PGNFERHWGIFGYDGQPKYELDLSGPLQNGGLVPAKNVQYLPPKWCVFKTNATDQSKILDSIKY
ACTYSDCTAMGYGSSCNNLDLYGNASYAFNMYFQVMNQYEINCDFTGLAMITEQNASQGTCKF
PIGIAYGAAERSIKIHSILAAVLLGVVTFILSFL

SEQ ID NO: 258
pinusRadiata_021803
MATSAMAVALHALVLLLLFGISFCSGPGKQKLYSSSRGNDTNLAAEEASFFLGNDSSTTTPSTPV
TAGTTWCVAKNNVDDNTLQVALDYACGLGGADCTPIQQGGVCFDPDNVQAHASYAFNNYYVK
NGMLPGSCDFGGSAAPTTLNPSYGKCTFETSTGTSSITSSPGSSITGAMGPSTFNPNGAAFMAP
SLVISSIITILYFSATL

SEQ ID NO: 259
pinusRadiata_024199
MEIIVRVSAITILLPLFIHCIRCGESIGRSRTLVEHSPALGVNYGQMADNLPSPSGVAKLVQSTTISK
LRIYGADPAILQAFANTGIGLLVGISNDQIPSLNQLAVAQNWVKSNIVPFVPATDIIGISVGNEVLFS
GDRVLISQLLPALQNLHTALVEVSLDQQIKVSTPHSMAILSASAPPSAGRFSGSFDMKALVDFLQ
KTGAPFMINPYPYFAYKSDPTDRTLAYALFEPNQGSYDTNTGLKYTNMFDAQLDAVYSAMKYLG
YTDIDIVVAETGWPSAGDPSETGASLQNAIAYNGNLIKHVTSMAGTPMMPNRSIEIYIFGLFNEDL
KPGPTSERNFGLFKTDMTMAYDVGLLRSQSASPSPAAPRTGGPVVAPPTAKVWCIAKPGVDEK
SLKQNLDYACGQGIDCKPIQQGGPCYLPNTMASHAAYAMNAYYQSAGRNSLNCDFAQTGTVTS
KDPSYGGCVYSTVNS

SEQ ID NO: 260
pinusRadiata_024166
MHFTTAALVSALAATPVVYGQLDSKFKAKGKKYFGTCSDSGLLSVSQNANIIKSDFGALTPENSA
KWDSIEPSRNGFNFGGFDTLVNFAQSNGKLVRGHTFVWHSQLPSWVSSIGDAATLTTVIQNHIT
TIATRYKGKIYGWDVVNEIFNEDGSLRSSIFSQRLGENFVSIAFKAARAADSNAKLYINDYNLDSV
NSKVNGLVALVNRQKSAGTPIDGIGSQTHLSAGGSGGVQAAIQKLATTGCDVAITELDIASAPTS
DYVAVVKACLNTPKCVGITVWGISDKDSWRTGANPLLFDSNYQKKAAYNSIISALA

SEQ ID NO: 261
pinusRadiata_000560
MENFVLVLFCIGIGVFFNGGSLVQSAGSFPCDPSTGLSSFPFCNTSLPIGDRVKDLVGRLTLQEK
VEQLVDQTTAIPRLGIPVYLWWSEALHGVSNVGHGTKFGGSIPGATSFPQVILTAASFNTSLWKE
IGQVVSTEARAMYNAGQAGLTFWSPNVNIFRDPRWGRGQETPGEDPLVASLYATNYVQGLQE
TNGADTNRLKVAACCKHYTAYDVDNWNGFQRYTFDAIVSQQDLEDTYDVPFKSCVLNGNVASV
MCSYNKVNGVPTCADKNLLAGTIRGNWSLNGYIVSDCDSVSVYYNQQHYGATPEDAAADAINA
GLDLDCGSFLGQHTEAAVNESKVTESAVDQALINTFTVLMRLGRFDGDPAQQPYGNLGPNDVC
TNENQQLALEAAREGIVLLKNDGSLPLAAKNISSLAVIGPNANVTKTMIGNYAGIPCKYTTPFQGL
SAYTQTLYAPGCANVACISNDSLIAEAVQTASSADATVLIVGGDLSLEAESLDRTSLLLPGQQQQ
LVTQVADASKGPVILVIMSGGPFDISFAKNSDKISGILWVGYPGQAGGAAIADVIFGEYNPGGRLP
VTWYPEEFSINVNMTNMTMRADPATGYPGRTYRFYTGQTVFEFGYGMSYTSFNITVVHAPELIS
VPLDEKYTCSPTQSESCETISLTNTKCDNMSLQVDVDVNNIGNRDGSHVLFLFSTAPSNNVDAP
NKQLIDFKKVYVEAGATERVIFTPDVCKDLSIVDKTGTRMLPVGSRLLYIGDLEHSVSLQISS

SEQ ID NO: 262
pinusRadiata_008324
MGLMENLVFVFVFCIVVFLKEGSLAQSVGNFPCSGQSSFPFCSTSLPIGDRVKDLVGRLTLPEKV
QQLVNTASAIPRLGIPKYEWWSEALHGVSNLGPGTRFGGSVPGATSFPQVIGTAASFNTSLWQ
AIGQVVSTEARAMYNAGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPVLASKYASNYVRGLQ
DTDGGDPNRLKVAACCKHYTAYDVDNWSGVQRYTFNAIVTQQDLEDTYNPPFQSCVADGNVA
SVMCSYNKVNGIPTCADKNLLAGTIRGKWNLNGYIVSDCDSVKVLFESQHYTPTPEDAAADAILA
GLDLNCGDFLGLHTEAAVKAGKLPESAVDAALVNIFTVLMRLGWFDGDPTKQPYGNLGPKDVC
TAEHQQLALEAARQGIVLLKNDGPLPLAANKVHSLAVIGPNANVTKTMIGNYAGIPCKYTTPLQG
LSAYTRTLYAAGCADVLCSGNNLLGAAVQTAGNADATVLIVGGDQTLEKESLDRMDLLLPGQQQ
QLISQVAAASKGPVILVIMSGGPFDISFAKDNNKISGILWVGYPGQAGGAAIADVIFGAYNPGGRL
PVTWYPQDFAAKIPMTNMNMRPDPATGYPGRTYRFYTGKTVYMFGDGLSYTNFKHTLVHAPKL
ISLPMDGKHSCSHKSSNSCEAIRVTHTKCQNLFLEVHVEVSNVGRREGGHVLFLFSSPPSKHHA
PKKQLLGFRKLHLQAGAMEKVHFTLNVCKDLSIVDKTGTRKLPVGSHLLHIGDVQHSVSLQISS

SEQ ID NO: 263
pinusRadiata_008526
MKSLWWLVNIVMMMVLGAIAEEPPFACDSRNPATRSYAFCDSSKPITVRVEDLISRLSLVEKVEQ
LTNNASAVQRLGIPKYEWWSEALHGVSQWGRGIHFNGPIHTATSFPQVILTAASFDVKLWYHIA
QAIGIEARAIYNAGQASGLTFWTPNINIFRDPRWGRGQETPGEDPLLSSRYSVAYVRGLQGDPL
SSSSKTNVRSSTHLRASACCKHFTAYDMDNWEGHTRFSFDAMVTKQDLLDTYQPPFKSCVELG
RASGIMCSYNSVNGVPTCGDFNLLTSTARRDWGFQGYITADCDAVATIYTSHRYTPTAEDAVAD
VLKAGMDVDCGNYLGKYTMSAIAKRKVNESDIDRALRNLFSVRMRLGLFDGDLNHQLEGKLKM
RVVCSAEHQRLALQAARQGIVLLKNSRKHLPLSKTRTKSLAVIGPNANNATTLLGNYYGLPCHTI
TPLQGLQRYVRDTLYYSGCEDLACISNNLFGEAVEIAKKVDEVVVVVGLDQTQEKEERDRIKLTL
PGQQEKLVYQVSHAAKRPVVLVILSGGPVDVSFAVNDPQISSIIWAGYPGQAGGQALAEIIFGDY
NPGGRLPVTWYPQDFVKIPMTDMNMRPNHHTGYPGRTYRFYTGKKVFDFGQGLSYSAYSYEF
SSTTIKKIDLNVTMEHVETLGDTGKAHVRVENSPCRKLKFRCSILVRNHDNMDGRHAVLLYSKSP
ATHKGAPQKQLIGFRSVHVPGKQTTNITFVVKPCDHFSTVEENGQRLLAIGSHSLIVGDTQYSVS
LVTKHSNRNP

SEQ ID NO: 264
pinusRadiata_013209
MGPLAIAIADLLLWMLFLCCGIHGQPMFPCDSRIPNAANYPFCRTTLPIKDRVNDLIGRLTLKEKA
QHLVSRSGAVSRLGIPVYEWWSEALHGVSNVGPGTHFDPRSVPAATSFPQVILTAASFNTALW
EVIGQAVSTEARAMYNAGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPLLSSKYATYYVRGLQ
SPDGRNPNRLKVAACCKHYTAYDLDNWNGVDRFHFDAKVSQQDLEDTYNPPFKSCVIDGHVA
SVMCSYNKINGVPSCADPKLLNGVIRGEWGLNGYIASDCDSVDVLYNTQHWTSTPERAVADVIN
AGLDIDCGTFLGDHAEAAVRVGKLRESLIDEALSHSLTVQMRLGLFDGNPAMQHYGNLGPRDIC
TNQHQQLALEAARQGIVLLKNNNRVLPLSATRIRSLAVIGPNADATNAMIGNYAGIPCRYSTPLHA
LGKYTATIYKPGCENVACNRNLPLIHAAAQAASRADATVIIVGADQSIEAEALDRVNLLLPGEQQQ
MVIETAAFSRGPVILVVMSGGPMDISFAKYNSKISSILWVGYPGEAGGDALADIIYGHHNPGGRL
PVTWYPQDFVAKAPMTNMNMRPDRATGYPGRTYRFYTGRTVYPFGYGLSYTTFSHTLVNAPE
LVSLSLHDSPLMPYNGTNNSCTSVHVENTKCQGLLFDIHMDVHNTGNRDGGHAVLLFFSPPTIH
RSPQKSLMDFRKVHVGAGATERVQFSIDVCKDLSIVDEIGVKKLALGSHILHVGDVQHSLNLQIE

SEQ ID NO: 265
pinusRadiata_013210
MGPKAISNIAGLILWMLFLCCGIHGQPNFPCDSRIPNAASYPFCKTSLPIRARVSDLIGRLTLKEKV
QQLVSKSAGVPRLGIPSYEWWSEALHGVSNIGPGTQFAAGSVPAATSFPQVILTAASFNTSLWE
AIGQAVSTEARAMYNAGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPLVVGRYGTYYVRGLQ
STGGKNRNRLKVAACCKHYTAYDLDNWNGFDRFHFDAKVTQQDLEDTYNPPFKSCVMDGHVA
SVMCSYNKVNGVPTCADPKLLNGIIRGQWKLNGYIASDCDSADVLYNTQHWTTTPERAVADVL
GAGLDVNCGTFLGDHAEAAVKVGKVKEALINRALINSFTVRMRLGVFDGNPATQPFGNLGPRDV
CSEQHQQLALEAAREGIVLLKNNNRVLPLFKTRTRTLAVIGPNADVTNVMIGNYAGIPCRYTTPR
QGLGKYATTIYKPGCQNVACQRNPTLIHDASQAASQADATVIIVGADQSVEREGLDRGSLLLPG
QQEQMVLEVTAASRGPVILVVMSGGPMDISFARDSNKISSILWVGYPGQAGGDALADIIFGHHN
PGGRLPVTWYPQDFVTRVPMTNMNMRPDRATGYPGRTYRFYTGKAVYPFGYGLSYTTFSHSL
VHAPEMVSLSLHENQLLSCHGTNNSCNSVNVENTKCEGLLLDVHLDVQNTGSRDGGHAVLLFS
SPPAVHGAPQKNMVGFRKVHVGAGTTERVHFSIDVCKDLSIADESGAKKLLLGSHLLHAGDVQH
SLNLQIE

SEQ ID NO: 266
pinusRadiata_018923
MRLLTVMSRQIQALCISIVLSLSIVIVISDSTDYACKEHDVNSVSYGFCNTSLPIKERVEDLIRRMTL
EEKVGQLSNGASDVQRLGIPRYEWWSESLHGIATNGPGVNFDGPITAATVFPQIILSAASFNSTL
WFRTAQAIAVEARAMYNVGQAGLTFWAPNINIFRDPRWGRGQETPGEDPLLTSEFAVAFVRGF
QGENESHDTMEKSQRSRARRELKMEGLNSLQTEPSRLMLSACCKHFTAYDLDSWQGHARYTF
NAVVSEQDLKDTFQPPFQRCVQDGHASCMMCSYNQLNGVPVCANYDLLTQMTRNDWGLEGYI
TSDCDAVAIISEDQHYATCAEDAVTDVLKAGMDINCGTYLLRNTMSAIKQGKLHESVIDQSLFNLF
SIRMRLGLFDGDPKQQEYGHLGPDHVCTNEHWQLALEGSRQGIVLLKNIGNALPVSKNKINSIAV
IGPNANATEEMLGDYIGIPCNPVTPFVALQNYIGNVSFSKGCENVACSSNAKFGEAVDIAAKADA
VVIVVGLDLTQETEDHDRVNLTLPGQQQRLVSEVAVASKGPVVLVLMCGGPVDVSFAKDDPRIS
SILWVGYPGEAGGQALAEIIFGDYNPGGRLPMTWYPQKFINVPMTDMNMRPNSSTGYPGRTYR
FYTGETVFQFGEGLSYSNYSYKFSSKDGHIILPFSSPSYGEWVSDYIDIDDIPCESFKFTTKLTVQ
NHGSMDGSHVVLLFSRYGGNFRGAPHEQLIDFKRVHIVAGKTTDVSFLVNPCKHFGMVMEDGR
RVLAIGNHELMVGDTRLSVSLKTSFLSRK

SEQ ID NO: 267
pinusRadiata_022167
MGASAVPIAGLILWILFFRCGIHGELMFACDSRIPNAANYPFCSTALPIKDRVNDLIGRLTLEEKIQ
QLVSKAAGVPRLGIPGYDWWSEALHGVSNVGPGTQFAAGSVPAATSFPQVILTAASFNISLWDA
IGQAVSTEARAMYNTGLAGLTYWSPNVNIFRDPRWGRGQETPGEDPLLVSQYAANYVRGLQLT
DSLDTNRLKVAACCKHYTAYDLDNWNGADRFHFDAQVTQQDLEDTYNPPFKNCVIDGQAASV
MCSYNKVNGVPTCADPKLLNGVIRGEWGLNGYIVSDCDSAEVMYNTQHWTSTPERAVADIMES
GLDVNCGNFLADHGEAAVKVGKLKETFIDTALFNSFTVQMRLGLFDGNPAFQPYGNLGPGDVC
SEQHQQLALEAARQGIVLLKNNNGALPLSPTQIRSLAVVGPNADVTNVMIGNYAGIPCRYTTPLQ
GLGKYTATIHKLGCENVACQSNSILLSEASEAATQADATVIIVGADQTVEAEMLDRVSLSLPGQQ
EQLVLDTADAARGTVILVVMSGGPMDISFARDNPKICGILWVGYPGQAGGDALADILFGQHNPG

GRLPVTWYPEEFAIKVPMTNMNMRPDPATGYPGRTYRFYTGNSVYPFGYGLSYTTFSHSLVRA
PKLVSLSLHESLLKSCRGMNNSCASVEVENTKCQGLLFDLHAEVHNTGSRDGDHVLLLFASPPA
IQGIPQKRLMGFRKVHVGAGGTERVHFSIDVCKDMSIVDGNGVKQLLLGSHLLHVGDTKHTLRV
EIE

SEQ ID NO: 268
pinusRadiata_005555
MGHICSCKWQFLILLCFVFFPFAAPTEGRRLAQTPKVRGVNLGGWLVVEGWIKPSLFDDIKDND
LLDGTKVQFKSAKLNTYVSAENGGGQNAVVNRDNASTWETFKMWRVSDGMYQLRVFSGQFLT
AENGGGGNMSAEADSPADWETFHIIRHHKHPNRVHIRVFNGMYMQAQSQEQLTADYQGDPG
WHDNSATFQMIIVANDLHGDYQLANGYGRDKAKKVYHRHRSSFITDKDFKFLSRNGINTVRIPV
GWWIAYDPNPPAPFVGGSLQSLDNAFKWADHYGLQVIVDLHAAPGSQNGMEHSASRDGSAD
WSNSSDHISQSLTVIDFLASRYSNNSMLLGIELLNEPLATTVPVDVLASYYSNGYQTVRKYSATT
YVIMCQRIGNADPHELYQINDAFSNIVVDVHYYNLFDDYFDNKTAQDNIDFISKNREPQVEALNST
NGPLIFVGEWTNEWKVQGASRSEYQQFGDAQLQAYEKASFGWSYWTLKNEEKHWDFEWNIK
HNYLRLGNSRATSNKSISWRIYAFLLIFGCIYV

SEQ ID NO: 269
pinusRadiata_006798
MVSRMNSGWYVFLCVVILCKCAGAIGYARYKDPSQPIDARVKDLLSRMTLEEKIGQMTQIERTD
ATADVMKHYYIGSVLSGGGSVPAPKASPATWINMVDELQKGAMSTRLQIPMIYGIDAVHGHNNV
YGATIFPHNIGLGATRDPDLARRIGAATALEVRATGIQYTFAPCVAVCRDPRWGRCYESYSEDP
KIVKAMTEIIVGLQGNPPANSTKGGPFIAGQSNVAACAKHFVGDGGTTKGIDENNTVINYQGLFNI
HMTPYFDAIAKGVSTIMVSYSSWNGQKMHANHFLVSQVLKKQLGFKGFVISDWQGIDRITSPPD
ANYSLSVLDGVGAGIDMVMVPDNFTDFISDLTSQVKGGFISMSRINDAVQRILRVKFTMGLFEHP
MADPSLANQLGSKEHRELAREAVRKSLVLLKNGKSASKPLLPLDKNAPKILVAGTHPDNLGYQC
GGWTIEWQGLSGNSTIGTTILEAIKFAVSPSTDVVYQQNPDANYVKGQGFSYAIVVVGEAPYAE
MKGDNFNLTIPLGGGDTIKNVCGSLKCLVILISGRPLVIEPYLPLVDAFVAAWLPGTEGQGVTDVI
FGDHGFQGKLPRTWFKSVDQLPMNVGDKHYDPLFPLGFGLT

SEQ ID NO: 270
pinusRadiata_006799
MDSIWCLFLFLVAFGKCADAAQYTLYKDPSQPVSARVDDLLARMSLEEKIGQMTQTERSVATPD
VMTNYYIGSVLSGGGSAPAPQASPATWMNMVDGLQKGAMATRLQIPMIYGIDAVHGHNNVYGA
TIFPHNVGLGATRDPDLVKRIGAATALEIRSTGIQYTFAPCVAVCRDPRWGRCYESYSEDPTIVK
AMTEIIYGLQGQPPANSTKGVPYVAGQSNVAACAKHFVGDGGTTQGVDESNTVTDYKQLVNIH
MTPYFDAIAKGVSTIMVSYSSWNGHKMHANRFLISHVLKKQLSFKGFVISDWQGIDRITSPPNAN
YSLSVLESVGAGIDMVMVPFNFADFINDLTSQVKGGFIPMSRINDAVQRILTVKFTMGLFEHPMG
DPSLANQLGSKEHRDLAREAVRKSLVLLKNGKSASQPLLPLNKNAPKILVAGTHPDNIGYQCGG
WTIEWQGLSGNITIGTTILSAIQSAVSSSTEVVYQQNPDANYVKEQGFSYAIVVVGEPPYTEMFG
DNLNLTIPLGGGDTINNVCGSLKCLVILISGRPLVIEPYLPLVDAFVAAWLPGTEGQGVTDVIFGDY
SSQGKLSRTWFKSADQLPMNAGDQHYDPQFPLGFGLTTTVAENISSSFGVL

SEQ ID NO: 271
pinusRadiata_006802
MANRMDSGWCLLLFVVVLCRCAEAVEYAKYKDSSQPIDARVDDLLARMTLEEKIGQMTQIERTV
ATADVMKNYYIGSVLSGGGSEPAPQASPATWINMVDGLQKSALSTRLQIPMIYGIDAVHGHNNV
YGATIFPHNIGLGATRDPDLVRRIGAATALEVRATGIPYTFAPCVAVCRDPRWGRCYESYSEDPT
VVKSMTQIILGLQGQPPAKYKRGIPFVAGESNTVACAKHFVGDGGTTDGINENNTVISYDGLVNI
HMAPYFDAIAKGVSTIMISYSSWNGVKMHANRFLVSQVLKKQLGFKGFVISDWQGIDRITSPAGA
NYSLSVFDGVSAGIDMVMVPYNFMDFIGDLTSQVKSGLISMTRINDAVRRILRVKFTMGLFEHPM
ANPSLANQLGSKAHRELAREAVRKSLVLLKNGKSDSKPLVPLDKNATKILVAGTHPDNLGYQCG
GWTITWQGLSGNTTKGTTILEAIQSAVSPSTEVVYQENPDANYVKGQGFSYAIVVVGEAPYAET
AGDNLNLTIPLGGGDTINNVCGSVKCLVILVSGRPLVITPYLPLVEAFVAAWLPGSEGQGVTDVIF
GDYGFQGKLSRTWFKSVDQLPMNVGDKHYDPLFPFGFGLTTTVAKNL

SEQ ID NO: 272
pinusRadiata_006803

MDSGWYLLLFVVVLCRCAEATEYAKYKDPSQSITARVDDLLARMTLEEKIGQMTQIERTVATADV
MKNYYIGSVLSGGGSAPAPKASPATWMNMVDELQKGAMSTRLQIPMIYGIDAVHGHNNVYGATI
FPHNVGLGATRDPDLARRIGVATALEVRATGIQYAFAPCIAVCRDPRWGRCYESYSEDPKIVKT
MTEIIFGLQGQPPANSTKGVPFLAGQSNVAACAKHFVGDGGTTEGINENNTVISYKGLVHIHMAA
YFDAIAKGVSTVMVSYSSWNGGKMHANRFLVSRVLKKQLGFKGFVISDWQGIDRITSPAGANYS
LSVFDGVSAGIDMVMIPYNFKDFINDLSSQVKSGLIPMTRINDAVRRILRVKFTMGLFEHPLGNPS
LANQLGSKEHRELAREAVRKSLVLLKNGKSANKPLLPLEKNASKVLVAGTHPDNLGYQCGGWT
MEWQGLSGNITVGTTILEAIKLAVSPSTEVVYEQNPDANYVKGQGFSYAIVVVGEAPYAETFGDN
LNLTIPLGGGDTIKTVCGSLKCLVILISGRPLVIEPYLPLVDAFVAAWLPGTEGQGVTDVIFGDYRF
QGKLARTWFKSVDQLPMNIGDQHYDPLFPLGFGLV

SEQ ID NO: 273
pinusRadiata_013555
MAACINIHARNCPQGCFKFVILVLITSCLAYGSEASEVRRLTIGTQKYHSVALGGWLVIEGWIKPS
LFDGIPDNDLLDGTQIQLKSMKLGTYIVAENGGGQKVAVNRTNPLKWETFRIWRVRDGYYQLRV
FNKQFLGADNGGGGVVKAVATTPRSWETFQIIRNNADRNRVHLKALNGMYLQANSKDQLTADF
KGEPAWDGNNAATFEMSFTGHMQGEFQISNGYGPERAAQVLKEHRSTFIREDDFVFLSKQGIS
AVRIPVGWWIASDPKPPAPFVGGSLECLDKAFSWAQNHGIKVIIDLHAAPGSQNGDEHGGGRD
GYIEWADSQKNIDTTLSTIDFLASRYAAHPALLGIELLNEPRSSGISLNNLTAYYTQGYNIVRKYSS
SAYVIMCNRIGPVDPKELFQINNGLFRTVVDVHYYNLFDDSTFKHMTVQQNIDYIKNTRAQTLQS
LVSANGPLIFVGEWVAEWEVQNATQSDYERYGDAQFQVYGTASFGWTYWTLRNIGNRHWDF
QWMVNNQYLRLPSIQI

SEQ ID NO: 274
pinusRadiata_014884
MAAYIDVHAKKLSQRCFGFVITLLVFTSSLAYGRKILEARRLTNDTQKYHSVNLGGWLVIEGWIKP
SLFDGIPDKDLLDGTQIQLKSMKLGTYVVAEDGGGTIMAVNRTNPSGWETFSLWRARDGYYQF
RVFNKQFVGADNGGGGIVEAVATTPNSSETFQIIRNPANSNSVHIKVFNGMYMQAQSKDQLTAD
FEGEPGWDDNNAATFEMTIVRTLQGEFQISNGYGPEKATQVLNEHRSTFITEDDFVFMSKNGIS
AVRIPVGWWIASDPYPPAPFVGGSLACLDKAFSWAQNHDIKVIIDLHAAPGSQNGDEHSGTRDG
FIEWPESQENIDKSLSVIDFLAARYAAHPALLGIELLNEPRSPAVSLNNVTDYYSRGYDIVRKYSS
SAYVIMCNRIGPADPKELFQMNNGLSRTVVDVHYYNLYDDATFKNMTVQQNIDYIKTTRAQTLQ
SLVSANGPLIFVGEWVDEWELNSATQSDYQRYGDAQLQVYGEASFGWAYWTLRNIGSRHWDL
EWMVQNQYLLLPASNQS

SEQ ID NO: 275
pinusRadiata_001975
MGFIHTMAIPESKVFWLLLAIVGGVIHAYAEDYTIGIDYGQLGDNLPSTEEAIHLIQRMKVGRVKIY
DTNPEILKALAHTGIKVSVMVKNEVIANVSANQSFADKWVKNNVVYFYPATKINIVLVGNEILSDY
SNNQTWYQLVPAMLRIRRALVRYKLHHIKVGTPSAMDVLNTSFPPSSGAFRDDVAETVMKPML
EFLTRTRSYFFIDVYPYFAWSSDPTNISLEYASFGDHDKNYTDPNGLVYTNLLDQQLDAVVAAM
SKLGYEDIRLIIAETGWPNAGDLNQLGANIFNSAHYNRRLIRRMLADPPLGTPRRPNQFIPTYIFSL
FNEDQKSGPGTERHWGLLYPNGTRVYEIDLTGELQDSEYKPLPPPPPPYTGKLWCVVDANANV
SSLPSAINYACSQGNNTCASIQPGKPCYQPNTVIDHASYAFNSYWQQFKNSGGTCYFNGAATL
VTQDPSRGSCTYPFT

SEQ ID NO: 276
pinusRadiata_003684
MRRRMGLLFSVLVMFVWVGWVRGLGVNWGTQASHPLPPDILVGLLKDNGIKKVKLFDAEERA
MRALAKSGIEVMAGIPNDQLQRMANSQKAAANWVEANATEFSLDGGVDIRYVAVGNEPFLKAY
NGTFIQYTFPALQNIQNALNKAGLKNIKATVPLNADVYQGDTPSEGQFRPDINDLMIQICQFLASN
GAPFTVNIYPFLSLYTNENFPVDFAFFDGTGQPVIDGNIQYTNVFDAALDTLFWALKRAGFPDLP
VLVGEVGWPTDGDKHANINFAQRFNQGLLKHIMNGRGTPLRPQNIETYLFSLVDEDAKSIAPGN
FERHWGIFQYDGTPKYALDLSGQTQNTALVSAKGVKYLPRRWCVFNPSASPSVLTQLPDSITYA
CTHGDCTSLGFGSSCNSLDYQGNASYAFNSYYQVNNQQNGACGFSSLAIVTESDPSQGTCKF
EIQIAVSAASNTMNSYL

SEQ ID NO: 277

pinusRadiata_008566
MATNIILIVCIAIFCCSILAESAQIGVNYGMLGTSLPPAGQVVTLMKSNNIGKMKIFQADKDALKAFA
NSGIEVIVGVGNNELQLISSSQDAANGWVNDNIRPFYPATNIKYIAVGNEVLIKTTYGSYLVPAMR
NIQTALQNANLQNNIKVSTTHSSDVSEGYPPSNGVFKDEVKDTMKSVLQFLLDHGSPFMGNIYP
YFSYINNRAQITLDYALFKSTSTVVPDKGRSYKYLFDALVDTLVSAMEALGYPNIPLIVTESGWPS
AEADVATVDNARTYNNNLIRHVLSNEGTPKRPGKSIETYIFALFNENKKNPGTEQHFGLFYPNQQ
HVYPVNFSP

SEQ ID NO: 278
pinusRadiata_013146
MATFKDQSRIFLIGCVAIFCCSVLADGDKIGVDYGMTADNLPSPDEVVTLMKSNNIGKTRIYQEN
DVVLQAFANSGIDVIVGVANEELKNISSSQDSANRWVNEHIVPFYPATNVKYIAVGNEVLITLDNV
QYVPYLVPAMNNIQTAIQNAKLQDSIKVSTTHRPDVSSGYPPSKGVFVDAVKDTMSQILNFLSQN
GGPFMADVYPYFSYIGNTKDISLDYALFKSTSTVVQDGDHSYTNLFDAMVDTLLSAMEASGYPNI
PIVITESGWPSAGAEVATIENAQTYNNNLIKHVLSNAGTPKRPGMSIDTYVFALFNEDLKPGDETE
KHFGLFDPNTKQPVYSVNFSP

SEQ ID NO: 279
pinusRadiata_014358
MKILSRFLLLLLLIASFSEVALGGPFVGVNIGTDVSNMPSASAVVALLKNQQITHVRLYDADRQML
TALANTGIEVVVSVPNNQLLGVGQSRSTAANWVNKNVAAYLPNTNITAIAVGSEVLTTIPNAALVL
VPAMRFLHSALVAANLDGQVKVSTPHPAELILDSFPPSQAFFNSSWNSVMIPLLAFLRDTKSYLM
LNVYPYYVYMQGNGVVPLDYALFRPLPPNKEAVDPNTLLHYTNVFDAVVDAAYYAMASLNFTNI
PVVVTETGWPSMGDANEPDATVDNADTYNSNLVRHVLNSTGTPKLPGVAVNTFIYELFNEDLRP
GGTSEENWGLFSANSTPVYVLHLNGAGSPLGNDTSAQTFCVALSGADNQLLQAALDWACGPG
QADCSAIQAGQSCYTPDTVADHASYAFDSYYHKMNMAPGSCDFNGVGTITNTDPSHGSCIFQG
SVSANGTSSVNGTVLGNETFPLTGTNITSLNSSAPHLQSQIHPILFPLVALPILFWNLPIL

SEQ ID NO: 280
pinusRadiata_014570
MGSLNRSMVCSMLISVFFCFVFGALHMVSADFANKQALGINYGQVANNLPSPAIAVQLMKSINV
GYVKIYDADSQVLTALANTSLPLVITVANEDIPNIASGSSNADQWVQKNVLPYYPATQIFMIMVGN
EVLSNPQIQSTWSQLVPAMENLQASLVKHNLDDSIKVTTSVAMDALASSYPPSNGSFKADIAASI
MQPMLSFLNRTDSYFFVDAYPYFAWSSNPVNISLNYVLFGVSTTEILDGQLQYSNMLDAQLDAV
VAAMADLGFPQVKLAVSETGWPTKGAADEPGANVANAAKYNRRLVSRFSASPPVGTPRRPGA
FIPVFVFALFNEDQKTGPVTERNWGVFYPNGTPVYNIDLSGGNQGSAYTPIIRSGTNNNTFSAPA
GAPASAAAPIPTAAPITTAAAPIPTAAPITTAAPTPSTLQQWCVAKSGVNNMTAVQQALDYACGA
GADCSAIQAGNACYQPNTVEAHASYAFNSYWQSTKSNGGTCYFNGVAALTTSDPSFQGCSFP
FQ

SEQ ID NO: 281
pinusRadiata_014985
MASSNKVGVCYGMVANNLPLPDQVANLIRSRNIGKVRLFQAHHEAQRALQNSGGIEVIVGVGND
ELQKIASDQAAANGWVNDNIRQFYPATNIKYIAVGNEVFSSENRQHLPYLVPAMRNIQTAVQNA
NLQSSIKVSTTHATSVLGNSYPPSQGEFADELKSSMSDVLNFLAENGSPFMANVYPYFSYIYNQ
AQISLDYALFKSADPVVSDEGRLYKSLFDALVDSLISAMEKSGHPDIPIVITESGWPSAGNEAATV
ENAQTYNNNLIKHVLSNAGTPKRPGQHIDTYIFALFNENLKGGDEPERHFGLFYPDQNLVYPVNF
SP

SEQ ID NO: 282
pinusRadiata_023047
MWVLPLLLLLLFLFCPFILGARVNGGAFVGVNIATDLSNMPSPSQVVSLLQTQQIKHVRLYDVER
DMLLALANTSIQVVISIPNNQVLAIGESNSSAANWVKKNVADYLPNTNITGIVVGNEVLTTLPNAAL
VLVSAMKFLQSALVAANLDQQVKISSSHSSDIILDAFPPSQAIFNQSFNDIIGPMLEFLQDTGSYF
MMNLYPYYTFMEGKGKVPLDYALFEPLTPDKEAVDPNTLLHYTNVFDALVDAAYYSMGNLNYT
NIPVVVAETGWPSDGDATEPYATINNADTYNSNLVIHVLNITGTPKRPTIPVNTYIYELYNEDLRP
GPLSEQNWGLFFANSSPVYVLHLTDAGEFLANDTTNQTFCIAKPGADLKLLQAALDWACGPGE

ANCTAIQGGEDCFNPDTVEAHSSYAFDSYYHNTGMAAGSCDFKGVAIITTTDPSHGSCVYPGS
GGANQTSASKNNTSVSGSMDMGHMDNSVLMMLHILLLFLWF

SEQ ID NO: 283
pinusRadiata_006216
MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAIGVDEVVLAINYQPEVMLSFLKAF
ETKLGIKITCSQETEPMGTAGPLALARDKLIDGSGDPFFVLNSDVISEYPLKQMIDFHTKHGGEAS
IMVTKVDEPSKYGVVILDEETGKVERFVEKPKVFVGNKINAGIYLLNPSVLDRIELRPTSIEKEVFP
KIAQEKQLYAMVLPGFWMDIGQPRDYISGLRLYLDSLRRNTSDKLATGVNIVGNVIVDSTAQIGE
GCLIGPDVAIGPGCVIEAGVRLSRCTIMRGVRIKKHACVSGSIIGWHSTVGQWARVENMTILGED
VHVSDEVYSNGGVVLPHKEIKSSILKPEIVM

SEQ ID NO: 284
pinusRadiata_013260
MSIGDRKSVAVIMVGGPTKGTRFRPLSLNLAKPLFPLAGQPMVHHPILACKKIPNLAHIYLIGFYE
EREFALYVSSISNELKIPVRYLREDKPHGSAGGLYHFKDLIMEDDPANIFLLNCDVCCSFPLADML
EAHCKYGGMGTILVIKVSAESANQFGELVADSVTGELLHYAEKPETFVSDRINCGVYVFTPDIFL
GIQDVSTQRKDRATMRRVSSFEALQSATKALPTDFVRLDQDILTPLAGKKKLYTYETSDFWEQIK
TPGMSLRCSSLYLSQYRLTSPELLAKSNGGRTATIVGDVYIHPSAKVHPTAKIGPNVSISANARIG
AGVRLIGCIILDDVELKENSIVMHSIVGWKSSIGRWSRVQGEANYTSKLGITILGEDVTVEDEVVV
ANCIVLPHKMLNMSVQEEIIL

SEQ ID NO: 285
pinusRadiata_014596
MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAIGVDEVVLAINYQPEVMLSFLKEF
EAKVGIKITCSQETEPMGTAGPLALARDKLDDGSGEPFFVLNSDVICEYPLKQMLEFHKKHGGE
ASIMVTKVDEPSKYGVVILDEETGRVDRFVEKPKIFVGNKINAGIYLLNPSVLNMIELRPTSIEKEV
FPKIASKKQLYAMILPGFWMDIGQPKDYISGLRLYLDSLRRNLPKKLSFGAHIIGNVIVDETAQIGE
GCLIGPDVAIGPGCVIEAGVRLSRCTVMRGVRIKKHACVSGSIIGWHCTVGQWARVENMTVLGE
DVHVCDEVYSNGGVVLPHKEIKSSITKPEIVM

SEQ ID NO: 286
pinusRadiata_021340
MAGEGKVIAVIMVGGPTKGTRFRPLSLNIAKPLFPLAGFPMVHHPILACKKIPNLAHIYLIGFYDER
LFSLYLSNVSSELKIPVRYLCEDKPHGSAGALFKFHDLLMEDNPKEIFVMHCDICCSFPLVDMQM
AHRNYGGIGTMLVKKVSTEATGKFGELVADPLTKELLHFAEKPETHVSDYINCGVYIFTPDIFVTM
QTLTPTRKERGIFRRLSSFESLEFSSPSVQKDVIRLDEDLFTPLVGKKMIYTFETSDFWEQIKTPG
MSLRCSSLYLKQYHMKTPELLSSADAIMTVNIIGDVYIHPSSKIHPTAKIGPNVSISANARIGPGVR
LRDCIILDDVEVQDNAIVMHAIIGWKASIGKWARVQGERNYGAKNGISILGEAVTVEDEVVVLSST
VLPHKALNQSVQGEIIL

SEQ ID NO: 287
pinusRadiata_022975
MKALILVGGFGTRLRPLTLSLPKPLVDFANKPMILHQIEALKEAGVDDVILAVNYQPESMMKFLTE
FEAKLGIRIQCSREIEPLGTAGPLALAKDKLIDGSGQPIFVLNSDVICEFPLKEMLEFHKSCGAEAS
VMVTRVDEPSKYGVVVLDEETGRVKRFVEKPQMFVGNKINAGIYLLNPSVLDRIELKPTSIEKDIF
PRIAEENQLYAMVLPGFWMDIGQPRDYLTGLRLYLDYLRTKSDVLASGSQFQGNVLIDESVQIG
EGCLIGPDVSIGPGCIIEAGVRLSNCAIMSGVRIKKHACVSWSIVGWHSTVGQWARAENMTILGE
DVHISDEIYSNGGVVLPHKEIKSNILKPEIVM

SEQ ID NO: 288
pinusRadiata_007714
MDCRKAGVLALFDVDGTLTPARKVVSQEMLEFMQELRKVVAVGVVGGSDLAKITEQLGKTVISD
YDYVFSENGLVAHKGSKAIGNQSFKAFLGDEKLKELINFTLHYIADLDIPVKRGTFIEFRSGMLNV
SPIGRNCSQEERDEFERYDKVHGIRTKMVEVLREKFAPLNLTYSIGGQISFDVFPQGWDKTYCL
RYVENDFQEIHFFGDKTYKGGNDHEIFESSKTIGHTVTSPEDTRRQCTELFFQ

SEQ ID NO: 289
pinusRadiata_013469
MAGNEWMNGYLEAILDGGGVGDDNDYTRQKKESSVKSGVTVIPQLGAFNPARYFIDEVVHGTD
ETDIHHFWVKVTATKNPEERNTRLENLCWRIWHISRRKKKGKLEQSKRLQKLRQERERGRRDV
TEDMSEDLSEGEKLGGDGQGLKFSESHYNLELLTEQSLKGKRLYVIMISLHGLVRGENMELGRD
SDTGGQVKYVVEFAKALAKMPEVYRVDLLTRQICSPDLDSSYGEPTEMLTSDQDDDILESGGAY
IVRIPCGCKEKYIQKELLWPYIPEFVDGALGHILNISKALGDLIGEDTPVWPHVIHGHYADAGDAA
CLLSGALNVPMVLTGHSLGRNKLEQLLKQGLHSKEDINATYKIMRRIEAEELCLDSAELVVTSTR
QEIEEQWGLYDGFDLELNRKLRQRAKRGVHSYGRYMPRMSVIPPGMDFSNVVVHDENSDNDL
DNDSVQLPESPLWGEIPRFLNNPSKPIILALARPDPKKNMATLVKAFGECIKLRKLANLMLIMGNR
DDIDQMPAASANVLTTVLKLIDKYDLYGEVAYPKHHKQSEVADIYRIAAKTKGVFINPALVEPFGL
TLIEAAAHGLPMVATKNGGPVDIQRTLNNGLLVDPHNDKEIAAALYRLVVDKNLWVECRQNGLQ
NIHLYSWPQHCRTYLSRISQCRMRHPQWQSENDQNENMDSESDSGSFKDAPDTSLRLSLDAD
RPSRSSSVNSPFDLDKLLQNEENVGGISEHIRMIIEKTKDNQSKLGDTNDVNSQEKQSIEHSNSL
GSSGKHLLRRRKRLFVIAVDCYDASGEPLLSRQAIIIQEIMNAVCSAGNFSSPGFILSTALTVPETI
SMLQSIGIKVSAFDALICSSGSQLLYTAGDNPDSPIYPDPDYDSHIDYRWGAEGLRKSMKKLRGP
ENSRFLAEDAEASNFHCLAYQVKNISTAPKADELRRQLRMRGLRCHVIYTQNCSRLRVLPLHAS
RSQALRYLYVRWGLDIANMYVFLGEKGDTGYEELIGGMHKTLILKGTVVDGSEKMLRSPTSYGS
GDVFPSESPNIVSVTVSDDNEEFNSQQIIASLHWFEGSAS

SEQ ID NO: 290
pinusRadiata_016491
MAGNDWINGYLEAILDAGAGFTEAETRPALTVADGGGFNPTKYFVEEVVTGFDESDLHRTWIKV
VAMRNSLERNNRLENMCWRIWHLARRQKQIEWDDAQRLAKRRIEREQGRRDATEDMSEDLSE
GEKADVATPRATPKRAFSRNFSDLQVWSDDNKGKRLYIVLISLHGLVRGENMELGRDSDTGGQ
VKYVVELARALSMMPGVYRVDLLTRQISSPDVDWSYGEPTEMLSSGSYDVDGHGGGESSGAYI
IRIPCGPRDKYIPKELLWPYIQEFVDGALGHILNMSKVLGDQAGKGDPVWPYVIHGHYADAGDSA
ALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINATYKIMRRIEAEELSLDAAELVITSTKQ
EIVEQWGLYDGFDVRLEKILRARAKRQVSCHGRFMPRMVVIPPGMDFSNVVVADQEPAEADGD
LAALINGDVNLSPKALPPIWSEVMRFFTNRHKPMILALSRPDPKKNLTTLVKAFGECRPLKELANL
TLVMGNRDDIDEMSGGNAAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINP
ALVEPFGLTLIEAAAYGLPMVATKNGGPVDIHSTLTNGLLVDPHDQKAIANALLELVADKNLWNE
CRRNGLRNIHLFSWPEHCRKYLSRVAVCRMRHPQWQTDTLMDTTMDEESMGDSLKDVQDMS
LRLSVDGEKYSVNGSLDNSAEVDKLLAAKGDPETYNQVKRILDKLKKGPPSSITQETEPKPDVNE
PRAPANNVSVSNKYLALRKKRKLFVIAVDCYDDTGNVSPRMLEIIQEIIKAVRSDATAARFAGLVL
STALTVDEILGMLNSGNILPHEFDALICSSGSELYYPTIPAYPDDGSNKKLCPDPDYDSHIDYRWG
GEGLRKTMSLLTASERDGQEKQERVIFEDAKHSNAHCLAYVVKDSTRVRKVDEFRQRLRMRGL
RCHPMFCRNSTQLHVIPLLASRSQALRYLFVRWGLDVANMHVFVGETGDTDYEEMLAGLHKTII
LKGAVDRGSEKLLRGSGSYQREDIVPSESPNIVSTEAGYNCEAILNEIRKFGHI

SEQ ID NO: 291
pinusRadiata_001007
MDTPLHLLFLLLASSAALASANFYNDVDITWGNDRAKILDNGQQLQLTLDRSSGCGIQSKQEYLF
AKIDIQMKLVPGNSAGTVTTFYLSSQGPKHDEIDFEFLGNLSGDPYILHTNVFAQGLGGREQQFY
LWFDPTLDFHTYSVLWTSNQIIFSVDGSPVRVFKNRETELGKVDSNYHYPKTQAMRVYSSLWN
ADDWATRGGLVKTDWTKAPFVASLRNFNAAATSSFDAAAEEVALESNQEQRQRLQWVRKNYM
IYDYCADTKRFPQGPPPECK

SEQ ID NO: 292
pinusRadiata_001008
MDTPLHLLFLLLASSAALASANFYNDVDITWGNDRAKIIDNGQELQLTLDRSSGCGIQSKQEYLF
AKIDIQIKLVPGNSAGTVTTFYLSSQGPKHDEIDFEFLGNLSGDPYILHTNVFAQGLGGREQQFYL
WFDPTLDFHTYSVLWTSNQIIFSVDGSPIRVFKNRETEMGKVDNNYHYPKSQAMSVYSSLWNA
DDWATRGGLVKTDWTKAPFVASFRNFSAATASSFDAAAEEAALESNQEQRLEWVRKNYMIYDY
CGDTKRFPQGPPPECK

SEQ ID NO: 293
pinusRadiata_001184
MEMGKPLLFLFLLISSSLLLIVSANFYNDVDVTWGNGRGQILDNGQQLQLTLDPTSGSGFQSKKE
YLFAKIDMQIKLVPGNSAGTVTAYYLSSQGPKHDEIDYEFLGNLSGDPYIMHTNIFAQGLGNREQ
QFYLWFDPTLAFHTYSVLWTPNQITLSVDGIPVRVFKNRETELAKVDSNYHYPKSQAMRVYSSL
WNADDWATRGGLVKTDWTKAPFVASFSDFNAATSSSNFAGEGALDSNQGQKLQWVRNKYMI
YDYCADTNRFPQGLPAECK

SEQ ID NO: 294
pinusRadiata_001186
MDTPLLFLLLLISSTLLLTVSANFYNDVDITWGNDRAKILDNGQQLQLTLDRTSGCGFQSKEEHLF
AKIDMQIKLVPGNSAGTVTAYYLSSQGPKHDEIDFEFLGNLSGDPYIMHTNVFAQGLGNREQQF
YLWFDPTLDFHTYSVLWTSNQIIFSVDETPVRVFKNRETELGKVDSNYHYPNSQAMRVYSSLWN
ADDWATRGGLVKTDWTKAPFVASFSDFNAATSSSNFDGEDVLDSNEEQKLQWVRKNYMIYDY
CADTKRFPQGLPAECK

SEQ ID NO: 295
pinusRadiata_001187
MDTGTPLLFLFLLITSSSLLVIVSANFYNDVDITWGDGRGKILDNGQQLQLTLDRTSGSGFQSKN
EYLFAKVDMQIKLVPGNSAGTVTAYYLSSQGPKHDEIDYEFLGNLSGDPYIMHTNIFAQGLGNRE
QQFYLWFDPTLAFHTYSVLWTPNQITFSVDETPVRVFKNRETELGKVDSNYHYPKSQAMRVYS
SLWNADDWATRGGLVKTDWTKAPFVASFRNFSAATSSSNFAAEEALDSNQEQKLQWVRNNY
MIYDYCADTKRFPQGLPAECK

SEQ ID NO: 296
pinusRadiata_001191
MQTHHSESSLLLLVLAFEIALFFLIFNRLLSIIITDMDTPLLFISLLSLASLVVTVSANFYNDFDITWG
NDHAQILDNGNQLQLTLDHTSGCGCQSKEEYLFAKIDMQIKLVPGNSAGTVTTYYLSSQGPKHD
EIDFEFLGNLSGDPYVMHTNIFAQGLGNREQQFYLWFDPTLDFHTYSVLWTPNQIIFSVDGTPVR
VFKNREKELGNNFHFPNSQAMRIYSSLWNADDWATRGGLIKSDWSKAPFVAYFSNFSAVISSS
NFVIEEDLDSNQEQKLQWVRNNYMIYDYCADTKRFPQGLPPECK

SEQ ID NO: 297
pinusRadiata_001197
MDMGMPLLFLFLLITSSSLLVTVSANFYNDVDITWGNGRGKILDNGQQLQLTLDRTSGCGFQSK
NEYLFAKIDMQIKLVPGNSAGTVTAYYLSSQGSEHDEIDYEFLGNLSGDPYIMHTNIFAQGLGNR
EQQFYLWFDPTLDFHTYSVLWTPNQIFSVDGIPVRVFKNRETELGKIDSNYHYPKSQAMRIYSSL
WNADDWATRGGLVKTDWTKAPFVASFSNFSAATSSSNFAGEEALDSNQEQKLQWVRKNYMV
YDYCADTKRFPHGLPAECK

SEQ ID NO: 298
pinusRadiata_001603
MMLAVALVCIWVCGLFSQPGSAVGSSRPRLAGKLVTENFAGLQFEEAYTSLFGDENVKVAEDG
KTVMLSLDKRTGSGLLSQDMYLYGLFSASMKLPDDYTAGVVAAFYTSNGDMFPGTHDELDFEF
LGNIRGKEWRIQTNVYGNGSTAYGREERYTLWFDPTEDFHQYTILWTEKSTVFFVDDVPIREIPR
TDAMGAHYPGKPMSVYATVWDGSDWATKGGRYRVNYKYSPFVVTLANLILEGCAVDPLEQFP
AVSCSADTTSSASLSKLAELSEDQKALMEWFRGKYISYSYCDDAVRYPSNPSDCPPRDPHKKIA
TAHVKFGHHQRHHKKNRKSRRSSSSSAASAAVSL

SEQ ID NO: 299

pinusRadiata_001604
MMLAVALVCIWVCGLFSQPGSAVGSSRPRLAGKLVTENFAGLQFEEAYTSLFGDENVKVAEDG
KTVMLSLDKRTGSGLLSQDMYLYGLFSASMKLPDDYTAGVVAAFYVSNGDMFPGTHDELDFEF
LGNIRGKEWRIQTNVYGNGSTAYGREERYTLWFDPTEDFHQYTILWTEKSTVFFVDDVPIREIPR
TDAMGAHYPGKPMSVYATVWDGSDWATKGGRYRVNYKYSPFVVTLANLILEGCAVDPLEQFP
AVSCSADTTSSASLSKLAELSEDQKALMEWFRGKYISYSYCDDAVRYPSNPSDCPPRDPHKKIA
TAHVKFGHHQRHHKKNRKSRRSSSSSAASAAVSL

SEQ ID NO: 300
pinusRadiata_002148
MARIIPIVLASAILLVASLQSEVNAANQIFNADFQILFASDHVKTSDDGQIWELMLDKKSGSGFQTK
NSYRFGFFTMKLKLVAGDSAGVVTTYYMASKDFETRDELDFEFLGNVSGQPYALQTNIYVNGV
GGREQRNELWFDPTADFHTYSFLWNDHQLIFFVDLVPLRVHRHTNVTDNVYPKNRPMSLLSSI
WNADNWATRGGLDKTNWSYAPFISSYQNFNADACMWEDPFPACVSTTGENWWDKPPAWTLT
DAQKLDYAWARRNFLIYDYCQDTKRFNGTLPVECSVGPW

SEQ ID NO: 301
pinusRadiata_005260
MGLVGRMMHWPCVLGSIVVLCSLIVGSQCAAFNDFFYPSWALDHVMYEGELLKLKLDNTSGAG
FASKSTYIFGKVNVQIKLVPEDSAGTVTAFYMSSQGDQHDEFDFEFLGNTSGEPYAVQTNVFSK
GVGKREQRIFLWFDPTTDFHSYSFLWNRQQVVFFVDDVPVRVFGNNEKVGVPYPQSQPMGVY
SSIWNADDWATQGGLVKTDWSHAPFVSTYTNFSIDACDYSLKTTCSSWWDEPAYASLDAKQRL
KLKWVQEKYMTYDYCKDSARFPTPPPECSA

SEQ ID NO: 302
pinusRadiata_005658
MCLQRICWVRAMLIKMVPKLLLVLLVAAMAAMAASPPKPVDVPFPKNYVPTWAADHIKYINGGN
EVQLSLDKWTGTGFQSKGTYLFGHFSMQIKMVPGDSAGTVTAFYLSSQNAEHDEIDFEFLGNR
SGQPYILQTNVFSGGKGNREQRIYLWFDPTKDYHAYSVLWNMHQIVFFVDDVPIRVFKNSRDLG
VRYPFNQPMKIYSSLWNADDWATRGGLEKTDWSKAPFVASYRGFHVDGCEASVTESTCATQG
RRWWDQKAFDDLDGMQWRKLKGVRNSYTIYNYCADKVRSPAMPPECTRDRDI

SEQ ID NO: 303
pinusRadiata_005659
MLINMVPNVLLFLLVAAMAATATPPPKPVDVPFQKNYVPTWASDHIKYINGGNEAQLSLDKWTG
TGFQSKGSYLFGHFSMQIKMVPGDSAGVVTAFYLSSQNSEHDEIDFEFLGNRSGQPYILQTNVF
SGGKGDREQRVYLWFDPTKDYHSYTVLWNMHQIVFFVDDVPIRVFKNSKDLGVRYPFNQPMKI
YSSLWNADDWATRGGLEKTDWSKAPFVASYKGFHVDGCEASMPHSACPTLGRRWWDQKAF
DDLDGQQWRKLKWVRDRYTIYNYCTDRVRYPKMSPECTRDRDI

SEQ ID NO: 304
pinusRadiata_005715
MGGTWRTVGLSFLFLVFSSLIASVCSQSQGDDSSAKVFDDNFQIMWAEDHFRTSENGQVWHL
VLDQNSGSGFKSKYKYRFGWFSMKLKLVPGDSAGVVTAYYMSSNTDMNRDELDFEFLGNRSG
EPYALQTNIYAKGVGGREQRHILWFDPTTQFHTYSILWNSHQIVFFVDQVPLRVHRHTEATSDVF
PKEQGMYMFSSIWNADNWATRGGLEKTNWTAAPFVSSYKKFHGLGCKWGDDNTTLLPCAND
KNASASHWWDEAVAWTLTKKQRENYRWVNSKYLLYDYCNDQSRYSIKPVECSVAPWD

SEQ ID NO: 305
pinusRadiata_005718
MGRTWRAMGMSFLVLVLIGLIACVSCQSDGDDSSPKVFDDNFQILWAQDHFRTSENGQVWHL
VLDQNSGSGFKSKNKYRFGWFSMKLKLVPGDSAGVVTAYYMSSDTDMNRDELDFEFLGNRSG
QPYGLQTNIYSNGVGGREQRHILWFDPTTEFHTYSILWNAHQIVFFVDQVPLRVHRHTKATRHV
FPRKQGMYMFSSIWNGDNWATRGGLEKTNWAAAPFVSSYKKFHGLGCKWEDQNTTQSSCAH
SNNASARHWWDKPEARTLTKKQREYYRWVNSKYLTYDYCHDQPRYPIKPVECSVAPWD

SEQ ID NO: 306
pinusRadiata_006166

MAGQRNWFKRIEFIVIFVVCLNSVSARPASFAEDFKVTWADDHVKTRSDNNSIDLILDQNSGAGF
ASKNQYMFGLVSMNIKLVAGDSAGTVTAFYMSSDKEEVRDELDFEFLGNRSGQPYTVQTNVFA
LGKGGREQRVNLWFDPSLEFHRYSILWNHYHIVFSVDDIPIRVYKNNEARGVPFPKNQSMGIFS
TLWEADNWATRGGLEKIDWSKAPFVASYRGFEIESCQYPGNASCVVNTSNWWEGLSYSGLRP
NQARLYKWVRTNYMIYDYCKDTPRYPVLPTECNAGI

SEQ ID NO: 307
pinusRadiata_008291
MEVSSASCLRGYVHFLLTAIICTAISPTVYADIYSDIDVTWGENNAWVLNNGQGLQLSLTNYSGS
GFQSYKEFLFGSVDISMKLVPGNSAGTVTTYYLSSTGEGHDEIDMEFLGNVSGEPYILHTNIYVN
CSADKEQQFYLWFDPTADFHNYSILWNPQQIAIFVDGLPIRVFANNENIGVPYPNEQAMRVFSSI
WNGDQWATQGGRVKIDWSSSPFVASYMNFNTDVCEWNGNGSTSQCWATNWWNQNNLNYG
QQGQLQWVRSNYLIYDYCKDYARFNYQLPAECAQQPQ

SEQ ID NO: 308
pinusRadiata_008343
MCSEAMKTAQFLGLFLILLLHSAAMAATPKPVSVPFGKNYGASWGSDHIKEFHGGRKVELLLNK
QYGAGFESKGTYLFGHFSMQIKLVPGDSAGTVTAFYLSSQTAEHDEIDFEFLGNRSGQPYILQT
NVFTGGKGEREHRIYLWFDPTKDYHSYAVLWNMYQIVFFVDSVPIRVFKNCKNLGIRFPFNQPM
KIYSSLWNADNWATRGGLEKTDWSKAPFTASYKQFHVDACEASVSESVCATQGRRWWDQVE
FRDLDGRQWRFLKWVRKHYTIYNYCTDAARNKKMPPECVRDRDNI

SEQ ID NO: 309
pinusRadiata_010682
MYDCKRQNTIKPFTGHFHALLVLAFVLIVSVCPNADHVRVSEAARRGHKGRYPRASQFPTVAFN
RGFHVLWGPQHQTIWNDQSGITIWLDRNSGSGFKSLRPYKSGYFSAAIKLQAGYTAGVNTAFYL
SNNEAHPDYHDEIDIEFLGNIPGRPYTLQTNIYVRAGNAGRGRIITGREQQIHLWFDPTKDFHRYS
ILWTPLKIIFFVDDIPIRKYRRTNPYTFPARPMWLYGSIWDASPWATDNGKYKVDYSYQPFVAQY
RGFVLA

SEQ ID NO: 310
pinusRadiata_011081
MAGYEGRRICIYWWVITVMLCRLVVGSQCAAFNDLFYASWAADHVMSQGDLLQLKLDHTSGAG
FASKSTYLFGKVNVQIKLVPGDSAGTVTAFYMSSQGDQHDEFDFEFLGNTSGEPYVVQTNVYS
NGVGNREQRIYLWFDPTANFHSYSFLWNRHQSVFFVDDVPIRVFSNNEKRGVPFPQTRPMGVY
SSIWNADDWATQGGRVKTDWSHAPFISTYTSFNIDACKYSPGSSCTSWWDQPAYASLTAKQR
MQLKWVHEKYMIYDYCKDPVRFGTPPAECTA

SEQ ID NO: 311
pinusRadiata_011726
MSTNGAYLWALVWASVISAGLGLGNGNFDDDFYIMWAPDHVTRLYNGHGVQISMDRQSGSGF
ATKKQYLFGKFEMQIKLPPGNSAGTVVAVYLYSNQPNRDEIDIEFLGNVDGKDIIMQTNVFANGY
DDREQRIKLWFDPTADFHTYTIFWNRYHIVFLVDGFPIRVHQNNAVRGIPFPRMQPMSLYTTIWN
GESWATNGGKTKITWEPYPFVAQFRNFYIDGCEWNGNPRFCKGGSTQNWWNKRTYAYFNAG
DRLKLHWVRKHYLVYDYCNDKVRFKVAPEECRYHI

SEQ ID NO: 312
pinusRadiata_013444
MAFIRKLPLLVLAFMLVLSVAHIQVSEAAGRPQSSHGTAYPLRSQLSAVKFNQAFDVLWGPQHE
QVSNDESGITIWLDRNSGSGFKSQRAYDSGYFSAAIKLQAGYTAGVNTAFYLSNNEVHPDSHDE
IDIEFLGTIPGQPYTLQTNIYVRAANGGTERIITGREQQIHLPFDPTSDFHRYSILWTPSKIVFSVDN
VPIRKYSRTGSAFPTRPMWLYGSIWDASSWATDNGKYKVDYNYQPFVARYTDFILTDCTQSRA
AECS

SEQ ID NO: 313
pinusRadiata_014144
MEAPNLSGYLHLVLMIVIIWSTGIYPTVHANFYNDIDIAWGYNNVNIFDNGEELQLSLNNASGSAF
QSKAQFLFGSVDMFMKLVPKNSAGTVTTFYLSSTGDRHDEIDLEFLGNVSGQPYILHTNIYTNGS
GNREQEFYLWFDPTSEFHNYSILWNPQQIVLFVDGLPIRVFGNNEDIGVPYANGQAMRAYSSIW
DGDSWATQGGRVKIDWSYSPFVASYRNFTADVCEWTGSGSSSQCWANIPSNWWNQAAYESL
TYAQQGQLQWVRNNFLVYDYCKDPARFNNQLPAECYRQP

SEQ ID NO: 314
pinusRadiata_014539
MGTSGTSSQYSSSAFLQPRSCMNIIAVLIIFTLLNSIIPVHGESEKHIPVTSRFQTINFYNGYSNLW
GPQHQQVSEDESSTTIWLDSSSGSGFKSLEAYKSGFFSAAIKLQAGYTAGVIAALYLSNNQEYP
GHHDEIDIEFLGTTPGKPYTLQTNVYINGTGDGQVLTGRELKFHLWFDPTEDFHNYSLLWTPSYII
FYVDDIAIRKYPRRISSTYPLRPLWVYGSIWDASSWATENGKYRADYRYQPFVAKFSKFILSGCP
VSDSTCSATFSNSLISTGTGGLTSQERSRMKSIQTNNLVYNYCKDRERYPTRLPECGKRYAPSLI
NGND

SEQ ID NO: 315
pinusRadiata_015716
MAFVGCQEGGRVMHCALLCIFVTLCNLLVSSQCASFDDFFYPSWAVDHVMSQGELLQLKLDNI
SGAGFASKSTYIFGKANVQIKLVPGDSAGTVTAFYMSSQGDQHDEFDFEFLGNTSGEPYAVQT
NVYSKGVGNREQRIFLWFDPTADFHSYSFLWNRQQVVFFVDDVPVRIFSNNEKRGVPYPQTQP
MGVYSSIWNADDWATQGGLVKTNWSHAPFISTYKNFSIDACQYSSKTNCSSWWDQPGYASLD
AKQRLKLKWVHEKYMTYDYCKDSARFPTPPAECE

SEQ ID NO: 316
pinusRadiata_016453
MASTGSQDDSAYRYTTIIRKQGHYQKHGSRHHLSASTGIQVVMVMAFFLVSSSSAARISSRPLL
RDQNRTATTVDFDQNYDITWGNQLVKFLDNRRSVELRMDQSSGSGFASKNKYLFGYFSTRIKL
VPGDSSGTVTAFYLSTQQTSKHDEMDFEFLGNKPGKPHYLSTNVFVNGVGNRESRIRLWFDPT
ADFHTYSLLWNRHQILFMVSGVVVRVFKNSETSLGVPYPSSKPMQVIASLWNGENWATDGGKS
KINWKQSPFIATFEGFDIEGHKCEGDSESSPFCPSSPSSEWWEDLGSKGLSAEQMRQLRWVR
RNYMDYDYCTDKTRFPKPPPECALNTI

SEQ ID NO: 317
pinusRadiata_017884
MLREAMKTAQFLGLFLILLLHSAAMAATPRTPVSVPFGNNYVASWGADHIKEFHGGRKVELLLN
KQYGAGFESKGTYLFGHFSMQIKLVPGDSAGTVTAYYLSSQTAEHDEIDFEFLGNRSGKPYILQT
NVFTGGKGEREHRIYLWFDPTKDYHSYAVLWNMYQIVFFVDSVPIRVFKNCKDLGVRYPFNQP
MKLYSSLWNADDWATRGGLEKTDWSKAPFLASYEQFHVDACEASAPQSACATQGRRWWDQE
EFRDLDGRQWRYLKWVRKQYTIYNYCTDISRNAKMPPECVRDRDNE

SEQ ID NO: 318
pinusRadiata_023707
MKRRAKLLGFGINWRKIVYISSVVNLILSSVESSSFNDNFDISWGTVQLLNNGQTAQLTMDKASG
SGFQSKDEYLFGSLSMSIKLVSGNSAGTVTSYYMSSDAASHDELDYEFLGNLPGNPYTLQTNVF
ANGVGNREQRLNLWFDPTADFHNYSILWNHNQIVFWVDSIPIRVFKNNEETAGIPYPNSRPMRIL
STLWNGENWATDGGRVKIDWSKAPFVASYQSFEVNACSAPSNSSLPCANNWWEQPEFQSLD
ESQLGKLDWVRKNYMTYDYCHDTSGRFSTTPAECAFNA

SEQ ID NO: 319
pinusRadiata_023708
MKSHISLLGSRRSSPELVYLSLLIILNLCTVKATFSDNFEISWGNVRLLNNGQTVQLTMDKASGSG
FQSKMDYLFGSLSMRIKLISGDSAGTVTSYYMSSEASQHDELDYEFLGNLPGQPYTMQTNVFAS
GIGNREQRLKLWFDPTADFHNYSILWNQKQIVFWIDSIPIRVFKNNEAAGVPYPDQRPMKIISTLW
NGEDWATDGGRVKIDWNDAPFIASYQSFEVDACSSSPCVNDWWDQSTFQSLNQQQLTQLDW
VRKNYMTYDYCNDASRYPTPPRECALNP
SEQ ID NO: 320

pinusRadiata_027337
MATSFSFYKLVLVVALLLTNGANVVVMLVSADQSLQPPLPSQPVTRYFKTMAFDEGFSNIWSPD
HQNVSQDRNSVTLKIDRYSGAGFKSKKTYLYGFFNAALKLQAGYTAGIVTTFYLSNSDVYPDLH
DELDFEFLGTIPGEPYTLHTNIYGNGSGDGNITSRIGREQRFHLWFDPTQEFHNYTILWTPHQIM
FFVDSIPIRQFRKLKSVRKQYPGKPMSIYATVWDGSDWATDGGKHRANYSYEPFLSTYTNFIISG
CTAGQPDCKPGRLDHRFPPILSKAQKEDLHFVRKNYMIYDYCHDTSRYPKGLPECPRSFPRRS
PVFRPRHV

SEQ ID NO: 321
pinusRadiata_001609
MAAPKSSNLSLLALIILLMGGTHHAVGMDLKKTEIEFYMHDVVTASKNFTTMKVAHSPEFGMIRVI
DNALTEDLQQNSKELGRARGMYVQDSFSGVNLLMVLTVIFQAGEHSGSTLCLQGQDGRKQREI
SVVGGTGHFRHATGHAILEKQLSMGENAILNFNVTVLHRSELAE

SEQ ID NO: 322
pinusRadiata_004488
MATKGFLETTIAVSAVLLLVCLHIAEAEVKTKLGREKISHLHFYFHDVVTGKNATAVQVASAPTTK
YSPTGFGAVVVMDDCLTAGPEATSKLVGRAQGIYVSSGQEDFHLLMATTFVFESGMYNGSTLA
MIGKNAPLEEVREMPIVGGSGLFRFARGYALAHTHSIDGTTAVVKYNVTVLHY

SEQ ID NO: 323
pinusRadiata_004489
MANKGYSAATITVAAVLLLSLFYLEAEAEAEAKLKLGREKISHLHFYFHDLVAGKNVTAVKVASAP
TTNSSATLFGAVMVMDDWLTEGPEATSKMVGRAQGIYVSSSQEDFHLLMATTFVFESGKYNGS
TLAMIGKNAALEQVREMPIVGGSGLFRFARGYALARTHAFELNTGNAVVEYNVTVLHY

SEQ ID NO: 324
pinusRadiata_005049
MGPRFLFLAIIANVLLMFAAGEGEVNMVFYLHDNLTGTNVTAVPVAGLNGSSSNAGKFGTVVTIS
DVITRRPEISESDSDNIIGRAQGMYVDTNPVTGLDFLMVFTLIFEDKKYRGSTLEFQGTDRFAQP
RREFAVVGGTGKFRFARGYAVANTESLSGVNAIIKFNGTIRTD

SEQ ID NO: 325
pinusRadiata_005790
MKGFSAVNTAMAAVVLLVCLYLAVAEAKVKLGPEKISHLHFYFHDLVDGTNVTAVEVASAPTTDS
YFTQFGLVRVMDDPLTEEPKATSKMVGRAQGIYVSSCQHRVQLLMATTFIFESGKYNGSTLAMV
GKNAVFDDVREMPILGGSGLFRLARGYALARTHSLDLKTGNAVVEYDVTVVHY

SEQ ID NO: 326
pinusRadiata_005791
MAIKGYSSVNITVAVYCYWFVLYLAAAEAEEKIGHGKISHLHFYFHDLVGGKNVTAVEVASAPTT
DSYFTQFGLVRVMDDRLTKGPKVTSKMVGRAQGIYVSSCQHRLQLLMATTFVFESGKYNGSTL
AMVGKNAVFDEVREMPIVGGSGFFRLARGYALARTHSFDLNTGNAIVEYNVTVLHY

SEQ ID NO: 327
pinusRadiata_006230
MAIKKYNRDVHLCFVCLVLFTVMLQTSNGHRWKKHSLPKPCRNLVLYFHDVIYNGSNAKNATST
LVGAPQGANLTLLAGKDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSSWLGFT
FVLNSTDYRGTITFSGADPILTKHRDISVVGGTGDFLMTRGIATISTDAYEGDVYFRLCVNITLYEC
Y

SEQ ID NO: 328
pinusRadiata_006231
MAIKNHNTAVHLGFIWLVVFSAMLLQSSDAHSYMKRPLPKPCRNLVLYFHDVIYNGLNAMNATS
TLVGAPQGANLTLLAGRDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSSWLGL
TFVLNSTDYKGTITFSGADPILKKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLCVNITLYE
CY

SEQ ID NO: 329
pinusRadiata_009358
MGSRVLLPAMATATIVIFLLHAAAGERETNLVFYMHDNVSGNNVTAFTVAGLNGTSSDPGKFGTI
VVNWDAATKGAQATGTADPDNIVGRIQGMYVNTNLVTGLDFLMLFTVIFEDMEYKGSTLEFHGT
DKFFAPHRELAVVGGTGKFRFARGYAILTTEVLSGPNAVVKFNTTLRY

SEQ ID NO: 330
pinusRadiata_011003
MRKFNDNARSNINNIAVAAAATTFLFWVALTIFERHEMKEKTSYLQFYFHDIVSGKNVTAVEVAS
SPTTGSSFTEFGLVRVMDDWLTEGPEPTSKMLGRAQGIYVSSCQEKVHLLMTLTFVFDSGKYN
GSTLAVVGKNAVFDEVREMPIVGGSGFFRFARGYALARTHSLDLTTGNAIVKYNVTVFHY

SEQ ID NO: 331
pinusRadiata_014809
MAIENNNRAVYLCFVWLLLFTVLLQASDGHGWNKDPFRRPSRNLVLYFHDVIYDGTNAKNATAT
LVGAPHGANLTHLTAKDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYNMKNTFNAWLGFT
FVLNSTHYKGTITFAGADPILTKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLRVNITLYE
WY

SEQ ID NO: 332
pinusRadiata_014810
MAIKNNNRAVYLCFLIWLLVFTLSLRSSDGHGWNKYPFRRPSRNLVFYFHDVIYDGTNAKNATST
LVGAPHGAKLTHLAAKDNHFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSAWLGFT
FVLNSTDYKGTITFAGADPILTKYRDTSVVGGTGDFLMARGIATISTDAYEGDVYFRLRVNITLYE
WY

SEQ ID NO: 333
pinusRadiata_018046
MAKLSAGVASNVNSIAVAATLLLLLLALTAEAKEGYDSKVEEKTSDLHFYFHDTVSGKNVTTMQV
ARASGTNSSPTLFGLAVVLDDIVTKGPEPASQLLGRMQGLYTLSGLEERAMQMVVTLVFSSGQY
NGSTLSLVGINRIYHPVREIPIVGGSGLFRLARGYVLARTHSLVQNGNAVVECNVTVLHY

SEQ ID NO: 334
pinusRadiata_018129
MAGKNYSTATIAVAVVLLFVCLHIAAVQAKVKLGNEKISHLHFYFHDLLVGKNVTAVQVASAPTTN
NYFTQFGMVRVMDDWLTEGPEGTSKMLGRAQGIYVSACQEKFQLLMATTFVFESGRYNGSTL
AMVGKNAVLEQVREMPIVGGSGFFRFARGYALAHTHSIDFKTGNAVVEYNVTVLHY

SEQ ID NO: 335
pinusRadiata_019464
MASRCLFATLATATLVMAAAGEGVLNMAFYMHDHLNRNKDQTAFPVAGVNGSSSEASKFGTLV
VISDMVTKRPQITEYDTENILGRAQGTYVNTNPVTGLDFLMVFSLIFQNAEYNGSTLEIQGTERFD
QPHREYAVVGGTGKLRFARGYAVGTTVSTSGENAVLKINATFCTV

SEQ ID NO: 336
pinusRadiata_019641
MASGILFPVMAIIVIVSLQPAAGESEMNMVFYLHDNLSGTNVTSFPVAGLNGSSSDAGKFGTLVV
TSDVKTKGPNSGSDNIAGRAQGTYVNTNMVNGLDFSMVFTLIFEDMEYGGSTLVIRGTDRFDQP
QCEYALVGGTGKFRFARGYAVVTTESVSAPNAVLKFNTTFLIPS

SEQ ID NO: 337

pinusRadiata_020854
MAGFKFLFPAMAVTILVVFLKKAAAAAIEGEMNMVFYMHDNVKGNNVTAIPVAGTNGSSSPPGH
FGTVVVISDVITKFPDVAESESQNIVGRAQGMYINTNLDTRRDFLMVFTVIFNNMEYNGSTLEVQ
GTDRFDQTQREYAVIGGTGKFRFARGYAVVTTESLSGQNSVLKFNTTLSTL

SEQ ID NO: 338
pinusRadiata_022079
MAIKSGRALHLSFVWLVLSTALLQTSDVYSWKKKPLRKPYRNLVLYFHDVIYDGTNADNATSTLV
GAPHWANLTHLTAKDHQFGDLAVFDDPITLDNNFHSPPVGRAQGFYFYDMKNTFSAWLGFTFV
LNSTDHRGTITFAGADPILTKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLCVNISLYE

SEQ ID NO: 339
pinusRadiata_026378
MGSGVLFSAVAKTTLVLVFVQAAAGISETNMVLYMHDNLTGRNVTSFPVAGLNGSSSDPGKFG
TVVIMSDPITKQPEVTDSDGNNYLGRAQGAYINTNPHTGMEFLMVFAITFESMEYNGSTLQIQGI
ERFDQPQREYFVVGGTGQFRYARGYVVCTMEYVSGENAVLRLNTTFRTD

SEQ ID NO: 340
pinusRadiata_027112
MPVKPSSRELVHLCILWLLVSTVLLQVTDGFVWKKREYEKPNWNKVFYFHDVLYNGNNAENAT
SAIVAAPQGANLTSLTDNNHFGDLVVFDDPITLDNDMHSPPVGRAQGFYFYDMKNTFSAWLGFT
FVLNSTEHRGTITFAGADPILTKYRDISVVGGTGDFLMARGIATISTDAYEGDVYFRLRVNTTLYE
CYNCLLSASASHDNQ

SEQ ID NO: 341
pinusRadiata_000134
MKIFNNPLLFAVWALSMVSAALSCDRCLRKSKVASFARANINGACGYGNSATSLTARGGLVMAS
ASAKIYRDGVGCGACYQIRCTDPGVCTKSGVKVLVTDFTKSTQTDFVLSARSFSKLAVASKAAQ
FLKMGTVDIDYKRIPCDYGSQNMTVKVDKSSKYPDYLAVQFLYQGGQTDITAVDIDRVGSSGWQ
YMTHKNGAIWGIQNPPIGSLSFRLLVTGGYDGSWVWPTRNLLPAIWRPGSVYDSGVQITEIAQE
GCSPCETGNWTDTRTP

SEQ ID NO: 342
pinusRadiata_003894
MAFLWLVSLGLLSMLRAAHGSGWTSAHATFYGGGDATGTMGGACGYGNLYSQGYGTNTAAL
STALFNNGFSCGACYEIQCNDDLQWCLPGSIVVTATNFCPPNNALPNDNGGWCNPPLEHFDLS
EPVFQHIAKFRAGIVPVQYRRVPCQRKGGIRFTINGHSYFNLVLITNVGGAGDVEAVSVKGAKTG
WQPMSRNWGQNWQSNSYLDGQSLSFKVTTSDGKTVTSYNVASSNWQFGQTFAGEQMN

SEQ ID NO: 343
pinusRadiata_005134
MRRTVGLQWPLVPNVCVNVTAFCFVLLLLFSCKEAALGLEHTELNRDDLEWRPATATWYGSPD
GDGSDGGACGYGGLVDQKPLRARVGAVSPVLFKGGEGCGACYKVKCMEKGLCSEKPVTVVIT
DECPGGYCAFGRTHFDLSGAAFGRMATNGKTPALLNTGELPVLYRRTLCEYPGKNITFHVTEGS
TAYWFSILIEYEDGDGDVGAMHLKQADSDAWMEMNHVWGANWCLLGGTPLKAPFSVRVTTLT
SKRTLSARNVIPDHWYPNATYKARLNFED

SEQ ID NO: 344
pinusRadiata_005738
MGALGFLVVGLLLVTTRATMASSWISAHATFYGGSDASGTMSGACGYGNLYSQGYGANTAALS
TALFNNGLSCGACFQVMCNDDPQWCLRGSVVVTATNFCPPGGWCNPPLRHFDLSRPVFLKIA
KYKAGVVPILYRRVPCHKKGGIRFTINGHSYFNLVLISNVGGAGDVHGVWIKGSRTGWQPMSRN
WGQNWQSNSYLNGQSLSFKVTTSDGRSVTSYNVASVNWQFGQTFSGAQFH

SEQ ID NO: 345
pinusRadiata_006938
MGFLAFIGLFVFNFLSMARFAHGWTNAHATFYGGGDASGTMGGACGYGNLYSQGYGTSTAAL
STALFNNGLSCGACFAIRCNDDPQWCLPGAIVVTATNFCPPNNALPNNAGGWCNPPLQHFDLS
EPVFQHIAKFRAGIVPVMYQRVPCHRSGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSRTG
WQPMSRNWGQNWQSNSYLNGQSLSFKVTTSDGRTVTSYNAAPSNWQFGQTFAGAQIR

SEQ ID NO: 346
pinusRadiata_007527
MATRTPNFFLFCSLGFMLIVTVPSPVLSCSSCVYQSKLAYYAYSGAVNVGACGYGSFAAKLYGG
NVGAASSDLYRNGVGCSACYQIRCTDPKLCNKSGTTIVVADFTQNNQTYFVVSRSTFSSLAIAD
KGSQLIKGGIIDIEYKRVPCQYKDQNLVVRVDGSSQYPHYLAVQFLYQGGQTDIVSVDVAQVGT
SGWHYMTRNHGAVWEIQKPPGGALQFRFVVTSGYDGKWLWAKKAVLPSDWKSEGLYDSGIQI
SDVALENCNPCNENNSGWADSSWIYV

SEQ ID NO: 347
pinusRadiata_008477
MATVKLATIFGLWWIASTAYALDYGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTA
ALSTALFNNGATCGACYQMKCNQQSDPQWCLPGTVTVTATNLCPPNSALPNDNGGWCNPPL
QHFDMAQPAFQQIAIYRSGIVPIMFRRVPCVRKGGVRFAINGHSYFNLVLITNVGGAGDVEAVSI
KGSNTGWQAMSRNWGQNWQSNSYLNGQTLSFQVTTSDGRTITSYNVASANWQFGQTFEGLQ
F

SEQ ID NO: 348
pinusRadiata_008478
MAPVKLATIFGLLWIVGTAYALDYGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTA
ALSTALFNNGATCGACYQMKCNQQSDPQWCLPGTVTVTATNLCPPNCWNVNSNCRLRGQRR
TWATMDSNSLPARISSQRPPRNHRSKPQNQPVSYRTTLQRKVVSVQRAPMQLGADNCPPSDA
GMTSATDTHRKVSLG

SEQ ID NO: 349
pinusRadiata_008479
MNSGRSLHSDHLFGCKMAPVKLVTMFSFLWVAGAAYALDSGWQSAHATFYGGSDASGTMGG
ACGYGNLYSQGYGTNTAALSTALFNNGATCGACYQMKCNHHSDPQWCLPGTVTVTATNLCPP
NSALPNDNGGWCNPPLQHFDMAQPAFQHIAIYRSGIVPIIFRRVPCVRKGGVRFTINGHSYFNLV
LITNVGGAGDVEAVSIKGSNTGWQAMSRNWGQNWQSNSYLNGQALSFQVTTSDGRTITSYNV
APANWQFGQTFEGLQF

SEQ ID NO: 350
pinusRadiata_008480
MAPLKLATMFSFLWIAGTAYAQDSGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTA
ALSTALFNNGATCGACYEMKCNDQSDSQWCLPGTVTVTATNLCPPNSALPNDNGGWCNPPLQ
HFDMAQPAFQQIAIYRSGIVPIMFRRIPCVREGGVRFTINGHSYFNLVLITNVGGAGDVEAVSIKG
SNTGWQTMSRNWGQNWQSNSYLNGQTLSFQVTTSDGRIITSYNVAPANWQFGHTFEGLQF

SEQ ID NO: 351
pinusRadiata_008481
MAPLKLATMFSFLWIAGTAYAQDSGWQSAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTA
ALSTALFNNGATCGACYEMKCNDQSDSQWCLPGTVTVTATNLCPPNSALPNDNGGWCNPPLQ
HFDMAQPAFQQIAIYRSGIVPIMFRRIPCVREGGVRFTINGHSYFNLVLITNVGGAGDVEAVSIKG
SNTGWQTMSRNWGQNWQSNSYLNGQTLSFQVSTSDGRIITSYNVAPANWQFGQTFEGVQF

SEQ ID NO: 352
pinusRadiata_009863
MKRFRCMSPCKFSAWLVIGAVSVFLCVKASWALEEEELEWHPATATWYGSPDGDGSDGGAC
GYGNLVDVKPYRKRVGAVSPVLFKGGEGCGACYKVKCTDERMCAKRAVTFVVTDECPGGPCA
FGKTHFDLSGSAFGRMAIADKTTTILNSGEIPVLYRRTLCEFPRKNVTFHVNEGSTAYWFSILIEY

EDGDGDVGAVHLREADSDEWMAMQHSWGANWCLLGGPMKAPFSLRVTTLSSNRTLSARNIIP
QNWYPTASYRSRLNFDR

SEQ ID NO: 353
pinusRadiata_009864
MKRFRCMSPCKFSAWLVIGAVSVFLCVKASWALEEEELEWHPATATWYGSPDGDGSDGGAC
GYGNLVDVKPYRKRVGAVSPVLFKGGEGCGACYKVKCTDERMCAKRAVTFVVTDECPGGPCA
FGKTHFDLSGSAFGRMAIADKTTTILNSGEIPVLYRRTLCEFPRKNVTFHVNEGSTAYWFSILIEY
EDGDGDVGAVHLREADSDEWMAMQHSWGANWCLLGGPMKAPFSLRVTTLSSNRTLSARNIIP
QNWYPTASYRSRLNFDR

SEQ ID NO: 354
pinusRadiata_011105
MQTRRGSWVAYLLLLLLLNLGWWKQLIIMPTSAAYANDGWKYAFATFYSESDALGTMAGACGF
GDLYRQGYGVNTAALSSVLYNGGQACGACFELRCVEDPLYCHPGTSIVVTATNFCPPNYGLPG
EDGGWCNPPRQHFVLPVTAFEKIAMWKIGTMNVQYRRVRCAKVGGMRFAINGKDFFLTVLISN
VAGDGAVSGVKVKGSKTGWLSMGTNWGQNWHVNADYRGQALSFEVTTSDGKTVTSYNVAPS
DWQFGHTYKGKQFS

SEQ ID NO: 355
pinusRadiata_012207
MLTSGFVLVAVAIIFANKFVSAHDYNGGWYYAHATFYGGADASGTMQGACGYGNLYSQGYGT
NTAALSTVLFNSGASCGSCFEIKCVDDPQWCLPGSPSIVVTATNFCPPNYALPNDNGGWCNPP
REHFDMAMPAFEQIGIWKAGIVPVQYRRVACVKEGGMRFTINGNYYFYLILVTNVGGDGVVADV
KVKGSNTGWLPLSRNWGQNWQCNTILKGQALSFRVTSSGGRTVTSYNVAPSHWQFGQTFEG
NQF

SEQ ID NO: 356
pinusRadiata_015481
MATQTPVVFVLYCILGVNLLIVFPSLALGCTSCVHQSKLAYYAYPGAVDVGACGYGSFAETLYGG
NVGGSSRDLYRNGVACGACYQMRCTDSKLCTKSGTTIVVTDFTESSQTDFVVTRSTFSSMALP
DHGDQLLKAGIIDIEYKRVPCQYKNQNMSVKVDKLSRYPNYLAVQFLYQGGQTDIVSVDVEQVG
SSEKHDLKRNYGAVWDIENPPEGALQFGFVIVSGYNGKRVWPTKSVLPSDWKVGGVYDSGLQ
TNDVSLEKCSPCDHNDRGWGDSRIP

SEQ ID NO: 357
pinusRadiata_015617
MISMTSMVRVKSVALVSMSTIIWLITRAHGYGDWESAHATFYGGSDASGTMGGACGYGNLNSQ
GYGTNTAALSTALFNDGLSCGACYEMQCNDDAQWCLPGTVTVTATNFCPPNNALPNDNGGW
CNPPLQHFDMAEPAFQQIAKYKGGIVPILYRRVPCVRKGGIRFTVNGHSYFNLVLITNVGGPGDV
HAVSIKGSRTGWQPMSRNWGQNWQSNSYLNGQSLSFQVTTSDGKTFVSYNAAPSSWQFGQT
FEGCQV

SEQ ID NO: 358
pinusRadiata_015619
MRSMELVKSIALASLLTFIWLLTGAHGYGGWESAHATFYGGSDASGTMGGACGYGNLYSQGY
GTNTAALSTALFNDGLSCGACYEMRCNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNP
PLQHFDMAEPAFLKIAKYRGGIVPILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVS
IKGSRSGWQPMSRNWGQNWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEG
SQV

SEQ ID NO: 359
pinusRadiata_016977
MAIGIIERQAASLVKGFVIALVFSISVAEGSGYTSSGWTSGHATFYGGSDASGTMGGACGYGDL
YSTGYGTKTAALSTALFNSGATCGACFQIQCDISKDPQWCLPGPKSITITATNFCPPNYALPSND
GGWCNPPLMHFDMAQPAWEQIAIYSGGIVPVQFRRVPCTPVGGVRFTINGRSYFELVLLSNVG
GAGDISAVSIKGSNTGWQPMSRNWGVNWQSNSYLSGQSLSFQVTTSDGNSITFYNVAPSNWQ
FGQTFATSQQFN

SEQ ID NO: 360
pinusRadiata_021768
MQSPLKSRVRYVLMVLAIIFAQTLAAADDCDGDWNSAHATLYGGGDAAGIMAGACGYGNLYSQ
GYGTNTAALSAILFDSGAACGACFEIKCVDDSQWCLPGSPSVVITATNFCPPNYALSNDNGGWC
NPPREHFDMAMPAFEQIAIWKAGIVPVQYRRVRCAKGGGIRFTIHGNRYFYLILITNVGGDGDVA
EVMVKGSNTDWLPLTRNWGQNWQSNTNLQGQALSFQVSSSSGHTITSYNVAPSDWQFGQTF
QGNQF

SEQ ID NO: 361
pinusRadiata_026140
MFSTKFFAAAAATFSLIRFSTAVYDPSSQRNLAMYWGSGSDQLDLAHFCDETNVDIIPIGFINFFP
PQANGLVAETFGDQCWDGNYTGPGYDGTNNPNDNFLYEQCPNLQRDLYYCQQNTNKKILLSL
GGAVGNYYLNGPSDGEYLAEFLWGAYGPYNESWTGVRPLDRGYYNTNLTEHIDFDGFDFDIEQ
TTPDQQAGYIACIKRLRQLFIEHKAVNPCSKDYIISGAPQCPLDEPYMSTAIAGAQFDVLWIQFYN
NGANGCTARNYTDSKALGKTSGFNYDSWVTKVNGGASAGAKLYIGLLAGQAASEFSPNDYIDG
PAIQTLVSQYHSHPQFGGIMLYEATVAENNAQFYNTVKGILNDTALAGTVTSSAKVCSSTTSTSS
KTSSTSTSTTSTSSKVTTTSSSTSSKASTTSSSSSTSSSSTSSTSSSKTSSSSSSSSSTKTSTSS
SVSSTSTTSSSSSSSSSSLSSSSSSSSTSAYPTTSSSSVISSTTSASSTSSSSSSSSEISSSTSV
SSTSSETPTSTPTPTTVPSVGSCTYLGCYTEATTTRALSGAVYDNYTLMSVEICAGFCTGFTYFG
VEYGGECYCGNEFGEGSVVSPPIDCSMTCAGTPTELCGAGDRLDVYSCAGSATTTSSSVSGSS
TSSIESSTSSSVSISSSSSVVSTSSSSVVSSTSSEVTPTTSSTSSSVSSTSSLSSTSVYSDSSSSV
TSTSTSSLSSSSSVSETLTSTSSSSIYSPTITSTAYTNSSSAIVTPTSSLYTNSSSVITTSSSSSSSK
SVCTRKTHTSSGSVSITSSYSVSGTATSISSYSVSSGSSSSSASGIISTPSSSLSGSATSSAQGTA
TSASTTQYTTSTVYTTSVHTITSCAATVTNCPARSTVLTTETIALYTTVCPVTATETGKGVPTTSS
PVKPTSSGSGSGETTSYTTSTVYATSVYTITSCAPTVTNCPARIGSVTTETIALYTTVCPVTATET
GKVAPSSTPSASSPVLPGKGGKSSSSAAGYPVSGTESVKHTTISSTTTSYVTVKVVKSTATVVAI
PSSSSTAGGVTTAPYPTGSGSATVGKPFGTAGPSVSLVVGKVSSSSTSTNAGVATSSSSPVPS
QFTGAASNVRSGMGALAAVVVGVVALMM

SEQ ID NO: 362
eucalyptusSpp_002590
MAMAGSTGRRQQQLLLLALALSSLAAIASAAVLFEERFEDGWETRWVKSDWKKDENMAGEWN
YTSGKWNGDSDDKGIQTSEDYRFYAISAEYPEFSNKDKTLVFQFSVKHEQKLDCGGGYMKLLS
GDVDQKKFGGDTPYSIMFGPDICGYSTKKVHAILTYNGTNQLIKKDVPCETDQLTHVYTFVLRPD
ATYTILIDNVEKQTGSLYSDWDLLPPKQIKDPEAKKPEDWDDKEYIPDPEDKKPEGYDDIPKEIPD
SDAKKPEDWDDEEDGEWTAPTIANPEYKGPWNPKKIKNPNYQGKWKAPMIDNPDFKDDPELY
VFPKLKYVGIELWQVKSGTLFDNVLICDDPEYAKKVAEETWGKNKDAEKAAFDEAEKKREEEEA
KDEPVDSDIEDEDDDADADDAEDDSDSVIKAEADESAESADSKDEVKDEL

SEQ ID NO: 363
eucalyptusSpp_003495
MMEGRRIRLLARALTVLLLSFQICASDVIFHESFDESFEGRWVVSEKEEYQGVWKHSKSEGHDD
YGLLVSEKARKYAIVKELDDVVSLKDGTVVLQYEVRLQDGLECGGAYLKYLRPQDAGWKVKEF
DNESPYTIMFGPDKCGATNKVHFIFKHKNPKTGEYVEHHLKHPASVPYDKLSHVYTAVLKPDNE
LRILIDGEEKKKANFLSAEDFEPALIPPKTIPDPDDKKPEDWDERAKIPDSDAVKPDDWDEDAPM
EIVDEDAVKPEGWLDDEPEEIDDPEATKPEDWDDEEDGEWEAPKIDNPKCETAPGCGEWKRPT
KSNPAYKGKWHAPLIDNPNYKGIWKPQEIPNPDYFELERPNFEPIAAIGIEIWTMQDGILFDNVLIA
SDEKVAESYRETAWKPKFEVEKEKQKEEDKATGSDGLSAIHKKVFDVLYKVADVSFLEPYKPKIL
ELIEKAEEKPNIAIGVLGSIVVVILTVFFKILFGGKKPVANVPEPRREAAAETSNNQGSQGDKEDE
DEKEDAGDAAAAAAPRKRPNRREI

SEQ ID NO: 364
eucalyptusSpp_013577
MEGSRIPRLVPALALVLISFAFLQIRASDVIFYDSFDQPFVGRWVVSVKDDYTGEWKHSKSEGHD
DYGLLVSEKARKYAIVKELDEIVSLKDGTIALQYEVRLQNGLECGGAYLKYLRPQDAGWKVKEFD
NDSPYTIMFGPDKCGSTNKVHFIFKHKNPKTGEYVEHHLKFPPSVPYDKLSHVYTAVLKPDNEL
RILIDGEEKKKANFLSAEDFEPPLIPPKTIPDPDDKKPEDWDEQEKIPDPDAVKPDDWDEDAPMEI
VDEDAVKPEGWLDDEPEEIDDPEATKPEDWDDEEDGEWEAPKIDNPKCELAPGCGEWKRPMK
RNPAYKGKWHAPLIDNPNYKGIWKPQEIPNPDYFELERPQFDPIAAIGIEIWTMQDGILFDNILIAS
DEKVAETYRETTWKPKFEVEKEKQKEEDKDSDSPGLSAVHKKAFDVLYMIADVPFLDPYKPKIL
DLIEKAEKQPNITIGVLVSIVVIILTLFFKILFGGKKPAVNVPEPRSEAAPETSDGPGSSGDKEDEDE
DEDEDEKEETAAAPRRRSIRREA

SEQ ID NO: 365
eucalyptusSpp_033927
MKALLFLSFVLFVAVATATVHFQEEFDAGWEKRWVYSTADDASGSAGKFTATPGQYYGDAQKD
SGVQTSTDARFYKASAQFPKFSNKDKPLVLQYSVKNEQELDCGGAYLKLSPPGVDQKSLTGET
PYNIMFGPDVCGYSTRRVHFIFNYKGTNHLIKKTVAPSSDKLTHLYTAIINPDQTYEIRIDNEKKES
GKLVDDWDFLPPKEINDPSISKPADWVEEKEIPDPEDKKPEGYDDIPKEIPDPDAKKPEDWDSEL
DGEWEPPTIPNPEYKGEWHPKLIPNPAYKGPWVHPQIPNPDYHYDDSIYAFEHEFVAFEIWQVK
SGTIFDHILVTDSLEEAEAFATGHFAAQQKAEKAMYDKQEEEKQEKEKAEREAEKQKLEEEGKK
EDDDEDEDEEEEEDEGKGHSHDEL

SEQ ID NO: 366
eucalyptusSpp_039632
MAGTERRQQLLFLLPTSPLCLALLLLLSSLARLALSEVIFEERFLDGWKRRWVVSDWKKSEGKA
GTFKYTAGKWPGDPDDKGIQTIKDAAHSAISAKLPEFSNKNRTLVLQYSIKFEQEIECGGGYIKLL
SGFVNQKKFGGDTPYSLMFGPDICGTQTKKLHVILSYQGQNYPIKKELECETGKLTHFYTFILRP
DATYSILVDNRERDSGSMYTDWDILPPRRIKDVNAKKPADWDDREYIEDPNEVKPEGYDSIPSEI
PDPKAKEPDNWDEEADGVWKPPKVPNPAFKGPWKRKKIKNPNYKGKWKIPWINNPEFEDDPD
LYVMKPIQYVGIEVWQVKAGAIFDNVLICDDPEYAKQVVEEVFANREAEKEAFEEAEKVRKAQEE
EEARRAREEGERRRRERGYDRRYRDRYRDKYRRHDRRDYMDDYHDEL

SEQ ID NO: 367
eucalyptusSpp_006372
MAAPKLGRIPSIRDRVEDTLAAHRNELVSLLSRYVAQGKGILQPHHLLDELENIISEDEGKSSLSD
GPFSEVLKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVHELSVEQLTVSEYLGFKEELVDGKSE
DSFVLELDFEPFNASFPRPNRSSSIGNGVQFLNRHLSSIMFRNKDCLEPLLNFLRAHKYKGHTLM
LNDRIPSISRLQSALAKAEEYLSKLPTDTPYSEFEYMLQGLGFERGWGDTAERVLEMIHLLLDILQ
APDPSTLETFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQKQ
GLDIAPKILIVTRLIPDSKGTTCNQRLERVSGTEHSHILRVPFRSDQGILRKWISRFDVWPYLETFA
LDAAHEITAELQGFPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFDEKY
HFSCQFTADLLAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVS
PGADMCIYFPYSEKQKRLTALHGSIEKLLYDPEQNDEHIGSLSDRSKPMIFSMARLDKVKNMTGL
VECYAKNSKLRELANLVVVAGYIDVKKSKDREEIAEIEKMHELMKEYNLDGQFRWMAAQTNRAR
NGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGVSGYHIDPYHPD
QAATLLADFFEQSKRDPNHWTKISAAGLQRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRE
TRRYLEMFYILKFRELVKTVPVAADEPH

SEQ ID NO: 368
eucalyptusSpp_006373
MAAPKLGRIPSIRDRVEDTLAAHRNELVSLLSRYVAQGKGILQPHHLLDELENIISEDEGKSSLSD
GPFSEVLKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVHELSVEQLTVSEYLGFKEELVDGKSE
DSFVLELDFEPFNASFPRPNRSSSIGNGVQFLNRHLSSIMFRNKDCLEPLLNFLRAHKYKGHTLM
LNDRIPSISRLQSALAKAEEYLSKLPTDTPYSEFEYMLQGLGFERGWGDTAERVLEMIHLLLDILQ
APDPSTLETFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQKQ
GLDIAPKILIVTRLIPDSKGTTCNQRLERVSGTEHSHILRVPFRSDQGILRKWISRFDVWPYLETFA
LDAAHEITAELQGFPDFIIGNYSDGNLVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFDEKY
HFSCQFTADLLAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVS

PGADMCIYFPYSEKQKRLTALHGSIEKLLYDPEQNDEHIGSLSDRSKPMIFSMARLDKVKNMTGL
VECYAKNSKLRELANLVVVAGYIDVKKSKDREEIAEIEKMHELMKEYNLDGQFRWMAAQTNRAR
NGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGVSGYHIDPYHPD
QAATLLADFFEQSKRDPNHWTKISAAGLQRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRE
TRRYLEMFYILKFRELVKTVPVAADEPH

SEQ ID NO: 369
eucalyptusSpp_006549
MAERLLTRVHSLRERLDETLLAHRNDILAFLTRIEAKGKGILQHHQLIAEFEAISEEHRKKLSEGAF
GEILRSSQEAIILPPWIALAVRPRPGVWEYIRVNIHALVVEELQVTEFLHFKEELVNGNLNGNFVLE
LDFEPFTAQFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESLHPLLEFLQVHCYKGKNMMVNTRIQ
NVFSLQHVLRKAEEYLSALKPETPYSQFEHKFQEIGLERGWGDTAERVLEMIRLLLDLLEAPDPC
TLENFLGRIPMVFNVVIMSPHGYFAQDDVLGYPDTGGQVVYILDQVRALESEMLHRIKQQGLDIT
PRILIVTRLLPDAVGTTCNQRLEKVFGTEYSHILRVPFRTEKGMVRKWISRFEVWPYLETYTEDV
ANEIAGELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFS
CQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGA
DMSIYFSYTEEKLRLKSFHAEIEELLFSDVENKEHLCVLKDRNKPILFTMARLDRVKNLTGLVEWY
GKNTRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYGLIETYNLNGQFRWISSQMNRVRNGEL
YRYICDMRGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGFHIDPYHGDQAA
ETLANFFEKCKVDPSHWDKISQGAMQRIKDKYTWQIYSERLLNLTAVYGFWKHVSNLDRLESRR
YLEMFYALKYRKLAESVPLAVE

SEQ ID NO: 370
eucalyptusSpp_019813
MDSSPALKTTEPVPDSMPEAPSQSRYHMKRCFAKYMEKGRRIMKFHHLMDELESAIDAKTERE
LVLGSDLGYILCYTQEALVVPPHMAFAVRRSPGNWEYVKVSSDSLSVEGMSAADYLKFKAMIYD
EEWAKDENALEVDFGALDFSVPHLTLSSSIGNGVDFISKYLSSKLSGTPDSAQPLVDFLASINYQ
GENLMINETLDTAPKLQMALIVAEASLASVPKDTPFQDFEMRFKEWGLEKGWGDTAEKVKDTIR
WLSEVLQAPDPTNMEKFFSRLPMIFNVVIFSPHGYFGQSDVLGLPDTGGQVVYILDQVRALEEE
LLLRIKEQGINAKPQILVVTRLIPDARGTKCNQELEPIIGTKHSNILRVPFRTEKGVLRQWVSRFDIY
PYLERFTQDATIKILDQLEGKPDLIIGNYSDGNLVASLMASKLGTTQGTIAHALEKTKYEHSDVKW
KELDPKYHFSCQFIADTIAMNATDFIITSTFQEIAGSHDRPGQYESHAAFTLPGLCRVVSGINVFD
PKFNIAAPGADQSVYFPYSEKQKRLTQLNRAIEELLYSRVDNDEHIGYLADKKKPIIFSMARLDTV
KNITGLVEWYGKNARLRSLVNLVIVGGFFDSSKSKDREEMAEIRKMHDLIAKYKLKDQIRWIAAQ
TDRYRNGELYRWIADTRGAFVQPALYEAFGLTVIEAMNCGLPTIATNQGGPAEIIVDGVSGFHID
PNHGEESSNKIADFFEKCKVDNEYWNKISAGGLKRINECYTWKIYANKMLNMGCIYTFWRQLNK
EQKQAKQRYIQMFYSLQLRNSMKTVPIKTDEPEQAAPKPPPKVQPTMSTRRTQSRIHK

SEQ ID NO: 371
eucalyptusSpp_033523
MADRVLNRSHSPRERLDEALFADRNDCLVFLSRLKAKGKGILQRHQILAVFEAIPEESRARLLDG
AFGKVLKSTQEAIVSSPWVALAVRARPGVWEHIRVNVHALLLEHFQVDEYLHFKEALVDGSLNP
DSEPLTATFGRPTLSTSIGNGVECIRRSLSDKLFPDKESLHPLLEFLQVHSYKGKNMMVNARVQ
NVSSLQPVLRQAEEYLNTLKPETPFPKFEHKLQEIGLEQGWGDTAEWVLDMIQDLLDLLMVPNP
GALEKFLGRIPMVFDVVIVSPHGYFAQDNVLGYPDTGGQVIYILDQVRALETEMLHRIKQQGLDIT
PRILIITRLLPDAVGTTCGQRLEKVFRTKHSRILRIPFRDKKGIVSEWISRFKVWPYLERFAEDVAK
ELRGELQRNPDLIIGNYSDGNIVAYSLAKKLGVTQCTIAHALEKGKYPGSDIYWKKFDNEYHLSC
QFTADLLTMNYTDFIIASTSEEIAGSKDTVGQYESYTNSTLPGLYRVVHGINVFDPKFNIVSPGAD
MSIYFPYTEQKRRLKSFHPEIKELLFSDVENKEHLCVLKDKNKPIIFTMARLDRVKNLTGLVEWYG
KNPKLREVANLVVVGGDRRKDSKDLEEQSEMKTMYDLIEKYKLNGQFRWISSQTNQVRNGELY
RYICDTKGVFVQPAIYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGYHIDPYHGDQAAEL
LVEFFEKCKVDKSHWDKISKGAMQRIEEKYTWKIYSERLLNLTAVYGFWKHVTSLDRRESRRYL
EMFHALVYRPLAQSVPPAVE

SEQ ID NO: 372
eucalyptusSpp_001430
MAASFLSNPSSLSFLLLLLLLHASRLAFSQSFVGVNYGQVADNLPPPESTAKLLQSTTIGKVRLY
GADPAIIKALANTGIGIVIGAANGDIPSLAADPNAAGQWVGANILPFYPASKITLVTVGNEVFMSND
ENLMSQLLPAMQNMQRAITAAGLGGKVKVSSVHAMSLLSQSDPPSSGRFHPSFEARMRDVLQ
FQRENGSPLPINPYPFFAYQSDPRPETLAFCLFQPNAGRVDSGTGIKYMNMFDAQVDAVYSALK
ALGYKDIEIMVAETGWPYNGDSNEVGTSVENAKAYNGNLIAHLRSLVGTPLMPGKSVDTYIFALY
DEDLKPGPTSERSFGMYKPDLTMTYDIGLAKSSQTPASPKAPVTPTPVTPTPKPTGPGWCVPK
SGVSDAQLQASLDYACSNNIDCSPIQPGGACFDPNTIASHAAFAMNLYYQTLGRNPWNCDFSQ
TATLTTNNPSYNGCVYPGGST

SEQ ID NO: 373
eucalyptusSpp_001556
MASSSSLLRALFLLLSLSDSATQILGLEFGINYGQIADDLPSPSRVATLLGSLNVSRVKLYDADPN
VLQAFSNSNVDFIIGIGNDNLQNMTILANAQDWIQQHVQPYIGQTQISCIVVGNEVLNSSNNQWM
PYLVPAMKTVYSALSNLGLNKQVAVTTAHSLNILATSYPPSAGSFWPNLAQYLQPLLNFQAQINT
PFLINAYPYFAYKGSPSEVSLNYVLFQPNEGLTDPVTNLHYDNMLYAQIDAVYSAIKAMGHTDITV
RISETGWPSKGDDDEAGATLENAHIYNENLLQRIEQKQGTPAKPSVPIDIYVFALFNENLKPGPT
SERNYGLYYPDGTPVYSLGLQGYLPELYSATGTRPGLYSATGTRVLPFSVVLVSIMTFLMNI

SEQ ID NO: 374
eucalyptusSpp_003619
MASSALPPSNLLLLLLLLLISGLACVAAMAAPIGVNYGQIANNLPSPDHAVTLVKSIGATRVKLYDA
DSRVLCAFAHTGVEFTVGLGNEFLVQMKDPKNALSWVKSNVQSFLPDTNITTIAVGNEVFTSND
TSLRDLLMPAMKNVHDALASLGLDKQVTVTTAHSLAILETSYPPSTGRFRRDVASRVSQVLDFQ
CQTGSSFLINAYPYFAYKANPKQVPLDFVLFQASQGITDPSTGLNYENMLFAQIDAVHSALAAVG
YANMTVHVSETGWPSRGDDDEVGATPENAKKYNGNLIKIVKQKKGTPMKPNSDLNIYVFALFNE
NMKPGPMSERNYGLFKPDGTPSYTLSSGGGGGGGGGGTSNGTSSGGFGGGGGGGGSASDG
TPPAPIGYLSVSSGANELRSLGAACLMLALFLIKLVF

SEQ ID NO: 375
eucalyptusSpp_006486
MAKSSPFAADSLSIPSMLLFALMVFTILHRTAAQTGVCYGMLGNNLPSAQEVVALYKQNNIPTMR
IYDPNPQALQALGGSNIELVLGLANPDLQSIASSQANASAWVQNNIKNHGNVRFKYVAVGNEVK
PSDSFAQFLVPAMRNIRTALAGAGLEQIKVSTSVDTGVLSESFPPSKGVFRSDYMPLLGPIIGLLV
ETQAPLLVNVYPYFSYIGDPQGIRLDYALFTAPSVVVTDGALGYQNLFDASLDAVYSALEKADGG
SLKIVVSETGWPSAGGGEATTLDNARTYNTNLAKHVKGGTPRRPRGPIETYVFAMFDENQKSP
ETEKYWGLFLPNKQPKYSIDLN

SEQ ID NO: 376
eucalyptusSpp_006939
MANPHLPPLSLLLLLLLLGSAHGVSAVGVNYGTIGNNLLPPKKVAQLLQSTLIDRVKIYDSNPDILD
AFSNTGIDLVVAVENPLVANLSKDPSAAAEWLASRVAPFLPATSVVSVAVGNEYLTSGDDKLEP
NDVVQAMQNLHAALVARGLDRKIKVSTPHSMAVLAASFPPSSSTFAMTLLPTMTSIVQFLADTG
APFMINAYPYFAYRDNPSSVDLEYALLGNKTTVRDPKGYVYTNMLDAQIDAVRSAIGALGFGNR
SIEITVSESGWPSKGEDGDKAATPENARTYNTRLIERAQANRGTPMRKEERVEIFVFALFNENKK
EGGVAERNFGLFAGDGSKAYDVDLSCQFCSGGVSGFGEKAAGSSGVALRGPSVWCVAKPHA
EEGVLQAVVDFCCGAGGVDCREVYEGGDCYAPEKVHAHASYAMNAYYQMHGRNYWNCDFK
GTGLVTFGDPSYGRCRYSQQ

SEQ ID NO: 377
eucalyptusSpp_006955
MQMGLLHLLVFSSLLLALCSAEILSKVGVNYGQLGNNLPSPTRSVWLIKHQLKAQRVKIYDANPSI
LRALKHTGIQVSVMVPNELINAIAVNQTLADSWVGSNVVPFHPATKIRYLLVGNEILSSADNTTWF
NLVPAMRKVKKALKRHKVHHKVKVGTPLAMDVLATSYPPSSGSFRPDVSDRVMKPMLQFLNRT
KSFFFIDVYPYFAWSSDPKTIDLNYALFESKNVTVKDPGTGLVYTNLFDQMVDAVTFAMKKLGYP
NIPIWIAETGWPNAGDYDQIGANIYNAATYNRNVVKKLSARPAIGTPARPGWVLPSFMFALYNEN
QKTGPGTERHFGLLYPNDSFVYDIDLSGETPDTEYGKLPAPTNNEPYEGKIWCVVAKRANRSAL

ASALSYACSQGNATCGPIQPGKACHRKGSLVRQASYAFSSYWAQFRKTGGSCYFNGLATQTIE
DPSYGSCEFPAVTL

SEQ ID NO: 378
eucalyptusSpp_007432
MMGERGLGRILLLLLPFLPIALGAFVGINIGTDVTNLPEASDIVAVLKSNEITHVRLYNADAHMLKA
LANSGINVMVGVTNEEVLGIGEYPATAAAWINKNVAAYLPATNITAIAVGSEVLTAIPHAAPVLVPA
MNNLHKALVASNLNFVVKVSTPQSTDVIPKPFPPSAAAFNSSWNSTLYQLLQFLKNTNSSYMLN
AYPYYGYTQGNGIFPLDYALFRSLPSVKQIVDPNTLFHYSSMFDAMVDATYYSIEAMNFSGIPVM
VTETGWPWFGGSNEPDATAENAQTFNNNLIKRVLNGSGPPSQSDVPINTYIYELFNEDKRPGPV
SEKNWGVFFTNGTSVYPLSLGTSGRITGNSSGIFCVAKQDADSDKLQDGLNWACGQGHANCA
AIQEGQPCYSPNTVANHASYAYNDYYQKMQGVGGTCDFQGTAMTTTVDPSYGSCKFTGSSNS
SSTVTTPVASAPFSPIGGGSPTSAVLASKLKYVICTISVVLTLL

SEQ ID NO: 379
eucalyptusSpp_007745
MGGKRVRYAIILLCHLLLCSGSGSLATRKEAVGYANEIAQGKKYPTSSPSGQKDITDPVTTVPTM
NPAPFASADPVVNPTSNPELAPPAVISPITYPAMATPPPSLSSSWCIASQSVSQTALQVALDYAC
GYGGADCSGIQPGGSCYYPNTVHDHASYAFNKYYQKNPVPTSCSFGGTAVVTSTDPSTSTCQF
QSTSTASSILNTTNSSGATVFGAVPSGPPASSASQLSCIVSLVMTLSWLSFASGIY

SEQ ID NO: 380
eucalyptusSpp_007776
MAISKLAPLLFLALVFLSIAEPGEPSLFADIKQGQDPDKEPYVGVNVGTDVSHLLSPPNLVSFLQV
QKITHVRVYDADPDLLKALAKTKIRVIIGVPNNQLLAIGSSNATAASWVGRNVVAYYPETSIIGIAV
GDEVLTTVPSSAPLLVPAIESLYSALVAANLHTQIKVSTPHAASIILDSFPPSQAYFNQSLVSVMLP
LLQFLSRTGSPLMMNLYPYYVFMQNKGVVPLDNALFKPLTPAKEMVDPNTLLHYTNVLDAMIDA
TYVSMKNLNVTDVVVLVSESGWPSKGDSKEPYATVDNADTYNSNLIKHVLDRTGTPLHPELTSS
VYIYELFNEDLRSPPMSEANWGLFYGNSTAVYLLHVSGSGGFLANDTTNQTYCIAMDNVDSRTL
QTALDWACGQGQANCSEIQPGEDCYQPSNVKNHASYAFDSYYQKEGKAAGSCDFKGVAMITT
TDPSHGSCIFPGSKKVSNATKQVVNSTVSSGATESSRFFIFSSNRRTAIDKALGSVFSVLFSFFLA
VALWTPI

SEQ ID NO: 381
eucalyptusSpp_008889
MEHLPLAFFFLLLSVLSLADGGSIGVNYGRVADNLPPATKVVQLLKSQGVQKVKIYDADPAVLHA
FAGTGIRLTVDLPNEKLFAAARSLSFSLDWVQQNVADYPTTQIEAIAVGNEVFVDTHNTTRFLVP
AMKNIHTALVKHNLHNAIKISSPIALSALQASYPSSAGSFRPELIEPVFKPMLEFLRQTGSYLMVN
AYPFFAYESNSDVISLDYALFRENPGVVDAGNGLRYFNLFDAQIDAVFAAMSALKYDDIKMVVTE
TGWPSKGDENEVGASKDNAAAYNGNLVRRILTGGGTPLRRQADLTVYLFALFNENKKPGPSSE
QNYGLFYPNQDKVYDVPLTVEGLKNYHDTGKSAPAGGGQRGVAAPVKGGRGGVSKSSSANT
WCVAKGEAGKEKLQAALDFACGEGGADCRPIQRGSTCYDPNTLEAHASYAFNSYYQMKGRAF
WTCDFGGAASIVSQPPKYGKCDFPTGY

SEQ ID NO: 382
eucalyptusSpp_009271
MITEMSKIIPRMLSDSVFDIVFLLLSSSFFMQGARAGIGVNYGTVADNLPPPAQVAHFLLESTTIDR
IRLFDADPDILKAFANTGIAVTVTVPNDLIPQLAKLSNAQDWVRTNVEPYVPATDIVRILVGNEVLA
TANRLLLGNLVMSMRMLHAALANASLDGRIKVSTPHSLGILSSSSPPSSGKFRLGYDVHILRPLL
NFLRETGSPFLVNPYPFFGFSKDTLDYALFRPNAGVMDENSKLVYTNMLDGQLDAVYSAMKVL
GFTDIEVVIAETGWPSLCDSTQVGVDAKTAAEYNSNLIRHVSSGAGTPLMPKRTFETYIFALFNE
NLKPGPTCERNFGLFRPDMTPVYDAGILRPTARSSVPIDPIPAPSSMTPPTSPASMSPPKGTQW
CLPKTGADPDALQRNIDYVCGLGLECRPIEEGGACFLPNTVRAHAAYAMNAYYQAMGGNNYDC
DFKGTGAVTAIDPSYGKCTYHG

SEQ ID NO: 383
eucalyptusSpp_010369
MANLFPLATAVFFLSVACPHLSRAAYTIGVNYGTVADNLPPPSQVATFLKTKTAIDRVKLFDANP
DILRAFAGTGIAVTVTVGNGDIISLSKLPAAQAWVSANILPFHPKTLINRIAVGNEILATSDKNLIARL
LPAMKALHSALQLVNVTNVQVTTPHSLGILSSSEPPSTGRFRRGYDRAIFAPILDFHRQTKSAFM
VNPYPFFGFTAKTLNYALFKPNAGIFDAATGKNYTNMFDAQMDAVYSAMKKVGYEDVEIVVGET
GWPSVGDANQPDVNMANAVSYNGNLVRHVNAGKGTPLMPNRKFETYVFALFNEDLKPSTSER
NYGLFKPDLTPVYDVGILRNEPAGGPAPASPSPTAQPSPTAPPTSSGKKWCVPRSDASDQALQ
ANIDYVCSAQVDCKPIQTGGACFDPNTVRSHAAYAMNAYYQSMGQHDYDCDFDKTGVVTAVD
PSTSSSIPCF

SEQ ID NO: 384
eucalyptusSpp_010420
MLQPRTKVATFSLLLVLSSSFPAAEPAIGVNWGTISFHRLRPSTVVDLLQQNKIQKVKLFDADPG
ALKALEGSGIEVMVGIPNEMLTVLGSSSVASDLWVRQNVSSFVGKGGVAIRYVAVGNEPFLSSY
AGQFQNYVMPALLNLQQSLAKANLAGYVKLVVPCNADAYEADLPSQGAFRPELTQIVTQLVSFL
NSNGSPFVVNIYPFLSLYGSTDFPQDYAFFGGTTHAVTDGANVYTNAFDGNFDTLVAALTKLGY
GQMPIVIGEVGWPTDGALNANLTAARAFNQGLINHVLSNRGTPLRPGVPPMDVYLFSLLDEGAK
SVLPGNFERHWGIFSFDGQAKYALNLGLGNRLLKDARNVQYLPSRWCVADPSKDLSAVMNHM
KLACSVADCTTLNYGGSCNGIGAKGNISYAFNSYYQLQMQNSQSCDFDGLGMVTFLDPSVGEC
RFLVGVTESTSAAVETYWRGVIVWVLVMWSVWVFEV

SEQ ID NO: 385
eucalyptusSpp_010726
MAIPPLATLVLLVVLSQASCFANSQSFIGVNYGQVADNLPQPSATAKLLQSTSIEKVRLYGTDPAII
GVLANTGIGIVIGAANGDIPALANDPNFAKNWVNANVVPFYPSSKIILITVGNEVMTSGDHNLMTQ
LLPAMQNMQNALNAVSLGGKIKVSSVHSMAVLKSSEPPSSGSFDPSDEMKGILGFNNATGSPF
AINPYPYFAYRSDPRPETLAFCLFQPNAGRLDTKTQIKYTNMFDAQVDAVRSALNSFGYKNVEIV
VAETGWPYKGDSNEVGPSIENAKAYNGNLIAHLRSLVGTPLMPGISVDTYLFALYDEDLKPGPTS
ERAFGLFKSDLSMNYDIGLSKSSQTPAAPKMPAAPSPNATVTPSPNATVTPSPKPDKANWCIPK
SGVSDAQLQANLDYACGQGIDCRPIQPGGACFEPNTLAAHAAYAMNLYYQNSNRSPTNCDFSQ
SATFSSNNPSYNGCVYPSGKS

SEQ ID NO: 386
eucalyptusSpp_011679
MAESISHYPFPTLGLIVLCFMTMFSIGSSVGVNWGTQSNHQLPPEKVVKMLKENGIKKLKLFEYD
EKILGALAGSKIEVMLAVPNYMLEIMSVDPSFAASWVDTNVTSYRYTGGVNIKYIAVGNEPFLQS
YNHKYVRQVLPALRNIHEALHRARLSSKVKVTVPFNADVYYSPPPNEYPSSGDFRPEVRDAAIEII
HFLYINDSPFTVNIYPFLSLYQNQNFPVDFAFFDGTTEPVKDGDRVYTNVFDANFDILVSALTKAG
YSDMEIIVGEIGWPTDGDKFANIKNAQRFNQGLLKHALSGDGTPARKGVINVYLFSLIDEDTKNID
PGNFERHWGLFEYDGKPKYELDLSGSEKDTRLVPVMGVSYMPRRWCILNPELNDLTDLGENID
YACKSSDCTALGYGSSCNNLSSQGNASYAFNRYYQMNDQRIMACDFQGLAVVTENDPSTEGC
QFPLMIASGDSMSWNQGLLHTSFRFYLWFLVFWVIL

SEQ ID NO: 387
eucalyptusSpp_036289
MEKFDLFKWVLCGSIVLFGVGCGRVDGLGVNWGTLATRKLPPKTVVQMLKDNGIQKVKLFDAD
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SYNGSFVNTTLPALQNIQKALNEAGLGDTVKATVPLNADVYESPEDNPLPSAGTFRSDISDVMT
QIVKFMAENNAPFTVNIYPFLSLYGNNDFPFNYAFFDGATPIVDKGIEYTNVFDANFDTLVSALKA
VGHGNMTIIIGEVGWPTEGDINANNGNAYRFYNGLFTKLGANRGTPLRPGYIEVYLFGLIDEDAK
SVAPGNFERHWGLFRYDGQPKFLIDLTGRGQNKLLIPAQNVEYQPQKWCTFNAGAKDVSKLVD
NINFACTYADCTTLGYGSSCNSLDANGNASYAFNAYFQTQNQDPDSCNFQGLATVTTKNISQG
SCNFTIQLVASSTSILRPLIVLTVISMAYTFLLQ

SEQ ID NO: 388
eucalyptusSpp_037751
MASLFPLTAAVVFLSVACPHLSRAAYTIGINYGTIADNLPPPSKVATFLKTKTTIDRVKIFHASPDIL
RAFAGTGIAVTVSVGNEDIVSLSKLPAAKSWVSANILPFYPKTLINRIAMGNEILATSDKTLIANLLP
AMKALHSALQLANVTNVQVTTPNSLGILASSYPPSNGSFRSGFDRTIFAPILKFHRQTNSSFMVN
PYPFFAITPENVNSLLNYSLFKPIPSSTFDAATGKNYTNMFDAQMDAVYSAMKKVGYEDVEIVVG
ETGWPSVGDPNQPGVSMANAESYNSNLVRHVNSGKGTPLMPNRKFETYIFALFNENKKPSTSE
RNYGLFKPDLTPVYDVGILRNSVNAVPLHLLG

SEQ ID NO: 389
eucalyptusSpp_011491
MRRVCACFLTSPAKTPPKHGTQRVSKQTAGNQKSESASNNSEVMANSSGSQGTNIIQNHNFSG
GLHSWHPNCCESWVVSAESGDCYAMVTNRKECWQGLEQDITSRVTPGSTYSVSACVGVSGS
LQGSADVLATLRLEHQDSAATYKRIGITSVSKERWDKVEGSFSLSSMPNRVVFYLEGPSSGIDLL
IKSVVITCQSANGKERVDREHIAAGDENIILNPIFDDGLKNWAGRGCKIVLHDSMADGKIVPQSGK
YFVSATERTQTWNGIQQEVTGRLQRKLAYEVTALVRIFGNNVSSTDVRITLWTQTPDLREQYIGV
ANVQATDKDWTQMQGKFLLNGSPSKVIIYIEGPPAGTDILVNSLTVKHAAKAAPSPPPVIQNPAF
GVNIIGNSDLDNGTNEWFPLGNCTLSVRAGSPHILPSSARDSLGPHEPLSGSYILVTNRTQTWM
GPAQMITDKLKLFLTYQVSAWVRIGSGASGPQNINVALGVDNQWVNGGQVEANDDRWHELSG
SFRIEKQPSKVMVYIQGPAPGVDLMVAGVQIFPVDRQARFNHLKHLTDKLRKRDVVLKFSGADS
SSLVGATVIVKQTQNSFPFGSCISRTNIDNEDFVDFFVKNFNWTVFGNELKWYWTEPQQGNFN
YRDADEMLDLCKSHGIETRGHCIFWEVESTVQAWVQSLNNNDLMSAVQNRLNGLLSRYKGKFS
HYDVNNEMLHGSFYQGRLGKDIRANMFKTANQLDPSATLFVNDYHVEDGCDTKSCPEGYIEHIL
GLQEQGAPVGGIGIQGHIDNPVGPIINSALDKLGILGLPIWFTELDVSSVNEYVRADDLEVMLREA
FAHPAVDGIMLWGFWELFMSRDNAHLVNAEGDVNEAGKRYLALRKEWSSHAHGHVNEQGEYT
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SEQ ID NO: 390
eucalyptusSpp_016710
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EKGMFYAFSAWVQASQGSETVAVVFRTRDGKFVRGGSVVAKQGCWSLLKGGIAANSSSPADV
LFESKNTSTEIWVDNVALQSFSKKQWRTHQEESIEKVTRKRKSTVRFQITSANERGLGVGGANV
LIKQIKPGFPFGCGMNFHILESADYQNWFASRFRYATFTNAMKWYSTEKEQGQEDYSVADAML
KFVQDNNISIRGHNVFWDDPKYQPDWVRTLSPDDLRKAAEKRINSVVSRYAGELIAWDVVNENL
HFSFFEDNLGENASSMYYSMAYKLDPTPRMFLNEYNTIEYSGDEKVSPGNYKKRFQEIFTYPGN
EDIPAGIGVQGHFGAGQPNSAYMRSGLDILATTGLPIWLTEVSVAPGANQQYLEEVLREAYSHP
GVEGIIMFAGPAYAGFNSTALADMNFDNTPTGDVVDQLIQEWRFKDLAARADDEGFFSTKLLHG
EYEITITDPISNSSSTSRFQVTKDSFKIIYHFHM

SEQ ID NO: 391
eucalyptusSpp_017035
MKDASAFISFLVFFLLLCSPWIAASLDDPQYDHTAYTKCKEEPEKPLYNGGILEPHQLPQFASSS
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DLPSNSATLSFESSDGRYIAIAISSTSLQPFTDQQWRRNQQDMINKVRKRAVMIHVSNHNGDRL
QGVEINVKQVYKDFPFGSAIAKTILGNEAYQNWFVERFNAAVFENELKWYATEPYPGQINYTIAD
EMLEFIRANRIVTRGHNIFWEDPKYNPEWVQNLSGPQLESAVDTRIQSLMSRYREEFVHWDVS
NEMLHFDFYERRLGPNATLHFFQTAHESDPLATLFMNEFNVLETCSDANSTVDSYISRMRDLKR
GGVSMDGIGLEGHFTVPNLPLMRAILDKLGTLRLPMWLTEVDISSTLSKESQALHLEEVLREGFS
HPSLNGIMLWTALHPNGCYQMCLTDADFRNLPAGDVADSLLGEWRTKEVNGKTNEHGSYSFE
GFLGEYEVSVMHGDQTANSTFALSQGVETRHVTILL

SEQ ID NO: 392
eucalyptusSpp_000843
MMTPAQNRAPKVSSVLLCLCCIHAFFSCAVRLVAGQTPKPVFACDVDGNPSLAAFGFCNTSWG
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SFPQVILTAASFNATLFETIGKVVSTEARAMHNVGLAGLTFWSPNVNIFRDPRWGRGQETPGED
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TFQPPFKSCVLDGNVASVMCSYNQVNGKPTCADPDLLAGTIRGKWKLNGYIVSDCDSVEVLYD
KQHYTKTPEEAAAKAILAGLDLNCGSFLGQHTEAAVKGGLLNESAVDKAISNNFATLMRLGFFD
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MIGNYEGTPCKYVTPLQGLAAIVSTMYVAGCADVGCSTAQTDDAKKAAASADATVLVMGADQSI
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GGAAMADVIFGDHNPSGRLPMTWYPQSYVDAVPMTNMNMRPDPATGYPGRTYRFYTGPTVY
SFGDGLSYSSFSHGQVQVPQLVSVPLDEGHICHSSACESLEAKSETCSNLVFDVHLNVKNVGR
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GTHVLHVGDLKHALSVQIGSSGLSLSPPRHF

SEQ ID NO: 393
eucalyptusSpp_005983
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SFGDGLSYSSVSHGQVQAPQLVSVPLDEGHICHSSACESLEAKSETCSNLVFDVHLNVKNVGR
FSGSHTVFLFSSPPSVHRSPQKHLLGFEKVFLASQSEAQVQFKVDVCKDLSVVDELGGRKVAL
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SEQ ID NO: 394
eucalyptusSpp_008977
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AASFNASLWEAIGQVVSDEARAMYNGGMGGLTYWSPNINILRDPRWGRGQETPGEDPVVVGQ
YAASYVRGLQGADGNGGGRLKVAACCKHFTAYDLDNWNGVDRYHFNARVSKQDMEDTFSVP
FRMCVMEGKVASVMCSYNQVNGIPTCADPNLLRKTVRGAWRLDGYVVSDCDSVGVFYGNQH
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PSAQPYGTLGPKDVCTPAHQELALEAARQGIVLLKNQGPALPLSPRRHRAVAIIGPNSDVTVTMI
GNYAGVACGYTTPLQGIGKYTKTIHQQGCADVACSDDKLFEGAIKAARGADATVLVMGLDQSIE
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GGTAIADILFGATNPGGKLPMTWYPQDYLASVPMTVMDMRPTRSNLYPGRTYRFYGGPVVYPF
GHGLSYTHFVHTLASAPSTVVVPLAGRRPANATMGPGKAVRVTHARCARLSLRVQLDVQNAGA
RDGAHTVLVFSTPPEDGGARWAPPRSQLVGFQRVHVAAGARERVGINIHVCKSLSVVDGAGVR
RIPMGEHRLQIGDVVHSVSLQAEPLRVI

SEQ ID NO: 395
eucalyptusSpp_023461
MRNRQVQILSLLITFASAATLLSTPAAAQPPPFSCDPSSPSTKSFPFCKASLPISKRAQDLVSRLT
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VQGDRPQGGGKSRGGLQASACCKHFTAYDLDRWKGVDRYDFDAQVTAQDMADTFQPPFQKC
IQDGKASGIMCAYNRVNGVPSCADYNLLSNIARRQWSFHGYITSDCDAVSIMYDNQKYAKTPED
AVADALKAGMDVNCGTYLQNHTKSAVEQRKVSVSEIDRALHNLFSVRMRLGLFNGDPKKQPFG
NIGPDQVCSQKHQDLALEAARSGIVLLKNKEKHLPLQRSKSASLAVIGPNANKASNLLGNYAGPP
CKSVTLLQALQSYVKDTRYQPGCDDVVCSSPQIAQAVEVAKAADHVVLIMGLDQTQEREDFDR
VDLVLPGRQQEFITTVAQAAKKPVILVILCGGPVDIRFARDDQNIGSILWAGYPGEAGGMALSEIIF
GEHNPGGRLPVTWYPQEFTRVPMTDMRMRPEPSTGYPGRTYRFYQGQSIFEYGHGLSYTEYS
YKFISVTRELFYLSQSAKSQPDEASDASPRYRLVSDLGADFCKKSNFVATVKVKNHGDMVGKHP
VLLFVRHAKPSSGSPMKQLVAFQSVELKGGETMKVQLALNPCDHLSRANENGVMILEEGWRFL
EVGDQEYPINVMA

SEQ ID NO: 396
eucalyptusSpp_009517
MSVMGRYSVPIKAFLLICCLAAVTTEAEYVKYRDAKQPMGARVRDLMRRMTLAEKIGQMTQIER
SVATPDVMKNYFIGSVLSGGGSVPAPKASPETWVNAVNEIQKAALSTRLGIPMIYGIDAVHGHNN
VYNATIFPHNVGLGVTRDPVLLKKIGDATALEVRATGIPYAFAPCIAVCRDPRWGRCYESYSEDH
RIVRMLTEIIPGLQGDLPANSPKGVPFVAGKNKVAACAKHFVGDGGTTKGINENNTVVDYNGLLS
IHMPAYLDAIRKGVATVMVSYSSWNGKKMHANGDLVTGFLKNKLKFKGFVISDWEGIDRITSPP
HANYSYSVQAGVGAGIDMVMVPYKVTEFLDDLTKQVQNNVIPMSRIDDAVKRILRVKFVMGLFD
NPLADNSLANQVGSPEHRELAREAVRKSLVLLKNGKSSGKPLIPLPKKAQKILVAGSHADNLGN
QCGGWTIAWQGLNGNDLTTGTTILNAVKSTVHPDTQVVYNENPDANFVKSNNFAYAIVVVGEPP
YAETFGDSLNLTIPEPGPSTIRNVCGSVKCVVVVISGRPVVIEPYVSNIDALVAAWLPGTEGQGV
ADLLFGDYGFTGKLARTWFRSVDQLPMNVGDPHYDPLYPFGFGLTTKGTKESDPTYS

SEQ ID NO: 397
eucalyptusSpp_019373
MAHCRHHPLVLLCSLFVFLPSILAQTADFNLPLRAINLGNWLVTEGWMMPSRFDGLIGQLLDGA
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GTPSASETFEIIRNPNRPNRVRLRASNELFLQAKTLTSVTADYNGDTNWNDNDPSIFDINIVGGL
QGEYQITNGYGPSTAPQLLRDHWNNYITEQDFRFMATNNVTAVRIPVGWWIAYDPTPPKPFVG
GSLYALDRAFTWAENYRMKVIVDLHAAPGSQNAESHSATRDGFVEWGDSYIQETVKVIEFLAAR
YCNRSALVAIELMNEPRAPDVKLNDLIDYYRLGYEAVRRYTMDAYVILSNRLGPADPLELFQFVR
GLSRVVIDVHYYNLYDPKFKQWNLQQNIGYIYVDRENDLSKITQKRGPLSFVGEWTSALDFDGA
TKEDSGRFAKAQQDVYRQATFGWAYRSYKCHYDTWSLEQMIEDGLIKIVA

SEQ ID NO: 398
eucalyptusSpp_021302
MGSAEDARCVYKDPNAAIEDRVNDLLSRMTLQEKVGQMTQIERRVATPSVLSGLSIGSILSAGG
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ATRDAELVRRIGVATALEVRASGIPYTFAPCVAVLKDPRWGRSYESYSEDTDIVRKMTPIVAGLQ
GQPPQGHPKGYPFVAGRNNVIACAKHFVGDGGTERGVNEGNTVTSYEDLERIHMAPYLDCISQ
GVCTVMASYSSWNGRRLHSDYFLLTEVLKDKLGFKGFVISDWEGLDRLSQPHGSNYRQSISLA
VNAGIDMIMVPFRHEQFAEDLTALAESGEVPMSRIDDAVQRILRVKFVSGLFEHPFSDRSLLQIV
GCKSHRELAREAVRKSLVLLKNGKDPMKPFLPLDKNAKKILVAGSHADDLGYQCGGWTATWHG
SSGRITIGTTILDAIKEAVGGNTEVIYEQNPSPSTLASHDYTFAIVAVGEGPYAETLGDNPELAIPF
NGTDVIKSVAERIPTLVLVVSGRPLVIEPHVLEKIDALVAAWLPGSEGTGITDVVFGDYDFEGQLPI
SWFRTVEQVPMDHKANSYDPLFPLGFGLKCKKEA

SEQ ID NO: 399
eucalyptusSpp_021738
MGSAEDARCVYKDPNAAIEDRVNDLLSRMTLQEKVGQMTQIERRVATPSVLSGLSIGSVLSGGG
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ATRDAELVRRIGVATALEVRASGIPYTFAPCVAVLKDPRWGRSYESYSEDTDIVKKMTAIVTGLQ
GQPPQGHPKGYPFVAGRNNVIACAKHFVGDGGTERGVNEGNTVTSYEDLERIHMAPYLDCISQ
GVCTVMASYSSCNGRRLHTDYFLLTEVLKNKLGFKGFVISDWEGLDRLSQPHGSNYRQSISLAV
NAGIDMIMVPFRHEQFAEDLIALAESGEVPISRIDDAVQRILRVKFVSGLFEHPFSDRSLLQIVGCK
SHRELAREAVRKSLVLLKNGKEPTKPFLPLDKNAKKILVAGSHADDLGYQCGGWTVAWHGSSG
RITIGTTILDAIKEAVGGNTEVIYEQNPSPSTLASHDYTFAIVAVGEGPYAETLGDNAELAIPFNGT
DVIKSVAERIPTLVLVVSGRPLVIEPHVLEKIDALVAAWLPGSEGTGITDVVFGDYDFEGQLPVSW
FRTVEQLPMDHKANSYDPLFPLGFGLKCKKEA

SEQ ID NO: 400
eucalyptusSpp_024123
MGSAEDARCVYKDPNAAIEDRVNDLLSRMTLQEKVGQMTQIERRVATPSVLSGLSIGSVLSGGG
SGPLGLAESASSERALLSDWTDMVDGFQKAALESRLGIPLIYGIDAVHGNNNIYGATIFPHNIGLG
ATRDAELVRRIGVATALEVRASGIPYTFAPCVAVLKDPRWGRSYESYSEDTDIVKKMTAIVTGLQ
GQPPQGHPKGYPFVAGRNNVIACAKHFVGDGGTERGVNEGNTVTSYEDLERIHMAPYLDCISQ
GVCTVMASYSSWNGRRLHTDYFLLTEVLKNKLGFKGFVISDWEGLDRLSQPHGSNCRQSISLA
VNAGIDMIMVPFRHEQFAEDLIALAESGEVPISRIDDAVQRILRVKFVSGLFEHPFSDRSLLQIVGC

KSHRELAREAVRKSLVLLKNGKEPMKPFLPLDKNAKKILVAGSHADDLGYQCGGWTVAWHGSS
GRITIGTTILDAIKEAVGGNTEVIYEQNPSPSTLASHDYTFAIVAVGEGPYAETLGDNPELAIPFNG
TDVIKSVAERIPTLVLVVSGRPLVIEPHVLEKIDALVAAWLPGSEGTGITDVVFGDYDFEGQLPIS
WFRTVEQVPMDHKANSYDPLFPLGFGLKCKKEAR

SEQ ID NO: 401
eucalyptusSpp_033744
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IVQAMTEIIPGLQGDLPAGSRKGVPYVAGKKNVAACSKHYVGDGGTTNGVNENNTVTDWHGLL
GIHMPGYYTSIIKGVSTVMVSYSSWNGVKMHANGNLVTGFLKNKLRFRGFVISDWEGIDRITSPP
HANYSYSIQAGISAGIDMVMVPSNFTEFIDGLTFQVKNKIIPMSRIDDAVRRILRVKFTMGLFEDPL
ADTSLVNQLGSQEHRELAREAVRRSLVLLKNGEGADAPLLPLPKKAPKILVAGSHADNLGYQCG
GWTIQWQGLSGNNLTSGTTILSAIKNTVDPKTKVVYEENPDTDTVKSGKFSYAIVVVGEHPYAET
FGDSSNLTIADPGTSTIGNVCGAVKCVVVIISGRPVVIQPYVAVMDAIVAAWLPGTEGQGVADVL
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SEQ ID NO: 402
eucalyptusSpp_041352
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NVYNATIFPHNIGLGATRDPKLVKKIGAATALEVRATGIPYVFAPCIAVCRDPRWGRCYESYSEN
EDIVRQMTEIIPGLQGDIPSGSRKGVPYVDGKNKVAACAKHFVGDGGTSKGINEDNTVVDMHGL
LSIHMPAYTDAIIKGVSTVMVSYSSWNGEKMHANRDLVTGFLKNTLKFKGFVISDWQGIDRITSP
PHANYTYSVEAGILAGIDMVMVPFNFTEFINDLTYLVKEKVIPMDRIDDAVGRILFVKFTMGLFEN
PLADLSLVNELGSQAHRELAREAVRNSLVLLKNGKNETDPLLPLPKKPKKILVAGSHADNLGYQC
GGWTITWQGFSGNNYTRGTTILSAINSTVDLSTEVVYQENPDKDFVKSTDFDYAIVVVGEHPYA
ETAGDSTTLTMADPGPTTITNVCEAMKCVVIVVSGRPLVIEPYISSIDALVAAWLPGTEGQGVAD
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RLLMVTACLAISLYVTGYRWRASKF

SEQ ID NO: 403
eucalyptusSpp_006312
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PAMNNVHASLVKYNLSDISVSSPIALSALQTSYPTSSGSFKSDLVEPVIKPMLEFLRKTGSYLMVN
VYPFFAYTANSDQISLDYALLKQNPGVVDSGNGLKYNSLFDAQVDAVYAAMSALQYNDLKLVVT
ETGWPSKGDANEVGAGTQNAAAYNGNLVRRALTGTGTPLRPNNTVDVYLFALFNENQKTGPT
SERNYGLFYPDEQKVYSIPLTLEQLASDPNNASKAQVPTAPVGQTWCVANGKAGEKKLQAALD
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GECDFPTGY

SEQ ID NO: 404
eucalyptusSpp_006494
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ENLMSQLLPAMQNMQKAITAAGLGGKVKVSSVHAMSLLSQSDPPSSGRFHPSFEARMRDVLQF
QRENGSPLPINPYPFFAYQSDPRPETLAFCLFQPNAGRVDSGTGIKYMNMFDAQVDAVYSALKA
LGYKDIEIVVAETGWPYNGDSNEVGPSVENAKAYNGNLIAHLRSLVGTPLMPGKSVDTYIFALYD
EDLKTGPTSERSFGMYKPDLTMSYDIGLAKSSQTPVTPTPKPTGPGWCVPKSGVSDAQLQASL
DYACSHNIDCGPIQPGGACFDPNTVASHAAFAMNLYYQTSGRNPWNCDFSQTATLTTNNPSYN
GCVYPGGST
SEQ ID NO: 405
eucalyptusSpp_008515
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NALKFIHSALVASNLDRQIKVSTPLSSSVILDSFPPSQAFFNKSLNPVLVPMLNFLQSSGSYLMLN

VYPYYDYMQSNGVIPLDYALFKPLPSNKEAVDANTLLHYSNVFDATVDAAYFAMAFLNFTNIPVV
VTETGWPSKGDSNEPDATVDNANTYNSNLIRHVLNKTGTPKHPGITVSTYIYELYNEDTKAGPLS
EKNWGLFDASGSPIYILHLTGSGSVLANDTTNQTYCTAKEGADPKMLQAALDWACGVGKVDCS
PMLQGESCYEPDTLSAHATYAFDTYYHQMGKAPGTCDFNGVAAITTTDPSHGTCIFSGSLGRN
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SEQ ID NO: 406
eucalyptusSpp_011678
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YNHKYVRQVLPALRNIHEALHRARLSSKVKVTVPFNADVYYSPPPNEYPSSGDFRPEVRDAAIEII
HFLYINDSPFTVNIYPFLSLYQNQNFPVDFAFFDGTTEPVKDGDRVYTNVFDANFDILVSALTKAG
YSDMEILVGEIGWPTDGDKFANIKNAQRFNQGLLKHALSGDGTPARKGVIDVYLFSLIDEDTKNID
PGNFERHWGLFEYDGKPKYELDLSGSEKDTRLVPVMGVSYMPRRWCILNPELNDLTDLGENID
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QFPLMLASGDSMSWNQGSLHTSFRFYLWFLVFWVIL

SEQ ID NO: 407
eucalyptusSpp_016980
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SPVNGGTAQFARFVLPAMRNIQAALRSSGLQNQIKVSTAIDMTLIGNSYPPSQGAFRGDVRSYL
DPIISFLVNNNSPLLANIYTYFSYVGNPKDISLPYALFTSPSVVVRDGAHEYRNLFDAMLDALYSAL
ERAGGASLRVVVSESGWPSAGAFAATVDNARTYNGNLIKHVKGGTPKRPNGAIETYIFALFDEN
QKQPELEKHFGLFFPNKQPKYPLSFAQGRIWDVYDNVTGPLKSDM

SEQ ID NO: 408
eucalyptusSpp_020029
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SVSYACANADCTSLGYGNSCSNLTAQGNISYAFNSYYQQHDQLDTACQFPNLSVITDNDPSVG
DCKFIIMIQSQSMSLVGSDGSRGRGIVPAILVSSLLYMILWMP

SEQ ID NO: 409
eucalyptusSpp_021882
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MKFIHSALVASNLDSRIKVSTPHSSSIIIDSFPPSQAFFNRTWDPVMVPLLKFLQSTGSYLMLNVY
PYYDYMQSNGAIPLDYALFRPLPPNKEAVDSNTLLHYNNVFDAVVDAAYFAMSYLNFTNVPIVVT
ESGWPSKGDSSEADATLENANTYNSNLIKHVLNNTGTPKHPGVAVSTYIYELYNEDQRPGSVSE
KNWGLFDANGVPIYILHLTGAGTVLANDTTNQTFCVGKDGADKKMLQAALDWACGPGKVDCSL
LLQGQACYEPDNVVAHATYAFNAYYQKMGKALGTCDFKGVATVTTTNPSHGSCIFPGSGGRNG
TSVNGTILAPSSNSTTSGCPPQYFFDVGSITSSLIITILHLALVLL

SEQ ID NO: 410
eucalyptusSpp_000640
MGSAEERVVAVIMVGGPTKGTRFRPLSLNIPKPLFPLAGQPMVHHPISACKRIPNLAQIYLVGFY
EEREFALYVSSISNELKVPVRYLKEDKPHGSAGGLYNFRDLIMEDSPSHIFLLNCDVCCSFPLPE
MLEAHISYGAMGTLLVIKVSAESASQFGELIADPSTKELLHYTEKPETFVSDLINCGVYIFTPEIFSA
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TPGMSLKCSGLYLAQFRSTSPHLLASGDGTKGATIIGDVYIHPSAKVHPTAKIGPNVSISANARVG
AGARLMNCIILDDVEIKENAVVTHSIIGWKSSIGKWSRAQGGGDYNAKLGITILGEAVTVEDEVVVI
NSIVLPNKTMNISVQEEIIL

SEQ ID NO: 411
eucalyptusSpp_012471
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FYDEKEFALYVSSISNELRVPVRYLKEDKPHGSAGGLYHFRNLIMEDSPSHIFLLNCDVCCNFPL
PDMLEAHKRYGGMGTMLVVKVSAESANQFDVFSAIEDVSNDREDRANLRRLSSIDISTSTRTNIP
TDFVRLDQDILSPLSGKKQLYTYETMDYWEQIKTPGISLKCSGLYLAQFRLTSPHLLASGDGTRS
ATVVGDVFVHPSAKVHPTAKIGPNVSISANVRVGPGVRLISCIILDDVELEDNAIVINSIVGWKSSL
GRWSRVQADGDYNSKLGITILGESVVVEQEVVVVNSIVLPNKILNVSVQDEIIL

SEQ ID NO: 412
eucalyptusSpp_028949
MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAIGVSEVVLAINYQPEIMLNFLKGF
EAKLGIKITCSQETEPLGTAGPLALARDKLLDDSGEPFFVLNSDVISEYPLKEMIQFHKAHGGEAS
IMVTKVDEPSKYGVVIMEESTGQVEKFVEKPKIFVGNKINAGIYLLNPSVLDRIQLRPTSIEKEVFP
KIAAEKQLFAMVLPGFWMDIGQPRDYITGLRLYLDSIRKKSSEKLATGPHIVGNVLVDETAKIGEG
CLIGPDVAIGPGCVVESGVRLSRCTVMRGVRIKKHACISSSIIGWHSTVGQWARVENMTILGEDV
HVGDEIYSNGGVVLPHKEIKSSILKPEIVM

SEQ ID NO: 413
eucalyptusSpp_010858
METRSSPKLRRLRCSVQKYDWGRRGAESRVAKLFALNSGAEADPDRPYAEFWMGTHGSGPS
FLLPAGCGNGGHKVSPDVTLKAWISSNPDVLGDKVVAEWGCDLPFLFKVLSIAKPLSIQAHPDK
ELARALHKARPDVYKDANHKPEMALALTKFEAICGFISMEELKQVLCDVPEIAELVGSTDVEKFIK
LGEQEVEKAKCLLQSIFTKLMSASADIVALAVSQINSRLELESQVRPLTDKEQLVLRLEKQYPADV
GVISAFFLNYVRLNPGEALYLGANEPHAYVSGECIECMATSDNVVRAGLTPKTKDIQTLCSMLTY
KQGFPDILKGVPLKTYITRYIPPFDEFEVDRCVLPKGSSAVFSAVLGPSIFLVTDGEGTINVGSVK
QDVVAEGYVLFVPANVEIHVTSVTELHVYRAGVNDRFLKSRELENGKKSQI

SEQ ID NO: 414
eucalyptusSpp_001308
MAGNDWINSYLEAILDVGPALDDKKSSLLLRERGRFSPTRYFVEEVITGFDETDLYRSWVKAQA
TRSPQERNTRLENMCWRIWNLARQKKQLEGEEAQRKSKRRLERERGRREATADMSEDLSEGE
KGDAVSDISTHGDSNRGRLPRISSVDAMETWVGQQKGKKLYLVLISLHGLIRGENMELGRDSDT
GGQVKYVVELARALGSMPGVYRVDLLTRQISSPDVDWSYGEPTEMLSPRNSEGLSDEMGESS
GAYIVRIPFGPRDKYVPKELLWPHIREFVDGALSHVIQMSKVLGEQVGGGQPVWPVAIHGHYAD
AGDSAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLSRDEINTTYKIMRRIEAEELSLDSSEIVI
TSTRQEIDEQWRLYDAFDPILEKKLRARIKRNVSCYGRFMPRMAIIPPGMEFHNIAPQDGDMDG
EMEGNDDHPTTQDPPIWTEIMRFFNNPRKPMILALARPDPKKNITTLVKAFGECRPLQELANLTLI
MGNRDGIDEMSSTSSSVLLSVLKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIE
PFGLTLIEAAAHGLPMVATKNGGPVDIHRVLDNGLLIDPHDQRSIADALLKLVADKHLWARCRQN
GLKNIHLFSWPEHCKTYLSRIASCKPRHPQWQRSEDGLGNSESDSPSDSLRDIQDLSLNLKFSL
DGEKNDASGNENSVGSEENSADRKNKLENAVMTWSKGVLKDKKTGLVEKSDPNANSSKFPPL
RRRKHIFVLAVDCDSLTDLLEIIQKVFSSVENERNEGSIGFILSTSLTMSEVHSFLVSGGLSPNDFD
AFICNSGSDLYYPSLNSENRPFVIDFYYHSHIEYRWGGEGLRKTLVRWATNINDKRAENEAQIVT
LAEKLSTDYCYTFKVEKLGMVPPVKEVRKMMRIQALRSHAVYCQNWTRLNVIPVLASRAQALRY
LYVRWGVDLSKMVVFVGECGDTDYEGLLGGLHKSVILKGVCGSASNQFHANRNYPLSDVMPF
DSANIVQTPQDCSSDDIASLENLGVLKE

SEQ ID NO: 415
eucalyptusSpp_034568
MAGNEWINGYLEAILDAGRYNVKRRGDGKIGGGGKGGVVATEFDGNEREGSLFSPTRYFVEEV
VNSFDESDLHKTWIKVIATRNTRERNNRLENMCWRIWHLARKKKQIAWDDAQRLAKRRLEREQ
GRSEAADDLSELSEGEKEKGDGSHSPEPAKDKIARINSDLQAWSDDEKPRQLYIVLISMHGLVR
GENMELGRDSDTGGQVKYVVELARALASTKGVYRVDLLTRQITSHEVDSSYGEPIEMLSCPADA
GDGCGAYIIRMPCGPSNEYIPKESLWPHVPEFVDGALNHIVNMARVLGEQIDGKPVWPYVIHGH
YADAAEAAALLSGVLNVPMVLTGHSLGRNKFEQLLKQGRLSREDINTTYKIMRRIEAEELGLDAA
EMVVTSTRQEIEEQWGLYDGFDLKLERKLRVRRRRGVSCYGRYMPRMVVIPPGMDFSNVKVE
DSTESESDLKSLISSDKTPNKRHLPRIWSEVMRRFFSNPHKPMILALSRPDPKKNVTTLLKAFGEC
QHLRELANLTLILGNRDDIEEMPEGSSVVLTNVLKLIDKYNLYGQVAYPKHHKQSDVPEIYRLAAK
TKGVFINPALVEPFGLTLIEAAAYGLPIVATRNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADK
SLWAECRKNGLKNIHCFSWTEHCHNYLSQVDHCRNRHPTSRFQIMPIPEEPLSESLRDVEDLSL
KFSIDGELKANGELDLATRQKELIEALTRKVHPNGGSPSISLSSRRQKIFAIALDPYDSGGLFTNIF
RVTIKNIMKVARGYSGLNRVGFVLLTGATLQETLNAFKGSDINVEEFEALSCNSGSSIYYPGRDFI
ADVDYEGHLEYRWPGDNVRSMVLRLAKAEDGMEDDIEELKAGCNSRCFAFSIKPGGKVRRIDD
LRQALRMRGFRCHIVYSCAGTRLSVMPLFASRIQALRYLSIRWGIDFADSVVFVGDKGDTDYEQ
LLGGLHKTIILNGTVECGSEKLLRSEENFKRVDVVALNSPRIRIVEDGSEEDISRALESLRMK

SEQ ID NO: 416
eucalyptusSpp_038142
MAGNEWVNSYLEAILDVGPALDDPKSSSLLLRERGRFSPTRYFVEQVITGFDETDLHRSWLRAA
ATRSPQERNTRLENMCWRIWNLARKKKQLEGEEAQRIAKRRLEHERGRREATADMSEDLSSE
GEKGDSATDISSQGGERMPRTGSVDIMDKWASRQKDCKLYLVLISLHGLVRGENLELGRDSDT
GGQVKYVVELARALGTIPGVYRVDLLTRQISAPDVDWSYGEPTEMLRTRNSEFPLQEIGESSGS
YIIRIPCGPRNKYVQKELLWPHIPEFVDGALSHITQMSKVLGEQIGGGRPVWPAAIHGHYADAGD
AAALLSGALNVPMLFTGHSLGRDKLEQLLKQGRLAEEINTAYKIRRRIEAEELSLDTSEIIITSTRQ
EIEQQWRLYDGFDPVLERKLRARIKRGVSCHGRYMPRFVVIPPGMEFRNIVPHDGDMNGEVEK
NPPIWPEIMRFFSNPRKPMILALARPDPKKNITTLVKAYGECHQLRELANLTLIMGNRDDLDEMS
TTNAAVLLSILKLIDKYNLYGQVSYPKHHKQSDVPDIYRLAAKTKGVFINPALIEPFGLTLIEAAAYG
LPVVATKNGGPVDILRVLDNGQLVDPHDQHAIANALLKLVSDKQLWSRCRENGLKNIHLFSWPE
HCRTYLSRIISCKPRGPQWQNNDDKLDKSESDSPGDSLRDIQDISLNLKFTLDGEKSEGNATFLE
ENADDAKSNVENTVLTLAKGVLRGIAKGTSTEKANEDIGAGDFSTFRRRKWIYVIAVDCDATADY
IDIIKRIMEATRKENAAGFILSTALTILEVHSLLTSGGLNLTDFDAFICSSGSDLLYPSSSSDDGPSG
LPFVIDLDYRSHIEYRWGGEGLRKTLVRWAASINDKKDGENIVAEDESGSSSYCFSFKVEDYDLI
PPVKELRKLMRIQALRCHVVCCQNGRKLNVIPVLASRVQALRYLFVRWGMDLSKFVVFVGECG
DTDYEGLIGGVHKTVILKGLGCESRKLHAHRGYPLEHVVPYDSPNVAEAEGSDVDSIKETLAKLG
VTRT

SEQ ID NO: 417
eucalyptusSpp_002364
MASPAWALFLGLVLMASGAMGAAPRKPVAVPFGRNYMPTWAFDHIKYFNGGSEIQLSLDKYTG
TGFQSKGSYLFGHFSMDIKLVAGDSAGTVTAFYLSSQNSEHDEIDFEFLGNRSGQPYIVQTNVF
TGGKGDREQRIYLWFDPTAAYHSYSVLWNMYQIVFFVDDVPIRVFKNSKDLGVKFPFNQPMKLY
SSLWNADDWATRGGLEKTDWSKAPFVASYRGFHIDGCEASVEAKFCATQGQRWWDQKEFQD
LDAFQYRRLRWVRSKYTIYNYCADRKRYPAMSPECRRDRDV

SEQ ID NO: 418
eucalyptusSpp_003103
MAFQGVLSNKMAMALVALGLLVAAAAASGNFNKDFDITWGDGRAQIPSSGQLLTLSLDKTSGS
GFRSKKQYLFGKIDMQLKLVPGNSAGTVTAYYLSSLGSAHDEIDFEFLGNLSGDPYTLHTNVFTQ
GKGNREQQFHLWFDPTKDFHTYSILWNPQSIIFSVDGTPIREFKNLESKGVAFPKSQAMWIYSSL
WNADDWATRGGLVKTDWTQAPFTASYRGFNDEQACVGSSGSSSCSSSSGDKSWLSQSLDAT
GQQRIKWVQKNYMIYNYCADTKRFSQGFPPECSLS

SEQ ID NO: 419
eucalyptusSpp_003487
MASPSAPSLCITTLLLVVVSWATSASARNFYQDFDITWGDGRAQILNNGDLLTLSLDKASGSGFQ
SKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSTWDEIDFEFLGNLSGDPYILHTNVFSQGK
GNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESIGVPFPKAQPMRIFSSLWN
ADDWATRGGLVKTDWTQAPFTASYRNFNADNTCIWSSGSSSCTSSSSSSDGNAWLSEELDST
SQERLKWVQSNYMIYNYCTDAKRFPQGLPRECAMS

SEQ ID NO: 420
eucalyptusSpp_003488
MASRSTSSLCRAALLLMVVSWATSASARNFYQDFDITWGDGRGQILNNGDLLTLSLDKASGSG
FQSKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSTWDEIDFEFLGNLSGDPYILHTNVFSQ
GKGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESIGVPFPKAQPMRIFSSL
WNADDWATRGGLVKTDWTQAPFTASYSNFNADNACVWSSGSSSCTSSSSSSDGNAWLSEEL
DSTSQESLKWVQSNYMIYNYCTDAKRFPQGFPPECSMS

SEQ ID NO: 421
eucalyptusSpp_003492
MASRSTSSLCTTALLLLVVSWAASAFARNFYQDFDITWGDGRAQILNSGDLLTLSLDKASGSGF
QSKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSTWDEIDFEFLGNLSGDPYILHTNVFSQG
KGNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESIGVPFPKAQPMRIFSSLW
NADDWATRGGLVKTDWTQAPFTASYRNFNADNACVSSSGSSSCTSSSSSSDGNAWLSEELDS
TSQERLKWVQSNYMIYNYCTDAKRFPQGVPPECTMS

SEQ ID NO: 422
eucalyptusSpp_003494
MASLSTSSLCIATLLLVVVSWGTFASARNFYQDFDITWGDGRAQILNNGDLLTLSLDKASGSGFQ
SKNEYLFGKIDMQLKLVPGNSAGTVTAYYLSSNGSAWDEIDFEFLGNLSGDPYILHTNVFSQGK
GNREQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESVGVPFPKAQPMRIFSSLWN
ADDWATRGGLVKTDWTQAPFTASYRNFNADNACVWSSGSASCTSSSSSSDGNA

SEQ ID NO: 423
eucalyptusSpp_004062
MAHEGGGPSASSMVVFVSLLLMAAASPAAGNFYQDFDLTWGGSDRAKIFSGGQLLSLSLDRVS
GSGFRSKKEYLFGRIDMQLKLVAGNSAGTVTAYYLSSQGPTHDEIDFEFLGNLSGDPYILHTNVF
TQGKGNREQQFYLWFDPTRNFHTYSVIWKPQHIIFLVDNIPIRVFKNGESIGVPFPKNQPMKIYSS
LWNADDWATRGGLIKTDWSKAPFTAYYRKFQATACTWSTGSSSCEIGRPASYSGSTWKINELD
AYGRRRLRWVQKYFMIYDYCADGKRFPQGIPAECKRSRF

SEQ ID NO: 424
eucalyptusSpp_004063
MAHEGGGPSASSMVVLVSLLLMAAASPAAGNFYQDFDLTWGGSDRAKIFSGGQLLSLSLDRVS
GSGFRSKKEYLFGRIDMQLKLVAGNSAGTVTAYYLSSQGPTHDEIDFEFLGNLSGDPYILHTNVF
TQGKGNREQQFYLWFDPTRNFHTYSVIWKPQHIIFLVDNIPIRVFKNGESIGVPFPKNQPMKIYSS
LWNADDWATRGGLIKTDWSKAPFTAYYRKFQATACTWSTGSSSCEIGRPASYSGSTWKINELD
AYGRRRLRWVQKYFMIYDYCADGKRFPQGIPAECKRSRF

SEQ ID NO: 425
eucalyptusSpp_005148
MAVPVFSKVSVSFGLFVGLALLVGLVAGARFEELYQPGWAMDHFVYEGEVLKLKLDNYSGAGF
GSKSKYMFGKVTIQIKLVEGDSAGTVTAFYMSSDGPNHNEFDFEFLGNTTGEPYLVQTNVYVNG
VGNREQRLGLWFDPTTDFHSYSVLWNQRQVVFLVDETPIRVHTNLEHRGIPYPKDQPMGVYSS
IWNADDWATQGGRIKTDWTHAPFITSYRNFEIDACECPATMAAADNAKRCSSAGRERRYWWD
EPTVSELSLHQNHQLKWVQAHHMVYDYCKDTARFPVMPAECEHHRH

SEQ ID NO: 426
eucalyptusSpp_007619
MASAALAMILFTSVLLKSLMVASAGNLNQEFDITWGDGRAQILNNGDLLTLSLDKASGSGFQSKN
EYLFGKIDMQLKLVPGNSAGTVTAYYLSSKGSTWDEIDFEFLGNLSGDPYILHTNVFSQGKGNR
EQQFYLWFDPTADFHTYSILWNPQRIIFSVDGTPIREFKNAESSGVPFPKSQPMRIYSSLWNADD
WATRGGLVKTDWSRAPFTASYRNFNADACVWSSGSSSCGSGAASSDGSSWLTQELDTTSQQ
RLKWVQQNYMIYNYCSDSKRFPQGPPPECNLS

SEQ ID NO: 427
eucalyptusSpp_010673
MQDSRMEKMVSPLSILLCISLVLLAEPRSSDAAPQSKGSFVDNFDIMWSEEHFKTSADGQIWYL
SLDKETGCGFQTKQRYRFGWFSMKLKLVGGDSAGVVTAYYMCSENGAGPERDELDFEFLGNR
SGQPYLIQTNVYKNGTGSREMRHMLWFDPTEDFHSYSILWNSHQIVFFVDQVPVRVFKNNGEA
NNFFPNEKPMYLFSSIWNADDWATRGGLEKTDWTKAPFVSTYKDFSFDGCQWEDPFPACVST
TTKNWWDQYSAWHLSEDQKKDYAWVQRNLVIYDYCKDTQRFPTLPWECSLSPWD

SEQ ID NO: 428
eucalyptusSpp_010807
MLHSHLGLLSLTCFAVLLVLASGSSPNLPIISFDEGYTQLFGDNNLALHGDGQSVHLALDERTGS
GFASQDLYLHGFFSASIKLPADYTAGVVVAFYMSNGDMYEKNHDEIDFEFLGNIREKNWRIQTNI
YGNGSTSVGREERYGLWFDPSDDFHQYGILWTDSQIIFYVDNVPIREFKRTEAMGGQFPSKPM
SLYATIWDGSDWATNGGKYRVNYKYAPYVAKFSDLVLHGCAVDPIEHQLSCNDVPSHKAIPQGI
SPRQRTKMEYFRKKHMTYSYCYDRARYKVPPPECVINPGEAEHLRVFDPVTFGDGRHHRPKR
HRQSRTSRADASI

SEQ ID NO: 429
eucalyptusSpp_011549
MSASWSVTSCLFFASCALLVVLAVGSPENSNSELPVVSFDEGYAHLFGDDNLVIHGDGKSVHLT
LDERTGSGFVSQDLYLHGFFSASIKLPADYTAGVVVAFYMSNGDMFEKTHDEIDFEFLGNIRGKE
WRVQTNVYGNGSVGVGREERYNLWFDPSDDFHQYSILWTDSLIVFYVDNVPIREVKRTKAMGG
DFPSKPMTLYATIWDGSSWATNGGKYRVSYKYAPYIVEFSDLVLHGCAVDPMEHSSACDAVLP
SGSIPTAITREQRVQMESFRKRHMTYSYCYDRARYKIPPPECILSVKEAKHLRSFDPVTFGQGKR
HFAKRRHRRVSATSM

SEQ ID NO: 430
eucalyptusSpp_012168
MALLYLSLLLVLLMLPICPGNAQWPPAPGYWPSSRFRSMSFYQGFKNLWGPQHQRVDQSALTI
WLDSTSGSGFKSVKPFRSGYFGASIKLQPGYTAGVITSFYLSNGEAHPGFHDEVDIEFLGTTFGK
PYTLQTNVYIRGSGDGRIIGREMKFHLWFDPTQAFHHYAILWRPNELIFLVDDIPIRRYPRKSAAT
FPMRPMWLYGSIWDASSWATEDGKYKADYRYQPFIARYTNFKASGCSAYSPAWCRPVSASPY
RSGGLTRQQYRVMRWVQAHHMVYNYCRDSRRDHSLTPECRI

SEQ ID NO: 431
eucalyptusSpp_012541
MKYLRSFLVIVSVLNLVCVSFSSVVSTGNFNKDFFVMWSPDHVNTSADGRTRSMVLDQESGAG
FSSNDMFLFGQIDMKIKLISGHSAGTVVAFYLTSDQPNRDEIDFEFLGNVSGQPYILQTNVYADG
FDNREERIYLWFDPTQDFHNYSILWNLHQIVFFVDSIPIRTYRNHADKGVAFPRWQPMGVKATL
WNGDSWATRGGHDKIDWSKGPFVASFGDYKMDACVWKGNPRFCRAESPTNWWNNEDFSSL
TSTQRRWFKWVRRYHMIYDYCQDNARFQNNLPKECSLPKY

SEQ ID NO: 432
eucalyptusSpp_012905
MTSPSTRLCVCLFHLAAISALASAGNFYKDFDITWGDHRSQILNGGQELTLSLDQASGSGFKSK
NEYLFGRIDMEIKLVEGNSAGTVNAYYLSSQGPTHDEIDFEFLGNLSGNPYTLHTNVFSQGKGN
REQQFHLWFDPTKAFHTYSIVWNTRRIIFLVDNSPIRVFNNLESIGVPFPSNQPMRIYSSLWNAD
DWATMGGRVKTDWTKAPFTASFRNFNANACVVSSGSSSCGSKSTNNLQTSAWQEQSLNAAG
RNRLRWVQQKYMIYNYCSDSKRFPQGLPPECKRSRFL
SEQ ID NO: 433

eucalyptusSpp_017386
MPTSISSYSFPRTTMLVVCAILIGSSVVALAGNFYQDFDVTFGDGRVKVLDNGQLVTLSLDKASG
SGFKSKNQYLYGKFDMQIKLVPGNSAGTVTTLYLHSDGSTWDEIDLEFLGNLSGDPYILHTNLYS
QGKGNREQQFYLWFDPTADFHTYSVLWNPVHVVYYVDGIPIREFKNLNAAGVPYPKSQPMTLY
STLWDAEDWATRGGLVKTDWSQAPFTASFSGFNASACVWSNGASTCLSSSAASAKYPWFSQ
QLDAASLQTMKSVQQKYMIYDYCKDTKRFPQGLPLECTLKTKS

SEQ ID NO: 434
eucalyptusSpp_022385
MALLQENTLFFSLLFLLCMAISVSSHNRPYSPPDVPRLTDLFPHVAVDQGFSKFFGAQNVRLLNN
GSYANLALDKSSGSGLVSRSKYHYGFFSAAVKLPAGLSSGVVVAFYLSNADAFPHSHDEIDIELL
GHDKRNDWVLQTNIYSNGSVSTGREEKFYFWFDPTQEHHYYSIIWNSHHIVFFVDNIPVREFPS
SGVFSSTYPSKPMSVYATIWDGSQWATHGGKYPVNYKYAPFVVSLAETEMVGCVSNPRQQPL
SSCSNQSTSSGSDPVEGQDFAALSQQQITAMQWARSKLMFYSYCKDTSRFKVMPPECK

SEQ ID NO: 435
eucalyptusSpp_033851
MDPLRRLVSLAVTTSSSSSSSSSLTLLLALLFYAASAAAAFDIVPITFDEAYAPLFGDSNVVRSGD
GKSVRLLLDRFSGSGFISSNLYKYGFFSARIKLPSDYTAGIVVAFYTSNGDVFEKTHDELDIEFLG
NIKGKKWRFQTNVYGNGSTSRGREERYTLWFDPTRAFHRYSILWTANNIIFYVDEVPIREIIRNDA
MGGDFPAKPMALYATIWDASDWATSGGRYKVNYKYAPFVAEFKDLVLQGCPVDPIDQYSSGH
CYDKLALLEAQDFATVTAQRHAAMRRFRQNYMYYSYCYDTVRYAIPPPECVILQSEKERFKDTG
RLKFGGSHKKRSRRRGHRIPLVSEEQPVM

SEQ ID NO: 436
eucalyptusSpp_034061
MDRHPPPHSRRFSLYQPPSYFSLSLLSIFIFSCFLSTSDAAFDVTPISFDEGYRPLFGDGNVVRS
PAGDGVRILLDRFTGSGFISSDMYQHGFFSAKIKLPSDYTAGVVVAFYTSNGDVFEKTHDELDIE
FLGNIRGKPWRFQTNVYGNGSTSRGREERYTLWFDPTKEYHRYSILWTANKIIFYVDEVPIREIV
KSEAMGGDFPSKPMSLYATIWDASDWATSGGRYKVNYKYAPFVAEFKDLVLEGCMADPIRQLP
ASGCHAKDAQLEARDFATITSSQRRAMRRFRERYMYYSYCYDTLRYPVPPPECMIIPSEKARFK
DTGRLKFGGSHKRRSRRRERIPAASVSDNQASM

SEQ ID NO: 437
eucalyptusSpp_036012
MSHPRTQMAISKRRSPSCSLIALTMMVWLWSSHVVPRVAGCDGFDELFQPNWAPEHFECEGD
QTKLTLDSSSGCGFGSRKAYLFGLTSVQIKLVQGDSAGTVTAFYMSSDGPNHDELDFEFLGNLS
GEPYLVQTNVYVNGTGDREQRHSLWFDPTTDFHTYSLFWNRRYITFLVDGIPIRVFANKEESHG
VPYPKNQPMRVLGSVWNADDWATQGGRVKTNWSHAPFVSSFRAFDIDACELSPETADVTTKC
GQLGRYWWDRPSFNELGRRQSRQLKWVCKKYLVYDYCEDKPRFSELPKECVG

SEQ ID NO: 438
eucalyptusSpp_002298
MAKPGLTAMVVAALALVVAMVATLAHAEADDPKKVDAWFNGLSHADRKTTRLHFYFHDTLSGR
NPTAVRVAEATMTEKSPTLFGVVNMIDDPLTEGPEPESPLVGRAQGFYGSVGLESMALHMNMN
LVFTTPEYNGSTLSILGHNPALETYREMPIVGGTGVFRLASGVVTAKTYFLNLTTGDAVVEYKVIA
LHY

SEQ ID NO: 439
eucalyptusSpp_002439
MAKPGLTAMVVAAVALVVAAVALVVAMVAKHAHAEADDPEKVDAWFNGLSHADRKTTRLHFYF
HDTLSGSNPTAVRIAEAKSPTGFGVVNMIDDPLTKGPEPESPLVGRAQGFYGSVGLESTALHMS
MNLVFTTPEYHGSTLSILGRNPALETYREMPIVGGTGVFRLASGVVTAKTYFLNLTTGDAVVEYK
VIALHY

SEQ ID NO: 440
eucalyptusSpp_008836
MGARVIVSLLFLFLIFGSNADAANKRIRNRRPCKRLVFFFHDVLYNGNNAKNATSAIIGAPAWAN
QTILAGQSHFGDLVVFDDPITLDNNLHSKPVGRAQGFYIYDKKDIFTAWLGFSFVFNSTQHTGSL
NFAGADPLMNKTRDISVIGGTGDFFMARGVATLMTDSFEGEVYFRLRTDIKLYECW

SEQ ID NO: 441
eucalyptusSpp_009914
MATLSPISSLLLLLLLLLSSGSPTLASAFATALDPSLMGINLGKEKLSHFRFYWHDVQSGPHPSSV
TVVPPPSNSSATFFGLINMIDNPLTLRPDPGSELVGRAQGLYSSASQEEVGLLMIMNFAFVAGKY
NGSGITVLGRNPVLQKVREMPVISGCGLFRFARGYAQATTHTFDRKTGDAVVEYNVYVLHY

SEQ ID NO: 442
eucalyptusSpp_009915
MATLIPISSLLLLVLLSSAAPAPASAFATALDPSLMGVHLGKEKLSHFRFYWHDVLSGPNPSSVR
VTTPPSNASATGFGLVNVIDNPLTLLPDPASELVGRAQGLYSSASQEEVALLMIMNFAFVSGKYN
GSGITVMGRNPVFHKVREMPVISGCGVLRFARGYAQASTHTFDLKTGNAVVEYNVYYVLHY

SEQ ID NO: 443
eucalyptusSpp_010326
MVKPGLTAMVVAALALALATAVALACAEVDDPEKVNAWFNRLSHAEHKTTHLHFYFHDTLSGKN
PTAVRIAEATMTEKSPTLFGVVNMIDDPLTEGPEPESPLIGRAQGFYGSVGLESLALHMNVNLVF
TTPEYNGSTLSILGRNPALETYREMPIVGGTGVFRLASGVATAKTYFFNLTTGDAVVEYKVIAMH
Y

SEQ ID NO: 444
eucalyptusSpp_017008
MALISAPKMLTATTFSQLLLLSTYSILMHSYSSKATVQHPHTTKLVLYFQDIIAGPNANDIPVVGIP
GKLWSFSQFGTVFVADEPITETPDPNSAMVGRAQGMYVISSLDGSNVKTVFSIVFTNQAYNGST
LELQGAGKQLQRVLEFAVVGGTGKFRFARGYTTLETISFSQGHGVIQFNVTVRHD

SEQ ID NO: 445
eucalyptusSpp_017185
MRNLVAHKSCFLVLFLLLLFTSQFSSATKKTFNRDQPCKRFVLYFHDILFGGNDVANATSAAVAN
ETGLGNFKFGKLFVFDDPMTKDKNYLSPAVARAQGFYFYDMKNDYNAWFAYSLVFNSTEHKGT
LNIMGADIMAAQTRDLSIVGGTGDFFMARGIATFETDLFQGAKYFRIKMDIKLYECY

SEQ ID NO: 446
eucalyptusSpp_019645
MAVHIAKLVAFSLLCMSTVFVAANSHTFARSLLPQELGLKKEKLSHLHFYFHDIVSGRNPTAVRV
AEAKMTNSSATGFGAVVMIDDPLTEGPEMSSKEVGRAQGIYALSSQNDVGLLMVQNYVFTEGK
YNGSTLSVLGRNAVFSGVREMSIVGGSGLFRFARGYAQAKTHTMDRKTGDTVVNYNVYVFHY

SEQ ID NO: 447
eucalyptusSpp_002197
MASVSRVVGLVSLILFSTLAEARIPGVYTGGPWQSAHATFYGGSDASGTMGGACGYGNLYSQG
YGVNTAALSTALFNNGFSCGACFEIKCANEPQWCHSGSPSILVTATNFCPPNYALPNDNGGWC
NPPRPHFDLAMPMFLKIAEYRAGIVPVSYRRVPCRKQGGIRFTINGFRYFNLVLVTNVAGAGDIN
KLWVKGSKTGWMSMSRNWGQNWQSNSVLAGQSLSFRVTAGDRRTSTSWNIVPSNWQFGQT
FTGKNFRV

SEQ ID NO: 448
eucalyptusSpp_002399
MAAARVMALALAFLGVALSATRMAEARIPGIYTGGPWQSAHATFYGGADASGTMGGACGYGN
LYSQGYGVNTAALSTALFNNGFSCGACFEIKCANDPQWCHSGSSSIFVTATNFCPPNYAQPSD
NGGWCNPPRPHFDLAMPMFLKIAEYRAGIVPVAYRRVPCRKRGGIRFTINGFRYFNLVLISNVAG
AGDIVRVSVKGSRTGWMSMSHNWGQNWQSNSVLVGQSLSFRVTGSDRRTSTSWNIVPAGW
QFGQTFTGKNFRV

SEQ ID NO: 449
eucalyptusSpp_002532
MTRASVVFAASLISFSLMWLADARIPGVYSGGPWQTAHATFYGGSDASGTMGGACGYGNLYS
QGYGVNTAALSTALFNNGLSCGACFEIKCANDPTWCHSGSPSIFVTATNFCPPNFAQPSDNGG
WCNPPRPHFDLAMPMFLKIAEYRAGIVPVSFRRVPCRKRGGMRFTINGFRYFNLVLISNVAGAG
DIVRVSVKGARTGWMSMSRNWGQNWQSNAVLAGQALSFRVTASDRRSSTSWNMVPAGWQF
GQTFTGKNFRV

SEQ ID NO: 450
eucalyptusSpp_006932
MQQRRRGSPSSSSSAAALLLGRLWLLLVLGAATTSASAQVKKRVPNARWKPATATWYGSPDG
DGSDGGACGYGSMVDVRPLRARVGAVSPVLFKNGEGCGACYKVKCLDRGICSRRAVTIIVTDE
CPGGYCSGGNTHFDLSGAAFGRMAIAGEAGPLRNRGVLPVQYRRTPCKYPGKNIAFHVNEGST
DYWLSLLVEFEDGDGDVGSMHIRPASSSEWIEMKHLWGANWCITGGPLQGPFSVKLTSLSTNR
TLSARDVIPGNWSPKATYTSRLNFF

SEQ ID NO: 451
eucalyptusSpp_013492
MANFAAISAVALVFLCLKSAFGDYGGWEGGHATFYGGGDASGTMGGACGYGNLYSQGYGTNT
AALSTALFNNGLSCGACYEMRCNDDPRWCLPGTIMVTATNFCPPNLALSNDNGGWCNPPLQH
FDMAEPAFLQIAQYKAGIVPVSFRRVPCVKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKG
SRTGWQAMSRNWGQNWQSNAYMNGQALSFQVTTSDGRTVTSYNAAPANWQFGQTFEGSQF

SEQ ID NO: 452
eucalyptusSpp_014985
MAVVGLLLVGCLAMWVCSVDGYGGGGWINAHATFYGGSDASGTMGGACGYGNLYSQGYGTN
TAALSTALFNNGLSCGSCYEIRCVNDRQWCLPASIVVTATNFCPPNNALPSNAGGWCNPPLQH
FDLSEPVFEHIARYRAGIVPVAYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHAVSVKG
SRTGWMSMSRNWGQNWQSNNYLNGQSLSFKVTTSDGRSVMSYNAAPAHWSFGQTFSGVQF
R

SEQ ID NO: 453
eucalyptusSpp_014986
MAVVGLLLVGCLAMWVCSVDGYGGGGWINAHATFYGGSDASGTMGGACGYGNLYSQGYGTN
TAALSTALFNNGLSCGSCYEIRCVNDRQWCLPASIVVTATNFCPPNNALPSNAGGWCNPPLQH
FDLSEPVFEHIARYRAGIVPVAYRRYVHCNARPSFFGRVKKLGACVKHMNSLVRLVNLQCPVW
GTFCRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHAVSVKGSRTGWMSMSRNWGQNW
QSNNYLNGQSLSFKVTTSDGRSVMSYNAAPAHWSFGQTFSGAQFR

SEQ ID NO: 454
eucalyptusSpp_015104
MALLLCFLLSLFISSATACDRCVHQSKAAYFSKASALSSGACGYGSLAVGLNSGFLAAAIPSLYK
DGAGCGACFQIRCKNANLCTKGGTRVIVTDLNRNNNTDFVLSSRAFAAMARQGMSQDILRQGIV
DVEYKRVPCDYKDRNLAVRVEESSRKPNYLAIKVLYQGGQTEIVAMDVAQVGSSYWTYMSRNH
GAVWNTSRVPDGALQFRFVVTPGYDGKWIWAKSVLPADWQNGVVYDSGVQITDIAQEGCSQC
DDGSW

SEQ ID NO: 455
eucalyptusSpp_018610
MALLQSPSICFPLALLLALLINSSHCFNPKSLNISKVQSNGDWSPAGATWYGSPNGAGSDGGAC
GYGSGVDQAPFSSMVSAGGPSLFKSGKGCGACYQVKCTENAACSGNPVTVVITDECPGGPCV
AESAHFDLSGTAFGAMASSGKADELRNAGVLQIQYQKVKCNFPGAKVAFHVDSGSNPNYFAALI
EYEDGDGELGAVNLKQALDSDSWLPMQQSWGAVWKLDGAGQLRAPFSIKLTSLDSGKTLVAN
NVIPAGWQPGQTYRSVVNFAV
SEQ ID NO: 456
eucalyptusSpp_020260

MEVKLQVLVALAMALSLFSAASATAGLAVYYAPQYYPAACPGFTLKNSGVMVAGVSDALWNNG
RACGRMLKVRCTRAANQFPNPCRAGVITVKVVDYCRQPCNGVINLSQDAFAKIANLDAGKVWV
DYS

SEQ ID NO: 457
eucalyptusSpp_028458
MLPKTISVATGDDGTASYYVPPYERTECYGEGSSQFPESNFFAAVGDNLWDLGAACGREYEVR
CISKAQSGPGPCKPGSDTIRVKVVDYALSVSSSAAAPKQSVTGADLVLSQIAFEAIANPSVDSITV
ELKEV

SEQ ID NO: 458
eucalyptusSpp_031108
MVPLGFLVVGLLSQFVPVSRAYGYYGGWTNAHATFYGGSDASGTMGGACGYGNLYSQGYGT
NTAALSTALFNNGLSCGACFELRCVNDPQWCLPGAIVVTATNFCPPGGWCDPPQLHFDLSQPV
FQHIAQYRAGIVPVAYRRVRCRRSGGIRFTVNGHSYFNLVLITNVGGAGDVHSVAIKGSRTRWQ
PMSRNWGQNWQSNSDLNGQSLSFLVTASDGRSVVSYNVAPSGWSFGQTYTGGQFRY

SEQ ID NO: 459
eucalyptusSpp_010481
MASKSSTSPAFLFSMILALVVGINGGGIAIYWGQNGNEGTLAEACASGNYKFVNLAFLNVFGNG
QTPMINVAGHCDPSSGGCTGLSSEIKSCQARGVKVMLSIGGGVGSYYLPSAEDARYVATYLWD
NFLGGQSSSRPLGDAVLDGIDFVIATGTNQHWDDLARYLSAYSISGKKVYLAAAPQCPYPDAWV
GGALQTGLYDYVWVQFYGNPPCEYSSGNMGNLEDAWNQWTSIPAGEIFLGLPASADASSGFIP
ASNLTSIVLPTIKGSAKYGGVMLWSRTVFPSSRASGHDSHVYARDGFPDSPIRRFPIRRFSVSIQ
LGYVMIVDGSSSQLLLKRRRLAIPDPMEAEPAKVLSLSLSHSIFSMLMLGL

SEQ ID NO: 460
eucalyptusSpp_019062
MPSPPPSKPSLSLLLLLFSSSLIRASHGGGIAIYWGQNGNEGTLASTCATGKYAYVNLAFLYKFG
GGQTPQINLAGHCDPTSGGCTSTSNGIRSCQNQGIKVMLSLGGGVGSYSLASQADARNVANYL
WNNFLGGTSSSRPLGDAVLDGIDFDIELGSTKYWDDLARYLSDYSKQGKKVYLTAAPQCPYPD
SHMGAALNTGLFDYVWVQFYNNPPCQYSSGDISKLTSSWSKWVASINAGKMFVGLPASTEAAG
SGYVPPNVLTSQILPVIKKSAKYGGIMLWSKYYDDKNGYSDSVKSSV

SEQ ID NO: 461
Pra_000420_O_1
TATGTAAGTCATAGGTAAAATAGGAGGAACGGTCAGAGAATCTGCGTCCCCATCATGCGT

SEQ ID NO: 462
Pra_009128_O_1
GAAACGGCTTTACAGAAAGGAGTAATAATTATTGTAGTCTCCCTTTTTAATGGTGAGCAA

SEQ ID NO: 463
Pra_000082_O_1
AAATGCTAGCTCTGTCTGTTTACTAGTGCCATAGCTAGCATGCCAAGCGATGAGAATGAT

SEQ ID NO: 464
Pra_000808_ORF_O2
TTTGTTATCCTGTAATGAATTGAATCTGGGCCTATTCTGCTCGCACCTTCACACGTTTGG

SEQ ID NO: 465
Pra_002641_O_1
TTCTATACTAAAACATGACAGCTTGAGCATCCTCACTTATTAACGAGTAACTGTTGTCAC

SEQ ID NO: 466
Pra_003151_O_4
ACAATACATAAATACCTAACCAAAAACCTGTTAGTCCATGTTTTCCCACATGTATTTTAT

SEQ ID NO: 467
Pra_003170_O_1
ACGGATGAGACATCGTAGTTTTATATTTAGTGGACTGGCCAGCTATATTTTCAAGGATAT

SEQ ID NO: 468
Pra_003171_O_1
GATGTATGAGGTACCTATTTTCAAAGTTGTGATAGCATATACATCATAAGATGTAATGTG

SEQ ID NO: 469
Pra_005830_O_2
GATACATATGTGATCATCCTGAAGTGTGAATTGTGTCCAAACCTTCATCTCAGTAATCTT

SEQ ID NO: 470
Pra_006138_O_2
ATGCTCTTGAATTAATTTTTGACGTCATTTTTTGTGAATGTGTTCGTTCAATGTGACTTC

SEQ ID NO: 471
Pra_006141_O_1
TTTAAGCTTTGTGCATGTGTTTTGCTCAACAACTGTGAAGATTAGAATCTTTATAACCAT

SEQ ID NO: 472
Pra_008153_O_1
CTTAAAGGACCTTGTCACTTGTTACTCTTGTAATTGATCGTAGGGAATCCTTACTCTATT

SEQ ID NO: 473
Pra_008677_O_1
ATTTGTATACGATTTGCCTTTACGTTTTGTAGCGATGTGGGTGTTATCGATGACTATTAA

SEQ ID NO: 474
Pra_008688_O_1
ATTTCATAACGATAGAATCAATTTATATACTAAATAGTTCGTCTACTGTGAAATGATAAT

SEQ ID NO: 475
Pra_008701_O_1
TTATGTTTTTCGTCCGCTATAGGCTAAGCACAGGCTATCGCAACCCAGTGGATTGGATAA

SEQ ID NO: 476
Pra_010276_O_1
ATATTACAGGAAACGGTTGGATCGTTTTAAAATACGAAACGACTGTCGTTACTATAGTTA

SEQ ID NO: 477
Pra_012343_O_2
GAGTGAGAGGTTATGGAAACTGTGAATATATATCGCAGTGAGTGATGAGTGAGAGATTGT

SEQ ID NO: 478
Pra_013199_O_2
TTTCATTCAACATCAGCTAAGACGACGAAACTCAGAGGAAATCTTGTGGTGGATAACTAA

SEQ ID NO: 479
Pra_014339_O_2
TATTCACTAAGTAATGGTAGAAGGTCAAGGCTCTGTTAATATAAGAGTACAATTCTTGTA

SEQ ID NO: 480
Pra_014357_O_1
GAATGCTTTGCTATAGTTCTCTTACTCGGAGAACATTCTTACATGGAGAACGTGCAGTTT

SEQ ID NO: 481
Pra_014389_O_1
ATTTTGTAGGGGTATTTCACAGGCTCTTAGGTTGGAATTCGAATCACTTGTGTGTGACTT

SEQ ID NO: 482
Pra_015733_ORF_O2
AAATATGGCAGCGTCTAATGAACAGATGAAAGAGAATCGTGATTGGGTTGATTGCCGTCT

SEQ ID NO: 483
Pra_015734_ORF_O1
GACACCCAAGAGGCCGGGTACGAACATCGAGACCTATATCTTCGCTCTTTTCAACGAAGA

SEQ ID NO: 484
Pra_019348_O_2
AATGCAGTGATTTATGTTATGGAGGATGCTACTTATACAATCGTCCTCCTAAATAAATTC

SEQ ID NO: 485
Pra_020304_O_2
GATTTCAAGTGGGTAATATACAAATAGTATTTTTTGTACTATGTCTCCAAATTTACATTT

SEQ ID NO: 486
Pra_020305_O_1
GAGATATTAATCTTATTTTTAGTTAGTTTTCTGATGTCAGTTAGGTGTCATCACGATTGA

SEQ ID NO: 487
Pra_021499_ORF_O1
GGAACCGTAGAAAGCTTTAAAACGAGCTCTGAAACGCCTCTGGGTGCTCGGATATAGGAT

SEQ ID NO: 488
Pra_021803_O_1
AGAGTCCTCATCTGAATGCATCAAATGGTGTAATATTCTTAGTAGGTATAGCTTTACCCT

SEQ ID NO: 489
Pra_024199_ORF_O2
AAATATCTGGGTTACACAGATATTGATATAGTGGTGGCAGAAACGGGATGGCCATCTGCA

SEQ ID NO: 490
Pra_024166_O_1
GTTGCGCGCAACAGAGTGCACGTATTTGGAAATCAATGCCTCTGCACAGAACGTTGTATC

SEQ ID NO: 491
Pra_000560_O_1
TTATTAGTTTGGTTCTCCGAAGGCAATTGTCAGGAGGCAGATTAAGGTTAGGTAATAAAC

SEQ ID NO: 492
Pra_008324_O_3
TAACTGGAATAAATTATTGTTTACTGTGTCCCCTTATCAGAAATTGTTGTCAACAACTGC

SEQ ID NO: 493
Pra_008526_O_2
TTATTTGATTACATGCTTTGTATTTCCATTTCTGTCATTGTGAACCCAAGTTATTAAGCT

SEQ ID NO: 494

Pra_013209_O_2
GCAGTAGGAATAAAACTTTTAGGAAAGTTTAGGAATGTCAAGCTGGTTGTATATCATTAT

SEQ ID NO: 495
Pra_013210_O_2
ATTTATTTAAGATTAGAGTGATGCTAACAGCTACAACTTGTAAAAGCTCCTGGTTGTTGC

SEQ ID NO: 496
Pra_018923_ORF_O1
AGATGGTCATGCTAGTTGTATGATGTGCTCATACAATCAGCTAAATGGAGTCCCTGTATG

SEQ ID NO: 497
Pra_022167_O_1
AATTATTGAGCAACGACTCCTAAAAATTGGGTGTGGTTGCTGTCGTGTAGTGTAATAATT

SEQ ID NO: 498
Pra_005555_O_2
CTCCTGAAGTGTGGAATAAACTTATAAGTTATGACAGAGGACATCACCAGGTTTAAACAG

SEQ ID NO: 499
Pra_006798_O_1
ATGTGGGCTACAAGCACCATGATCCCCTGTTTCCCTTGGATTTTGAATTGACCACAACAG

SEQ ID NO: 500
Pra_006799_O_2
CATAGATGATAGAACCAATTGTTTGTAAAACAGTAGAATAATCTTGTACTTTATATCTGG

SEQ ID NO: 501
Pra_006802_O_1
GTTATTTAGGCTTACCCGTCTCTTATTTATTTAATAATGGTCGCACTGTGTAACAAATTT

SEQ ID NO: 502
Pra_006803_O_2
ACAGTAGCTGAAATTCCAAGGGAGTAATTTAGGTTCATCTCTTATTTAAAAGAATGAATG

SEQ ID NO: 503
Pra_013555_O_1
CTGCGCGAGCTTAGCTCAATAAATTTGGAGTAATCTTTTTTATACCACCTATTAGGTATA

SEQ ID NO: 504
Pra_014884_O_2
CAGTGCGACACAGTCGGATTATCAAAGGTACGGAGATGCACAGTTACAAGTATACGGTGA

SEQ ID NO: 505
Pra_001975_ORF_O1
GCATCAGTGGATGCGCTCAGGGCTCCAATATAACTGTACTGGATAGATTATATACATCAA

SEQ ID NO: 506
Pra_003684_ORF_O_3
CTGAAAGACAATGGTATAAAGAAGGTGAAACTGTTTGATGCAGAGGAGCGCGCGATGAGA

SEQ ID NO: 507
Pra_008566_O_2
ATTCTGCAGCTTGTGAGTCCAACATTCAAATAAAACCGATGTGGACTGGTCCTCCTCTAT

SEQ ID NO: 508
Pra_013146_O_1
CCACATCACATGTGACCCGAGTCGATGTAGACAAGCCCTTATCTGCAGACAAGCCCTTAT

SEQ ID NO: 509
Pra_014358_O_2
TTCATTGTTGTACGCAGAATAGAGGTATCAGAGTTTACTGCCATTCATTGATAGGTATTC

SEQ ID NO: 510
Pra_014570_O_2
ATATCTGTGTAATTATAAAGTGAAAATAGTGACTGAGACTCTGGATACGGCCTTATCCAG

SEQ ID NO: 511
Pra_014985_O_1
GTAACGCCATGCATTCACTATACCAATGTGATAAGGACGTCACTATACTGCTGTAATCTG

SEQ ID NO: 512
Pra_023047_O_2
AATCCTACGATGTAACGTTAGGAAATCTTTCAAACGGTATGTAACAGATGGATAAAATTA

SEQ ID NO: 513
Pra_006216_O_1
AAAGACCAATCAAGTAAACTGACAACCAAATAAGCTCCCTACAGTACTGACAACTCTAGA

SEQ ID NO: 514
Pra_013260_O_3
TTCTTTCTTAACACATTTGAGAACATGGCTAGCCATTTTAGGCTCGATACTGTATCAATT

SEQ ID NO: 515
Pra_014596_O_1
TCTCTTTCATGTTTATCTCGAGAATTGTAGGATATACCACAGGCTACATAATCTCTGGTT

SEQ ID NO: 516
Pra_021340_O_1
TTGGAGGTGCTTTATTCCATTCTCCTAGAGTTAGGCTGTCAGCTATATGATCTATTATAT

SEQ ID NO: 517
Pra_022975_O_1
TATGAATCGAATTGAGAATAGTAGCAATTTAATTTGCTATCGGACAATATGCTCCTAAGT

SEQ ID NO: 518
Pra_007714_O_1
ATCCTGGTTTAATCCCCAACTGGCATAGAGCTTTGACGAGATTCATATGCGGCATTAAAT

SEQ ID NO: 519
Pra_013469_O_1
ATTCCTAGCCAATTTTAGATGAGAACTACTGATGAAATCTTATAGAAGTTGTAAGAACCC

SEQ ID NO: 520
Pra_016491_O_1
GTAAAATAGAGTTAGGAGAATACATTATTATTTCATATATGTCTATTTCATTATATGTTT

SEQ ID NO: 521
Pra_001007_O_1
TTCTCAGACACACATGTAAAATATTAGAGGGTATCAATCATTTCATTTTGGTACTGCTAT

SEQ ID NO: 522
Pra_001008_O_1
CAGAAACGCATGTAACACAATCGATTCATTTTGGGTACTGGTAATACAAAATCGAGATTC

SEQ ID NO: 523
Pra_001184_O_1
AGCATTCCTGACTCAAGTACTCGGTCGTCTGATTGATGTATTTTAGATGCGCTGTCCTTC

SEQ ID NO: 524
Pra_001186_O_1
TGACTCAACTCTGTCGCCTGATTGACGTATTTTAGATGCCTTCTTCTTTGAACCATTCTT

SEQ ID NO: 525
Pra_001187_O_1
AGCACTCTCGACTCAACTCCTCGTCTAATTGATGAATTCTAGATGCCCTGCCCTTACAAG

SEQ ID NO: 526
Pra_001191_O_2
GCAACTACTATTACATATTTCTACATATACAGGAGTGTACCAATCAAAGGGAATGAGTGG

SEQ ID NO: 527
Pra_001197_O_1
AATTGATTCACGTGATTAATCCATCTTATCGAGTTCGAAAACCATTGATCGAGTTCGTAT

SEQ ID NO: 528
Pra_001603_O_1
GAGGGCGATACAGAGTCAATTACAAGTATTCCCCTTTCGTTGTCACGCTAGCTAACCTTA

SEQ ID NO: 529
Pra_001604_O_1
TCCGCTGCTGTGATGATGGTGGTATTAGACCATACGATTGTAATTCTACGCAGTTATTAT

SEQ ID NO: 530
Pra_002148_O_1
AGGAATCTCAATCTTGTGTTACAGAGATACACAGGGAACAGTAGCCTTGAATAAAGCTGG

SEQ ID NO: 531
Pra_005260_O_2
TGCTGTCCAGGGCACAATTGGACTTGTAAATTGCCATCCACGACACAATATTTACCTATT

SEQ ID NO: 532
Pra_005658_O_1
GTTATTTATGTCATCGTTACTGTTTTGCAGTCACAAGATGACTTATCTCTGTAATGCTTG

SEQ ID NO: 533
Pra_005659_O_1
GGCTGTTCTAATTATGTTATAACTGCCATTTCGTAGTAACAAAATGGCTTATGTGTGTGG

SEQ ID NO: 534
Pra_005715_O_2
AACACGATGATCTCACTCTCATATTTTCTCCGCCGGTTTGAACAAGAAGCTAAAAATCCG

SEQ ID NO: 535
Pra_005718_O_2
AACTCGAAGAACCATCTCGAACAGTCAATTAAATTATTAAGATAGACCTGCATTGAAAAG

SEQ ID NO: 536
Pra_006166_O_1
ATCGGCCACTCCCCACATAAGTATTAGGCTATGTTCTGTAATTGTGAATTTTCGAAATAT

SEQ ID NO: 537
Pra_008291_O_1
AATCTTAATGTATGCCGTTGAGGTTGGATTCCTTTCCGATTCCATTAAAATCCTATTCTA

SEQ ID NO: 538
Pra_008343_O_1
TTGTTAGCGATGATGGACGCCATCAGCATCTTATGCTACCGTCGGACTATCAAATGTTTG

SEQ ID NO: 539
Pra_010682_ORF_O_1
ATTTTGCAAATAGATCAAAATTGAAGATAAGGCGCGTGTCTAATTTAATGTAGCACCCAA

SEQ ID NO: 540
Pra_011081_O_1
GTTCCACTTGTATTAGTTTTAGTAGAGTCCTGTGCATTCCTGATAGCTTGGATAGTGAAA

SEQ ID NO: 541
Pra_011726_O_1
TTGGTAATAAGACAGTCTGGTGGAGGAGAGGCACTTTCCATTACCGGATGCTACAGAACC

SEQ ID NO: 542
Pra_013444_O_1
ATATCAGTGGATTCATGCGGTATTCGGCGCTACAAGTGTATATAAGTATATCCTGTAAGC

SEQ ID NO: 543
Pra_014144_O_2
ACGTTTTGAAACCCACGGGATTCATTGTAGGTCAACATATATCATGCATGTTCCTAAAAT

SEQ ID NO: 544
Pra_014539_O_2
TTTATTTATGGCCATCTATAATATAGGCCATTGAAGAGTGCTTCTGTATGGGTGTGTAAG

SEQ ID NO: 545
Pra_015716_O_1
AAAGGAGCTCACATCTAAGCGCGAGTATGTATGAAGTGTAGGATGATTTACATGTGAGAA

SEQ ID NO: 546
Pra_016453_O_1
GCCGTCATATAGATAACCACAACCTTAAGAACGGACGCCATATAGAAATGAATTAGTCAG

SEQ ID NO: 547
Pra_017884_O_1
GAGCTCGTTCATTATTACCAGTGGGCTTGTTATTCGACCTTCGGATTATCGAATGTTTGG

SEQ ID NO: 548
Pra_023707_O_2
TACAATCTGTATTTACACTGTTGTATTAGAAAGGCTGTCACCAACGGGAGCCAATAAAA

SEQ ID NO: 549
Pra_023708_O_2
ATAGACTGGAATGACGCTCCCTTTATTGCCTCTTATCAATCGTTTGAAGTCGATGCATGC

SEQ ID NO: 550
Pra_027337_O_2
GATATAGCTTAAACCTTTTCGTAATCTTTGTACCATTATAAAATGCTGCGTGCTGCTCAT

SEQ ID NO: 551
Pra_001609_O_1
AAGTATTTAATATATGGATTAGTAGGGAATATCTAATTCTATATTCATAGAAAGTAGATA

SEQ ID NO: 552
Pra_004488_O_1
GGGTTTATGTAGTTCTTTTGTTACCCATACAACTAGCTCTGTTTTACGTTTAGATGTAAT

SEQ ID NO: 553
Pra_004489_O_1
TTGTGGCGTTATGCTTTTTTCGCTATACCTATGTAGTACGAAACCCTTAGTGTTATGATC

SEQ ID NO: 554
Pra_005049_O_1
TTTTCCTTAGTGCTATAAATAAAGTCCCGAGGGCACCCGGATTATAAAGCCCCGAAGGCA

SEQ ID NO: 555
Pra_005790_O_1
TGTAGGGTATATTTCTTTATGTTCTGTCCACCTGCCTGCGTGGCTTTCTAGCGTATACTT

SEQ ID NO: 556
Pra_005791_O_1
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SEQ ID NO: 557
Pra_006230_O_2
TTTTGCTTACCCATATTGTAGTTCGATTTTGTGGAAACTCCTCGGCAGTCTATTAAATAT

SEQ ID NO: 558
Pra_006231_O_2
CTTCGGTTTTGCGTTTCTATGTTCATCTAATTTGAATTAGTGTATTCCATACGGCATATG

SEQ ID NO: 559
Pra_009358_O_2
GAGGTTCGGTGTCTATAAGTCTAGGTTCCGATTCTGCAAGTCTAGAGGTTTACTCTCATG

SEQ ID NO: 560
Pra_011003_O_1
ACATTAAACCATAGTTACTAAATTCGAATTCGAATTCGAATTCGGATTCGAATTCGATAC

SEQ ID NO: 561
Pra_014809_O_2
GAATCTCCAATAGTGTTGCTGTTTAGCTTTAGAGTAATGTAATCCACCCATATCCAATAA

SEQ ID NO: 562
Pra_014810_O_1
TCCTGCCCGCTCTTCGTTTCTTACATCGATTTTAGTGTTCCACTCTACGAGTATGTGCTT

SEQ ID NO: 563
Pra_018046_O_1
GGTGTAATGGCCGCCCACTGCTCTTTGAAAATAGCCTGTGGCATAACATCATTTGTGTGA

SEQ ID NO: 564
Pra_018129_O_1
TCATGTTTTGCTACCGGAAACGTTTTTTCATGTAACGATGGAATATCAACAGCTGTTTTA

SEQ ID NO: 565
Pra_019464_O_1
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SEQ ID NO: 566
Pra_019641_O_1
TTCTTCTAACTAAGTACCTACTAAATAAGGTCATGGTATGATCAATAACGGATAAGGGTG

SEQ ID NO: 567
Pra_020854_O_1
TCTCAATAATAATGCCGTGATTATAAAGTCCGGCGATATAACTATAACTTGTTTGTATGT

SEQ ID NO: 568
Pra_022079_O_1
CCTACTATGGTTTATCATAGGTCAATGTTATGGTACTATTGAACTGATGAGGTTAGGGAT

SEQ ID NO: 569
Pra_026378_O_2
GTTATTATTATACGTCGTACTGATTCGTTATTATTATAAGTTTCATACCTGCTTTATTTC

SEQ ID NO: 570
Pra_027112_O_2
GGCAGGTTAAATCTTCTTTTTAGATGTTAAGAGTTTGAAATTTGATTAATCATAAAGGTT

SEQ ID NO: 571
Pra_000134_O_1
CATAATCCAATTGTTTGAGGCATAGGGCTGAGATTGTTTTCTAATTGGCTAGCATAGTAA

SEQ ID NO: 572
Pra_003894_O_2
TTGTTTATCACCACATTAACCAACCTTACAAGCGTTTACCCTTCTAGATGTAGCAAGGTT

SEQ ID NO: 573
Pra_005134_O_1
ATGGTAACTTTAGAAACTGGCATCCTGTCAGGAGAACAAATGTCGTTTAGTGTATGCATA

SEQ ID NO: 574
Pra_005738_O_2
TGATACGGATTGTCCTCCGGGTATCCATGTAGCTTTATATGAGGATGACGCGTTATTATC

SEQ ID NO: 575
Pra_006938_O_1
TCCTTATGTCTACTTATGTCGCCCGTGATAACTACTAAAGTATGTTGTGTGTGCAAGGTA

SEQ ID NO: 576
Pra_007527_O_2
AAAACACAATATGTATTAGTGGCATGCACTGGTGGAAACACTGGTACCATTTAACCATTA

SEQ ID NO: 577
Pra_008477_O_1
AAGGAGTTTTACGTACTAATAGATATGGGGGACAATACAAGCATATTGAGTTGTACGATC

SEQ ID NO: 578
Pra_008478_O_2
TGAAAATTAATGTTGCGTGGAATAAGGTCTGTTGAAAATTAAATGCAGCGTGGAGAAAAG

SEQ ID NO: 579
Pra_008479_O_2
TGCTGCTCTGTAATATTGATATACACTTTGCGTATATTTCTGCGCTGAGTCAGGATGGTG

SEQ ID NO: 580
Pra_008480_O_2
CATTTACTGTATGTTGCCGCGCTGACTCGACGCGGTGATATATTGTATCAGTGATATATT

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