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- (73) Patenthaver: **DSM IP Assets B.V., Het Overloon 1, 6411 THE Heerlen, Holland**
- (72) Opfinder: **LOS, Alrik Pieter, c/o DSM Intellectual Property, P.O. Box 4, 6100 AA Echt, Holland**
DE JONG, René Marcel, c/o DSM Intellectual Property, P.O. Box 4, 6100 AA Echt, Holland
APPELDOORN, Maaïke, c/o DSM Intellectual Property, P.O. Box 4, 6100 AA Echt, Holland
- (74) Fuldmægtig i Danmark: **RWS Group, Europa House, Chiltern Park, Chiltern Hill, Chalfont St Peter, Bucks SL9 9FG, Storbritannien**
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DESCRIPTION

Field of the invention

[0001] The invention relates to sequences comprising genes that encode polypeptides having lignocellulosic material degrading activity. The invention features the full-length coding sequence of the novel gene as well as the amino acid sequence of the full-length functional protein, and variants and fragments of the gene or the amino acid sequence. The invention also relates to methods for using these proteins in industrial processes. Also included in the invention are cells transformed with a polynucleotide according to the invention suitable for producing these proteins. Also the invention relates to the successful expression of the genes that encode polypeptides having lignocellulosic material degrading activity in a host organism such as *Aspergillus niger* and/or *Rasamsonia emersonii*.

Background of the invention

[0002] Carbohydrates constitute the most abundant organic compounds on earth. However, much of this carbohydrate is sequestered in complex polymers including starch (the principle storage carbohydrate in seeds and grain), and a collection of carbohydrates and lignin known as lignocellulose. The main carbohydrate components of lignocellulose are cellulose, hemicellulose, and pectins. These complex polymers are often referred to collectively as lignocellulose.

[0003] Bioconversion of renewable lignocellulosic biomass to a fermentable sugar that is subsequently fermented to produce alcohol (e.g., ethanol) as an alternative to liquid fuels has attracted an intensive attention of researchers since 1970s, when the oil crisis broke out because of decreasing the output of petroleum by OPEC. Ethanol has been widely used as a 10% blend to gasoline in the USA or as a neat fuel for vehicles in Brazil in the last two decades. More recently, the use of E85, an 85% ethanol blend has been implemented especially for clean city applications. The importance of fuel bioethanol will increase in parallel with increases in prices for oil and the gradual depletion of its sources.

[0004] Additionally, fermentable sugars are being used to produce plastics, polymers and other bio-based products and this industry is expected to grow substantially therefore increasing the demand for abundant low cost fermentable sugars which can be used as a feed stock in lieu of petroleum based feedstocks.

[0005] The sequestration of such large amounts of carbohydrates in plant biomass provides a plentiful source of potential energy in the form of sugars, both five carbon and six carbon sugars that could be utilized for numerous industrial and agricultural processes. However, the enormous energy potential of these carbohydrates is currently under-utilized because the

sugars are locked in complex polymers, and hence are not readily accessible for fermentation. Methods that generate sugars from plant biomass would provide plentiful, economically-competitive feedstocks for fermentation into chemicals, plastics, such as for instance succinic acid and (bio) fuels, including ethanol, methanol, butanol synthetic liquid fuels and biogas.

[0006] Regardless of the type of cellulosic feedstock, the cost and hydrolytic efficiency of enzymes are major factors that restrict the commercialization of the biomass bioconversion processes. The production costs of microbially produced enzymes are tightly connected with a productivity of the enzyme-producing strain and the final activity yield in the fermentation broth.

[0007] In spite of the continued research of the last few decades to understand enzymatic lignocellulosic biomass degradation and cellulase production, it remains desirable to discover or to engineer new highly active cellulases and hemicellulases. It would also be highly desirable to construct highly efficient enzyme compositions capable of performing rapid and efficient biodegradation of lignocellulosic materials, in particular such cellulases and hemicellulases that have increased thermostability.

[0008] Such enzymes may be used to produce sugars for fermentation into chemicals, plastics, such as for instance succinic acid and (bio) fuels, including ethanol, methanol, butanol, synthetic liquid fuels and biogas, for ensiling, and also as enzyme in other industrial processes, for example in the food or feed, textile, pulp or paper or detergent industries and other industries.

[0009] WO 2007/091231 describes *Talaromyces mersonii* enzymes including alpha-arabinofuranosidases.

[0010] WO 2012/125925 describes methods for reducing viscosity of biomass mixtures using a composition comprising a polypeptide having glycosyl hydrolase family 61/endoglucanase activity.

Summary of the invention

[0011] The present invention provides a polypeptide having hemicellulase activity or an activity according to Table 1 which comprises the amino acid sequence set out in SEQ ID NO: 37 or an amino acid sequence encoded by the nucleotide sequence of SEQ ID NO: 36 SEQ ID NO: 39 or a variant polypeptide or variant polynucleotide thereof, wherein the variant polypeptide has at least 85% sequence identity with the sequence set out in SEQ ID NO: 37 or the variant polynucleotide encodes a polypeptide that has at least 85% sequence identity with the sequence set out in SEQ ID NO: 37.

Table 1: Temer numbers of the proteins of the invention and their activity

	Temer number	activity	activity
1	Temer00088	beta-xylosidase	GH3

	Temer number	activity	activity
2	Temer09484	beta-xylosidase	GH3
3	Temer08028	alpha-galactosidase	GH27
4	Temer02362	alpha-galactosidase	GH27
5	Temer08862	alpha-galactosidase	GH27
6	Temer04790	xyloglucanase	GH12
7	Temer05249	alpha-arabinofuranosidase	GH51
8	Temer06848	alpha-arabinofuranosidase	GH51
9	Temer02056	alpha-arabinofuranosidase	GH51
10	Temer03124	endo-xylanase	GH43
11	Temer09491	mannosidase/xylosidase	GH31
12	Temer06400	feruloyl esterase	CE1
13	Temer08570	endo-xylanase	GH39
14	Temer08163	endo-exo-xylanase	GH30
15	Temer07305	alpha-glucuronidase	GH115

[0012] The polypeptide of the invention has alpha-arabinofuranosidase.

[0013] Furthermore, the invention provides a nucleic acid sequence coding for an hemicellulase, whereby the nucleic acid sequence is selected from the group consisting of:

1. (a) a nucleic acid sequence having at least 70% identity with the nucleic acid sequence of SEQ ID NO: 36, SEQ ID NO: 39 or SEQ ID NO: 40;
2. (b) a nucleic acid sequence encoding (i) the amino acid sequence of SEQ ID NO: 37 (ii) an amino acid sequence having at least 85% identity with the amino acid sequence of SEQ ID NO: 37 or (iii) an amino acid sequence that differs in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acids from the amino acid sequence of SEQ ID NO: 37; or
3. (c) a nucleotide sequence which is the reverse complement of a nucleotide sequence as defined in (a) or (b).

[0014] The invention also provides a nucleic acid construct or vector comprising the polynucleotide of the invention and a cell comprising a polypeptide of the invention or a nucleic acid construct or vector of the invention.

[0015] According to an aspect of the invention the cell is a fungal cell, preferably a fungal cell selected from the group consisting of the genera *Acremonium*, *Agaricus*, *Aspergillus*, *Aureobasidium*, *Chrysosporium*, *Coprinus*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*,

Piromyces, Panerochaete, Pleurotus, Schizophyllum, Talaromyces, Rasamsonia, Thermoascus, Thielavia, Tolypocladium, and Trichoderma.

[0016] According to another aspect of the invention one or more gene of the cell of the invention is deleted, knocked-out or disrupted in full or in part, wherein optionally the gene encodes for a protease.

[0017] The invention also provides a method for the preparation of a polypeptide according to the invention having hemicellulase or an activity according to Table 1, which method comprises cultivating a cell of the invention under conditions which allow for expression of said polypeptide and, optionally, recovering the expressed polypeptide. Furthermore the invention provides a composition comprising: (i) a polypeptide of the invention and; (ii) a cellulase and/or an additional hemicellulase and/or a pectinase, preferably the cellulase is a GH61, cellobiohydrolase, cellobiohydrolase I, cellobiohydrolase II, endo- β -1,4-glucanase, β -glucosidase or β -(1,3)(1,4)-glucanase and/or the hemicellulase is an endoxylanase, β -xylosidase, α -L-arabinofuranosidase, α -D-glucuronidase feruloyl esterase, coumaroyl esterase, α -galactosidase, β -galactosidase, β -mannanase or β -mannosidase.

[0018] Additionally, the invention provides a method for the treatment of a substrate comprising hemicellulose, optionally a plant material, which method comprises contacting the substrate with a polypeptide of the invention and/or a composition of the invention.

[0019] Another aspect of the invention relates to the use of a polypeptide of the invention and/or a composition of the invention to produce sugar from a lignocellulosic material.

[0020] The invention also provides:

a method for the preparation of a polypeptide having carbohydrate material degrading or carbohydrate hydrolysing activity, which method comprises cultivating a cell of the invention under conditions which allow for expression of said polypeptide and, optionally, recovering the expressed polypeptide;

a polypeptide obtainable by such a method; and

a composition comprising: (i) a polypeptide of the invention and; (ii) a cellulase and/or a hemicellulase and/or a pectinase;

[0021] The polypeptides of the invention having carbohydrate material degrading or carbohydrate hydrolysing activity may be used in industrial processes. Thus, the invention provides a method for the treatment of a substrate comprising carbohydrate material which method comprises contacting the substrate with a polypeptide or a composition of the invention.

[0022] In particular, the invention provides a method for producing a sugar or sugars from lignocellulosic material which method comprises contacting the lignocellulosic material with a polypeptide or a composition of the invention.

[0023] Sugars produced in this way may be used in a fermentation process. Accordingly, the invention provides a method for producing a fermentation product, which method comprises: producing a fermentable sugar using the described above; and fermenting the resulting fermentable sugar, thereby to produce a fermentation product.

[0024] A polypeptide or a composition of the invention may also be used, for example, in the preparation of a food product, in the preparation of a detergent, in the preparation of an animal feed, in the treatment of pulp or in the manufacture of a paper or in the preparation of a fabric or textile or in the cleaning thereof.

Brief description of the drawings

[0025]

Fig 1: Map of pGBTOP for expression of genes in *A. niger*. Depicted are the gene of interest (GOI) expressed from the glucoamylase promoter (PglaA). In addition, the glucoamylase flank (3'glaA) of the expression cassette is depicted. In this application a gene of interest is the coding sequence of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 as defined hereinafter.

Fig. 2 shows a schematic diagram of plasmid Te pep.bbn, which is the basis for Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 overexpression construct in *R. emersonii* that is targeted to the *RePepA* locus. The vector comprises a 1500 bp 5' flanking region 1.5 kb upstream of the *RePepA* ORF for targeting in the *RePepA* locus, a lox66 site, the non-functional 5' part of the ble coding region (5'ble) driven by the *A. nidulans* *gpdA* promoter, and a *ccdB* gene.

Fig. 3 shows a schematic diagram of plasmid pEBA1006 that was used in bipartite gene-targeting method in combination with the pEBA expression vector containing Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 with the goal to replace the *RePepA* ORF and approximately 1500 nucleotides upstream of the start ATG codon by the expression cassette of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 in *Rasamsonia emersonii*. The vector comprises the 3' part of the ble coding region, the *A. nidulans* *trpC* terminator, a lox71 site, a 2500 bp 3' flanking region of the *RePepA* ORF, and the backbone of pUC19 (Invitrogen, Breda, The Netherlands). The *E.*

coli DNA was removed by digestion with restriction enzyme *NotI*, prior to transformation of the *R. emersonii* strains.

Fig. 4 shows a schematic diagram of pEBA expression plasmid containing Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 that was used in bipartite gene-targeting method in combination with the pEBA1006 vector with the goal to replace the *RePepA* ORF and approximately 1500 nucleotides upstream of the start ATG codon by the expression cassette of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 in *Rasamsonia emersonii*. The vector comprises a 1500 bp 5' flanking region 1.5 kb upstream of the *RePepA* ORF for targeting in the *RePepA* locus, Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 expression cassette consisting of *R. emersonii* promoter 2, Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 coding region and the *A.nidulans amdS* terminator (TamdS), a lox66 site, the non-functional 5' part of the ble coding region (5' ble) driven by the *A.nidulans gpdA* promoter. The *E. coli* DNA was removed by digestion with restriction enzyme *NotI*, prior to transformation of the *R. emersonii* strains.

Fig. 5 Chromatogram obtained by High-performance anion exchange chromatography showing oligomer formation by *Rasamsonia emersonii* Temer04790 in comparison with a commercial cellulase mix after incubation on xyloglucan for 24h incubation at pH 4.5 and 60°C.

Brief description of the sequence listing

[0026]

Table 2 shows codon-pair optimised coding sequence SEQ ID NO's, amino acid sequence SEQ ID NO's, signal sequence SEQ ID NO's, genomic DNA sequence SEQ ID NO's and wild-type coding sequence SEQ ID NO's of the the present invention.

	Temer number	Codon-pair optimized coding sequence SEQ ID NO:	Amino acid sequence SEQ ID NO:	Signal sequence SEQ ID NO:	Genomic DNA sequence SEQ ID NO:	Wild-type coding sequence SEQ ID NO:
1	Temer00088	1	2	3	4	5
2	Temer09484	6	7	8	9	10
3	Temer08028	11	12	13	14	15

	Temer number	Codon-pair optimized coding sequence SEQ ID NO:	Amino acid sequence SEQ ID NO:	Signal sequence SEQ ID NO:	Genomic DNA sequence SEQ ID NO:	Wild-type coding sequence SEQ ID NO:
4	Temer02362	16	17	18	19	20
5	Temer08862	21	22	23	24	25
6	Temer04790	26	27	28	29	30
7	Temer05249	31	32	33	34	35
8	Temer06848	36	37	38	39	40
9	Temer02056	41	42	43	44	45
10	Temer03124	46	47	48	49	50
11	Temer09491	51	52	53	54	55
12	Temer06400	56	57	58	59	60
13	Temer08570	61	62	63	64	65
14	Temer08163	66	67	68	69	70
15	Temer07305	71	72	73	74	75

SEQ ID NO: 76 *R. emersonii* RePepA (genomic sequence including flanks)

SEQ ID NO: 77 *R. emersonii* RePepA (cDNA)

SEQ ID NO: 78 *R. emersonii* RePepA (protein)

SEQ ID NO: 79 *A. nidulans* gpdA promoter and 5' part of the ble coding region

SEQ ID NO: 80 3' part of the *ble* coding region and *A. nidulans* TrpC terminator

SEQ ID NO: 81 *R. emersonii* promoter 2

SEQ ID NO: 82 *A. nidulans* AmdS terminator

Detailed description of the invention

[0027] Throughout the present specification and the accompanying claims, the words "comprise" and "include" and variations such as "comprises", "comprising", "includes" and "including" are to be interpreted inclusively. That is, these words are intended to convey the possible inclusion of other elements or integers not specifically recited, where the context allows.

[0028] The articles "a" and "an" are used herein to refer to one or to more than one (i.e. to one

or at least one) of the grammatical object of the article. By way of example, "an element" may mean one element or more than one element.

[0029] The present invention provides polynucleotides encoding polypeptides, e.g. enzymes which have the ability to modify, for example degrade, a carbohydrate material. A carbohydrate material is a material which comprises, consists of or substantially consists of one or more carbohydrates. Enzymes are herein a subclass of polypeptides.

[0030] Substrate (also called feedstock) herein is used to refer to a substance that comprises carbohydrate material, which may be treated with enzymes according to the invention, so that the carbohydrate material therein is modified. In addition to the carbohydrate material the substrate may contain any other component, including but not limited to non-carbohydrate material and starch.

[0031] The present invention provides polynucleotides encoding polypeptides, e.g. enzymes which have the ability to modify, for example degrade, a carbohydrate material. A carbohydrate material is a material which comprises, consists of or substantially consists of one or more carbohydrates. Enzymes are herein a subclass of polypeptides.

[0032] A β -xylosidase (EC 3.2.1.37) is any polypeptide which is capable of catalyzing the hydrolysis of 1,4- β -D-xylans, to remove successive D-xylose residues from the non-reducing termini. Such enzymes may also hydrolyze xylobiose. This enzyme may also be referred to as xylan 1,4- β -xylosidase, 1,4- β -D-xylan xylohydrolase, exo-1,4- β -xylosidase or xylobiase.

[0033] Herein, an α -galactosidase (EC 3.2.1.22; GH27) is any polypeptide which is capable of catalyzing the hydrolysis of terminal, non-reducing α -D-galactose residues in α -D-galactosides, including galactose oligosaccharides, galactomannans, galactans and arabinogalactans. Such a polypeptide may also be capable of hydrolyzing α -D-fucosides. This enzyme may also be referred to as melibiase.

[0034] Herein, a xyloglucanase is an xyloglucan-specific endo- β -1,4-glucanase, which catalyzes the cleavage of xyloglucan, a backbone of β 1 $\rightarrow$ 4-linked glucose residues, most of which substituted with 1-6 linked xylose side chains.

TEMER06848

[0035] Typically, a polypeptide of the invention encodes a polypeptide having at least alpha-arabinofuranosidase activity, tentatively called TEMER06848, having an amino acid sequence according to SEQ ID NO: 37, or a sequence which is a variant thereof, typically functionally equivalent to the polypeptide having the sequence of SEQ ID NO: 37, or a sequence which is a fragment of either thereof.

[0036] Herein, an α -L-arabinofuranosidase (EC 3.2.1.55) is any polypeptide which is capable

of acting on α -L-arabinofuranosides, α -L-arabinans containing (1,2) and/or (1,3)- and/or (1,5)-linkages, arabinoxylans and arabinogalactans. This enzyme may also be referred to as α -N-arabinofuranosidase, arabinofuranosidase or arabinosidase.

[0037] A polypeptide of the invention may have one or more alternative and/or additional carbohydrate degrading and/or carbohydrate hydrolysing activities other than that of alpha-arabinofuranosidase activity, for example one of the other carbohydrate degrading and/or carbohydrate hydrolysing activities mentioned herein.

[0038] Herein, an endoxylanase (EC 3.2.1.8) is any polypeptide which is capable of catalyzing the endo-hydrolysis of 1,4- β -D-xylosidic linkages in xylans. This enzyme may also be referred to as endo-1,4- β -xylanase or 1,4- β -D-xylan xylanohydrolase. An alternative is EC 3.2.1.136, a glucuronoarabinoxylan endoxylanase, an enzyme that is able to hydrolyze 1,4 xylosidic linkages in glucuronoarabinoxylans.

[0039] Herein, a β -mannosidase (EC 3.2.1.25) is any polypeptide which is capable of catalyzing the hydrolysis of terminal, non-reducing β -D-mannose residues in β -D-mannosides. This enzyme may also be referred to as mannanase or mannase.

[0040] Herein, a feruloyl esterase (EC 3.1.1.73; CE1) is any polypeptide which is capable of catalyzing a reaction of the form: feruloyl-saccharide + H₂O = ferulate + saccharide. The saccharide may be, for example, an oligosaccharide or a polysaccharide. It may typically catalyze the hydrolysis of the 4-hydroxy-3-methoxycinnamoyl (feruloyl) group from an esterified sugar, which is usually arabinose in 'natural' substrates. p-nitrophenol acetate and methyl ferulate are typically poorer substrates. This enzyme may also be referred to as cinnamoyl ester hydrolase, ferulic acid esterase or hydroxycinnamoyl esterase. It may also be referred to as a hemicellulase accessory enzyme, since it may help xylanases and pectinases to break down plant cell wall hemicellulose and pectin.

[0041] Herein, an α -D-glucuronidase (EC 3.2.1.139; GH115) is any polypeptide which is capable of catalyzing a reaction of the following form: alpha-D-glucuronoside + H₂O = an alcohol + D-glucuronate. This enzyme may also be referred to as alpha-glucuronidase or alpha-glucosiduronase. These enzymes may also hydrolyze 4-O-methylated glucuronic acid, which can also be present as a substituent in xylans. Alternative is EC 3.2.1.131: xylan alpha-1,2-glucuronosidase, which catalyses the hydrolysis of alpha-1,2-(4-O-methyl)glucuronosyl links.

[0042] Carbohydrate in this context includes all saccharides, for example polysaccharides, oligosaccharides, disaccharides or monosaccharides.

[0043] A polypeptide according to the invention may modify a carbohydrate material by chemically degrading or physically degrading such material or hydrolysing the carbohydrate. Chemical modification of the carbohydrate material may result in the degradation of such material, for example by hydrolysis, oxidation or other chemical modification such as by the

action of a lyase. Physical modification may or may not be accompanied by chemical modification.

Suitable carbohydrate materials

[0044] Lignocellulolytic or lignocellulosic materials or biomass are abundant in nature and have great value as alternative energy source. Second generation biofuels, also known as advanced biofuels, are fuels that can be manufactured from various types of biomass. Biomass is a wide-ranging term meaning any source of organic carbon that is renewed rapidly as part of the carbon cycle. Biomass is derived from plant materials but can also include animal materials. The composition of lignocellulosic biomass varies, the major component is cellulose (35-50%), followed by xylan (20-35%, a type of hemicellulose) and lignin (10-25%), in addition to minor components such as proteins, oils and ash that make up the remaining fraction of lignocellulosic biomass. Lignocellulosic biomass contains a variety of carbohydrates. The term carbohydrate is most common in biochemistry, where it is a synonym of saccharide. Carbohydrates (saccharides) are divided into four chemical groupings: monosaccharides, disaccharides, oligosaccharides, and polysaccharides. In general, monosaccharides and disaccharides, which are smaller (lower molecular weight) carbohydrates, are commonly referred to as sugars.

[0045] A non-starch carbohydrate suitable for modification by a polypeptide of the invention is lignocellulose. The major polysaccharides comprising different lignocellulosic residues, which may be considered as a potential renewable feedstock, are cellulose (glucans), hemicelluloses (xylans, heteroxylans and xyloglucans). In addition, some hemicellulose may be present as glucomannans, for example in wood-derived feedstocks. The enzymatic hydrolysis of these polysaccharides to soluble sugars, for example glucose, xylose, arabinose, galactose, fructose, mannose, rhamnose, ribose, D-galacturonic acid and other hexoses and pentoses occurs under the action of different enzymes acting in concert.

[0046] Lignin fills the spaces in the cell wall between cellulose, hemicellulose, and pectin components, especially in xylem tracheids, vessel elements and sclereid cells. It is covalently linked to hemicellulose and, therefore, crosslinks different plant polysaccharides, conferring mechanical strength to the cell wall and by extension the plant as a whole. Lignin is a highly hydrophobic crosslinked aromatic polymeric material that is formed by different monolignol monomers, which can be methoxylated to various degrees. There are three monolignol monomers, methoxylated to various degrees: p-coumaryl alcohol, coniferyl alcohol, and sinapyl alcohol. These lignols are incorporated into lignin in the form of the phenylpropanoids p-hydroxyphenyl (H), guaiacyl (G), and syringyl (S), respectively. Biodegradation of lignin is a prerequisite for processing biofuel from plant raw materials. Lignin can be degraded by applying different pretreatment methods, or by using ligninases or lignin-modifying enzymes (LME's). The improving of lignin degradation would drive the output from biofuel processing to better gain or better efficiency factor, for example by improving the accessibility to the (hemi)cellulosic components or by removing lignin-(hemi)cellulose linkages in oligosaccharides

released by the action of (hemi)cellulases.

[0047] In addition, pectins and other pectic substances such as arabinans may make up considerably proportion of the dry mass of typically cell walls from non-woody plant tissues (about a quarter to half of dry mass may be pectins).

[0048] Cellulose is a linear polysaccharide composed of glucose residues linked by β -1,4 bonds. The linear nature of the cellulose fibers, as well as the stoichiometry of the β -linked glucose (relative to α) generates structures more prone to interstrand hydrogen bonding than the highly branched α -linked structures of starch. Thus, cellulose polymers are generally less soluble, and form more tightly bound fibers than the fibers found in starch.

[0049] Hemicellulose is a complex polymer, and its composition often varies widely from organism to organism and from one tissue type to another. In general, a main component of hemicellulose is (3-1,4-linked xylose, a five carbon sugar. However, this xylose is often branched at O-3 and/or O-2 and can be substituted with linkages to arabinose, galactose, mannose, glucuronic acid, galacturonic acid or by esterification to acetic acid (and esterification of ferulic acid to arabinose). Hemicellulose can also contain glucan, which is a general term for β -linked six carbon sugars (such as the β -(1,3)(1,4) glucans and heteroglucans mentioned previously) and additionally glucomannans (in which both glucose and mannose are present in the linear backbone, linked to each other by β -linkages).

[0050] The composition, nature of substitution, and degree of branching of hemicellulose is very different in dicotyledonous plants (dicots, i.e., plant whose seeds have two cotyledons or seed leaves such as lima beans, peanuts, almonds, peas, kidney beans) as compared to monocotyledonous plants (monocots; i.e., plants having a single cotyledon or seed leaf such as corn, wheat, rice, grasses, barley). In dicots, hemicellulose is comprised mainly of xyloglucans that are 1,4- β -linked glucose chains with 1,6- β -linked xylosyl side chains. In monocots, including most grain crops, the principal components of hemicellulose are heteroxylans. These are primarily comprised of 1,4- β -linked xylose backbone polymers with 1,3 - α linkages to arabinose, galactose, mannose and glucuronic acid or 4-O-methyl-glucuronic acid as well as xylose modified by ester-linked acetic acids. Also present are β glucans comprised of 1,3- and 1,4- β -linked glucosyl chains. In monocots, cellulose, heteroxylans and β -glucans may be present in roughly equal amounts, each comprising about 15-25% of the dry matter of cell walls. Also, different plants may comprise different amounts of, and different compositions of, pectic substances. For example, sugar beet contains about 19% pectin and about 21% arabinan on a dry weight basis.

[0051] Accordingly, a composition of the invention may be tailored in view of the particular feedstock (also called substrate) which is to be used. That is to say, the spectrum of activities in a composition of the invention may vary depending on the feedstock in question.

[0052] Enzyme combinations or physical treatments can be administered concomitantly or sequentially. The enzymes can be produced either exogenously in microorganisms, yeasts,

fungi, bacteria or plants, then isolated and added to the lignocellulosic feedstock. Alternatively, the enzymes are produced, but not isolated, and crude cell mass fermentation broth, or plant material (such as corn stover), and the like are added to the feedstock. Alternatively, the crude cell mass or enzyme production medium or plant material may be treated to prevent further microbial growth (for example, by heating or addition of antimicrobial agents), then added to the feedstock. These crude enzyme mixtures may include the organism producing the enzyme. Alternatively, the enzyme may be produced in a fermentation that uses feedstock (such as corn stover) to provide nutrition to an organism that produces an enzyme(s). In this manner, plants that produce the enzymes may serve as the lignocellulosic feedstock and be added into lignocellulosic feedstock.

Enzymatic activity

[0053] Endo-1,4- β -glucanases (EG) and exo-cellobiohydrolases (CBH) catalyze the hydrolysis of insoluble cellulose to celooligosaccharides (cellobiose as a main product), while β -glucosidases (BGL) convert the oligosaccharides, mainly cellobiose and cellotriose to glucose.

[0054] Xylanases together with other accessory enzymes, for example α -L-arabinofuranosidases, feruloyl and acetylxytan esterases, glucuronidases, and β -xylosidases) catalyze the hydrolysis of part of the hemicelluloses.

[0055] Pectic substances include pectins, arabinans, galactans and arabinogalactans. Pectins are the most complex polysaccharides in the plant cell wall. They are built up around a core chain of α (1,4)-linked D-galacturonic acid units interspersed to some degree with L-rhamnose. In any one cell wall there are a number of structural units that fit this description and it has generally been considered that in a single pectic molecule, the core chains of different structural units are continuous with one another.

[0056] Pectinases include, for example an endo-polygalacturonase, a pectin methyl esterase, an endo-galactanase, a β -galactosidase, a pectin acetyl esterase, an endo-pectin lyase, pectate lyase, α -rhamnosidase, an exo-galacturonase, an exo-polygalacturonate lyase, a rhamnogalacturonan hydrolase, a rhamnogalacturonan lyase, a rhamnogalacturonan acetyl esterase, a rhamnogalacturonan galacturonohydrolase, a xylogalacturonase, an α -arabinofuranosidase.

[0057] The principal types of structural unit are: galacturonan (homogalacturonan), which may be substituted with methanol on the carboxyl group and acetate on O-2 and O-3; rhamnogalacturonan I (RGI), in which galacturonic acid units alternate with rhamnose units carrying (1,4)-linked galactan and (1,5)-linked arabinan side chains. The arabinan side chains may be attached directly to rhamnose or indirectly through the galactan chains; xylogalacturonan, with single xylosyl units on O-3 of galacturonic acid (closely associated with RGI); and rhamnogalacturonan II (RGII), a particularly complex minor unit containing unusual sugars, for example apiose. An RGII unit may contain two apiosyl residues which, under

suitable ionic conditions, can reversibly form esters with borate.

[0058] As set out above, a polypeptide of the invention will typically have an activity according to Table 1. However, a polypeptide of the invention may have one or more of the activities set out above in addition to or alternative to that activity. Also, a composition of the invention as described herein may have one or more of the activities mentioned above in addition to that provided by a polypeptide of the invention having an activity according to Table 1.

Polynucleotide sequence

[0059] The invention provides genomic polynucleotide sequences comprising the gene encoding the Temer06848 as well as its coding sequence. Accordingly, the invention relates to an isolated polynucleotide comprising the genomic nucleotide sequence according to the coding nucleotide sequence according to SEQ ID NO: 36 or SEQ ID NO: 39 or SEQ ID NO: 40 and to variants, such as functional equivalents, of either thereof.

[0060] In particular, the invention relates to an isolated polynucleotide which is capable of hybridizing selectively, for example under stringent conditions, preferably under highly stringent conditions, with the reverse complement of a polynucleotide comprising the sequence set out in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40.

[0061] More specifically, the invention relates to a polynucleotide comprising or consisting essentially of a nucleotide sequence according to SEQ ID NO: 36 or SEQ ID NO: 39 or SEQ ID NO: 40.

[0062] The invention also relates to an isolated polynucleotide comprising or consisting essentially of a sequence which encodes at least one functional domain of a polypeptide according to SEQ ID NO: 37 or a variant thereof, such as a functional equivalent, or a fragment of either thereof.

[0063] As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules which may be isolated from chromosomal DNA, which include an open reading frame encoding a protein, e.g. the activity according to the present invention.

[0064] A gene may include coding sequences, non-coding sequences, introns and/or regulatory sequences. Moreover, the term "gene" may refer to an isolated nucleic acid molecule as defined herein.

[0065] A nucleic acid molecule of the present invention, such as a nucleic acid molecule having the nucleotide sequence of SEQ ID NO: 36 or SEQ ID NO: 39 or SEQ ID NO: 40 or a variant thereof, such as a functional equivalent, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, using all or a portion of the nucleic acid sequence of SEQ ID NO: 36 as a hybridization probe, nucleic acid

molecules according to the invention can be isolated using standard hybridization and cloning techniques (e. g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. Molecular Cloning: A Laboratory Manual.2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

[0066] Moreover, a nucleic acid molecule encompassing all or a portion of SEQ ID NO: 36 or SEQ ID NO: 39 or SEQ ID NO: 40 may be isolated by the polymerase chain reaction (PCR) using synthetic oligonucleotide primers designed based upon the sequence information contained in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40.

[0067] A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis.

[0068] Furthermore, oligonucleotides corresponding to or hybridizable to a nucleotide sequence according to the invention can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

[0069] In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises the nucleotide sequence shown in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40.

[0070] In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is the reverse complement of the nucleotide sequence shown in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40 or a variant, such as a functional equivalent, of either such nucleotide sequence.

[0071] A nucleic acid molecule which is complementary to another nucleotide sequence is one which is sufficiently complementary to the other nucleotide sequence such that it can hybridize to the other nucleotide sequence thereby forming a stable duplex.

[0072] One aspect of the invention pertains to isolated nucleic acid molecules that encode a polypeptide of the invention or a variant, such as a functional equivalent thereof, for example a biologically active fragment or domain, as well as nucleic acid molecules sufficient for use as hybridization probes to identify nucleic acid molecules encoding a polypeptide of the invention and fragments of such nucleic acid molecules suitable for use as PCR primers for the amplification or mutation of nucleic acid molecules.

[0073] A polynucleotide according to the invention may be "isolated". In the context of this invention, an "isolated polynucleotide" or "isolated nucleic acid" is a DNA or RNA that is not immediately contiguous with one or both of the coding sequences with which it is immediately contiguous (one on the 5' end and one on the 3' end) in the naturally occurring genome of the organism from which it is derived. Thus, in one embodiment, an isolated nucleic acid includes

some or all of the 5' non-coding (e.g. promotor) sequences that are immediately contiguous to the coding sequence. The term therefore includes, for example, a recombinant DNA that is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other sequences. It also includes a recombinant DNA that is part of a hybrid gene encoding an additional polypeptide that is substantially free of cellular material, viral material, or culture medium (when produced by recombinant DNA techniques), or chemical precursors or other chemicals (when chemically synthesized). Moreover, an "isolated nucleic acid fragment" is a nucleic acid fragment that is not naturally occurring as a fragment and would not be found in the natural state.

[0074] As used herein, the terms "polynucleotide" or "nucleic acid molecule" are intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. The nucleic acid may be synthesized using oligonucleotide analogs or derivatives (e.g., inosine or phosphorothioate nucleotides). Such oligonucleotides can be used, for example, to prepare nucleic acids that have altered base-pairing abilities or increased resistance to nucleases.

[0075] Another embodiment of the invention provides an isolated nucleic acid molecule which is antisense to a Temer06848 nucleic acid molecule, e.g., the coding strand of a Temer06848 nucleic acid molecule. Also included within the scope of the invention are the complementary strands of the nucleic acid molecules described herein.

[0076] Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer 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 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule.

[0077] 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 will 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.

[0078] The person skilled in the art is capable of identifying such erroneously identified bases and knows how to correct for such errors.

[0079] A nucleic acid molecule according to the invention may comprise only a portion or a fragment of the nucleic acid sequence shown in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40 (or of a variant of either thereof), for example a fragment which can be used as a probe or primer or a fragment encoding a portion of a Temer06848 protein.

[0080] The nucleotide sequence determined from the cloning of the Temer06848 gene and cDNA allows for the generation of probes and primers designed for use in identifying and/or cloning other Temer06848 family members, as well as Temer06848 homologues from other species.

[0081] The probe/primer typically comprises a substantially purified oligonucleotide which typically comprises a region of nucleotide sequence that hybridizes preferably under highly stringent conditions to at least from about 12 to about 15, preferably from about 18 to about 20, preferably from about 22 to about 25, more preferably about 30, about 35, about 40, about 45, about 50, about 55, about 60, about 65, or about 75 or more consecutive nucleotides of a nucleotide sequence shown in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40 or of a variant, such as a functional equivalent, of either thereof.

[0082] Probes based on the Temer06848 nucleotide sequences can be used to detect transcripts or genomic Temer06848 sequences encoding the same or homologous proteins for instance in other organisms. In preferred embodiments, the probe further comprises a label group attached thereto, e.g., the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme cofactor. Such probes can also be used as part of a diagnostic test kit for identifying cells which express a TEMER09484 protein.

[0083] The polynucleotides herein may be synthetic polynucleotides. The synthetic polynucleotides may be optimized in codon use, preferably according to the methods described in WO2006/077258 and/or PCT/EP2007/055943. PCT/EP2007/055943 addresses codon-pair optimization. Codon-pair optimization is a method wherein the nucleotide sequences encoding a polypeptide have been modified with respect to their codon-usage, in particular the codon-pairs that are used, to obtain improved expression of the nucleotide sequence encoding the polypeptide and/or improved production of the encoded polypeptide. Codon pairs are defined as a set of two subsequent triplets (codons) in a coding sequence.

[0084] The invention further relates to a nucleic acid construct comprising the polynucleotide as described before. "Nucleic acid construct" is defined herein as a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acid which are combined and juxtaposed in a manner which would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains all the control sequences required for expression of a coding sequence. The term "coding sequence" as defined herein is a sequence, which is transcribed into mRNA and translated into a transcriptional activator of a protease promoter of the invention. The boundaries of the

coding sequence are generally determined by the ATG start codon at the 5' end of the mRNA and a translation stop codon sequence terminating the open reading frame at the 3' end of the mRNA. A coding sequence can include, but is not limited to, DNA, cDNA, and recombinant nucleic acid sequences. Preferably, the nucleic acid has high GC content. The GC content herein indicates the number of G and C nucleotides in the construct, divided by the total number of nucleotides, expressed in %. The GC content is preferably 56% or more, 57% or more, 58% or more, 59% or more, 60% or more, or in the range of 56-70% or the range of 58-65%. Preferably, the DNA construct comprises a promoter DNA sequence, a coding sequence in operative association with said promoter DNA sequence and control sequences such as:

- one translational termination sequence orientated in 5' towards 3' direction selected from the following list of sequences: TAAG, TAGA and TAAA, preferably TAAA, and/or
- one translational initiator coding sequence orientated in 5' towards 3' direction selected from the following list of sequences: GCTACCCCC; GCTACCTCC; GCTACCCTC; GCTACCTTC; GCTCCCCCC; GCTCCCTCC; GCTCCCCTC; GCTCCCTTC; GCTGCCCCC; GCTGCCTCC; GCTGCCCTC; GCTGCCTTC; GCTTCCCCC; GCTTCCTCC; GCTTCCCTC; and GCTTCCTTC, preferably GCT TCC TTC, and/or
- one translational initiator sequence selected from the following list of sequences: 5'-mwChkyCAAA-3'; 5'-mwChkyCACA-3' or 5'-mwChkyCAAG-3', using ambiguity codes for nucleotides: m (A/C); w (A/T); y (C/T); k (G/T); h (A/C/T), preferably 5'-CACCGTCAAA-3' or 5'-CGCAGTCAAG-3'.

[0085] In the context of this invention, the term "translational initiator coding sequence" is defined as the nine nucleotides immediately downstream of the initiator or start codon of the open reading frame of a DNA coding sequence. The initiator or start codon encodes for the AA methionine. The initiator codon is typically ATG, but may also be any functional start codon such as GTG.

[0086] In the context of this invention, the term "translational termination sequence" is defined as the four nucleotides starting from the translational stop codon at the 3' end of the open reading frame or nucleotide coding sequence and oriented in 5' towards 3' direction.

[0087] In the context of this invention, the term "translational initiator sequence" is defined as the ten nucleotides immediately upstream of the initiator or start codon of the open reading frame of a DNA sequence coding for a polypeptide. The initiator or start codon encodes for the AA methionine. The initiator codon is typically ATG, but may also be any functional start codon such as GTG. It is well known in the art that uracil, U, replaces the deoxynucleotide thymine, T, in RNA.

Homology and identity

[0088] Amino acid or nucleotide sequences are said to be homologous when exhibiting a certain level of similarity. Two sequences being homologous indicate a common evolutionary origin. Whether two homologous sequences are closely related or more distantly related is indicated by "percent identity" or "percent similarity", which is high or low respectively. Although disputed, to indicate "percent identity" or "percent similarity", "level of homology" or "percent homology" are frequently used interchangeably.

[0089] The terms "homology", "percent homology", "percent identity" or "percent similarity" are used interchangeably herein. For the purpose of this invention, it is defined here that in order to determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the complete sequences are aligned for optimal comparison purposes. In order to optimize the alignment between the two sequences gaps may be introduced in any of the two sequences that are compared. Such alignment is carried out over the full length of the sequences being compared. Alternatively, the alignment may be carried out over a shorter length, for example over about 20, about 50, about 100 or more nucleic acids/bases or amino acids. The identity is the percentage of identical matches between the two sequences over the reported aligned region.

[0090] A comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. The skilled person will be aware of the fact that several different computer programs are available to align two sequences and determine the homology between two sequences (Kruskal, J. B. (1983) An overview of sequence comparison In D. Sankoff and J. B. Kruskal, (ed.), Time warps, string edits and macromolecules: the theory and practice of sequence comparison, pp. 1-44 Addison Wesley). The percent identity between two amino acid sequences can be determined using the Needleman and Wunsch algorithm for the alignment of two sequences. (Needleman, S. B. and Wunsch, C. D. (1970) J. Mol. Biol. 48, 443-453). The algorithm aligns amino acid sequences as well as nucleotide sequences. The Needleman-Wunsch algorithm has been implemented in the computer program NEEDLE. For the purpose of this invention the NEEDLE program from the EMBOSS package was used (version 2.8.0 or higher, EMBOSS: The European Molecular Biology Open Software Suite (2000) Rice, P. Longden, I. and Bleasby, A. Trends in Genetics 16, (6) pp276-277, <http://emboss.bioinformatics.nl/>). For protein sequences, EBLOSUM62 is used for the substitution matrix. For nucleotide sequences, EDNAFULL is used. Other matrices can be specified. The optional parameters used for alignment of amino acid sequences are a gap-open penalty of 10 and a gap extension penalty of 0.5. The skilled person will appreciate that all these different parameters will yield slightly different results but that the overall percentage identity of two sequences is not significantly altered when using different algorithms.

Global Homology Definition

[0091] The homology or identity is the percentage of identical matches between the two full sequences over the total aligned region including any gaps or extensions. The homology or identity between the two aligned sequences is calculated as follows: Number of corresponding

positions in the alignment showing an identical amino acid in both sequences divided by the total length of the alignment including the gaps. The identity defined as herein can be obtained from NEEDLE and is labelled in the output of the program as "IDENTITY".

Longest Identity Definition

[0092] The homology or identity between the two aligned sequences is calculated as follows: Number of corresponding positions in the alignment showing an identical amino acid in both sequences divided by the total length of the alignment after subtraction of the total number of gaps in the alignment. The identity defined as herein can be obtained from NEEDLE by using the NOBRIEF option and is labelled in the output of the program as "longest-identity". For purposes of the invention the level of identity (homology) between two sequences (amino acid or nucleotide) is calculated according to the definition of "longest-identity" as can be carried out by using the program NEEDLE.

[0093] The protein sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases, for example to identify other family members or related sequences. Such searches can be performed using the BLAST programs. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov>). BLASTP is used for amino acid sequences and BLASTN for nucleotide sequences. The BLAST program uses as defaults:

- Cost to open gap: default = 5 for nucleotides/ 11 for proteins
- Cost to extend gap: default = 2 for nucleotides/ 1 for proteins
- Penalty for nucleotide mismatch: default = -3
- Reward for nucleotide match: default = 1
- Expect value: default = 10
- Wordsize: default = 11 for nucleotides/ 28 for megablast/ 3 for proteins

[0094] Furthermore, the degree of local identity (homology) between the amino acid sequence query or nucleic acid sequence query and the retrieved homologous sequences is determined by the BLAST program. However only those sequence segments are compared that give a match above a certain threshold. Accordingly, the program calculates the identity only for these matching segments. Therefore, the identity calculated in this way is referred to as local identity.

Vectors

[0095] Another aspect of the invention pertains to vectors, including cloning and expression vectors, comprising a polynucleotide of the invention encoding a TEMER09484 protein or a functional equivalent thereof and methods of growing, transforming or transfecting such

vectors in a suitable host cell, for example under conditions in which expression of a polypeptide of the invention occurs. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked.

[0096] Polynucleotides of the invention can be incorporated into a recombinant replicable vector, for example a cloning or expression vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus, in a further embodiment, the invention provides a method of making polynucleotides of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about replication of the vector. The vector may be recovered from the host cell. Suitable host cells are described below.

[0097] The vector into which the expression cassette or polynucleotide of the invention is inserted may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of the vector will often depend on the host cell into which it is to be introduced.

[0098] A vector according to the invention may be an autonomously replicating vector, i. e. a vector which exists as an extra-chromosomal entity, the replication of which is independent of chromosomal replication, e. g. a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome (s) into which it has been integrated.

[0099] One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. The terms "plasmid" and "vector" can be used interchangeably herein as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as cosmid, viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses) and phage vectors which serve equivalent functions.

[0100] Vectors according to the invention may be used in vitro, for example for the production of RNA or used to transfect or transform a host cell.

[0101] A vector of the invention may comprise two or more, for example three, four or five, polynucleotides of the invention, for example for overexpression.

[0102] The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vector includes one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed.

[0103] Within a vector, such as an expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell), i.e. the term "operably linked" refers to a juxtaposition wherein the components described are in a relationship permitting them to function in their intended manner. A regulatory sequence such as a promoter, enhancer or other expression regulation signal "operably linked" to a coding sequence is positioned in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences or the sequences are arranged so that they function in concert for their intended purpose, for example transcription initiates at a promoter and proceeds through the DNA sequence encoding the polypeptide.

[0104] A vector or expression construct for a given host cell may thus comprise the following elements operably linked to each other in a consecutive order from the 5'-end to 3'-end relative to the coding strand of the sequence encoding the polypeptide of the first invention: (1) a promoter sequence capable of directing transcription of the nucleotide sequence encoding the polypeptide in the given host cell; (2) optionally, a signal sequence capable of directing secretion of the polypeptide from the given host cell into a culture medium; (3) a DNA sequence of the invention encoding a mature and preferably active form of a polypeptide having cellobiohydrolase activity; and preferably also (4) a transcription termination region (terminator) capable of terminating transcription downstream of the nucleotide sequence encoding the polypeptide.

[0105] Downstream of the nucleotide sequence according to the invention there may be a 3' untranslated region containing one or more transcription termination sites (e. g. a terminator). The origin of the terminator is less critical. The terminator can, for example, be native to the DNA sequence encoding the polypeptide. However, preferably a yeast terminator is used in yeast host cells and a filamentous fungal terminator is used in filamentous fungal host cells. More preferably, the terminator is endogenous to the host cell (in which the nucleotide sequence encoding the polypeptide is to be expressed). In the transcribed region, a ribosome binding site for translation may be present. The coding portion of the mature transcripts expressed by the constructs will include a translation initiating AUG at the beginning and a termination codon appropriately positioned at the end of the polypeptide to be translated.

[0106] Enhanced expression of the polynucleotide of the invention may also be achieved by the selection of heterologous regulatory regions, e. g. promoter, secretion leader and/or

terminator regions, which may serve to increase expression and, if desired, secretion levels of the protein of interest from the expression host and/or to provide for the inducible control of the expression of a polypeptide of the invention.

[0107] It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The vectors, such as expression vectors, of the invention can be introduced into host cells to thereby produce proteins or peptides, encoded by nucleic acids as described herein (e.g. TEMER09484 proteins, mutant forms of TEMER09484 proteins, fragments, variants or functional equivalents thereof. The vectors, such as recombinant expression vectors, of the invention can be designed for expression of TEMER09484 proteins in prokaryotic or eukaryotic cells.

[0108] For example, TEMER09484 proteins can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), filamentous fungi, yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Representative examples of appropriate hosts are described hereafter.

[0109] Appropriate culture mediums and conditions for the above-described host cells are known in the art.

[0110] The recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

[0111] For most filamentous fungi and yeast, the vector or expression construct is preferably integrated in the genome of the host cell in order to obtain stable transformants. However, for certain yeasts also suitable episomal vectors are available into which the expression construct can be incorporated for stable and high level expression, examples thereof include vectors derived from the 2 μ and pKD1 plasmids of *Saccharomyces* and *Kluyveromyces*, respectively, or vectors containing an AMA sequence (e.g. AMA1 from *Aspergillus*). In case the expression constructs are integrated in the host cells genome, the constructs are either integrated at random loci in the genome, or at predetermined target loci using homologous recombination, in which case the target loci preferably comprise a highly expressed gene.

[0112] Accordingly, expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors e.g., vectors derived from bacterial plasmids, bacteriophage, yeast episome, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids.

[0113] The term "control sequences" or "regulatory sequences" is defined herein to include at least any component which may be necessary and/or advantageous for the expression of a

polypeptide. Any control sequence may be native or foreign to the nucleic acid sequence of the invention encoding a polypeptide. Such control sequences may include, but are not limited to, a promoter, a leader, optimal translation initiation sequences (as described in Kozak, 1991, J. Biol. Chem. 266:19867-19870), a secretion signal sequence, a pro-peptide sequence, a polyadenylation sequence, a transcription terminator. At a minimum, the control sequences typically include a promoter, and transcriptional and translational stop signals. As set out above, the term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the production of a polypeptide.

[0114] The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleic acid sequence encoding a polypeptide. The term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the production of a polypeptide.

[0115] The control sequence may be an appropriate promoter sequence, a nucleic acid sequence, which is recognized by a host cell for expression of the nucleic acid sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polypeptide. The promoter may be any nucleic acid sequence, which shows transcriptional activity in the cell including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the cell.

[0116] The term "promoter" is defined herein as a DNA sequence that binds RNA polymerase and directs the polymerase to the correct downstream transcriptional start site of a nucleic acid sequence encoding a biological compound to initiate transcription. RNA polymerase effectively catalyzes the assembly of messenger RNA complementary to the appropriate DNA strand of a coding region. The term "promoter" will also be understood to include the 5'-non-coding region (between promoter and translation start) for translation after transcription into mRNA, cis-acting transcription control elements such as enhancers, and other nucleotide sequences capable of interacting with transcription factors. The promoter may be any appropriate promoter sequence suitable for a eukaryotic or prokaryotic host cell, which shows transcriptional activity, including mutant, truncated, and hybrid promoters, and may be obtained from polynucleotides encoding extra-cellular or intracellular polypeptides either homologous (native) or heterologous (foreign) to the cell. The promoter may be a constitutive or inducible promoter.

[0117] Preferably the promoter is an inducible promoter. More preferably the promoter is a carbohydrate inducible promoter. Carbohydrate inducible promoters that are preferably used are selected from a starch-inducible promoter (i.e. a promoter inducible by starch, a monomer, a dimer, a oligomer thereof, such as for example a maltose-inducible promoter, an isomaltose-inducible promoter), a cellulose-inducible promoter (i.e. a promoter inducible by cellulose, a

monomer, a dimer and/or oligomer thereof, such as for example a cellobiose-inducible promoter, a sophorose-inducible promoter), a hemicellulose inducible promoter (i.e. a promoter inducible by hemicellulose, a monomer, a dimer, and/or an oligomer thereof, such as e.g. a xylan-inducible promoter, an arabionose-inducible promoter, a xylose-inducible promoter), a pectin-inducible promoter (i.e. a promoter inducible by pectin, a monomer, a dimer and/or an oligomer thereof such as for example a galacturonic acid-inducible promoter, a rhamnose-inducible promoter), an arabinan-inducible promoter (i.e. a promoter inducible by arabinan, a monomer, a dimer, and/or an oligomer thereof such as for example an arabinose-inducible promoter), a glucose-inducible promoter, a lactose-inducible promoter, a galactose-inducible promoter. Other inducible promoters are copper-, oleic acid- inducible promoters.

[0118] Promoters suitable in filamentous fungi are promoters which may be selected from the group, which includes but is not limited to promoters obtained from the polynucleotides encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus gpdA* promoter, *A. niger* neutral alpha-amylase, *A. niger* acid stable alpha-amylase, *A. niger* or *A. awamori* glucoamylase (glaA), *A. niger* or *A. awamori* endoxylanase (*xlnA*) or beta-xylosidase (*xlnD*), *T. reesei* cellobiohydrolase I (*CBHI*), *R. miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase, *A. nidulans* acetamidase, *Fusarium venenatum* amyloglucosidase (WO 00/56900), *Fusarium venenatum* Dania (WO 00/56900), *Fusarium venenatum* Quinn (WO 00/56900), *Fusarium oxysporum* trypsin-like protease (WO 96/00787), *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase IV, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* beta-xylosidase, as well as the NA2-tpi promoter (a hybrid of the promoters from the polynucleotides encoding *A. niger* neutral alpha-amylase and *A. oryzae* triose phosphate isomerase), and mutant, truncated, and hybrid promoters thereof. Other examples of promoters are the promoters described in WO2006/092396 and WO2005/100573. An even other example of the use of promoters is described in WO2008/098933. Preferred carbohydrate inducible promoters which can be used in filamentous fungi are the *A. oryzae* TAKA amylase, *A. niger* neutral alpha-amylase, *A. niger* acid stable alpha-amylase, *A. niger* or *A. awamori* glucoamylase (glaA), *A. niger* or *A. awamori* endoxylanase (*xlnA*) or beta-xylosidase (*xlnD*), *T.*, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase IV, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* beta-xylosidase, as well as the NA2-tpi promoter (a hybrid of the promoters from the polynucleotides encoding *A. niger* neutral alpha-amylase and *A. oryzae* triose phosphate isomerase) as defined above.

[0119] Examples of such promoters from Gram-positive microorganisms include, but are not limited to, gnt (gluconate operon promoter); penP from *Bacillus licheniformis*; glnA (glutamine synthetase); xylAB (xylose operon); araABD (L-arabinose operon) and Pspac promoter, a hybrid SPO1/lac promoter that can be controlled by inducers such as isopropyl- β -D-

thiogalactopyranoside [IPTG] ((Yansura D.G., Henner D.J. Proc Natl Acad Sci U S A. 1984 81(2):439-443). Activators are also sequence-specific DNA binding proteins that induce promoter activity. Examples of such promoters from Gram-positive microorganisms include, but are not limited to, two-component systems (PhoP-PhoR, DegU-DegS, Spo0A-Phosphorelay), LevR, Mry and GltC. (ii) Production of secondary sigma factors can be primarily responsible for the transcription from specific promoters. Examples from Gram-positive microorganisms include, but are not limited to, the promoters activated by sporulation specific sigma factors: σ^F , σ^E , σ^G and σ^K and general stress sigma factor, σ^B . The σ^B -mediated response is induced by energy limitation and environmental stresses (Hecker M, Völker U. Mol Microbiol. 1998; 29(5):1129-1136.). (iii) Attenuation and antitermination also regulates transcription. Examples from Gram-positive microorganisms include, but are not limited to, trp operon and sacB gene. (iv) Other regulated promoters in expression vectors are based the sacR regulatory system conferring sucrose inducibility (Klier AF, Rapoport G. Annu Rev Microbiol. 1988; 42:65-95).

[0120] Suitable inducible promoters useful in bacteria, such as *Bacilli*, include: promoters from Gram-positive microorganisms such as, but are not limited to, SP01-26, SP01-15, veg, pyc (pyruvate carboxylase promoter), and amyE. Examples of promoters from Gram-negative microorganisms include, but are not limited to, tac, tet, trp-tet, lpp, lac, lpp-lac, lacIq, T7, T5, T3, gal, trc, ara, SP6, λ -PR, and λ -PL.

[0121] Additional examples of promoters useful in bacterial cells, such as *Bacilli*, include the α -amylase and SPo2 promoters as well as promoters from extracellular protease genes.

[0122] Another example of a suitable promoter is the promoter obtained from the *E. coli* lac operon. Another example is the promoter of the *Streptomyces coelicolor* agarase gene (dagA). Another example is the promoter of the *Bacillus lentus* alkaline protease gene (aprH). Another example is the promoter of the *Bacillus licheniformis* alkaline protease gene (subtilisin Carlsberg gene). Another example is the promoter of the *Bacillus subtilis* levansucrase gene (sacB). Another example is the promoter of the *Bacillus subtilis* alphaamylase gene (amyF). Another example is the promoter of the *Bacillus licheniformis* alphaamylase gene (amyL). Another example is the promoter of the *Bacillus stearothermophilus* maltogenic amylase gene (amyM). Another example is the promoter of the *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ). Another example is a "consensus" promoter having the sequence TTGACA for the "-35" region and TATAAT for the "-10" region. Another example is the promoter of the *Bacillus licheniformis* penicillinase gene (penP). Another example are the promoters of the *Bacillus subtilis* xylA and xylB genes.

[0123] Preferably the promoter sequence is from a highly expressed gene. Examples of preferred highly expressed genes from which promoters may be selected and/or which are comprised in preferred predetermined target loci for integration of expression constructs, include but are not limited to genes encoding glycolytic enzymes such as triose-phosphate isomerases (TPI), glyceraldehyde-phosphate dehydrogenases (GAPDH), phosphoglycerate kinases (PGK), pyruvate kinases (PYK or PKI), alcohol dehydrogenases (ADH), as well as genes encoding amylases, glucoamylases, proteases, xylanases, cellobiohydrolases, β -

galactosidases, alcohol (methanol) oxidases, elongation factors and ribosomal proteins. Specific examples of suitable highly expressed genes include e. g. the LAC4 gene from *Kluyveromyces* sp., the methanol oxidase genes (AOX and MOX) from *Hansenula* and *Pichia*, respectively, the glucoamylase (glaA) genes from *A. niger* and *A. awamori*, the *A. oryzae* TAKA-amylase gene, the *A. nidulans* gpdA gene and the *T. reesei* cellobiohydrolase genes.

[0124] Promoters which can be used in yeast include e.g. promoters from glycolytic genes, such as the phosphofructokinase (PFK), triose phosphate isomerase (TPI), glyceraldehyde-3 -phosphate dehydrogenase (GPD, TDH3 or GAPDH), pyruvate kinase (PYK), phosphoglycerate kinase (PGK) promoters from yeasts or filamentous fungi; more details about such promoters from yeast may be found in (WO 93/03159). Other useful promoters are ribosomal protein encoding gene promoters, the lactase gene promoter (LAC4), alcohol dehydrogenase promoters (ADH1, ADH4, and the like), and the enolase promoter (ENO). Other promoters, both constitutive and inducible, and enhancers or upstream activating sequences will be known to those of skill in the art. The promoters used in the host cells of the invention may be modified, if desired, to affect their control characteristics. Suitable promoters in this context include both constitutive and inducible natural promoters as well as engineered promoters, which are well known to the person skilled in the art. Suitable promoters in eukaryotic host cells may be *GAL7*, *GAL10*, or *GAL1*, *CYC1*, *HIS3*, *ADH1*, *PGL*, *PH05*, *GAPDH*, *ADC1*, *TRP1*, *URA3*, *LEU2*, *ENO1*, *TPI1*, and *AOX1*. Other suitable promoters include *PDC1*, *GPD1*, *PGK1*, *TEF1*, and *TDH3*. Examples of carbohydrate inducible promoters which can be used are *GAL* promoters, such as *GAL1* or *GAL10* promoters.

[0125] All of the above-mentioned promoters are readily available in the art.

[0126] Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of the replication origin at bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

[0127] The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a filamentous fungal cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleic acid sequence encoding the polypeptide. Any terminator, which is functional in the cell, may be used in the present invention.

[0128] The control sequence may also be a terminator. Preferred terminators for filamentous fungal cells are obtained from the genes encoding *A. oryzae* TAKA amylase, *A. niger* glucoamylase (glaA), *A. nidulans* anthranilate synthase, *A. niger* alpha-glucosidase, *trpC* gene and *Fusarium oxysporum* trypsin-like protease.

[0129] The control sequence may also include a suitable leader sequence, a non-translated region of a mRNA which is important for translation by the filamentous fungal cell. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the polypeptide. Any leader sequence, which is functional in the cell, may be used in the present invention. Preferred leaders for filamentous fungal cells are obtained from the genes encoding *A. oryzae* TAKA amylase and *A. nidulans* triose phosphate isomerase and *A. niger* glaA. Other preferred sequences are isolated and/or disclosed in WO2006/077258.

[0130] Other control sequences may be isolated from the *Penicillium* IPNS gene, or pcbC gene, the beta tubulin gene. All the control sequences are cited in WO 01/21779.

[0131] The control sequence may also be a polyadenylation sequence, a sequence which is operably linked to the 3' terminus of the nucleic acid sequence and which, when transcribed, is recognized by the filamentous fungal cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence, which is functional in the cell, may be used in the present invention. Preferred polyadenylation sequences for filamentous fungal cells are obtained from the genes encoding *A. oryzae* TAKA amylase, *A. niger* glucoamylase, *A. nidulans* anthranilate synthase, *Fusarium oxysporum* trypsin-like protease and *A. niger* alpha-glucosidase.

[0132] When the polypeptide according to the invention is to be secreted from the host cell into the cultivation medium, an appropriate signal sequence can be added to the polypeptide in order to direct the de novo synthesized polypeptide to the secretion route of the host cell. The person skilled in the art knows to select an appropriate signal sequence for a specific host. The signal sequence may be native to the host cell, or may be foreign to the host cell. As an example, a signal sequence from a protein native to the host cell can be used. Preferably, said native protein is a highly secreted protein, i.e. a protein that is secreted in amounts higher than 10% of the total amount of protein being secreted. The signal sequences preferably used according to the invention are for example: pmeA.

[0133] As an alternative for a signal sequence, the polypeptide of the invention can be fused to a secreted carrier protein, or part thereof. Such chimeric construct is directed to the secretion route by means of the signal sequence of the carrier protein, or part thereof. In addition, the carrier protein will provide a stabilizing effect to the polypeptide according to the invention and or may enhance solubility. Such carrier protein may be any protein. Preferably, a highly secreted protein is used as a carrier protein. The carrier protein may be native or foreign to the polypeptide according to the invention. The carrier protein may be native or may be foreign to the host cell. Examples of such carrier proteins are glucoamylase, prepro sequence of alpha-Mating factor, cellulose binding domain of *Clostridium cellulovorans* cellulose binding protein A, glutathione S-transferase, chitin binding domain of *Bacillus circulans* chitinase A1, maltose binding domain encoded by the malE gene of *E. coli* K12, beta-galactosidase, and alkaline phosphatase. A preferred carrier protein for expression of such chimeric construct in *Aspergillus* cells is glucoamylase. The carrier protein and polypeptide according to the invention may contain a specific amino acid motif to facilitate isolation of the polypeptide; the

polypeptide according to the invention may be released by a special releasing agent. The releasing agent may be a proteolytic enzyme or a chemical agent. An example of such amino acid motif is the KEX protease cleavage site, which is well-known to the person skilled in the art.

[0134] A signal sequence can be used to facilitate secretion and isolation of a protein or polypeptide of the invention. Signal sequences are typically characterized by a core of hydrophobic amino acids, which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by known methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence, which facilitates purification, such as with a GST domain. Thus, for instance, the sequence encoding the polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide, which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (Qiagen, Inc.), among others, many of which are commercially available. As described in Gentz et al, Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. The HA tag is another peptide useful for purification which corresponds to an epitope derived of influenza hemagglutinin protein, which has been described by Wilson et al., Cell 37:767 (1984), for instance.

[0135] Preferably, a TEMER09484 fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers, which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Current Protocols in Molecular Biology, eds. Ausubel et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A TEMER09484 -encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the TEMER09484 protein.

(Over)expression

[0136] In a preferred embodiment, the polynucleotides of the present invention as described herein may be over-expressed in a microbial strain of the invention compared to the parent microbial strain in which said gene is not over-expressed. Over-expression of a polynucleotide sequence is defined herein as the expression of the said sequence gene which results in an activity of the enzyme encoded by the said sequence in a microbial strain being at least about 1.5-fold the activity of the enzyme in the parent microbial; preferably the activity of said enzyme is at least about 2-fold, more preferably at least about 3-fold, more preferably at least about 4-fold, more preferably at least about 5-fold, even more preferably at least about 10-fold and most preferably at least about 20-fold the activity of the enzyme in the parent microbial.

[0137] The vector may further include sequences flanking the polynucleotide giving rise to RNA which comprise sequences homologous to eukaryotic genomic sequences or viral genomic sequences. This will allow the introduction of the polynucleotides of the invention into the genome of a host cell.

[0138] An integrative cloning vector may integrate at random or at a predetermined target locus in the chromosome(s) of the host cell into which it is to be integrated. In a preferred embodiment of the invention, an integrative cloning vector may comprise a DNA fragment which is homologous to a DNA sequence in a predetermined target locus in the genome of host cell for targeting the integration of the cloning vector to this predetermined locus. In order to promote targeted integration, the cloning vector may be preferably linearized prior to transformation of the host cell. Linearization may preferably be performed such that at least one but preferably either end of the cloning vector is flanked by sequences homologous to the target locus. The length of the homologous sequences flanking the target locus is preferably at least about 0.1kb, such as about at least 0.2kb, more preferably at least about 0.5 kb, even more preferably at least about 1 kb, most preferably at least about 2 kb. Preferably, the parent host strains may be modified for improved frequency of targeted DNA integration as described in WO05/095624 and/or WO2007/115886.

[0139] The deletion example provided in the present invention, uses the promoter of the gene as 5'-flank and the gene as the 3'-flank to insert a selection marker between the promoter and gene, thereby disturbing (i.e. functionally inactivating) gene transcription. The gene sequences given above can be used to make similar functionally inactivated genes. The genes may be split in two, yielding a 5'-flank and a 3'-flank, but the gene may also be used to clone a larger piece of genomic DNA containing the promoter and terminator regions of the gene, which than can function as 5'-flank and a 3'-flanks.

[0140] The vector system may be a single vector, such as a single plasmid, or two or more vectors, such as two or more plasmids, which together contain the total DNA to be introduced into the genome of the host cell.

[0141] The vector may contain a polynucleotide of the invention oriented in an antisense direction to provide for the production of antisense RNA.

[0142] Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, transduction, infection, lipofection, cationic lipid-mediated transfection or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, et al. (Molecular Cloning: A Laboratory Manual, 2nd, ed. Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), Davis et al., Basic Methods in Molecular Biology (1986) and other laboratory manuals.

[0143] The person skilled in the art knows how to transform cells with the one or more expression cassettes and the selectable marker. For example, the skilled person may use one or more expression vectors, wherein the one or more cloning vectors comprise the expression cassettes and the selectable marker.

[0144] Transformation of the mutant microbial host cell may be conducted by any suitable known methods, including e.g. electroporation methods, particle bombardment or microprojectile bombardment, protoplast methods and *Agrobacterium* mediated transformation (AMT). Preferably the protoplast method is used. Procedures for transformation are described by J.R.S. Fincham, Transformation in fungi. 1989, Microbiological reviews. 53, 148-170.

[0145] Transformation may involve a process consisting of protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known *per se*. Suitable procedures for transformation of *Aspergillus* cells are described in EP 238 023 and Yelton et al., 1984, Proceedings of the National Academy of Sciences USA 81:1470-1474. Suitable procedures for transformation of *Aspergillus* and other filamentous fungal host cells using *Agrobacterium tumefaciens* are described in e.g. De Groot et al., *Agrobacterium tumefaciens*-mediated transformation of filamentous fungi. Nat Biotechnol. 1998, 16:839-842. Erratum in: Nat Biotechnol 1998 16:1074. A suitable method of transforming *Fusarium* species is described by Malardier et al., 1989, Gene 78:147156 or in WO 96/00787. Other methods can be applied such as a method using biolistic transformation as described in: Christiansen et al., Biolistic transformation of the obligate plant pathogenic fungus, *Erysiphe graminis* f.sp. *hordei*. 1995, Curr Genet. 29:100-102. Yeast may be transformed using the procedures described by Becker and Guarente, In Abelson, J. N. and Simon, M. I., editors, Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito et al., 1983, Journal of Bacteriology 153: 163; and Hinnen et al., 1978, Proceedings of the National Academy of Sciences USA 75: 1920.

[0146] In order to enhance the amount of copies of the polynucleotide coding for the compound of interest or coding for a compound involved in the production by the cell of the compound of interest (the gene) in the mutated microbial host cell, multiple transformations of the host cell may be required. In this way, the ratios of the different enzymes produced by the host cell may be influenced. Also, an expression vector may comprise multiple expression

cassettes to increase the amount of copies of the polynucleotide(s) to be transformed.

[0147] Another way could be to choose different control sequences for the different polynucleotides, which - depending on the choice - may cause a higher or a lower production of the desired polypeptide(s).

[0148] The cells transformed with the selectable marker can be selected based on the presence of the selectable marker. In case of transformation of (*Aspergillus*) cells, usually when the cell is transformed with all nucleic acid material at the same time, when the selectable marker is present also the polynucleotide(s) encoding the desired polypeptide(s) are present.

[0149] For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include, but are not limited to, those which confer resistance to drugs or which complement a defect in the host cell. They include e. g. versatile marker genes that can be used for transformation of most filamentous fungi and yeasts such as acetamidase genes or cDNAs (the *amdS*, *niaD*, *facA* genes or cDNAs from *A. nidulans*, *A. oryzae* or *A. niger*), or genes providing resistance to antibiotics like G418, hygromycin, bleomycin, kanamycin, methotrexate, phleomycin or benomyl resistance (*benA*). Alternatively, specific selection markers can be used such as auxotrophic markers which require corresponding mutant host strains: e.g. *URA3* (from *S. cerevisiae* or analogous genes from other yeasts), *pyrG* or *pyrA* (from *A. nidulans* or *A. niger*), *argB* (from *A. nidulans* or *A. niger*) or *trpC*. In a preferred embodiment the selection marker is deleted from the transformed host cell after introduction of the expression construct so as to obtain transformed host cells capable of producing the polypeptide which are free of selection marker genes.

[0150] Other markers include ATP synthetase, subunit 9 (*oliC*), orotidine-5'-phosphate decarboxylase (*pvrA*), the bacterial G418 resistance gene (this may also be used in yeast, but not in fungi), the ampicillin resistance gene (*E. coli*), the neomycin resistance gene (*Bacillus*) and the *E. coli uidA* gene, coding for β -glucuronidase (GUS). Vectors may be used in vitro, for example for the production of RNA or used to transfect or transform a host cell.

[0151] Expression of proteins in prokaryotes is often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, e.g. to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable

separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein.

[0152] As indicated, the expression vectors will preferably contain selectable markers. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline or ampicillin resistance for culturing in *E. coli* and other bacteria.

[0153] Vectors preferred for use in bacteria are for example disclosed in WO-A1-2004/074468, which are hereby enclosed by reference. Other suitable vectors will be readily apparent to the skilled artisan.

[0154] For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signal may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

[0155] The TEMER09484 polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification

[0156] The invention provides an isolated polypeptide having the amino acid sequence according to SEQ ID NO: 37 and an amino acid sequence obtainable by expressing the polynucleotide of SEQ ID NO: 36 or SEQ ID NO: 39 or SEQ ID NO: 40 in an appropriate host. Also, a peptide or polypeptide comprising a variant of the above polypeptides, such as a functional equivalent, is comprised within the present invention. The above polypeptides are collectively comprised in the term "polypeptides according to the invention"

[0157] The term "variant peptide" or "variant polypeptide" is defined herein as a peptide or polypeptide, respectively, comprising one or more alterations, such as substitutions, insertions, deletions and/or truncations of one or more specific amino acid residues at one or more specific positions in the peptide or polypeptide, respectively. Accordingly, a variant signal peptide is a signal peptide comprising one or more alterations, such as substitutions, insertions, deletions and/or truncations of one or more specific amino acid residues at one or more specific positions in the signal peptide.

[0158] The term "polynucleotide" is identical to the term "nucleic acid molecule" and can herein be read interchangeably. The term refers to a polynucleotide molecule, which is a ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) molecule, either single stranded or double stranded. A polynucleotide may either be present in isolated form, or be comprised in recombinant nucleic acid molecules or vectors, or be comprised in a host cell.

[0159] The term "variant polynucleotide" is defined herein as a polynucleotide comprising one or more alterations, such as substitutions, insertions, deletions and/or truncations of one or more nucleotides at one or more specific positions in the polynucleotide.

[0160] The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably, as the context requires, to indicate a chain of at least two amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than seven amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus. The one-letter code of amino acids used herein is commonly known in the art and can be found in Sambrook, et al. (Molecular Cloning: A Laboratory Manual, 2nd, ed. Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989)

[0161] By "isolated" polypeptide or protein is intended a polypeptide or protein removed from its native environment. For example, recombinantly produced polypeptides and proteins expressed in host cells are considered isolated for the purpose of the invention as are native or recombinant polypeptides which have been substantially purified by any suitable technique such as, for example, the single-step purification method disclosed in Smith and Johnson, Gene 67:31-40 (1988).

[0162] The Temer06848 protein according to the invention can be recovered and purified from recombinant cell cultures by methods known in the art. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

[0163] Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

[0164] The invention also features biologically active fragments of the polypeptides according to the invention.

[0165] Biologically active fragments of a polypeptide of the invention include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the Temer06848 protein (e.g., the amino acid sequence of SEQ ID NO: 37), which include fewer amino acids than the full length protein but which exhibit at least one biological activity of the corresponding full-length protein. Typically, biologically active fragments comprise a domain or motif with at least one activity of the Temer06848 protein.

[0166] A biologically active fragment of a protein of the invention can be a polypeptide which is,

for example, about 10, about 25, about 50, about 100 or more amino acids in length or at least about 100 amino acids, at least 150, 200, 250, 300, 350, 400 amino acids in length, or of a length up to the total number of amino acids of polypeptide of the invention.

[0167] Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the biological activities of the native form of a polypeptide of the invention. The invention also features nucleic acid fragments which encode the above biologically active fragments of the Temer06848 protein.

Proteins

[0168] In another aspect of the invention, improved Temer06848 proteins are provided. Improved Temer06848 proteins are proteins wherein at least one biological activity is improved. Such proteins may be obtained by randomly introducing mutations along all or part of the Temer06848 coding sequence, such as by saturation mutagenesis, and the resulting mutants can be expressed recombinantly and screened for biological activity. For instance, the art provides for standard assays for measuring the enzymatic activity of the protein of the invention and thus improved proteins may easily be selected.

[0169] Improved variants of the amino acid sequences of the present invention leading to an improved cellobiohydrolase function may be obtained by the corresponding genes of the present invention. Among such modifications are included:

1. 1. Error prone PCR to introduce random mutations, followed by a screening of obtained variants and isolating of variants with improved kinetic properties
2. 2. Family shuffling of related variants of the genes encoding the cellobiohydrolase, followed by a screening of obtained variants and isolating of variants with improved kinetic properties

[0170] Variants of the genes of the present invention leading to an increased level of mRNA and/or protein, resulting in more an activity according to Table 1 may be obtained by the polynucleotide sequences of said genes. Among such modifications are included:

1. 1. Improving the codon usage in such a way that the codons are (optimally) adapted to the parent microbial host.
2. 2. Improving the codon pair usage in such a way that the codons are (optimally) adapted to the parent microbial host
3. 3. Addition of stabilizing sequences to the genomic information encoding the cellobiohydrolase resulting in mRNA molecules with an increased half life

[0171] Preferred methods to isolate variants with improved catalytic properties or increased levels of mRNA or protein are described in WO03/010183 and WO03/01311. Preferred methods to optimize the codon usage in parent microbial strains are described in PCT/EP2007/05594. Preferred methods for the addition of stabilizing elements to the genes encoding the cellobiohydrolase of the invention are described in WO2005/059149.

[0172] In a preferred embodiment the protein of the invention has an amino acid sequence according to SEQ ID NO: 37. In another embodiment, the polypeptide of the invention is substantially homologous to the amino acid sequence according to SEQ ID NO: 37 and retains at least one biological activity of a polypeptide according to SEQ ID NO: 37 yet differs in amino acid sequence due to natural variation or mutagenesis as described.

[0173] In a further preferred embodiment, the protein of the invention has an amino acid sequence encoded by an isolated nucleic acid fragment capable of hybridizing to a nucleic acid according to SEQ ID NO: 36 or SEQ ID NO: 39 or SEQ ID NO: 40 preferably under highly stringent hybridization conditions.

[0174] Accordingly, the Temer06848 protein or the protein of the invention is preferably a protein which comprises an amino acid sequence at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, 92%, 93%, 94%, 95%, 96%, 95%, 96%, 97%, 98%, 97%, 98%, 99%, 99.8%, 99.9% or more homologous to the amino acid sequence shown in SEQ ID NO: 37 and, typically, retains at least one functional activity of the polypeptide according to SEQ ID NO: 37.

[0175] According to one aspect of the invention the polypeptide of the invention may comprise the amino acid sequence set out in SEQ ID NO: 37 or an amino acid sequence that differs in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acids from the amino acid sequence set out in SEQ ID NO: 37 and whereby the polypeptide still has the activity or function of the polypeptide of the invention. The skilled person will appreciate that these minor amino acid changes in the polypeptide of the invention may be present (for example naturally occurring mutations) or made (for example using r-DNA technology) without loss of the protein function or activity. In case these mutations are present in a binding domain, active site, or other functional domain of the polypeptide a property of the polypeptide may change (for example its thermostability) but the polypeptide may keep its hemicellulase activity. In case a mutation is present which is not close to the active site, binding domain, or other functional domain, less effect may be expected.

[0176] Functional equivalents of a protein according to the invention can also be identified e.g. by screening combinatorial libraries of mutants, e.g. truncation mutants, of the protein of the invention for an activity according to Table 1. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein

sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g. for phage display). There are a variety of methods that can be used to produce libraries of potential variants of the polypeptides of the invention from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477).

[0177] In addition, libraries of fragments of the coding sequence of a polypeptide of the invention can be used to generate a variegated population of polypeptides for screening a subsequent selection of variants. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the protein of interest.

[0178] Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations of truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify variants of a protein of the invention (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave et al. (1993) *Protein Engineering* 6(3): 327-331).

[0179] In addition to the Temer06848 gene sequence shown in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40 it will be apparent for the person skilled in the art that DNA sequence polymorphisms may exist within a given population, which may lead to changes in the amino acid sequence of the Temer06848 protein. Such genetic polymorphisms may exist in cells from different populations or within a population due to natural allelic variation. Allelic variants may also include functional equivalents.

[0180] Fragments of a polynucleotide according to the invention may also comprise polynucleotides not encoding functional polypeptides. Such polynucleotides may function as probes or primers for a PCR reaction.

[0181] Nucleic acids according to the invention irrespective of whether they encode functional or non-functional polypeptides can be used as hybridization probes or polymerase chain reaction (PCR) primers. Uses of the nucleic acid molecules of the present invention that do not

encode a polypeptide having a Temer06848 activity include, inter alia, (1) isolating the gene encoding the Temer06848 protein, or allelic variants thereof from a cDNA library e.g. from suitable microorganisms; (2) in situ hybridization (e.g. FISH) to metaphase chromosomal spreads to provide precise chromosomal location of the Temer06848 gene as described in Verma et al., Human Chromosomes: a Manual of Basic Techniques, Pergamon Press, New York (1988); (3) Northern blot analysis for detecting expression of Temer06848 mRNA in specific tissues and/or cells and 4) probes and primers that can be used as a diagnostic tool to analyse the presence of a nucleic acid hybridizable to the Temer06848 probe in a given biological (e.g. tissue) sample.

[0182] Also encompassed by the invention is a method of obtaining a functional equivalent of a Temer06848 gene. Such a method entails obtaining a labelled probe that includes an isolated nucleic acid which encodes all or a portion of the protein sequence according to SEQ ID NO: 37 or a variant thereof; screening a nucleic acid fragment library with the labelled probe under conditions that allow hybridization of the probe to nucleic acid fragments in the library, thereby forming nucleic acid duplexes, and preparing a full-length gene sequence from the nucleic acid fragments in any labelled duplex to obtain a gene related to the Temer06848 gene.

[0183] In one embodiment, a Temer06848 nucleic acid of the invention is at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more homologous to a nucleic acid sequence shown in SEQ ID NO: 36 or in SEQ ID NO: 39 or in SEQ ID NO: 40 or the complement thereof.

[0184] Provided also are host cells comprising a polynucleotide or vector of the invention. The polynucleotide may be heterologous to the genome of the host cell. The term "heterologous", usually with respect to the host cell, means that the polynucleotide does not naturally occur in the genome of the host cell or that the polypeptide is not naturally produced by that cell.

[0185] In another embodiment, the invention features cells, e.g., transformed host cells or recombinant host cells that contain a nucleic acid encompassed by the invention. A "transformed cell" or "recombinant cell" is a cell into which (or into an ancestor of which) has been introduced, by means of recombinant DNA techniques, a nucleic acid according to the invention. Both prokaryotic and eukaryotic cells are included, e.g., bacteria, fungi, yeast, and the like, especially preferred are cells from filamentous fungi, such as *Aspergillus niger*.

[0186] A host cell can be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in a specific, desired fashion. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may facilitate optimal functioning of the protein.

[0187] Various host cells have characteristic and specific mechanisms for post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems familiar to those of skill in the art of molecular biology and/or microbiology can be

chosen to ensure the desired and correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product can be used. Such host cells are well known in the art.

[0188] If desired, a cell as described above may be used to in the preparation of a polypeptide according to the invention. Such a method typically comprises cultivating a host cell (e. g. transformed or transfected with an expression vector as described above) under conditions to provide for expression (by the vector) of a coding sequence encoding the polypeptide, and optionally recovering the expressed polypeptide. Polynucleotides of the invention can be incorporated into a recombinant replicable vector, e. g. an expression vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus, in a further embodiment, the invention provides a method of making a polynucleotide of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about the replication of the vector. The vector may be recovered from the host cell.

[0189] Preferably the polypeptide is produced as a secreted protein in which case the nucleotide sequence encoding a mature form of the polypeptide in the expression construct is operably linked to a nucleotide sequence encoding a signal sequence. Preferably the signal sequence is native (homologous) to the nucleotide sequence encoding the polypeptide. Alternatively, the signal sequence is foreign (heterologous) to the nucleotide sequence encoding the polypeptide, in which case the signal sequence is preferably endogenous to the host cell in which the nucleotide sequence according to the invention is expressed. Examples of suitable signal sequences for yeast host cells are the signal sequences derived from yeast α -factor genes. Similarly, a suitable signal sequence for filamentous fungal host cells is e. g. a signal sequence derived from a filamentous fungal amyloglucosidase (AG) gene, e. g. the *A. niger* glaA gene. This may be used in combination with the amyloglucosidase (also called (gluco) amylase) promoter itself, as well as in combination with other promoters. Hybrid signal sequences may also be used with the context of the present invention.

[0190] Preferred heterologous secretion leader sequences are those originating from the fungal amyloglucosidase (AG) gene (glaA-both 18 and 24 amino acid versions e. g. from *Aspergillus*), the α -factor gene (yeasts e. g. *Saccharomyces* and *Kluyveromyces*) or the α -amylase gene (*Bacillus*).

[0191] The vectors may be transformed or transfected into a suitable host cell as described above to provide for expression of a polypeptide of the invention. This process may comprise culturing a host cell transformed with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the polypeptide.

Host cells

[0192] The invention thus provides host cells transformed or transfected with or comprising a polynucleotide or vector of the invention. Preferably the polynucleotide is carried in a vector for the replication and expression of the polynucleotide. The cells will be chosen to be compatible with the said vector and may for example be prokaryotic (for example bacterial), fungal, yeast or plant cells.

[0193] A heterologous host may also be chosen wherein the polypeptide of the invention is produced in a form which is substantially free from other cellulose-degrading or hemicellulose degrading enzymes. This may be achieved by choosing a host which does not normally produce such enzymes.

[0194] The invention encompasses processes for the production of the polypeptide of the invention by means of recombinant expression of a DNA sequence encoding the polypeptide. For this purpose, the DNA sequence of the invention can be used for gene amplification and/or exchange of expression signals, such as promoters, secretion signal sequences, in order to allow economic production of the polypeptide in a suitable homologous or heterologous host cell. A homologous host cell is a host cell which is of the same species or which is a variant within the same species as the species from which the DNA sequence is derived.

[0195] Suitable host cells are preferably prokaryotic microorganisms such as bacteria, or more preferably eukaryotic organisms, for example fungi, such as yeasts or filamentous fungi, or plant cells. In general, yeast cells are preferred over fungal cells because they are easier to manipulate. However, some proteins are either poorly secreted from yeasts, or in some cases are not processed properly (e. g. hyperglycosylation in yeast). In these instances, a fungal host organism should be selected.

[0196] The host cell may over-express the polypeptide, and techniques for engineering over-expression are well known. The host may thus have two or more copies of the encoding polynucleotide (and the vector may thus have two or more copies accordingly).

[0197] In the context of the present invention the "parent microbial host cell" and the "mutant microbial host cell" may be any type of host cell. The specific embodiments of the mutant microbial host cell are hereafter described. It will be clear to those skilled in the art that embodiments applicable to the mutant microbial host cell are as well applicable to the parent microbial host cell unless otherwise indicated.

[0198] The mutant microbial host cell according to the present invention may be a prokaryotic cell. Preferably, the prokaryotic host cell is bacterial cell. The term "bacterial cell" includes both Gram-negative and Gram-positive microorganisms. Suitable bacteria may be selected from e.g. *Escherichia*, *Anabaena*, *Caulobacter*, *Gluconobacter*, *Rhodobacter*, *Pseudomonas*, *Paracoccus*, *Bacillus*, *Brevibacterium*, *Corynebacterium*, *Rhizobium* (*Sinorhizobium*), *Flavobacterium*, *Klebsiella*, *Enterobacter*, *Lactobacillus*, *Lactococcus*, *Methylobacterium*, *Staphylococcus* or *Streptomyces*. Preferably, the bacterial cell is selected from the group

consisting of *B. subtilis*, *B. amyloliquefaciens*, *B. licheniformis*, *B. pumilus*, *B. megaterium*, *B. halodurans*, *G. oxydans*, *Caulobacter crescentus* CB 15, *Methylobacterium extorquens*, *Rhodobacter sphaeroides*, *Pseudomonas zeaxanthinifaciens*, *Paracoccus denitrificans*, *E. coli*, *C. glutamicum*, *Staphylococcus carnosus*, *Streptomyces lividans*, *Sinorhizobium meliloti* and *Rhizobium radiobacter*.

[0199] According to an embodiment, the mutant microbial host cell according to the invention is a eukaryotic host cell. Preferably, the eukaryotic cell is a mammalian, insect, plant, fungal, or algal cell. Preferred mammalian cells include e.g. Chinese hamster ovary (CHO) cells, COS cells, 293 cells, PerC6 cells, and hybridomas. Preferred insect cells include e.g. Sf9 and Sf21 cells and derivatives thereof. More preferably, the eukaryotic cell is a fungal cell, i.e. a yeast cell, such as *Candida*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia strain*. More preferably the eukaryotic host cell is a *Kluyveromyces lactis*, *S. cerevisiae*, *Hansenula polymorpha*, *Yarrowia lipolytica* or *Pichia pastoris*, or a filamentous fungal cell. Most preferably, the eukaryotic cell is a filamentous fungal cell.

[0200] Filamentous fungi include all filamentous forms of the subdivision *Eumycota* and *Oomycota* (as defined by Hawksworth et al., In, Ainsworth and Bisby's Dictionary of The Fungi, 8th edition, 1995, CAB International, University Press, Cambridge, UK). The filamentous fungi are characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. Filamentous fungal strains include, but are not limited to, strains of *Acremonium*, *Agaricus*, *Aspergillus*, *Aureobasidium*, *Chrysosporium*, *Coprinus*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Piromyces*, *Panerochaete*, *Pleurotus*, *Schizophyllum*, *Talaromyces*, *Rasamsonia*, *Thermoascus*, *Thielavia*, *Tolypocladium*, and *Trichoderma*.

[0201] Preferred filamentous fungal cells belong to a species of an *Acremonium*, *Aspergillus*, *Chrysosporium*, *Myceliophthora*, *Penicillium*, *Talaromyces*, *Rasamsonia*, *Thielavia*, *Fusarium* or *Trichoderma* genus, and most preferably a species of *Aspergillus niger*, *Acremonium alabamense*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus sojae*, *Aspergillus fumigatus*, *Talaromyces emersonii*, *Rasamsonia emersonii*, *Aspergillus oryzae*, *Chrysosporium lucknowense*, *Fusarium oxysporum*, *Myceliophthora thermophila*, *Trichoderma reesei*, *Thielavia terrestris* or *Penicillium chrysogenum*. A more preferred host cell belongs to the genus *Aspergillus* or *Rasamsonia*, more preferably the host cell belongs to the species *Aspergillus niger* or *Rasamsonia emersonii*. When the host cell according to the invention is an *Aspergillus niger* host cell, the host cell preferably is CBS 513.88, CBS124.903 or a derivative thereof.

[0202] Several strains of filamentous fungi are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Centraalbureau Voor Schimmelcultures

(CBS), Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL), and All-Russian Collection of Microorganisms of Russian Academy of Sciences, (abbreviation in Russian - VKM, abbreviation in English - RCM), Moscow, Russia. Useful strains in the context of the present invention may be *Aspergillus niger* CBS 513.88, CBS124.903, *Aspergillus oryzae* ATCC 20423, IFO 4177, ATCC 1011, CBS205.89, ATCC 9576, ATCC14488-14491, ATCC 11601, ATCC12892, *P. chrysogenum* CBS 455.95, *P. chrysogenum* Wisconsin54-1255(ATCC28089), *Penicillium citrinum* ATCC 38065, *Penicillium chrysogenum* P2, *Thielavia terrestris* NRRL8126, *Talaromyces emersonii* CBS 124.902, *Acremonium chrysogenum* ATCC 36225 or ATCC 48272, *Trichoderma reesei* ATCC 26921 or ATCC 56765 or ATCC 26921, *Aspergillus sojae* ATCC 11906, *Myceliophthora thermophila* C1, Garg 27K, VKM-F 3500 D, *Chrysosporium lucknowense* C1, Garg 27K, VKM-F 3500 D, ATCC44006 and derivatives thereof.

[0203] According to one embodiment of the invention, when the mutant microbial host cell according to the invention is a filamentous fungal host cell, the mutant microbial host cell may comprise one or more modifications in its genome such that the mutant microbial host cell is deficient in the production of at least one product selected from glucoamylase (glaA), acid stable alpha-amylase (amyA), neutral alpha-amylase (amyBI and amyBII), oxalic acid hydrolase (oahA), a toxin, preferably ochratoxin and/or fumonisin, a protease transcriptional regulator prtT, PepA, a product encoded by the gene hdfA and/or hdfB, a non-ribosomal peptide synthase *npsE* if compared to a parent host cell and measured under the same conditions.

[0204] Therefore, when the mutant microbial host cell according to the invention is a filamentous fungal host cell the host cell may comprise one or more modifications in its genome to result in a deficiency in the production of the major extracellular aspartic protease PepA. For example, the host cell according to the invention may further comprise a disruption of the *pepA* gene encoding the major extracellular aspartic protease PepA.

[0205] When the mutant microbial host cell according to the invention is a filamentous fungal host cell the host cell according to the invention may additionally comprises one or more modifications in its genome to result in a deficiency in the production of the product encoded by the *hdfA* and/or *hdfB* gene. For example, the host cell according to the invention may further comprise a disruption of the *hdfA* and/or *hdfB* gene. Filamentous fungal host cells which are deficient in a product encoded by the *hdfA* and/or *hdfB* gene have been described in WO 2005/095624.

[0206] When the mutant microbial host cell according to the invention is a filamentous fungal host cell the host cell according to the invention may additionally comprise a modification in its genome which results in the deficiency in the production of the non-ribosomal peptide synthase *npsE*. Such host cells deficient in the production of non-ribosomal peptide synthase *npsE* have been described in WO 2012/001169 (*npsE* has a genomic sequence as depicted in SEQ ID NO: 35, a coding sequence depicted in SEQ ID NO: 36, the mRNA depicted in SEQ ID NO: 37 and the *nrps* protein depicted in SEQ ID NO: 38 of WO 2012/001169).

[0207] When the mutant microbial host cell according to the invention is a filamentous fungal host cell the host cell may additionally comprise at least two substantially homologous DNA domains suitable for integration of one or more copies of a polynucleotide encoding a compound of interest wherein at least one of the at least two substantially homologous DNA domains is adapted to have enhanced integration preference for the polynucleotide encoding a compound of interest compared to the substantially homologous DNA domain it originates from, and wherein the substantially homologous DNA domain where the adapted substantially homologous DNA domain originates from has a gene conversion frequency that is at least 10% higher than one of the other of the at least two substantially homologous DNA domains. These cells have been described in WO2011/009700. Strains containing two or more copies of these substantially homologous DNA domains are also referred hereafter as strain containing two or more amplicons. Examples of host cells comprising such amplicons are e.g. described in van Dijck et al, 2003, *Regulatory Toxicology and Pharmacology* 28; 27-35: *On the safety of a new generation of DSM Aspergillus niger enzyme production strains*. In van Dijck et al, an *Aspergillus niger* strain is described that comprises 7 amplified glucoamylase gene loci, i.e. 7 amplicons. Preferred host cells within this context are filamentous fungus host cells, preferably *A. niger* host cells, comprising two or more amplicons, preferably two or more $\Delta glaA$ amplicons (preferably comprising 3, 4, 5, 6, 7 $\Delta glaA$ amplicons) wherein the amplicon which has the highest frequency of gene conversion, has been adapted to have enhanced integration preference for the polynucleotide encoding a compound of interest compared to the amplicon it originates from. Adaptation of the amplicon can be performed according to any one of the methods described in WO 2011/009700. An example of these host cells, described in WO2011/009700, are host cells comprising three $\Delta glaA$ amplicons being a BamHI truncated amplicon, a SalI truncated amplicon and a BglII truncated amplicon and wherein the BamHI amplicon has been adapted to have enhanced integration preference for a polynucleotide encoding a compound of interest compared to the BamHI amplicon it originates from. Host cells comprising two or more amplicons wherein one amplicon has been adapted to have enhanced integration preference for a polynucleotide encoding a compound of interest compared to the amplicon it originates from are hereafter referred as host cells comprising an adapted amplicon.

[0208] When the mutant microbial host cell according to the invention is a filamentous fungal host cell the host cell according to the invention may additionally comprises a modification of Sec61. A preferred SEC61 modification is a modification which results in a one-way mutant of SEC61; i.e. a mutant wherein the de novo synthesized protein can enter the ER via SEC61, but the protein cannot leave the ER via SEC61. Such modifications are extensively described in WO 2005/123763. Most preferably, the SEC 61 modification is the S376W mutation in which Serine 376 is replaced by Tryptophan.

[0209] Host cells according to the invention include plant cells, and the invention therefore extends to transgenic organisms, such as plants and parts thereof, which contain one or more cells of the invention. The cells may heterologously express the polypeptide of the invention or may heterologously contain one or more of the polynucleotides of the invention. The

transgenic (or genetically modified) plant may therefore have inserted (e. g. stably) into its genome a sequence encoding one or more of the polypeptides of the invention. The transformation of plant cells can be performed using known techniques, for example using a Ti or a Ri plasmid from *Agrobacterium tumefaciens*. The plasmid (or vector) may thus contain sequences necessary to infect a plant, and derivatives of the Ti and/or Ri plasmids may be employed.

[0210] Alternatively, direct infection of a part of a plant, such as a leaf, root or stem can be affected. In this technique the plant to be infected can be wounded, for example by cutting the plant with a razor or puncturing the plant with a needle or rubbing the plant with an abrasive. The wound is then inoculated with the *Agrobacterium*. The plant or plant part can then be grown on a suitable culture medium and allowed to develop into a mature plant. Regeneration of transformed cells into genetically modified plants can be achieved by using known techniques, for example by selecting transformed shoots using an antibiotic and by sub-culturing the shoots on a medium containing the appropriate nutrients, plant hormones and the like.

[0211] The invention also includes cells that have been modified to express the cellobiohydrolase of the invention or a variant thereof. Such cells include transient, or preferably stable higher eukaryotic cell lines, such as mammalian cells or insect cells, lower eukaryotic cells, such as yeast and (e. g. filamentous) fungal cells or prokaryotic cells such as bacterial cells.

[0212] It is also possible for the proteins of the invention to be transiently expressed in a cell line or on a membrane, such as for example in a baculovirus expression system. Such systems, which are adapted to express the proteins according to the invention, are also included within the scope of the present invention.

[0213] According to the present invention, the production of the polypeptide of the invention can be affected by the culturing of microbial expression hosts, which have been transformed with one or more polynucleotides of the present invention, in a conventional nutrient fermentation medium.

Polypeptide/Enzyme production

[0214] The recombinant host cells according to the invention may be cultured using procedures known in the art. For each combination of a promoter and a host cell, culture conditions are available which are conducive to the expression the DNA sequence encoding the polypeptide. After reaching the desired cell density or titer of the polypeptide the culture is stopped and the polypeptide is recovered using known procedures.

[0215] The fermentation medium can comprise a known culture medium containing a carbon source (e. g. glucose, maltose, molasses, starch, cellulose, xylan, pectin, lignocellolytic

biomass hydrolysate, etc.), a nitrogen source (e. g. ammonium sulphate, ammonium nitrate, ammonium chloride, etc.), an organic nitrogen source (e. g. yeast extract, malt extract, peptone, etc.) and inorganic nutrient sources (e. g. phosphate, magnesium, potassium, zinc, iron, etc.). Optionally, an inducer (e. g. cellulose, pectin, xylan, maltose, maltodextrin or xylogalacturonan) may be included.

[0216] The selection of the appropriate medium may be based on the choice of expression host and/or based on the regulatory requirements of the expression construct. Such media are known to those skilled in the art. The medium may, if desired, contain additional components favoring the transformed expression hosts over other potentially contaminating microorganisms.

[0217] The fermentation can be performed over a period of from about 0.5 to about 30 days. It may be a batch, continuous or fed-batch process, suitably at a temperature in the range of 0-100°C or 0-80°C, for example, from about 0 to about 50°C and/or at a pH, for example, from about 2 to about 10. Preferred fermentation conditions are a temperature in the range of from about 20 to about 45°C and/or at a pH of from about 3 to about 9. The appropriate conditions are usually selected based on the choice of the expression host and the protein to be expressed.

[0218] After fermentation, if necessary, the cells can be removed from the fermentation broth by means of centrifugation or filtration. After fermentation has stopped or after removal of the cells, the polypeptide of the invention may then be recovered and, if desired, purified and isolated by conventional means.

Polypeptide/enzyme compositions

[0219] The invention provides a composition comprising a polypeptide of the invention and a cellulase and/or a hemicellulase and/or a pectinase and/or ligninase or a lignin-modifying enzyme.

[0220] When the polypeptide of the invention is a cellulase, a composition of the invention will typically comprise a hemicellulase and/or a pectinase and/or ligninase or a lignin-modifying enzyme in addition to the polypeptide of the invention.

[0221] When the polypeptide of the invention is a hemicellulase, a composition of the invention will typically comprise a cellulase and/or a pectinase and/or ligninase or a lignin-modifying enzyme in addition to the polypeptide of the invention.

[0222] When the polypeptide of the invention is a pectinase, a composition of the invention will typically comprise a cellulase and/or a hemicellulase and/or ligninase or a lignin-modifying enzyme in addition to the polypeptide of the invention.

[0223] When the polypeptide of the invention is a ligninase or a lignin-modifying enzyme, a composition of the invention will typically comprise a cellulase and/or a hemicellulase and/or a pectinase in addition to the polypeptide of the invention.

[0224] A composition of the invention may comprise one, two or three or more classes of cellulase, for example one, two or all of a GH61, an endo-1,4- β -glucanase (EG), an exo-cellobiohydrolase (CBH) and a β -glucosidase (BGL).

[0225] A composition of the invention may comprise a polypeptide which has the same enzymatic activity, for example the same type of cellulase, hemicellulase and/or pectinase activity as that provided by a polypeptide of the invention.

[0226] A composition of the invention may comprise a polypeptide which has a different type of cellulase activity and/or hemicellulase activity and/or pectinase activity than that provided by a polypeptide of the invention. For example, a composition of the invention may comprise one type of cellulase and/or hemicellulase activity and/or pectinase activity provided by a polypeptide of the invention and a second type of cellulase and/or hemicellulase activity and/or pectinase activity provided by an additional hemicellulase/pectinase.

[0227] Herein, a cellulase is any polypeptide which is capable of degrading or cellulose. A polypeptide which is capable of degrading cellulose is one which is capable of catalysing the process of breaking down cellulose into smaller units, either partially, for example into cellodextrins, or completely into glucose monomers. A cellulase according to the invention may give rise to a mixed population of cellodextrins and glucose monomers when contacted with the cellulase. Such degradation will typically take place by way of a hydrolysis reaction.

[0228] Herein, a hemicellulase is any polypeptide which is capable of degrading or hemicellulose. That is to say, a hemicellulase may be capable of degrading or one or more of xylan, glucuronoxylan, arabinoxylan, glucomannan and xyloglucan. A polypeptide which is capable of degrading a hemicellulose is one which is capable of catalysing the process of breaking down the hemicellulose into smaller polysaccharides, either partially, for example into oligosaccharides, or completely into sugar monomers, for example hexose or pentose sugar monomers. A hemicellulase according to the invention may give rise to a mixed population of oligosaccharides and sugar monomers when contacted with the hemicellulase. Such degradation will typically take place by way of a hydrolysis reaction.

[0229] Herein, a pectinase is any polypeptide which is capable of degrading or pectin. A polypeptide which is capable of degrading pectin is one which is capable of catalysing the process of breaking down pectin into smaller units, either partially, for example into oligosaccharides, or completely into sugar monomers. A pectinase according to the invention may give rise to a mixed population of oligosaccharides and sugar monomers when contacted with the pectinase. Such degradation will typically take place by way of a hydrolysis reaction.

[0230] Herein, a ligninase or a lignin-modifying enzyme is any polypeptide which is capable of

degrading or modifying lignin or degradation components thereof. A polypeptide which is capable of degrading or modifying lignin is one which is capable of catalysing the process of breaking down lignin into smaller units, either partially, for example into monophenolic compounds. A ligninase or a lignin-modifying enzyme according to the invention may give rise to a mixed population of phenolic compounds when contacted with the lignin. Such degradation will typically take place by way of an oxidation reaction. Herein, a ligninase or a lignin-modifying enzyme may also be any polypeptide which is capable of degrading phenolic degradation products of lignin. A polypeptide which is capable of degrading phenolic degradation products of lignin is one which is capable of catalysing the process of breaking down phenolic degradation products of lignin into even smaller units, for example by catalysing a ring opening reaction of the phenolic ring. A ligninase or a lignin-modifying enzyme according to the invention may give rise to a mixed population of ring-opened degradation products of phenolic compounds when contacted with the phenolic degradation products of lignin. Such degradation will typically take place by way of an oxidation reaction. The ligninase or lignin-modifying enzyme may further be capable of breaking linkages between cellulose or hemicellulose and the lignin or degradation products thereof. Enzymes that can break down lignin include lignin peroxidases, manganese peroxidases, laccases and feruloyl esterases, and other enzymes described in the art known to depolymerize or otherwise break lignin polymers. Also included are enzymes capable of hydrolyzing bonds formed between hemicellulosic sugars (notably arabinose) and lignin. Ligninases include but are not limited to the following group of enzymes: lignin peroxidases (EC 1.11.14), manganese peroxidases (EC 1.11.1.13), laccases (EC 1.10.3.2) and feruloyl esterases (EC 3.1.1.73).

[0231] Accordingly, a composition of the invention may comprise any cellulase, for example, a GH61, a cellobiohydrolase, an endo- β -1,4-glucanase, a β -glucosidase or a β -(1,3)(1,4)-glucanase.

[0232] GH61 (glycoside hydrolase family 61 or sometimes referred to EGIV) proteins are oxygen-dependent polysaccharide monooxygenases (PMO's) according to the latest literature. Often in literature these proteins are mentioned to enhance the action of cellulases on lignocellulose substrates. GH61 was originally classified as endoglucanase based on measurement of very weak endo-1,4- β -D-glucanase activity in one family member. The term "GH61" as used herein, is to be understood as a family of enzymes, which share common conserved sequence portions and foldings to be classified in family 61 of the well-established CAZY GH classification system (<http://www.cazy.org/GH61.html>). The glycoside hydrolase family 61 is a member of the family of glycoside hydrolases EC 3.2.1. GH61 is used herein as being part of the cellulases.

[0233] Herein, a cellobiohydrolase (EC 3.2.1.91) is any polypeptide which is capable of catalysing the hydrolysis of 1,4- β -D-glucosidic linkages in cellulose or cellotetraose, releasing cellobiose from the non-reducing ends of the chains. This enzyme may also be referred to as cellulase 1,4- β -cellobiosidase, 1,4- β -cellobiohydrolase, 1,4- β -D-glucan cellobiohydrolase, avicelase, exo-1,4- β -D-glucanase, exocellobiohydrolase or exoglucanase. It may have the EC code EC 3.2.1.91.

[0234] Herein, an endo- β -1,4-glucanase (EC 3.2.1.4) is any polypeptide which is capable of catalysing the endohydrolysis of 1,4- β -D-glucosidic linkages in cellulose, lichenin or cereal β -D-glucans. Such a polypeptide may also be capable of hydrolyzing 1,4-linkages in β -D-glucans also containing 1,3-linkages. This enzyme may also be referred to as cellulase, avicelase, β -1,4-endoglucan hydrolase, β -1,4-glucanase, carboxymethyl cellulase, celludextrinase, endo-1,4- β -D-glucanase, endo-1,4- β -D-glucanohydrolase, endo-1,4- β -glucanase or endoglucanase. The endo-glucanase may also catalyze the cleavage of xyloglucan, a backbone of P1 $\rightarrow$ 4-linked glucose residues, most of which substituted with 1-6 linked xylose side chains, and the enzyme is then referred to as a xyloglucan-specific endo- β -1,4-glucanase or a xyloglucanase.

[0235] Herein, a β -glucosidase (EC 3.2.1.21) is any polypeptide which is capable of catalysing the hydrolysis of terminal, non-reducing β -D-glucose residues with release of β -D-glucose. Such a polypeptide may have a wide specificity for β -D-glucosides and may also hydrolyze one or more of the following: a β -D-galactoside, an α -L-arabinoside, a β -D-xyloside or a β -D-fucoside. This enzyme may also be referred to as amygdalase, β -D-glucoside glucohydrolase, cellobiase or gentobiase.

[0236] Herein a β -(1,3)(1,4)-glucanase (EC 3.2.1.73) is any polypeptide which is capable of catalyzing the hydrolysis of 1,4- β -D-glucosidic linkages in β -D-glucans containing 1,3- and 1,4-bonds. Such a polypeptide may act on lichenin and cereal β -D-glucans, but not on β -D-glucans containing only 1,3- or 1,4-bonds. This enzyme may also be referred to as licheninase, 1,3-1,4- β -D-glucan 4-glucanohydrolase, β -glucanase, endo- β -1,3-1,4 glucanase, lichenase or mixed linkage β -glucanase. An alternative for this type of enzyme is EC 3.2.1.6, which is described as endo-1,3(4)-beta-glucanase. This type of enzyme hydrolyses 1,3- or 1,4-linkages in beta-D-glucans when the glucose residue whose reducing group is involved in the linkage to be hydrolyzed is itself substituted at C-3. Alternative names include endo-1,3-beta-glucanase, laminarinase, 1,3-(1,3;1,4)-beta-D-glucan 3 (4) glucanohydrolase; substrates include laminarin, lichenin and cereal beta-D-glucans.

[0237] A composition of the invention may comprise any hemicellulase, for example, an endo-xylanase, a β -xylosidase, a α -L-arabionofuranosidase, an α -D-glucuronidase, a cellobiohydrolase, a feruloyl esterase, a coumaroyl esterase, an α -galactosidase, a β -galactosidase, a β -mannanase or a β -mannosidase.

[0238] Herein, an endoxylanase (EC 3.2.1.8) is any polypeptide which is capable of catalyzing the endo-hydrolysis of 1,4- β -D-xylosidic linkages in xylans. This enzyme may also be referred to as endo-1,4- β -xylanase or 1,4- β -D-xylan xylanohydrolase. An alternative is EC 3.2.1.136, a glucuronoarabinoxylan endoxylanase, an enzyme that is able to hydrolyze 1,4 xylosidic linkages in glucuronoarabinoxylans.

[0239] Herein, a β -xylosidase (EC 3.2.1.37; GH3) is any polypeptide which is capable of catalyzing the hydrolysis of 1,4- β -D-xylans, to remove successive D-xylose residues from the non-reducing termini. Such enzymes may also hydrolyze xylobiose. This enzyme may also be

referred to as xylan 1,4- β -xylosidase, 1,4- β -D-xylan xylohydrolase, exo-1,4- β -xylosidase or xylobiase.

[0240] Herein, an α -L-arabinofuranosidase (EC 3.2.1.55) is any polypeptide which is capable of acting on α -L-arabinofuranosides, α -L-arabinans containing (1,2) and/or (1,3)- and/or (1,5)-linkages, arabinoxylans and arabinogalactans. This enzyme may also be referred to as α -N-arabinofuranosidase, arabinofuranosidase or arabinosidase.

[0241] Herein, an α -D-glucuronidase (EC 3.2.1.139) is any polypeptide which is capable of catalyzing a reaction of the following form: α -D-glucuronoside + H(2)O = an alcohol + D-glucuronate. This enzyme may also be referred to as α -glucuronidase or α -glucosiduronase. These enzymes may also hydrolyze 4-O-methylated glucuronic acid, which can also be present as a substituent in xylans. Alternative is EC 3.2.1.131: xylan α -1,2-glucuronosidase, which catalyses the hydrolysis of α -1,2-(4-O-methyl)glucuronosyl links.

[0242] Herein, an acetyl xylan esterase (EC 3.1.1.72) is any polypeptide which is capable of catalyzing the deacetylation of xylans and xylo-oligosaccharides. Such a polypeptide may catalyze the hydrolysis of acetyl groups from polymeric xylan, acetylated xylose, acetylated glucose, α -naphthyl acetate or p-nitrophenyl acetate but, typically, not from triacetyl glycerol. Such a polypeptide typically does not act on acetylated mannan or pectin.

[0243] Herein, a feruloyl esterase (EC 3.1.1.73) is any polypeptide which is capable of catalyzing a reaction of the form: feruloyl-saccharide + H(2)O = ferulate + saccharide. The saccharide may be, for example, an oligosaccharide or a polysaccharide. It may typically catalyze the hydrolysis of the 4-hydroxy-3-methoxycinnamoyl (feruloyl) group from an esterified sugar, which is usually arabinose in 'natural' substrates. p-nitrophenol acetate and methyl ferulate are typically poorer substrates. This enzyme may also be referred to as cinnamoyl ester hydrolase, ferulic acid esterase or hydroxycinnamoyl esterase. It may also be referred to as a hemicellulase accessory enzyme, since it may help xylanases and pectinases to break down plant cell wall hemicellulose and pectin.

[0244] Herein, a coumaroyl esterase (EC 3.1.1.73) is any polypeptide which is capable of catalyzing a reaction of the form: coumaroyl-saccharide + H(2)O = coumarate + saccharide. The saccharide may be, for example, an oligosaccharide or a polysaccharide. This enzyme may also be referred to as trans-4-coumaroyl esterase, trans-p-coumaroyl esterase, p-coumaroyl esterase or p-coumaric acid esterase. This enzyme also falls within EC 3.1.1.73 so may also be referred to as a feruloyl esterase.

[0245] Herein, an α -galactosidase (EC 3.2.1.22) is any polypeptide which is capable of catalyzing the hydrolysis of terminal, non-reducing α -D-galactose residues in α -D-galactosides, including galactose oligosaccharides, galactomannans, galactans and arabinogalactans. Such a polypeptide may also be capable of hydrolyzing α -D-fucosides. This enzyme may also be referred to as melibiase.

[0246] Herein, a β -galactosidase (EC 3.2.1.23) is any polypeptide which is capable of catalyzing the hydrolysis of terminal non-reducing β -D-galactose residues in β -D-galactosides. Such a polypeptide may also be capable of hydrolyzing α -L-arabinosides. This enzyme may also be referred to as exo-(1 $\rightarrow$ 4)- β -D-galactanase or lactase.

[0247] Herein, a β -mannanase (EC 3.2.1.78) is any polypeptide which is capable of catalyzing the random hydrolysis of 1,4- β -D-mannosidic linkages in mannans, galactomannans and glucomannans. This enzyme may also be referred to as mannan endo-1,4- β -mannosidase or endo-1,4-mannanase.

[0248] Herein, a β -mannosidase (EC 3.2.1.25) is any polypeptide which is capable of catalyzing the hydrolysis of terminal, non-reducing β -D-mannose residues in β -D-mannosides. This enzyme may also be referred to as mannanase or mannase.

[0249] A composition of the invention may comprise any pectinase, for example an endo polygalacturonase, a pectin methyl esterase, an endo-galactanase, a beta galactosidase, a pectin acetyl esterase, an endo-pectin lyase, pectate lyase, alpha rhamnosidase, an exo-galacturonase, an exo-polygalacturonate lyase, a rhamnogalacturonan hydrolase, a rhamnogalacturonan lyase, a rhamnogalacturonan acetyl esterase, a rhamnogalacturonan galacturonohydrolase or a xylogalacturonase.

[0250] Herein, an endo-polygalacturonase (EC 3.2.1.15) is any polypeptide which is capable of catalyzing the random hydrolysis of 1,4- α -D-galactosiduronic linkages in pectate and other galacturonans. This enzyme may also be referred to as polygalacturonase pectin depolymerase, pectinase, endopolygalacturonase, pectolase, pectin hydrolase, pectin polygalacturonase, poly- α -1,4-galacturonide glycanohydrolase, endogalacturonase; endo-D-galacturonase or poly(1,4- α -D-galacturonide) glycanohydrolase.

[0251] Herein, a pectin methyl esterase (EC 3.1.1.11) is any enzyme which is capable of catalyzing the reaction: pectin + n H₂O = n methanol + pectate. The enzyme may also be known as pectinesterase, pectin demethoxylase, pectin methoxylase, pectin methylesterase, pectase, pectinoesterase or pectin pectylhydrolase.

[0252] Herein, an endo-galactanase (EC 3.2.1.89) is any enzyme capable of catalyzing the endohydrolysis of 1,4- β -D-galactosidic linkages in arabinogalactans. The enzyme may also be known as arabinogalactan endo-1,4- β -galactosidase, endo-1,4- β -galactanase, galactanase, arabinogalactanase or arabinogalactan 4- β -D-galactanohydrolase.

[0253] Herein, a pectin acetyl esterase is defined herein as any enzyme which has an acetyl esterase activity which catalyzes the deacetylation of the acetyl groups at the hydroxyl groups of GalUA residues of pectin

[0254] Herein, an endo-pectin lyase (EC 4.2.2.10) is any enzyme capable of catalyzing the eliminative cleavage of (1 $\rightarrow$ 4)- α -D-galacturonan methyl ester to give oligosaccharides with 4-

deoxy-6-O-methyl- α -D-galact-4-enuronosyl groups at their non-reducing ends. The enzyme may also be known as pectin lyase, pectin trans-eliminase; endo-pectin lyase, polymethylgalacturonic transeliminase, pectin methyltranseliminase, pectolyase, PL, PNL or PMGL or (1 $\rightarrow$ 4)-6-O-methyl- α -D-galacturonan lyase.

[0255] Herein, a pectate lyase (EC 4.2.2.2) is any enzyme capable of catalyzing the eliminative cleavage of (1 $\rightarrow$ 4)- α -D-galacturonan to give oligosaccharides with 4-deoxy- α -D-galact-4-enuronosyl groups at their non-reducing ends. The enzyme may also be known polygalacturonic transeliminase, pectic acid transeliminase, polygalacturonate lyase, endopectin methyltranseliminase, pectate transeliminase, endogalacturonate transeliminase, pectic acid lyase, pectic lyase, α -1,4-D-endopolygalacturonic acid lyase, PGA lyase, PPase-N, endo- α -1,4-polygalacturonic acid lyase, polygalacturonic acid lyase, pectin trans-eliminase, polygalacturonic acid trans-eliminase or (1 $\rightarrow$ 4)- α -D-galacturonan lyase.

[0256] Herein, an alpha rhamnosidase (EC 3.2.1.40) is any polypeptide which is capable of catalyzing the hydrolysis of terminal non-reducing α -L-rhamnose residues in α -L-rhamnosides or alternatively in rhamnogalacturonan. This enzyme may also be known as α -L-rhamnosidase T, α -L-rhamnosidase N or α -L-rhamnoside rhamnohydrolase.

[0257] Herein, exo-galacturonase (EC 3.2.1.82) is any polypeptide capable of hydrolysis of pectic acid from the non-reducing end, releasing digalacturonate. The enzyme may also be known as exo-poly- α -galacturonosidase, exopolygalacturonosidase or exopolygalacturanosidase.

[0258] Herein, exo-galacturonase (EC 3.2.1.67) is any polypeptide capable of catalyzing: (1,4- α -D-galacturonide)_n + H₂O = (1,4- α -D-galacturonide)_{n-1} + D-galacturonate. The enzyme may also be known as galacturan 1,4- α -galacturonidase, exopolygalacturonase, poly(galacturonate) hydrolase, exo-D-galacturonase, exo-D-galacturonanase, exo-poly-D-galacturonase or poly(1,4- α -D-galacturonide) galacturonohydrolase.

[0259] Herein, exo-polygalacturonate lyase (EC 4.2.2.9) is any polypeptide capable of catalyzing eliminative cleavage of 4-(4-deoxy- α -D-galact-4-enuronosyl)-D-galacturonate from the reducing end of pectate, i.e. de-esterified pectin. This enzyme may be known as pectate disaccharide-lyase, pectate exo-lyase, exopectic acid transeliminase, exo-pectate lyase, exopolygalacturonic acid-trans-eliminase, PATE, exo-PATE, exo-PGL or (1 $\rightarrow$ 4)- α -D-galacturonan reducing-end-disaccharide-lyase.

[0260] Herein, rhamnogalacturonan hydrolase is any polypeptide which is capable of hydrolyzing the linkage between galactosyluronic acid and rhamnopyranosyl in an endo-fashion in strictly alternating rhamnogalacturonan structures, consisting of the disaccharide [(1,2- α -L-rhamnoyl-(1,4)- α -galactosyluronic acid)].

[0261] Herein, rhamnogalacturonan lyase is any polypeptide which is any polypeptide which is capable of cleaving α -L-Rhap-(1 $\rightarrow$ 4)- α -D-GalpA linkages in an endo-fashion in

rhamnogalacturonan by beta-elimination.

[0262] Herein, rhamnogalacturonan acetyl esterase is any polypeptide which catalyzes the deacetylation of the backbone of alternating rhamnose and galacturonic acid residues in rhamnogalacturonan.

[0263] Herein, rhamnogalacturonan galacturonohydrolase is any polypeptide which is capable of hydrolyzing galacturonic acid from the non-reducing end of strictly alternating rhamnogalacturonan structures in an exo-fashion.

[0264] Herein, xylogalacturonase is any polypeptide which acts on xylogalacturonan by cleaving the β -xylose substituted galacturonic acid backbone in an endo-manner. This enzyme may also be known as xylogalacturonan hydrolase.

[0265] Herein, an α -L-arabinofuranosidase (EC 3.2.1.55) is any polypeptide which is capable of acting on α -L-arabinofuranosides, α -L-arabinans containing (1,2) and/or (1,3)- and/or (1,5)-linkages, arabinoxylans and arabinogalactans. This enzyme may also be referred to as α -N-arabinofuranosidase, arabinofuranosidase or arabinosidase.

[0266] Herein, endo-arabinanase (EC 3.2.1.99) is any polypeptide which is capable of catalyzing endohydrolysis of 1,5- α -arabinofuranosidic linkages in 1,5-arabinans. The enzyme may also be known as endo-arabinase, arabinan endo-1,5- α -L-arabinosidase, endo-1,5- α -L-arabinanase, endo- α -1,5-arabanase; endo-arabanase or 1,5- α -L-arabinan 1,5- α -L-arabinanohydrolase.

[0267] A composition of the invention will typically comprise at least one cellulase and/or at least one hemicellulase and/or at least one pectinase (one of which is a polypeptide according to the invention). A composition of the invention may comprise a cellobiohydrolase, an endoglucanase and/or a β -glucosidase. Such a composition may also comprise one or more hemicellulases and/or one or more pectinases.

[0268] One or more (for example two, three, four or all) of an amylase, a protease, a lipase, a ligninase, a hexosyltransferase or a glucuronidase may be present in a composition of the invention.

[0269] "Protease" includes enzymes that hydrolyze peptide bonds (peptidases), as well as enzymes that hydrolyze bonds between peptides and other moieties, such as sugars (glycopeptidases). Many proteases are characterized under EC 3.4, and are suitable for use in the invention incorporated herein by reference. Some specific types of proteases include, cysteine proteases including pepsin, papain and serine proteases including chymotrypsins, carboxypeptidases and metalloendopeptidases.

[0270] "Lipase" includes enzymes that hydrolyze lipids, fatty acids, and acylglycerides, including phosphoglycerides, lipoproteins, diacylglycerols, and the like. In plants, lipids are used

as structural components to limit water loss and pathogen infection. These lipids include waxes derived from fatty acids, as well as cutin and suberin.

[0271] "Hexosyltransferase" (2.4.1-) includes enzymes which are capable of transferring glycosyl groups, more specifically hexosyl groups. In addition to transfer of a glycosyl-group from a glycosyl-containing donor to another glycosyl-containing compound, the acceptor, the enzymes can also transfer the glycosyl-group to water as an acceptor. This reaction is also known as a hydrolysis reaction, instead of a transfer reaction. An example of a hexosyltransferase which may be used in the invention is a β -glucanosyltransferase. Such an enzyme may be able to catalyze degradation of (1,3)(1,4)glucan and/or cellulose and/or a cellulose degradation product.

[0272] "Glucuronidase" includes enzymes that catalyze the hydrolysis of a glucuronoside, for example β -glucuronoside to yield an alcohol. Many glucuronidases have been characterized and may be suitable for use in the invention, for example β -glucuronidase (EC 3.2.1.31), hyaluronoglucuronidase (EC 3.2.1.36), glucuronosyl-disulfoglucosamine glucuronidase (3.2.1.56), glycyrrhizinate β -glucuronidase (3.2.1.128) or α -D-glucuronidase (EC 3.2.1.139).

[0273] A composition of the invention may comprise an expansin or expansin-like protein, such as a swollenin (see Salheimo et al., Eur. J. Biochem. 269, 4202-4211, 2002) or a swollenin-like protein.

[0274] Expansins are implicated in loosening of the cell wall structure during plant cell growth. Expansins have been proposed to disrupt hydrogen bonding between cellulose and other cell wall polysaccharides without having hydrolytic activity. In this way, they are thought to allow the sliding of cellulose fibers and enlargement of the cell wall. Swollenin, an expansin-like protein contains an N-terminal Carbohydrate Binding Module Family 1 domain (CBD) and a C-terminal expansin-like domain. For the purposes of this invention, an expansin-like protein or swollenin-like protein may comprise one or both of such domains and/or may disrupt the structure of cell walls (such as disrupting cellulose structure), optionally without producing detectable amounts of reducing sugars.

[0275] A composition of the invention may comprise the polypeptide product of a cellulose integrating protein, scaffoldin or a scaffoldin-like protein, for example CipA or CipC from *Clostridium thermocellum* or *Clostridium cellulolyticum* respectively.

[0276] Scaffoldins and cellulose integrating proteins are multi-functional integrating subunits which may organize cellulolytic subunits into a multi-enzyme complex. This is accomplished by the interaction of two complementary classes of domain, i.e. a cohesion domain on scaffoldin and a dockerin domain on each enzymatic unit. The scaffoldin subunit also bears a cellulose-binding module (CBM) that mediates attachment of the cellulosome to its substrate. A scaffoldin or cellulose integrating protein for the purposes of this invention may comprise one or both of such domains.

[0277] A composition of the invention may comprise a cellulose induced protein or modulating protein, for example as encoded by cip1 or cip2 gene or similar genes from *Trichoderma reesei* / *Hypocrea jecorina* (see Foreman et al., J. Biol. Chem. 278(34), 31988-31997, 2003). The polypeptide product of these genes are bimodular proteins, which contain a cellulose binding module and a domain which function or activity can not be related to known glycosyl hydrolase families. Yet, the presence of a cellulose binding module and the co-regulation of the expression of these genes with cellulases components indicates previously unrecognized activities with potential role in biomass degradation.

[0278] A composition of the invention may be composed of a member of each of the classes of the polypeptides mentioned above, several members of one polypeptide class, or any combination of these polypeptide classes.

[0279] A composition of the invention may be composed of polypeptides, for example enzymes, from (1) commercial suppliers; (2) cloned genes expressing polypeptides, for example enzymes; (3) complex broth (such as that resulting from growth of a microbial strain in media, wherein the strains secrete proteins and enzymes into the media; (4) cell lysates of strains grown as in (3); and/or (5) plant material expressing polypeptides, for example enzymes. Different polypeptides, for example enzymes in a composition of the invention may be obtained from different sources.

Use of the polypeptides

[0280] The polypeptides and polypeptide compositions according to the invention may be used in many different applications. For instance, they may be used to produce fermentable sugars. The fermentable sugars can then, as part of a biofuel process, be converted into biogas or ethanol, butanol, isobutanol, 2 butanol or other suitable substances. Alternatively, the polypeptides and their compositions may be used as enzyme, for instance in production of food products, in detergent compositions, in the paper and pulp industry and in antibacterial formulations, in pharmaceutical products such as throat lozenges, toothpastes, and mouthwash. Some of the uses will be illustrated in more detail below.

[0281] In the uses and methods described below, the components of the compositions described above may be provided concomitantly (i.e. as a single composition per se) or separately or sequentially.

[0282] The invention also relates to the use of the cellobiohydrolase according to the invention and compositions comprising such an enzyme in industrial processes.

[0283] Despite the long-term experience obtained with these processes, the cellobiohydrolase according to the invention may feature a number of significant advantages over enzymes currently used. Depending on the specific application, these advantages may include aspects such as lower production costs, higher specificity towards the substrate, reduced antigenicity,

fewer undesirable side activities, higher yields when produced in a suitable microorganism, more suitable pH and temperature ranges, non-inhibition by hydrophobic, lignin-derived products or less product inhibition or, in the case of the food industry a better taste or texture of a final product as well as food grade and kosher aspects.

[0284] In principle, a cellobiohydrolase or composition of the invention may be used in any process which requires the treatment of a material which comprises polysaccharide.

[0285] Thus, a polypeptide or composition of the invention may be used in the treatment of polysaccharide material. Herein, polysaccharide material is a material which comprises or consists essential of one or, more typically, more than one polysaccharide.

[0286] Typically, plants and material derived therefrom comprise significant quantities of non-starch polysaccharide material. Accordingly, a polypeptide of the invention may be used in the treatment of a plant or fungal material or a material derived therefrom.

Lignocellulose

[0287] An important component of plant non-starch polysaccharide material is lignocellulose (also referred to herein as lignocellulolytic biomass). Lignocellulose is plant material that comprises cellulose and hemicellulose and lignin. The carbohydrate polymers (cellulose and hemicelluloses) are tightly bound to the lignin by hydrogen and covalent bonds. Accordingly, a polypeptide of the invention may be used in the treatment of lignocellulolytic material. Herein, lignocellulolytic material is a material which comprises or consists essential of lignocellulose. Thus, in a method of the invention for the treatment of a non-starch polysaccharide, the non-starch polysaccharide may be a lignocellulosic material/biomass.

[0288] Accordingly, the invention provides a method of treating a substrate comprising non-starch polysaccharide in which the treatment comprises the degradation and/or hydrolysis and/or modification of cellulose and/or hemicellulose and/or a pectic substance.

[0289] Degradation in this context indicates that the treatment results in the generation of hydrolysis products of cellulose and/or hemicellulose and/or a pectic substance, i.e. saccharides of shorter length are present as result of the treatment than are present in a similar untreated non-starch polysaccharide. Thus, degradation in this context may result in the liberation of oligosaccharides and/or sugar monomers.

[0290] All plants contain non-starch polysaccharide as do virtually all plant-derived polysaccharide materials. Accordingly, in a method of the invention for the treatment of substrate comprising a non-starch polysaccharide, said substrate may be provided in the form of a plant or a plant derived material or a material comprising a plant or plant derived material, for example a plant pulp, a plant extract, a foodstuff or ingredient therefore, a fabric, a textile or an item of clothing.

[0291] Lignocellulolytic biomass suitable for use in the invention includes biomass and can include virgin biomass and/or non-virgin biomass such as agricultural biomass, commercial organics, construction and demolition debris, municipal solid waste, waste paper and yard waste. Common forms of biomass include trees, shrubs and grasses, wheat, wheat straw, sugar cane bagasse, corn, corn husks, corn cobs, corn kernel including fiber from kernels, products and by-products from milling of grains such as corn, wheat and barley (including wet milling and dry milling) often called "bran or fiber" as well as municipal solid waste, waste paper and yard waste. The biomass can also be, but is not limited to, herbaceous material, agricultural residues, forestry residues, municipal solid wastes, waste paper, and pulp and paper mill residues. "Agricultural biomass" includes branches, bushes, canes, corn and corn husks, energy crops, forests, fruits, flowers, grains, grasses, herbaceous crops, leaves, bark, needles, logs, roots, saplings, short rotation woody crops, shrubs, switch grasses, trees, vegetables, fruit peels, vines, sugar beet pulp, wheat middlings, oat hulls, and hard and soft woods (not including woods with deleterious materials). In addition, agricultural biomass includes organic waste materials generated from agricultural processes including farming and forestry activities, specifically including forestry wood waste. Agricultural biomass may be any of the aforesaid singularly or in any combination or mixture thereof. Further examples of suitable biomass are orchard primings, chaparral, mill waste, urban wood waste, municipal waste, logging waste, forest thinnings, short- rotation woody crops, industrial waste, wheat straw, oat straw, rice straw, barley straw, rye straw, flax straw, soy hulls, rice hulls, rice straw, corn gluten feed, oat hulls, sugar cane, corn stover, corn stalks, corn cobs, corn husks, prairie grass, gamagrass, foxtail; sugar beet pulp, citrus fruit pulp, seed hulls, cellulosic animal wastes, lawn clippings, cotton, seaweed, trees, shrubs, grasses, wheat, wheat straw, sugar cane bagasse, corn, corn husks, corn hobs, corn kernel, fiber from kernels, products and by-products from wet or dry milling of grains, municipal solid waste, waste paper, yard waste, herbaceous material, agricultural residues, forestry residues, municipal solid waste, waste paper, pulp, paper mill residues, branches, bushes, canes, corn, corn husks, an energy crop, forest, a fruit, a flower, a grain, a grass, a herbaceous crop, a leaf, bark, a needle, a log, a root, a sapling, a shrub, switch grass, a tree, a vegetable, fruit peel, a vine, sugar beet pulp, wheat middlings, oat hulls, hard or soft wood, organic waste material generated from an agricultural process, forestry wood waste, or a combination of any two or more thereof.

[0292] Apart from virgin biomass or feedstocks already processed in food and feed or paper and pulping industries, the biomass/feedstock may additionally be pretreated with heat, mechanical and/or chemical modification or any combination of such methods in order to enhance enzymatic degradation.

Pretreatment

[0293] Before enzymatic treatment, the feedstock may optionally be pre-treated with heat, mechanical and/or chemical modification or any combination of such methods in order to enhance the accessibility of the substrate to enzymatic hydrolysis and/or hydrolyse the

hemicellulose and/or solubilize the hemicellulose and/or cellulose and/or lignin, in any way known in the art. The pretreatment may comprise exposing the lignocellulosic material to (hot) water, steam (steam explosion), an acid, a base, a solvent, heat, a peroxide, ozone, mechanical shredding, grinding, milling or rapid depressurization, or a combination of any two or more thereof. This chemical pretreatment is often combined with heat-pretreatment, e.g. between 150-220 °C for 1 to 30 minutes.

Presaccharification

[0294] After the pretreatment step, a liquefaction/hydrolysis or presaccharification step involving incubation with an enzyme or enzyme mixture can be utilized. The presaccharification step can be performed at many different temperatures but it is preferred that the presaccharification step occur at the temperature best suited to the enzyme mix being tested, or the predicted enzyme optimum of the enzymes to be tested. The temperature of the presaccharification step may range from about 10 °C to about 95 °C, about 20 °C to about 85 °C, about 30 °C to about 70 °C, about 40 °C to about 60 °C, about 37 °C to about 50 °C, preferably about 37 °C to about 80 °C, more preferably about 60-70°C even more preferably around 65° C. The pH of the presaccharification mixture may range from about 2.0 to about 10.0, but is preferably about 3.0 to about 7.0, more preferably about 4.0 to about 6.0, even more preferably about 4.0 to about 5.0. Again, the pH may be adjusted to maximize enzyme activity and may be adjusted with the addition of the enzyme. Comparison of the results of the assay results from this test will allow one to modify the method to best suit the enzymes being tested.

[0295] The liquefaction/hydrolysis or presaccharification step reaction may occur from several minutes to several hours, such as from about 1 hour to about 120 hours, preferably from about 2 hours to about 48 hours, more preferably from about 2 to about 24 hours, most preferably for from about 2 to about 6 hours. The cellulase treatment may occur from several minutes to several hours, such as from about 6 hours to about 120 hours, preferably about 12 hours to about 72 hours, more preferably about 24 to 48 hours.

Saccharification

[0296] The invention provides a method for producing a sugar from a lignocellulosic material which method comprises contacting a polypeptide of the invention to a composition of the invention with the lignocellulosic material.

[0297] Such a method allows free sugars (monomers) and/or oligosaccharides to be generated from lignocellulosic biomass. These methods involve converting lignocellulosic biomass to free sugars and small oligosaccharides with a polypeptide or composition of the invention.

[0298] The process of converting a complex carbohydrate such as lignocellulose into sugars preferably allows conversion into fermentable sugars. Such a process may be referred to as "saccharification." Accordingly, a method of the invention may result in the liberation of one or more hexose and/or pentose sugars, such as one or more of glucose, xylose, arabinose, galactose, galacturonic acid, glucuronic acid, mannose, rhamnose, ribose and fructose.

[0299] Accordingly, another aspect of the invention includes methods that utilize the polypeptide of composition of the invention described above together with further enzymes or physical treatments such as temperature and pH to convert the lignocellulosic plant biomass to sugars and oligosaccharides.

[0300] While the composition has been discussed as a single mixture it is recognized that the enzymes may be added sequentially where the temperature, pH, and other conditions may be altered to increase the activity of each individual enzyme. Alternatively, an optimum pH and temperature can be determined for the enzyme mixture.

[0301] The enzymes are reacted with substrate under any appropriate conditions. For example, enzymes can be incubated at about 25°C, about 30 °C, about 35 °C, about 37 °C, about 40 °C, about 45 °C, about 50 °C, about 55 °C, about 60°C, about 65°C, about 70°C, about 75°C, about 80°C, about 85°C, about 90°C or higher. That is, they can be incubated at a temperature of from about 20°C to about 95 °C, for example in buffers of low to medium ionic strength and/or from low to neutral pH. By "medium ionic strength" is intended that the buffer has an ion concentration of about 200 millimolar (mM) or less for any single ion component. The pH may range from about pH 2.5, about pH 3.0, about pH 3.5, about pH 4.0, about pH 4.5, about pH 5, about pH 5.5, about pH 6, about pH 6.5, about pH 7, about pH 7.5, about pH 8.0, to about pH 8.5. Generally, the pH range will be from about pH 3.0 to about pH 7. For the production of ethanol an acidic medium is preferred, e.g. pH=4, whereas for the production of biogas neutral pH, e.g. pH=7 is desirable. Incubation of enzyme combinations under these conditions results in release or liberation of substantial amounts of the sugar from the lignocellulose. By substantial amount is intended at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more of available sugar.

[0302] The polypeptides, such as enzymes, can be produced either exogenously in microorganisms, yeasts, fungi, bacteria or plants, then isolated and added, for example, to lignocellulosic feedstock. Alternatively, the enzymes are produced, but not isolated, and crude cell mass fermentation broth, or plant material (such as corn stover), and the like may be added to, for example, the feedstock. Alternatively, the crude cell mass or enzyme production medium or plant material may be treated to prevent further microbial growth (for example, by heating or addition of antimicrobial agents), then added to, for example, a feedstock. These crude enzyme mixtures may include the organism producing the enzyme. Alternatively, the enzyme may be produced in a fermentation that uses feedstock (such as corn stover) to provide nutrition to an organism that produces an enzyme(s). In this manner, plants that produce the enzymes may themselves serve as a lignocellulosic feedstock and be added into lignocellulosic feedstock.

Fermentation of sugars

[0303] The fermentable sugars can be converted to useful value-added fermentation products, non-limiting examples of which include amino acids, vitamins, pharmaceuticals, animal feed supplements, specialty chemicals, chemical feedstocks, plastics, solvents, fuels, or other organic polymers, lactic acid, and ethanol, including fuel ethanol. In particular the sugars may be used as feedstocks for fermentation into chemicals, plastics, such as for instance succinic acid and (bio) fuels, including ethanol, methanol, butanol synthetic liquid fuels and biogas.

[0304] For instance, in the method of the invention, an enzyme or combination of enzymes acts on a lignocellulosic substrate or plant biomass, serving as the feedstock, so as to convert this complex substrate to simple sugars and oligosaccharides for the production of ethanol or other useful fermentation products.

[0305] Sugars released from biomass can be converted to useful fermentation products such as one of those including, but not limited to, amino acids, vitamins, pharmaceuticals, animal feed supplements, specialty chemicals, chemical feedstocks, plastics, and ethanol, including fuel ethanol.

[0306] Accordingly, the invention provides a method for the preparation of a fermentation product, which method comprises:

1. a. degrading lignocellulose using a method as described herein; and
2. b. fermentation of the resulting material,

thereby to prepare a fermentation product.

[0307] The fermentation may be carried out under aerobic or anaerobic conditions. Preferably, the process is carried out under micro-aerophilic or oxygen limited conditions.

[0308] An anaerobic fermentation process is herein defined as a fermentation process run in the absence of oxygen or in which substantially no oxygen is consumed, preferably about 5 or less, about 2.5 or less or about 1 mmol/L/h or less, and wherein organic molecules serve as both electron donor and electron acceptors.

[0309] An oxygen-limited fermentation process is a process in which the oxygen consumption is limited by the oxygen transfer from the gas to the liquid. The degree of oxygen limitation is determined by the amount and composition of the ingoing gas flow as well as the actual mixing/mass transfer properties of the fermentation equipment used. Preferably, in a process under oxygen-limited conditions, the rate of oxygen consumption is at least about 5.5, more preferably at least about 6 and even more preferably at least about 7 mmol/L/h.

[0310] A method for the preparation of a fermentation product may optionally comprise recovery of the fermentation product.

SSF

[0311] Fermentation and Saccharification may also be executed in Simultaneous Saccharification and Fermentation (SSF) mode. One of the advantages of this mode is reduction of the sugar inhibition on enzymatic hydrolysis (Sugar inhibition on cellulases is described by Caminal B&B Vol XXVII Pp 1282-1290).

Fermentation products

[0312] Fermentation products which may be produced according to the invention include amino acids, vitamins, pharmaceuticals, animal feed supplements, specialty chemicals, chemical feedstocks, plastics, solvents, fuels, or other organic polymers, lactic acid, and ethanol, including fuel ethanol (the term "ethanol" being understood to include ethyl alcohol or mixtures of ethyl alcohol and water).

[0313] Specific value-added products that may be produced by the methods of the invention include, but not limited to, biofuels (including ethanol and butanol and a biogas); lactic acid; a plastic; a specialty chemical; an organic acid, including citric acid, succinic acid, fumaric acid, itaconic acid and maleic acid; 3-hydroxy-propionic acid, acrylic acid; acetic acid; 1,3-propanediol; ethylene, glycerol; a solvent; an animal feed supplement; a pharmaceutical, such as a β -lactam antibiotic or a cephalosporin; vitamins; an amino acid, such as lysine, methionine, tryptophan, threonine, and aspartic acid; an industrial enzyme, such as a protease, a cellulase, an amylase, a glucanase, a lactase, a lipase, a lyase, an oxidoreductases, a transferase or a xylanase; and a chemical feedstock.

Biogas

[0314] The invention also provides use of a polypeptide or composition as described herein in a method for the preparation of biogas. Biogas typically refers to a gas produced by the biological breakdown of organic matter, for example non-starch carbohydrate containing material, in the absence of oxygen. Biogas originates from biogenic material and is a type of biofuel. One type of biogas is produced by anaerobic digestion or fermentation of biodegradable materials such as biomass, manure or sewage, municipal waste, and energy crops. This type of biogas is comprised primarily of methane and carbon dioxide. The gas methane can be combusted or oxidized with oxygen. Air contains 21% oxygen. This energy release allows biogas to be used as a fuel. Biogas can be used as a low-cost fuel in any country for any heating purpose, such as cooking. It can also be utilized in modern waste

management facilities where it can be used to run any type of heat engine, to generate either mechanical or electrical power.

[0315] The first step in microbial biogas production consists in the enzymatic degradation of polymers and complex substrates (for example non-starch carbohydrate). Accordingly, the invention provides a method for preparation of a biogas in which a substrate comprising non-starch carbohydrate is contacted with a polypeptide or composition of the invention, thereby to yield fermentable material which may be converted into a biogas by an organism such as a microorganism. In such a method, a polypeptide of the invention may be provided by way of an organism, for example a microorganism which expresses such a polypeptide.

Use of enzymes in food products

[0316] The polypeptides and compositions of the invention may be used in a method of processing plant material to degrade or modify the cellulose or hemicellulose or pectic substance constituents of the cell walls of the plant or fungal material. Such methods may be useful in the preparation of food product. Accordingly, the invention provides a method for preparing a food product which method comprises incorporating a polypeptide or composition of the invention during preparation of the food product.

[0317] The invention also provides a method of processing a plant material which method comprises contacting the plant material with a polypeptide or composition of the invention to degrade or modify the cellulose in the (plant) material. Preferably, the plant material is a plant pulp or plant extract, such as juices.

[0318] The present invention also provides a method for reducing the viscosity, clarity and/or filterability of a plant extract which method comprises contacting the plant extract with a polypeptide or composition of the invention in an amount effective in degrading cellulose or hemicellulose or pectic substances contained in the plant extract.

[0319] Plant and cellulose/hemicellulose/pectic substance-containing materials include plant pulp, parts of plants and plant extracts. In the context of this invention an extract from a plant material is any substance which can be derived from plant material by extraction (mechanical and/or chemical), processing or by other separation techniques. The extract may be juice, nectar, base, or concentrates made thereof. The plant material may comprise or be derived from vegetables, e. g., carrots, celery, onions, legumes or leguminous plants (soy, soybean, peas) or fruit, e. g., pome or seed fruit (apples, pears, quince etc.), grapes, tomatoes, citrus (orange, lemon, lime, mandarin), melons, prunes, cherries, black currants, redcurrants, raspberries, strawberries, cranberries, pineapple and other tropical fruits, trees and parts thereof (e. g. pollen, from pine trees), or cereal (oats, barley, wheat, maize, rice). The material (to be hydrolysed) may also be agricultural residues, such as sugar beet pulp, corn cobs, wheat straw, (ground) nutshells, or recyclable materials, e. g. (waste) paper.

[0320] The polypeptides of the invention can thus be used to treat plant material including plant pulp and plant extracts. They may also be used to treat liquid or solid foodstuffs or edible foodstuff ingredients, or be used in the extraction of coffee, plant oils, starch or as a thickener in foods.

[0321] Typically, the polypeptides of the invention are used as a composition/enzyme preparation as described above. The composition will generally be added to plant pulp obtainable by, for example mechanical processing such as crushing or milling plant material. Incubation of the composition with the plant will typically be carried out for at time of from 10 minutes to 5 hours, such as 30 minutes to 2 hours, preferably for about 1 hour. The processing temperature is preferably from about 10°C to about 55°C, e. g. from about 15°C to about 25°C, optimally about 20°C and one can use from about 10 g to about 300 g, preferably from about 30 g to about 70 g, optimally about 50 g of enzyme per ton of material to be treated.

[0322] All of the enzyme(s) or their compositions used may be added sequentially or at the same time to the plant pulp. Depending on the composition of the enzyme preparation the plant material may first be macerated (e. g. to a pure) or liquefied. Using the polypeptides of the invention processing parameters such as the yield of the extraction, viscosity of the extract and/or quality of the extract can be improved.

[0323] Alternatively, or in addition to the above, a polypeptide of the invention may be added to the raw juice obtained from pressing or liquefying the plant pulp. Treatment of the raw juice will be carried out in a similar manner to the plant pulp in respect of dosage, temperature and holding time. Again, other enzymes such as those discussed previously may be included. Typical incubation conditions are as described in the previous paragraph.

[0324] Once the raw juice has been incubated with the polypeptides of the invention, the juice is then centrifuged or (ultra) filtered to produce the final product.

[0325] After treatment with the polypeptide of the invention the (end) product can be heat treated, e.g. at about 100°C for a time of from about 1 minute to about 1 hour, under conditions to partially or fully inactivate the polypeptide(s) of the invention.

[0326] A composition containing a polypeptide of the invention may also be used during the preparation of fruit or vegetable purees.

[0327] The polypeptide of the invention may also be used in brewing, wine making, distilling or baking. It may therefore be used in the preparation of alcoholic beverages such as wine and beer. For example it may improve the filterability or clarity, for example of beers, wort (e.g. containing barley and/or sorghum malt) or wine.

[0328] Furthermore, a polypeptide or composition of the invention may be used for treatment of brewers spent grain, i.e. residuals from beer wort production containing barley or malted barley or other cereals, so as to improve the utilization of the residuals for, e.g., animal feed.

[0329] The protein may assist in the removal of dissolved organic substances from broth or culture media, for example where distillery waste from organic origin is bioconverted into microbial biomass. The polypeptide of the invention may improve filterability and/or reduce viscosity in glucose syrups, such as from cereals produced by liquefaction (e.g. with α -amylase).

[0330] In baking the polypeptide may improve the dough structure, modify its stickiness or suppleness, improve the loaf volume and/or crumb structure or impart better textural characteristics such as break, shred or crumb quality.

[0331] The present invention thus relates to methods for preparing a dough or a cereal-based food product comprising incorporating into the dough a polypeptide or composition of the present invention. This may improve one or more properties of the dough or the cereal-based food product obtained from the dough relative to a dough or a cereal-based food product in which the polypeptide is not incorporated.

[0332] The preparation of the cereal-based food product according to the invention further can comprise steps known in the art such as boiling, drying, frying, steaming or baking of the obtained dough.

[0333] Products that are made from a dough that is boiled are for example boiled noodles, dumplings, products that are made from fried dough are for example doughnuts, beignets, fried noodles, products that are made for steamed dough are for example steamed buns and steamed noodles, examples of products made from dried dough are pasta and dried noodles and examples of products made from baked dough are bread, cookies and cake.

[0334] The term "improved property" is defined herein as any property of a dough and/or a product obtained from the dough, particularly a cereal-based food product, which is improved by the action of the polypeptide according to the invention relative to a dough or product in which the polypeptide according to the invention is not incorporated. The improved property may include, but is not limited to, increased strength of the dough, increased elasticity of the dough, increased stability of the dough, improved machinability of the dough, improved proofing resistance of the dough, reduced stickiness of the dough, improved extensibility of the dough, increased volume of the cereal-based food product, reduced blistering of the cereal-based food product, improved crumb structure of the baked product, improved softness of the cereal-based food product, improved flavour of the cereal-based food product, improved anti-staling of the cereal-based food product. Improved properties related to pasta and noodle type of cereal-based products are for example improved firmness, reduced stickiness, improved cohesiveness and reduced cooking loss.

[0335] The improved property may be determined by comparison of a dough and/or a cereal-based food product prepared with and without addition of a polypeptide of the present invention. Organoleptic qualities may be evaluated using procedures well established in the

baking industry, and may include, for example, the use of a panel of trained taste-testers.

[0336] The term "dough" is defined herein as a mixture of cereal flour and other ingredients firm enough to knead or roll. Examples of cereals are wheat, rye, corn, maize, barley, rice, groats, buckwheat and oat. Wheat is here and hereafter intended to encompass all known species of *Triticum* genus, for example *aestivum*, *durum* and/or *spelt*. Examples of suitable other ingredients are: the cellobiohydrolase according to the present invention, additional enzymes, chemical additives and/or processing aids. The dough may be fresh, frozen, prepared, or pre-baked. The preparation of a dough from the ingredients described above is well known in the art and comprises mixing of said ingredients and processing aids and one or more moulding and optionally fermentation steps. The preparation of frozen dough is described by Kulp and Lorenz in *Frozen and Refrigerated Doughs and Batters*.

[0337] The term "cereal-based food product" is defined herein as any product prepared from a dough, either of a soft or a crisp character. Examples of cereal-based food products, whether of a white, light or dark type, which may be advantageously produced by the present invention are bread (in particular white, whole-meal or rye bread), typically in the form of loaves or rolls, French baguette-type bread, pasta, noodles, doughnuts, bagels, cake, pita bread, tortillas, tacos, cakes, pancakes, biscuits, cookies, pie crusts, steamed bread, and crisp bread, and the like.

[0338] The term "baked product" is defined herein as any cereal-based food product prepared by baking the dough.

[0339] Non-starch polysaccharides (NSP) can increase the viscosity of the digesta which can, in turn, decrease nutrient availability and animal performance. The use of the cellobiohydrolase of the present invention can improve phosphorus utilization as well as cation minerals and protein during animal digesta.

[0340] Adding specific nutrients to feed improves animal digestion and thereby reduces feed costs. A lot of feed additives are being currently used and new concepts are continuously developed. Use of specific enzymes like non-starch carbohydrate degrading enzymes could breakdown the fibre releasing energy as well as increasing the protein digestibility due to better accessibility of the protein when the fibre gets broken down. In this way the feed cost could come down as well as the protein levels in the feed also could be reduced.

[0341] Non-starch polysaccharides (NSPs) are also present in virtually all feed ingredients of plant origin. NSPs are poorly utilized and can, when solubilized, exert adverse effects on digestion. Exogenous enzymes can contribute to a better utilization of these NSPs and as a consequence reduce any anti-nutritional effects. Non-starch carbohydrate degrading enzymes of the present invention can be used for this purpose in cereal-based diets for poultry and, to a lesser extent, for pigs and other species.

[0342] A non-starch carbohydrate degrading polypeptide/enzyme of the invention (of a

composition comprising the polypeptide/enzyme of the invention) may be used in the detergent industry, for example for removal from laundry of carbohydrate-based stains. A detergent composition may comprise a polypeptide/enzyme of the invention and, in addition, one or more of a cellulase, a hemicellulase, a pectinase, a protease, a lipase, a cutinase, an amylase or a carbohydrase.

Use of enzymes in detergent compositions

[0343] A detergent composition comprising a polypeptide or composition of the invention may be in any convenient form, for example a paste, a gel, a powder or a liquid. A liquid detergent may be aqueous, typically containing up to about 70% water and from about 0 to about 30% organic solvent or non-aqueous material.

[0344] Such a detergent composition may, for example, be formulated as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dish washing operations.

[0345] In general, the properties of the enzyme should be compatible with the selected detergent (for example, pH-optimum, compatibility with other enzymatic and/or non-enzymatic ingredients, etc.) and the enzyme(s) should be present in an effective amount.

[0346] A detergent composition may comprise a surfactant, for example an anionic or nonionic surfactant, a detergent builder or complexing agent, one or more polymers, a bleaching system (for example an H₂O₂ source) or an enzyme stabilizer. A detergent composition may also comprise any other conventional detergent ingredient such as, for example, a conditioner including a clay, a foam booster, a sud suppressor, an anti-corrosion agent, a soil-suspending agent, an anti-soil redeposition agent, a dye, a bactericide, an optical brightener, a hydrotropes, a tarnish inhibitor or a perfume.

Use of enzymes in paper and pulp processing

[0347] A polypeptide or composition of the present invention may be used in the paper and pulp industry, inter alia in the bleaching process to enhance the brightness of bleached pulps whereby the amount of chlorine used in the bleaching stages may be reduced, and to increase the freeness of pulps in the recycled paper process (Eriksson, K. E. L., Wood Science and Technology 24 (1990):79-101; Paice, et al., Biotechnol. and Bioeng. 32 (1988):235-239 and Pommier et al., Tappi Journal (1989):187-191). Furthermore, a polypeptide or composition of the invention may be used for treatment of lignocellulosic pulp so as to improve the bleachability thereof. Thereby the amount of chlorine needs to obtain a satisfactory bleaching

of the pulp may be reduced.

[0348] A polypeptide or composition of the invention may be used in a method of reducing the rate at which cellulose-containing fabrics become harsh or of reducing the harshness of cellulose-containing fabrics, the method comprising treating cellulose-containing fabrics with a polypeptide or composition as described above. The present invention further relates to a method providing colour clarification of coloured cellulose-containing fabrics, the method comprising treating coloured cellulose-containing fabrics with a polypeptide or composition as described above, and a method of providing a localized variation in colour of coloured cellulose-containing fabrics, the method comprising treating coloured cellulose-containing fabrics with a polypeptide or composition as described above. The methods of the invention may be carried out by treating cellulose-containing fabrics during washing. However, if desired, treatment of the fabrics may also be carried out during soaking or rinsing or simply by adding the polypeptide or composition as described above to water in which the fabrics are or will be immersed.

Other enzyme uses

[0349] In addition, a polypeptide or composition of the present invention can also be used in antibacterial formulation as well as in pharmaceutical products such as throat lozenges, toothpastes, and mouthwash.

[0350] The following Examples illustrate the invention:

EXAMPLES

Experimental information

Strains and enzyme compositions

[0351] *Aspergillus niger* strain is deposited at the CBS Institute under the deposit number CBS 513.88.

[0352] *Rasamsonia (Talaromyces) emersonii* strain TEC-142 is deposited at CENTRAAL BUREAU VOOR SCHIMMELCULTURES, Uppsalalaan 8, P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands on 1st July 2009 having the Accession Number CBS 124902. TEC-142S is a single isolate of TEC-142.

[0353] *Rasamsonia (Talaromyces) emersonii* strain was deposited at CENTRAAL BUREAU

VOOR SCHIMMELCULTURES, Uppsalalaan 8, P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands in December 1964 having the Accession Number CBS 393.64. Other suitable strains can be equally used in the present examples to show the effect and advantages of the invention. For example, TEC-101, TEC-147, TEC-192, TEC-201 or TEC-210 are suitable *Rasamsonia* strains which are described in WO2011/000949.

[0354] TEC-210 cellulase-containing composition was produced according to the procedures such as inoculation and fermentation as described in WO2011/000949.

[0355] Beta-glucosidase (BG) is produced by overexpression of EBA4 in *Aspergillus niger* as described in WO2011/098577 followed by fermentation of the *Aspergillus niger* transformant. EBA4 is a *Rasamsonia emersonii* (*Talaromyces emersonii*) BG and is identified in WO2011/098577 as *T. emersonii* beta-glucosidase (BG) and represented by SEQ ID NO: 5 in WO2011/098577.

Celluclast (*Trichoderma* cellulase) was obtained from Sigma

Molecular biology techniques

[0356] In these strains, using molecular biology techniques known to the skilled person (see: Sambrook & Russell, MolecularCloning: A Laboratory Manual, 3rd Ed., CSHL Press, Cold Spring Harbor, NY, 2001), several genes were over expressed and others were down regulated as described below. Examples of the general design of expression vectors for gene over expression and disruption vectors for down-regulation, transformation, use of markers and selective media can be found in WO199846772, WO199932617, WO2001121779, WO2005095624, WO2006040312, EP 635574B, WO2005100573, WO2011009700, WO2012001169 and WO2011054899. All gene replacement vectors comprise approximately 1 - 2 kb flanking regions of the respective ORF sequences, to target for homologous recombination at the predestined genomic loci. In addition, *A. niger* vectors contain the *A. nidulans* bi-directional *amdS* selection marker for transformation, in-between direct repeats. The method applied for gene deletion in all examples herein uses linear DNA, which integrates into the genome at the homologous locus of the flanking sequences by a double cross-over, thus substituting the gene to be deleted by the *amdS* gene. After transformation, the direct repeats allow for the removal of the selection marker by a (second) homologous recombination event. The removal of the *amdS* marker can be done by plating on fluoro-acetamide media, resulting in the selection of marker-gene-free strains. Using this strategy of transformation and subsequent counter-selection, which is also described as the "MARKER-GENE FREE" approach in EP 0 635 574, the *amdS* marker can be used indefinitely in strain modification programs.

Media and solutions:

[0357] Potato dextrose agar, PDA, (Fluka, Cat. No. 70139): per litre: Potato extrac 4 g; Dextrose 20 g; Bacto agar 15 g; pH 5.4; Sterilize 20 min at 120°C.

[0358] Rasamsonia agar medium: per litre: Salt fraction no.3 15 g; Cellulose 30 g; Bacto peptone 7.5 g; Grain flour 15 g; KH₂PO₄ 5 g; CaCl₂·2aq 1 g; Bacto agar 20 g; pH 6.0; Sterilize 20 min at 120°C.

[0359] Salt fraction composition: The "salt fraction no.3" was fitting the disclosure of WO98/37179, Table 1. Deviations from the composition of this table were CaCl₂·2aq 1.0 g/l, KCl 1.8 g/L, citric acid 1aq 0.45 g/L (chelating agent).

Shake flask media for *Rasamsonia*

[0360] Rasamsonia medium 1: per litre: Glucose 20 g; Yeast extract (Difco) 20 g; Clerol FBA3107 (AF) 4 drops; pH 6.0; Sterilize 20 min at 120°C.

[0361] Rasamsonia medium 2: per litre: Salt fraction no.3 15 g; Cellulose 20 g; Bacto peptone 4 g; Grain flour 7.5 g; KH₂PO₄ 10 g; CaCl₂·2H₂O 0.5 g; Clerol FBA3107 (AF) 0.4 ml; pH 5; Sterilize 20 min at 120°C.

[0362] Rasamsonia medium 3: per litre: Salt fraction no.3 15 g; glucose 50 g; Bacto peptone 7.5 g; KH₂PO₄ 10 g; CaCl₂·2H₂O 0.5 g; Clerol FBA3107 (AF) 0.4 ml; pH 5; Sterilize 20 min at 120°C.

Spore batch preparation for *Rasamsonia*

[0363] Strains were grown from stocks on Rasamsonia agar medium in 10 cm diameter Petri dishes for 5-7 days at 40°C. For MTP fermentations, strains were grown in 96-well plates containing Rasamsonia agar medium. Strain stocks were stored at -80°C in 10% glycerol.

Chromosomal DNA isolation

[0364] Strains were grown in YGG medium (per liter: 8 g KCl, 16 g glucose, H₂O, 20 ml of 10% yeast extract, 10 ml of 100x pen/strep, 6.66 g YNB+amino acids, 1.5 g citric acid, and 6 g K₂HPO₄). for 16 hours at 42°C, 250 rpm, and chromosomal DNA was isolated using the DNeasy plant mini kit (Qiagen, Hilden, Germany).

MTP fermentation of *Rasamsonia*

[0365] 96 wells microtiter plates (MTP) with sporulated *R. emersonii* strains were used to harvest spores for MTP fermentations. To do this, 200 µl of 10 times diluted Rasamsonia medium 1 was added to each well and after resuspending the mixture, 100 µl of spore suspension was incubated in humidity shakers (Infors) for 44°C at 550 rpm, and 80% humidity for 16 hours. Subsequently, 50 µl of pre-culture was used to inoculate 250 µl of Rasamsonia medium 2 in MTP plates. The 96-well plates were incubated in humidity shakers (Infors) for 44°C at 550 rpm, and 80% humidity for 6 days. Plates were centrifuged and supernatants were harvested.

Shake flask growth protocol of *Rasamsonia*

[0366] Spores were directly inoculated into 500 ml shake flasks containing 100 ml of either Rasamsonia medium 2 or 3 and incubated at 45°C at 250 rpm in an incubator shaker for 3-4 days. Alternatively, spores were inoculated in 100 ml shake flasks containing Rasamsonia medium 1 and incubated at 45°C at 250 rpm in an incubator shaker for 1 day (preculture) and, subsequently, 5 or 10 ml of biomass from the pre-culture was transferred to 500 ml shake flasks containing 100 ml of Rasamsonia medium 2 or 3 and grown under conditions as described above.

Protein analysis

[0367] Protein samples were separated under reducing conditions on NuPAGE 4-12% Bis-Tris gel (Invitrogen, Breda, The Netherlands) and stained. Gels were stained with either InstantBlue (Expedeon, Cambridge, United Kingdom), SimplyBlue safestain (Invitrogen, Breda, The Netherlands) or Sypro Ruby (Invitrogen, Breda, The Netherlands) according to manufacturer's instructions.

Total protein content

[0368] Protein content of the recovered supernatant was determined according to Bradford method. The amount of protein in the enzyme samples was determined with Bradford Protein assay, using Coomassie protein reagent. 25 µl of appropriately diluted enzyme sample was mixed with 1.2 ml Coomassie reagent. After 10 minutes at room temperature the absorbance of the mixture at 595 nm was determined using a spectrophotometer (Uvikon XL). Protein content was calculated in comparison to BSA standard.

Sugar-release activity assay from acid pretreated corn stover feedstock

[0369] For each (hemi-)cellulase assay condition, the enzyme culture supernatant was analysed in duplicate according to the following procedure: 5 mg protein /g dry matter feedstock of the enzyme culture supernatant was transferred to a suitable vial containing 800 μL 2.5 % (w/w) dry matter of a mildly acid pre-treated corn stover substrate in a 50 mM citrate buffer, buffered at pH 3.5 or pH 4.5 or 5.0. Additionally, as a blank sample the same amount of enzyme culture supernatant was added to another vial, where the 800 μL 2.5 % (w/w) dry matter of a mildly acid pre-treated corn stover substrate in a 50 mM citrate buffer was replaced by 800 μL 50 mM citrate buffer, buffered at pH 4.5. The assay samples buffered at pH 3.5 were incubated at 65°C for 72 hours. The assay samples buffered at pH 5.0 were incubated at 50°C for 72 hours. The assay samples buffered at pH 4.5, and blank samples for correction of the monomeric sugar content in the enzyme supernatants were incubated at 65°C for 72 hours. Also, assay samples buffered at pH 4.5 were incubated at 75°C for 72 hours.

[0370] In addition to the individual incubations as described above, the enzyme culture supernatant was also tested in combination with two different hemicellulase mixtures; TEC-210 (*Rasamsonia emersonii*) to which additional beta-glucosidase (BG) (*Aspergillus niger* strain expressing a BG from *Rasamsonia emersonii*) was added (0.08 mg/g dry matter) and Celluclast (*Trichoderma reesei*) to which additional BG (Novozym-188) was added (0.08 mg/g dry matter). The mixtures were added to a concentration of 1 mg protein/ g dry matter of the feedstock. These incubations were performed at the same conditions as described above.

[0371] For each procedure, an assay was performed where the enzyme supernatant was replaced by demineralized water, in order to correct for possible monomeric sugars present in the feedstock after incubation.

[0372] After incubation of the assay samples, a fixed volume of an internal standard, maleic acid (20 g/L), EDTA (40 g/L) and DSS (2,2-Dimethyl-2-silapentane-5-sulfonate) (0.5g/L), was added to each vial. After centrifugation, 650 μL of the supernatant was transferred to a new vial.

[0373] The supernatant of the samples is lyophilized overnight, subsequently 50 μL D₂O is added to the dried residue and lyophilized once more. The dried residue is dissolved in 600 μL of D₂O. 1D 1H NMR spectra are recorded on a Bruker Avance III HD 400 MHz, equipped with a N₂ cooled cryo-probe, using a pulse program without water suppression at a temperature of 17°C with a 90 degrees excitation pulse, acquisition time of 2.0 s and relaxation delay of 10 s. The analyte concentrations are calculated based on the following signals (δ relative to DSS (4,4-dimethyl-4-silapentane-1-sulfonic acid)): 1/2 of β -glucose peak at 4.63 ppm (d, 0.31 H, J = 8 Hz), 1/2 of β -xylose peak at 4.56 ppm (d, 0.315 H, J = 8 Hz), Xylo-oligo peak at 4.45 ppm (d, 1H, J=8Hz), 1/2 of β anomer of the reducing end of cellobiose peak at 4.66 ppm (d, 0.31H, J=8Hz). The signal user for the standard: Maleic acid peak at 6.26 ppm (s, 2H)

[0374] The (hemi-)cellulase enzyme solution may contain residual sugars. Therefore, the

results of the assay are corrected for the sugar content measured after incubation of the enzyme solution.

β-xylosidase activity measurement

[0375] This assay measures the release of p-nitrophenol by the action of β-xylosidase on p-nitrophenyl-β-D-xylopyranoside (PNPX). One β-xylosidase unit of activity is the amount of enzyme that liberates 1 micromole of p-nitrophenol in one minute at 60°C and pH 4.5. Acetate buffer (0.1 M, pH 4.5) is prepared as follows: 8.2 g of anhydrous sodium acetate is dissolved in distilled water so that the final volume of the solution is 1000 ml (Solution A). In a separate flask, 6.0 g (5.72 ml) of glacial acetic acid is mixed with distilled water to make the total volume of 1000 ml (Solution B). The final 0.1 M acetate buffer, pH 4.5 is prepared by mixing Solution A with Solution B until the pH of the resulting solution is equal to 4.5. A drop (~ 25 µL) Triton X-100 is added/ L buffer solution. PNPX (Sigma) is used as the assay substrate.

[0376] 100 mg of PNPX is dissolved in 84 mL of 0.1 M acetate buffer to obtain a 4.4 mM stock solution. The stop reagent (1 M sodium carbonate solution) is prepared as follows: 10.6 g of anhydrous sodium carbonate is dissolved in 50 ml of distilled water, and the solution volume is adjusted to 100 ml. This reagent is used to terminate the enzymatic reaction.

[0377] For the incubation with enzyme, 0.1 mL of 4.4 mM PNPX stock solution is mixed with 0.1 mL of the appropriate diluted enzyme sample and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as A_S

[0378] For the substrate blank, 0.1 mL of 4.4 mM PNPX stock solution is mixed with 0.1 mL of 0.1 M acetate buffer, pH 4.5 and treated the same as the samples: incubated at 60°C for 60 minutes after which 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance at 405 nm is measured in microtiter plates as A_{SB} .

[0379] Enzyme blanks (without addition of substrate) are measured to correct for background color originating from the enzymes. 0.1 mL of the appropriate diluted enzyme sample is mixed with 0.1 mL 0.1 M acetate buffer, pH 4.5 and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as A_{EB} .

[0380] A calibration curve of p-nitrophenol (appropriate diluted in 0.1 M acetate buffer, pH 4.5) mixed in a ratio of 1:1 with 1 M sodium carbonate solution is used to quantify its release from PNPX by the action of the enzyme.

[0381] After the incubation of enzyme with substrate the corrected absorbance ($= A_S - A_{EB} - A_{SB}$), is used to calculate the amount of p-nitrophenol released by the enzyme.

[0382] The activity is expressed as the amount of enzyme required to release 1 μ M *p*-nitrophenol /min under the assay conditions.

[0383] This assay can be used to test the activity of enzymes such as, but not limited to, GH3, GH30, GH39, GH43, GH52, and GH54 enzymes.

β -xylosidase activity assay 2

[0384] This assay measures the release of xylose by the action of β -xylosidase on xylobiose.

[0385] Sodium acetate buffer (0.05 M, pH 4.5) was prepared as follows. 4.1 g of anhydrous sodium acetate or 6.8 g of sodium acetate $\cdot$ 3H₂O was dissolved in distilled water to a final volume of 1000 mL (Solution A). In a separate flask, 3.0 g (2.86 mL) of glacial acetic acid was mixed with distilled water to make the total volume of 1000 mL (Solution B). The final 0.05 M sodium acetate buffer, pH 4.5, was prepared by mixing Solution A with Solution B until the pH of the resulting solution was equal to 4.5. Xylobiose was purchased from Sigma and dissolved in sodium acetate buffer pH 4.5 to a concentration of 100 μ g/mL

[0386] The assay was performed as detailed below.

[0387] The enzyme culture supernatant was added to the substrate in a dosage of 1 and 5 mg protein/ g substrate which was then incubated at 62°C for 24 hours. The reaction was stopped by heating the samples for 10 minutes at 100°C. The release of xylose was analyzed by High Performance Anion Exchange Chromatography.

Substrate Blank

[0388] Instead of enzyme culture supernatant the same amount of buffer was added to the substrate solution which was then incubated at 62°C for 24 hours. The reaction was stopped by heating the samples for 10 minutes at 100°C. The sample was analyzed by High Performance Anion Exchange Chromatography. The analysis was performed using a Dionex HPLC system equipped with a Dionex CarboPac PA-1 (2 mm ID $\times$ 250 mm) column in combination with a CarboPac PA guard column (2 mm ID $\times$ 50 mm) and a Dionex PAD-detector (Dionex Co. Sunnyvale). A flow rate of 0.3 mL/min was used with the following gradient of sodium acetate in 0.1 M NaOH: 0-20 min, 0-180 mM. Each elution was followed by a washing step of 5 min 1000 mM sodium acetate in 0.1 M NaOH and an equilibration step of 15 min 0.1 M NaOH.

[0389] In case interfering compounds were present that complicate xylose identification the analysis was performed by running isocratic on H₂O for 30 min a gradient (0.5M NaOH was

added post-column at 0.1 mL/min for detection) followed by a washing step of 5 min 1000 mM sodium acetate in 0.1 M NaOH and an equilibration step of 15 min H₂O.

[0390] Standards of xylose and xylobiose (Sigma) were used for identification of the substrate and product formed by the enzyme.

[0391] This assay can be used to test the activity of enzymes such as, but not limited to, GH3, GH30, GH39, GH43, GH52, and GH54 enzymes.

β-xylosidase activity assay 3

[0392] The same assay as described above was performed with xylan substrates like Oat arabinoxylan, Beech wood xylan and Birch wood xylan (Sigma) instead of xylobiose to measure xylosidase activity on polymeric substrates.

[0393] Assay conditions were the same with the exception that all substrates were solved to a concentration of 2 mg/mL. The incubation was performed at 60°C for 24h at a dosage of 10 mg/g. Next to xylose and xylobiose also xylotriose and xylotetraose were quantified.

α-galactosidase activity measurement

[0394] This assay measures the release of p-nitrophenol by the action of α-galactosidase on p-nitrophenyl-α-D-galactopyranoside (PNPG). One α-galactosidase unit of activity is the amount of enzyme that liberates 1 micromole of p-nitrophenol in one minute at 60°C and pH 4.5. Acetate buffer (0.1 M, pH 4.5) is prepared as follows: 8.2 g of anhydrous sodium acetate is dissolved in distilled water so that the final volume of the solution is 1000 ml (Solution A). In a separate flask, 6.0 g (5.72 ml) of glacial acetic acid is mixed with distilled water to make the total volume of 1000 ml (Solution B). The final 0.1 M acetate buffer, pH 4.5 is prepared by mixing Solution A with Solution B until the pH of the resulting solution is equal to 4.5. A drop (~ 25 µL) Triton X-100 is added/ L buffer solution. PNPG (Sigma) is used as the assay substrate.

[0395] A stock solution of 4.4 mM PNPG is made in 0.1 M acetate buffer. The stop reagent (1 M sodium carbonate solution) is prepared as follows: 10.6 g of anhydrous sodium carbonate is dissolved in 50 ml of distilled water, and the solution volume is adjusted to 100 ml. This reagent is used to terminate the enzymatic reaction.

[0396] For the incubation with enzyme, 0.1 mL of 4.4 mM PNPG stock solution is mixed with 0.1 mL of the appropriate diluted enzyme sample and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as As

[0397] For the substrate blank, 0.1 mL of 4.4 mM PNPG stock solution is mixed with 0.1 mL of 0.1 M acetate buffer, pH 4.5 and treated the same as the samples: incubated at 60°C for 60 minutes after which 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance at 405 nm is measured in microtiter plates as A_{SB} .

[0398] Enzyme blanks (without addition of substrate) are measured to correct for background color originating from the enzymes. 0.1 mL of the appropriate diluted enzyme sample is mixed with 0.1 mL 0.1 M acetate buffer, pH 4.5 and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as A_{EB} .

[0399] A calibration curve of p-nitrophenol (appropriate diluted in 0.1 M acetate buffer, pH 4.5) mixed in a ratio of 1:1 with 1 M sodium carbonate solution is used to quantify its release from PNPG by the action of the enzyme.

[0400] After the incubation of enzyme with substrate the corrected absorbance ($= A_S - A_{EB} - A_{SB}$), is used to calculate the amount of p-nitrophenol released by the enzyme.

[0401] The activity is expressed as the amount of enzyme required to release 1 μ M p-nitrophenol /min under the assay conditions.

[0402] This assay can be used to test the activity of enzymes such as, but not limited to, GH4, GH27 and GH36 enzymes.

xyloglucanase activity assay 1

[0403] Sodium acetate buffer (0.05 M, pH 4.5) was prepared as follows. 4.1 g of anhydrous sodium acetate was dissolved in distilled water to a final volume of 1000 mL (Solution A). In a separate flask, 3.0 g (2.86 mL) of glacial acetic acid was mixed with distilled water to make the total volume of 1000 mL (Solution B). The final 0.05 M sodium acetate buffer, pH 4.5, was prepared by mixing Solution A with Solution B until the pH of the resulting solution is 4.5.

[0404] Tamarind xyloglucan was solved in sodium acetate buffer to obtain 2.0 mg/mL. The enzyme culture supernatant was added to the substrate in a dosage of 10 mg protein/ g substrate which was then incubated at 60°C for 24 hours. The reaction was stopped by heating the samples for 10 minutes at 100°C. The release of oligosaccharides was analyzed by High Performance Anion Exchange Chromatography

[0405] As a blank sample the substrate was treated and incubated in the same way but then without the addition of enzyme.

[0406] As a reference the substrate was also incubated under the same conditions with a

commercial cellulase preparation from *Trichoderma Reesei* (Celluclast; Sigma) which was diluted 50 times after which 20 µL was added to the incubation.

[0407] The analysis was performed using a Dionex HPLC system equipped with a Dionex CarboPac PA-1 (2 mm ID × 250 mm) column in combination with a CarboPac PA guard column (2 mm ID × 50 mm) and a Dionex PAD-detector (Dionex Co. Sunnyvale). A flow rate of 0.3 mL/min was used with the following gradient of sodium acetate in 0.1 M NaOH: 0-40 min, 0-150 mM. Each elution was followed by a washing step of 5 min 1000 mM sodium acetate in 0.1 M NaOH and an equilibration step of 15 min 0.1 M NaOH.

[0408] This assay can be used to test the activity of enzymes such as, but not limited to, GH5, GH12, GH16, GH44, and GH74 enzymes.

xyloglucanase activity assay 2

[0409] The following example illustrates the assay to measure xyloglucanase activity. Such activity was demonstrated by using xyloglucan as substrate and a reducing sugars assay (PAHBAH) as detection method. The values were compared to a standard, which was prepared using a commercial cellulase preparation from *Trichoderma Reesei* (Celluclast; Sigma).

[0410] Reagent A: 5 g of p-Hydroxybenzoic acid hydrazide (PAHBAH) was suspended in 60 mL water, 4.1 mL of concentrated hydrochloric acid was added and the volume was adjusted to 100 mL. Reagent B: 24.9 g of trisodium citrate was dissolved in 500 mL of water. To this solution 2.2 g of calcium chloride and 40 g sodium hydroxide was added. The volume was adjusted to 2 L with water. Both reagents were stored at room temperature. Working Reagent: 10 mL of Reagent A was added to 40 mL of Reagent B. This solution was prepared freshly every day, and was stored on ice between uses. Using the above reagents, the assay was performed as detailed below

[0411] Next to xyloglucan also carboxymethylcellulose was used as a substrate to determine the specificity of the enzyme.

[0412] After incubation 10 µL of each well was mixed with 200 µL working reagent. These solutions were heated at 70°C for 30. After cooling down, the samples were analyzed by measuring the absorbance at 405 nm. Glucose was used as a standard to quantify reducing ends formed as glucose equivalents.

[0413] As controls the substrates were also incubated without addition of enzyme culture supernatant and the enzyme culture supernatants were incubated without substrate.

[0414] This assay can be used to test the activity of enzymes such as, but not limited to, GH5, GH12, GH16, GH44, and GH74 enzymes.

xyloglucanase activity assay 3

[0415] Sodium acetate buffer (0.05 M, pH 4.5) is prepared as follows. 4.1 g of anhydrous sodium acetate is dissolved in distilled water to a final volume of 1000 mL (Solution A). In a separate flask, 3.0 g (2.86 mL) of glacial acetic acid is mixed with distilled water to make the total volume of 1000 mL (Solution B). The final 0.05 M sodium acetate buffer, pH 4.5, is prepared by mixing Solution A with Solution B until the pH of the resulting solution is 4.5.

[0416] Tamarind xyloglucanase is solved in sodium acetate buffer to obtain 2.0 mg/mL. The enzyme is added to the substrate in a dosage of 10 mg protein/ g substrate which is then incubated at 60°C for 24 hours. The reaction is stopped by heating the samples for 10 minutes at 100°C. The formation of lower molecular weight oligosaccharides is analyzed by High Performance size-exclusion Chromatography

[0417] As a blank sample the substrate is treated and incubated in the same way but then without the addition of enzyme.

[0418] As a reference the substrate is also incubated under the same conditions with a commercial cellulase preparation from e.g. *Aspergillus niger* or *Trichoderma Reesei* (the cellulase standard at its own optimal temperature in case of inactivity at 60°C).

[0419] The analysis is performed using High-performance size-exclusion chromatography (HPSEC) performed on three TSK-gel columns (6.0 mm×15.0 cm per column) in series SuperAW4000, SuperAW3000, SuperAW2500; Tosoh Bioscience), in combination with a PWXguard column (Tosoh Bioscience). Elution is performed at 55 C with 0.2 M sodium nitrate at 0.6 mL/min. The eluate was monitored using a Shodex RI-101 (Kawasaki) refractive index (RI) detector. Calibration was performed by using pullulans (Associated Polymer Labs Inc., New York, USA) with a molecular weight in the range of 0.18-788 kDa.

[0420] This assay can be used to test the activity of enzymes such as, but not limited to, GH5, GH12, GH16, GH44, and GH74 enzymes.

α-arabinofuranosidase activity assay

[0421] The following example illustrates an assay to measure the ability of α-arabinofuranosidases to remove the α-L-arabinofuranosyl residues from substituted xylose residues.

[0422] For the complete degradation of arabinoxylans to arabinose and xylose, several enzyme activities are needed, including endo-xylanases and arabinofuranosidases. The

arabinoxylan molecule from wheat is highly substituted with arabinosyl residues. These can be substituted either to the C2 or the C3 position of the xylosyl residue (single substitution), or both to the C2 and C3 position of the xylose (double substitution).

[0423] Single and double substituted oligosaccharides were prepared by incubating wheat arabinoxylan (WAX; 10 mg/mL; Megazyme, Bray, Ireland) in 50 mM acetate buffer pH 4.5 with an appropriate amount of endo-xylanase (from *Aspergillus awamori*, Kormelink F. et al; Journal of Biotechnology (1993) 27: 249-265) 48 hours at 40°C to produce a sufficient amount of arabinoxyloligosaccharides. The reaction was stopped by heating the samples at 100°C for 10 minutes. The samples were centrifuged for 5 minutes at 10,000 × g. The supernatant was used for further experiments. Degradation of the arabinoxylan was followed by analysis of the formed reducing sugars and High Performance Anion Exchange Chromatography (HPAEC).

[0424] The enzyme culture supernatant was added to the single and double substituted arabinoxyloligosaccharides (endo-xylanase treated WAX; 2 mg/mL) in a dosage of 10 mg protein/ g substrate in 50 mM sodium acetate buffer which was then incubated at 65°C for 24 hours. The reaction was stopped by heating the samples at 100°C for 10 minutes. The samples were centrifuged for 5 minutes at 10,000 × g. The release of arabinose was followed by HPAEC analysis.

[0425] The analysis was performed using a Dionex HPLC system equipped with a Dionex CarboPac PA-1 (2 mm ID × 250 mm) column in combination with a CarboPac PA guard column (2 mm ID × 50 mm) and a Dionex PAD-detector (Dionex Co. Sunnyvale). A flow rate of 0.3 mL/min was used with the following gradient of sodium acetate in 0.1 M NaOH: 0-40 min, 0-400 mM. Each elution was followed by a washing step of 5 min 1000 mM sodium acetate in 0.1 M NaOH and an equilibration step of 15 min 0.1 M NaOH. Arabinose release was identified and quantified by a standard (Sigma).

[0426] This assay can be used to test the activity of enzymes such as, but not limited to, GH3, GH43, GH51, GH54, and GH62 enzymes.

Endo-xylanase activity assay

[0427] Endo-xylanases are enzyme able to hydrolyze β -1,4 bond in the xylan backbone, producing short xylooligosaccharides. This assay measures the release of xylose and xylooligosaccharides by the action of xylanases on wheat arabinoxylan (WAX) (Megazyme, Medium viscosity 29 cSt), Oat arabinoxylan, Beech wood xylan and Birch wood xylan (Sigma).

[0428] Sodium acetate buffer (0.05 M, pH 4.5) was prepared as follows; 4.1 g of anhydrous sodium acetate was dissolved in distilled water to a final volume of 1000 mL (Solution A). In a separate flask, 3.0 g (2.86 mL) of glacial acetic acid was mixed with distilled water to make the total volume of 1000 mL (Solution B). The final 0.05 M sodium acetate buffer, pH 4.5, was prepared by mixing Solution A with Solution B until the pH of the resulting solution was 4.5.

Each substrate was solved in sodium acetate buffer to obtain 2.0 mg/mL. The enzyme culture supernatant was added to the substrate in a dosage of 10 mg protein/ g substrate which was then incubated at 60°C for 20 hours. The reaction was stopped by heating the samples for 10 minutes at 100°C. The release of xylose and xylooligosaccharides was analyzed by High Performance Anion Exchange Chromatography.

[0429] As a blank sample the substrate was treated and incubated in the same way but then without the addition of enzyme.

[0430] The analysis was performed using a Dionex HPLC system equipped with a Dionex CarboPac PA-1 (2 mm ID × 250 mm) column in combination with a CarboPac PA guard column (2 mm ID × 50 mm) and a Dionex PAD-detector (Dionex Co. Sunnyvale). A flow rate of 0.3 mL/min was used with the following gradient of sodium acetate in 0.1 M NaOH: 0-40 min, 0-400 mM. Each elution was followed by a washing step of 5 min 1000 mM sodium acetate in 0.1 M NaOH and an equilibration step of 15 min 0.1 M NaOH. Standards of xylose, xylobiose and xylotriose (Sigma) were used to identify these oligomers released by the action of the enzyme.

[0431] This assay can be used to test the activity of enzymes such as, but not limited to, GH5, GH8, GH10, and GH11.

α/B -xylosidase activity measurement

[0432] This assay measures the release of p-nitrophenol by the action of α/β -xylosidase on p-nitrophenyl- α/β -D-xylopyranoside (PNPX). One β-xylosidase unit of activity is the amount of enzyme that liberates 1 micromole of p-nitrophenol in one minute at 60°C and pH 4.5. Acetate buffer (0.1 M, pH 4.5) is prepared as follows: 8.2 g of anhydrous sodium acetate is dissolved in distilled water so that the final volume of the solution is 1000 ml (Solution A). In a separate flask, 6.0 g (5.72 ml) of glacial acetic acid is mixed with distilled water to make the total volume of 1000 ml (Solution B). The final 0.1 M acetate buffer, pH 4.5 is prepared by mixing Solution A with Solution B until the pH of the resulting solution is equal to 4.5. A drop (~ 25 µL) Triton X-100 is added/ L buffer solution. PNPX (Sigma) is used as the assay substrate.

[0433] 100 mg of PNPX is dissolved in 84 mL of 0.1 M acetate buffer to obtain a 4.4 mM stock solution. The stop reagent (1 M sodium carbonate solution) is prepared as follows: 10.6 g of anhydrous sodium carbonate is dissolved in 50 ml of distilled water, and the solution volume is adjusted to 100 ml. This reagent is used to terminate the enzymatic reaction.

[0434] For the incubation with enzyme, 0.1 mL of 4.4 mM PNPX stock solution is mixed with 0.1 mL of the appropriate diluted enzyme sample and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as As

[0435] For the substrate blank, 0.1 mL of 4.4 mM PNPX stock solution is mixed with 0.1 mL of

0.1 M acetate buffer, pH 4.5 and treated the same as the samples: incubated at 60°C for 60 minutes after which 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance at 405 nm is measured in microtiter plates as A_{SB} .

[0436] Enzyme blanks (without addition of substrate) are measured to correct for background color originating from the enzymes. 0.1 mL of the appropriate diluted enzyme sample is mixed with 0.1 mL 0.1 M acetate buffer, pH 4.5 and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as A_{EB} .

[0437] A calibration curve of p-nitrophenol (appropriate diluted in 0.1 M acetate buffer, pH 4.5) mixed in a ratio of 1:1 with 1 M sodium carbonate solution is used to quantify its release from PNPX by the action of the enzyme.

[0438] After the incubation of enzyme with substrate the corrected absorbance ($= A_S - A_{EB} - A_{SB}$), is used to calculate the amount of p-nitrophenol released by the enzyme.

[0439] The activity is expressed as the amount of enzyme required to release 1 μ M p-nitrophenol /min under the assay conditions.

[0440] This assay can be used to test the activity of enzymes such as, but not limited to, GH3, GH30, GH31, GH39, GH43, GH52, and GH54 enzymes.

α/β -mannosidase activity measurement

[0441] This assay measures the release of p-nitrophenol by the action of α/β -mannosidase on p-nitrophenyl- α/β -D-mannopyranoside (PNPM). One α/β -mannosidase unit of activity is the amount of enzyme that liberates 1 micromole of p-nitrophenol in one minute at 60°C and pH 4.5. Acetate buffer (0.1 M, pH 4.5) is prepared as follows: 8.2 g of anhydrous sodium acetate is dissolved in distilled water so that the final volume of the solution is 1000 ml (Solution A). In a separate flask, 6.0 g (5.72 ml) of glacial acetic acid is mixed with distilled water to make the total volume of 1000 ml (Solution B). The final 0.1 M acetate buffer, pH 4.5 is prepared by mixing Solution A with Solution B until the pH of the resulting solution is equal to 4.5. A drop (~ 25 μ L) Triton X-100 is added/ L buffer solution. PNPM (Sigma) is used as the assay substrate.

[0442] A stock solution of 4.4 mM PNPM is made in 0.1 M acetate buffer. The stop reagent (1 M sodium carbonate solution) is prepared as follows: 10.6 g of anhydrous sodium carbonate is dissolved in 50 ml of distilled water, and the solution volume is adjusted to 100 ml. This reagent is used to terminate the enzymatic reaction.

[0443] For the incubation with enzyme, 0.1 mL of 4.4 mM PNPM stock solution is mixed with 0.1 mL of the appropriate diluted enzyme sample and incubated at 60°C for 60 minutes. After

60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as A_S

[0444] For the substrate blank, 0.1 mL of 4.4 mM PNPM stock solution is mixed with 0.1 mL of 0.1 M acetate buffer, pH 4.5 and treated the same as the samples: incubated at 60°C for 60 minutes after which 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance at 405 nm is measured in microtiter plates as A_{SB} .

[0445] Enzyme blanks (without addition of substrate) are measured to correct for background color originating from the enzymes. 0.1 mL of the appropriate diluted enzyme sample is mixed with 0.1 mL 0.1 M acetate buffer, pH 4.5 and incubated at 60°C for 60 minutes. After 60 minutes of incubation, 0.1 mL of the reaction mixture is mixed with 0.1 mL of 1 M sodium carbonate solution and the absorbance is measured at 405 nm in microtiter plates as A_{EB} .

[0446] A calibration curve of p-nitrophenol (appropriate diluted in 0.1 M acetate buffer, pH 4.5) mixed in a ratio of 1:1 with 1 M sodium carbonate solution is used to quantify its release from PNPM by the action of the enzyme.

[0447] After the incubation of enzyme with substrate the corrected absorbance ($= A_S - A_{EB} - A_{SB}$), is used to calculate the amount of p-nitrophenol released by the enzyme.

[0448] The activity is expressed as the amount of enzyme required to release 1 μ M *p*-nitrophenol /min under the assay conditions.

[0449] This assay can be used to test the activity of enzymes such as, but not limited to, GH1, GH2, GH5, GH38, GH47, GH92, and GH125 enzymes.

feruloyl esterase activity measurement

[0450] Synthetic substrates: Methyl caffeate, methyl coumarate, methyl sinapinate and methyl ferulate are obtained from Apin Chemicals. Activity towards these synthetic substrates is determined by incubating the enzyme with the substrate at a dosage of about 5 mg/g DM at a pH of 5.0 (50 mM sodium acetate buffer). The reaction will be done at 60°C for up to 24 h.

[0451] At the end of the incubation the samples are boiled for 5 minutes to inactivate the enzymes and centrifuged at room temperature (10 min, 10,000 $\times$ g). Hydroxycinnamic acid release from the substrate is measured by RP-UHPLC-MS analysis in negative ion mode as described earlier (Appeldoorn et al., 2010) on an Accela UHPLC system (Thermo Scientific) equipped with a Hypersyl GOLD column (2.1 mm $\times$ 150 mm, 1.9 μ m particle size; Thermo Scientific). The mobile phase is composed of (A) H₂O + 1% (v/v) acetonitrile + 0.2% (v/v) acetic acid and (B) acetonitrile + 0.2% (v/v) acetic acid. The flow rate is 0.4 mL/min, and the column temperature is 30°C. The elution profile is as follows: first 5 min, isocratic 0%B; 5-23 min, linear

from 0 to 50% B; 23-24 min, linear from 50 to 100% B; 24-27min, isocratic at 100%B; 27-28 min, linear from 100 to 0% B, followed by reconditioning of the column for 7 min. Spectral data are collected from 200 to 600 nm, and quantification is performed at 320 nm. Ferulic, caffeic, sinapic and coumaric acid contents are identified and quantified on the basis of standards.

[0452] MS data are collected in the negative mode with an ion spray voltage of 3.5 kV, a capillary voltage of -20 V, and a capillary temperature of 350 C. Full MS scans are made within the range m/z 150-1500, and MS2 data of the most intense ions is obtained.

[0453] This assay can be used to test the activity of enzymes such as, but not limited to, CE1 enzymes.

feruloyl esterase activity measurement

[0454] Natural occurring substrate: Arabinoxylan oligomers purified from pretreated corn fibre (CF) (1 mg/ml each) (Appeldoorn et al 2010) are incubated with ferulic acid esterases at a dosage of about 5 mg/g DM at a pH of 5.0 (50 mM sodium acetate buffer). The reaction will be done at 60°C for up to 24 h.

[0455] At the end of the incubation the samples are boiled for 5 minutes to inactivate the enzymes and centrifuged at room temperature (10 min, 10,000 × g). Hydroxycinnamic acid release from the substrate is measured by RP-UHPLC-MS analysis in negative ion mode as described earlier (Appeldoorn et al., 2010) on an Accela UHPLC system (Thermo Scientific) equipped with a Hypersyl GOLD column (2.1 mm × 150 mm, 1.9 µm particle size; Thermo Scientific). The mobile phase is composed of (A) H₂O + 1% (v/v) acetonitrile + 0.2% (v/v) acetic acid and (B) acetonitrile + 0.2% (v/v) acetic acid. The flow rate is 0.4 mL/min, and the column temperature is 30°C. The elution profile is as follows: first 5 min, isocratic 0%B; 5-23 min, linear from 0 to 50% B; 23-24 min, linear from 50 to 100% B; 24-27min, isocratic at 100%B; 27-28 min, linear from 100 to 0% B, followed by reconditioning of the column for 7 min. Spectral data are collected from 200 to 600 nm, and quantification is performed at 320 nm. Ferulic and coumaric acid contents are identified and quantified on the basis of standards.

[0456] MS data are collected in the negative mode with an ion spray voltage of 3.5 kV, a capillary voltage of -20 V, and a capillary temperature of 350 C. Full MS scans are made within the range m/z 150-1500, and MS2 data of the most intense ions is obtained.

[0457] The total amount of ester-linked ferulic acid in corn oligomers was determined after alkaline hydrolysis and ethylether extraction using the UHPLC method described above.

[0458] Reference: MAAIKE M. APPELDOORN et al, J. Agric. Food Chem. 2010, 58, 11294-11301

[0459] This assay can be used to test the activity of enzymes such as, but not limited to, CE1

enzymes.

α -glucuronidase activity assay

[0460] The following example illustrates the assay to measure the **α -glucuronidase** activity towards aldouronic acids(megazyme). This assay measures the release of xylose and xylooligomers by the action of the **α -glucuronidase** on the glucuronoxylan oligosaccharides.

[0461] Sodium acetate buffer (0.05 M, pH 4.5) was prepared as follows. 4.1 g of anhydrous sodium acetate was dissolved in distilled water to a final volume of 1000 mL (Solution A). In a separate flask, 3.0 g (2.86 mL) of glacial acetic acid was mixed with distilled water to make the total volume of 1000 mL (Solution B). The final 0.05 M sodium acetate buffer, pH 4.5, was prepared by mixing Solution A with Solution B until the pH of the resulting solution was 4.5.

[0462] To determine the activity on small oligomers the aldouronic acids are solved in sodium acetate buffer to obtain 1.0 mg/mL. The enzyme culture supernatant was added to the substrate in a dosage of 1 and 10 mg protein/ g substrate which was then incubated at 60°C for 24 hours. The reaction was stopped by heating the samples for 10 minutes at 100°C. The release of xylooligomers as a result of the removal of 4-O-methyl glucuronic acid were analyzed by High Performance Anion Exchange Chromatography

[0463] As a blank sample the substrate was treated and incubated in the same way but then without the addition of enzyme.

[0464] The analysis was performed using a Dionex HPLC system equipped with a Dionex CarboPac PA-1 (2 mm ID × 250 mm) column in combination with a CarboPac PA guard column (2 mm ID × 50 mm) and a Dionex PAD-detector (Dionex Co. Sunnyvale). A flow rate of 0.3 mL/min was used with the following gradient of sodium acetate in 0.1 M NaOH: 0-40 min, 0-400 mM. Each elution was followed by a washing step of 5 min 1000 mM sodium acetate in 0.1 M NaOH and an equilibration step of 15 min 0.1 M NaOH.

[0465] Standards of xylose, xylobiose and xylotriose (Sigma) were used to identify the xylooligomers released by the action of the enzyme that removes 4-O-methyl-Glucuronic acid from these oligomers.

[0466] This assay can be used to test the activity of enzymes such as, but not limited to, GH67 and GH115 enzymes.

Example 1: Construction of *A.niger* expression vectors

[0467] This Example describes the construction of an expression construct for overexpression

of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 in *A.niger*. Genomic DNA of *Rasamsonia emersonii* strain CBS393.64 was sequenced and analysed. The gene with translated protein annotated as activity according in Table 1 was identified. Sequences of the *R. emersonii* Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 and Temer07305 gene, comprising the codon-pair optimised ORF sequence, protein sequence, signal sequence, genomic sequence and wild-type cDNA sequence are shown in sequence listings SEQ ID NO: 1 to 75.

Construction of expression plasmids

[0468] The sequence having SEQ ID NO: 1, 6, 11, 16, 21, 26, 31, 36, 41, 46, 51, 56, 61, 66 or 71 is cloned into the pGBTOP vector (Fig. 1) using EcoRI and *PacI* sites, comprising the glucoamylase promoter and terminator sequence. The *E.coli* part was removed by *NotI* digestion prior to transformation of *A. niger* CBS 513.88.

Transformation of *A. niger* and shake flask fermentations

[0469] *A. niger* strain CBS513.88 is co-transformed with the expression constructs and an appropriate selection marker (*amdS* or phleomycin) containing plasmid according to method described in the experimental information section. Of recombinant and control *A. niger* strains a large batch of spores is generated by plating spores or mycelia onto PDA plates (Potato Dextrose Agar, Oxoid), prepared according to manufacturer's instructions. After growth for 3-7 days at 30 degrees Celsius, spores are collected after adding 0.01% Triton X-100 to the plates. After washing with sterile water about 10^7 spores of selected transformants and control strains are inoculated into 100 ml shake flasks with baffles containing 20 ml of liquid pre-culture medium consisting of per liter: 30 g maltose.H₂O; 5 g yeast extract; 10 g hydrolyzed casein; 1 g KH₂PO₄; 0.5 g MgSO₄.7H₂O; 0.03 g ZnCl₂; 0.02 g CaCl₂; 0.01 g MnSO₄.4H₂O; 0.3 g FeSO₄.7H₂O; 3 g Tween 80; 10 ml penicillin (5000 IU/ml)/Streptomycin (5000UG/ml); pH5.5. These cultures are grown at 34 degrees Celsius for 16-24 hours. 10 ml of this culture was inoculated into 500 ml shake flasks with baffles containing 100 ml fermentation medium consisting of per liter: 70 g glucose.H₂O; 25 g hydrolyzed casein; 12.5 g yeast extract; 1 g KH₂PO₄; 2 g K₂SO₄; 0.5 g MgSO₄.7H₂O; 0.03 g ZnCl₂; 0.02 g CaCl₂; 0.01 g MnSO₄.4H₂O; 0.3 g FeSO₄.7H₂O; 10 ml penicillin (5000 IU/ml)/Streptomycin (5000UG/ml); adjusted to pH5.6. These cultures are grown at 34 degrees Celsius until all glucose was depleted (usually after 4-7 days). Samples taken from the fermentation broth are centrifuged (10 min at 5000 × g) in a swinging bucket centrifuge and supernatants collected and filtered over a 0.2 µm filter (Nalgene)

[0470] Supernatants are analysed for expression of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 and Temer07305 by SDS-PAGE and total protein measurements.

Example 2: Construction of a *R. emersonii* expression vectors.

[0471] This Example describes the construction of an expression construct for overexpression Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 in *R. emersonii*. The expression cassette was targeted integrated into the *RePepA* locus.

[0472] In order to target the promoter-reporter constructs into the *pepA* locus, expression vectors were cloned for targeting. The gene with translated protein annotated as protease *pepA* was identified in the genome. Sequences of *Rasamsonia emersonii pepA (RePepA)*, comprising the genomic sequence of the ORF and approximately 3000 bp of the 5' region and 2500 bp of the 3' flanking regions, cDNA and protein sequence, are shown in sequence listings 76, 77 and 78, respectively.

[0473] Two vectors were constructed according to routine cloning procedures for targeting into the *RePepA* locus. The insert fragments of both vectors together can be applied in the so-called "bipartite gene-targeting" method (Nielsen et al., 2006, 43: 54-64). This method is using two non-functional DNA fragments of a selection marker which are overlapping (see also WO2008113847 for further details of the bipartite method) together with gene-targeting sequences. Upon correct homologous recombination the selection marker becomes functional by integration at a homologous target locus. As also detailed in WO 2008113847, two different deletion vectors, Te *pep.bbn* and pEBA1006, were designed and constructed to be able to provide the two overlapping DNA molecules for bipartite gene-targeting. The first vector Te *pep.bbn* (General layout as in Fig. 2) comprises a 1500 bp 5' flanking region approximately 1.5 kb upstream of the *RePepA* ORF for targeting in the *RePepA* locus (ORF and approximately 1500 bp of the *RePepA* promoter), a *lox66* site, and the non-functional 5' part of the *ble* coding region driven by the *A. nidulans gpdA* promoter (P*gpdA*-*ble* sequence missing the last 104 bases of the coding sequence at the 3' end of *ble*, SEQ ID NO: 79). To allow efficient cloning of promoter-reporter cassettes in *E. coli*, a *ccdB* gene was inserted in between the 5' *RePepA* flanking region and the *lox66* site. The second pEBA1006 vector (General layout as in Fig. 3) comprises the non-functional 3' part of the *ble* coding region and the *A. nidulans trpC* terminator (*ble*-*TrpC* sequence missing the first 12 bases of the coding sequence at the 5' end of *ble*, SEQ ID NO: 80), a *lox71* site, and a 2500 bp 3' flanking region of the *RePepA* ORF for targeting in the *RePepA* locus. Upon homologous recombination, the first and second non-functional fragments become functional producing a functional *ble* cassette. Both *RePepA* upstream and downstream gene flanking regions target for homologous recombination of the

bipartite fragments at the predestined *RePepA* genomic locus.

[0474] The *ccdB* gene in vector Te pep.bbn is replaced by Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 expression cassettes according to routine cloning procedures. *R. emersonii* promoter 2, represented by SEQ ID NO: 81, is cloned upstream of the *R. emersonii* Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 coding region with *A. nidulans amdS* terminator, generating construct pEBA. The *A. nidulans amdS* terminator sequence is represented by SEQ ID NO: 82. A schematic representation of pEBA for overexpression of the Gene of interest (GOI) being Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 is shown in Figure 4.

Example 3: Overexpression of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 gene in *Rasamsonia emersonii*

[0475] Linear DNA of pEBA and pEBA1006 are isolated and used to transform *Rasamsonia emersonii* using method as described earlier in WO2011/054899. The linear DNAs can integrate together into the genome at the *RePepA* locus, thus substituting the *RePepA* gene by the Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 and *ble* gene. Transformants are selected on phleomycin media and colony purified and tested according to procedures as described in WO2011/054899. Growing colonies are diagnosed by PCR for integration at the *RePepA* locus using a primer in the *gpdA* promoter of the deletion cassette and a primer directed against the genomic sequence directly upstream of the 5' targeting region. Candidate transformants in which *RePepA* is replaced by Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 */ble* cassettes are obtained.

Example 4: enzymatic activity in Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 overexpressing *Rasamsonia emersonii* strains

[0476] Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 overexpressing strains are fermented in shake flask in Rasamsonia medium 3 and supernatants are analysed for activity according to Table 1 in a suitable assay. An increase in activity is observed in supernatants of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 overexpressing strains compared to the wild-type strain, indicating that overexpression of Temer00088, Temer09484, Temer08028, Temer02362, Temer08862, Temer04790, Temer05249, Temer06848, Temer02056, Temer03124, Temer09491, Temer06400, Temer08570, Temer08163 or Temer07305 improves activity in *R. emersonii*.

Example 5: *Aspergillus niger* shake flask fermentation

[0477] About 10^7 spores of selected transformants and control strains were inoculated into 100 ml shake flasks with baffles containing 20 ml of liquid pre-culture medium consisting of per liter: 30 g maltose.H₂O; 5 g yeast extract; 10 g hydrolyzed casein; 1 g KH₂PO₄; 0.5 g MgSO₄.7H₂O; 0.03 g ZnCl₂; 0.02 g CaCl₂; 0.01 g MnSO₄.4H₂O; 0.3 g FeSO₄.7H₂O; 3 g Tween 80; 10 ml penicillin (5000 IU/ml)/Streptomycin (5000UG/ml); pH5.5. These cultures were grown at 34 degrees Celsius for 16-24 hours. 10 ml of this culture was inoculated into 500 ml shake flasks with baffles containing 100 ml fermentation medium consisting of per liter: 70 g glucose.H₂O; 25 g hydrolyzed casein; 12.5 g yeast extract; 1 g KH₂PO₄; 2 g K₂SO₄; 0.5 g MgSO₄.7H₂O; 0.03 g ZnCl₂; 0.02 g CaCl₂; 0.01 g MnSO₄.4H₂O; 0.3 g FeSO₄.7H₂O; 10 ml penicillin (5000 IU/ml)/Streptomycin (5000UG/ml); adjusted to pH5.6. These cultures were grown at 34 degrees Celsius until all glucose was depleted (usually after 4-7 days). Samples taken from the fermentation broth were centrifuged (10 min at 5000 × g) in a swinging bucket centrifuge and supernatants collected and filtered over a 0.2 µm filter (Nalgene)

Shake flask concentration and protein concentration determination with TCA-biuret method

[0478] In order to obtain greater amounts of material for further testing the fermentation supernatants obtained as described above (volume between 75 and 100 ml) were concentrated using a 10 kDa spin filter to a volume of approximately 5 ml. Subsequently, the protein concentration in the concentrated supernatant was determined via a TCA-biuret method.

[0479] Concentrated protein samples (supernatants) were diluted with water to a concentration between 2 and 8 mg/ml. Bovine serum albumin (BSA) dilutions (0, 1, 2, 5, 8 and 10 mg/ml)

were made and included as samples to generate a calibration curve. Of each diluted protein sample 270 µl was transferred into a 10 ml tube containing 830 µl of a 12% (w/v) trichloro acetic acid solution in acetone and mixed thoroughly. Subsequently, the tubes were incubated on ice water for one hour and centrifuged for 30 minutes, at 4°C and 6000 rpm. The supernatant was discarded and pellets were dried by inverting the tubes on a tissue and letting them stand for 30 minutes at room temperature. Next, 3 ml BioQuant Biuret reagent mix was added to the pellet in the tube and the pellet was solubilized upon mixing followed by addition of 1 ml water. The tube was mixed thoroughly and incubated at room temperature for 30 minutes. The absorption of the mixture was measured at 546 nm with a water sample used as a blank measurement and the protein concentration was calculated via the BSA calibration line.

Example 6: Identification of thermophilic *Rasamsonia emersonii* Temer09484 beta-xylosidase activity on xylobiose

[0480] The beta-xylosidase activity of *Rasamsonia emersonii* Temer09484 was analysed as described above. The supernatant of the Temer09484 *A. niger* shake flask fermentation was concentrated and assayed in two dosages for xylose release from xylobiose after incubation for 24 hours at pH 4,5 and 62°C. The enzyme showed significant xylose release from xylobiose as shown in Table 3. This shows that Temer09484 has beta-xylosidase activity.

Table 3: Effect of *Rasamsonia emersonii* Temer09484 on release of xylose from xylobiose (100 ug/mL) after 24h incubation at pH 4.5 and 62 °C.

Protein ID	Dosage (mg/g DM)	Product xylose (ug/mL)
No enzyme	0	0
Temer09484	1	100
Temer09484	5	100

Example 7: Identification of thermophilic *Rasamsonia emersonii* Temer09484 beta-xylosidase activity on polymeric xylan substrates

[0481] As a second experiment the activity of the beta-xylosidase activity of *Rasamsonia emersonii* Temer09484 was also analysed on polymeric xylan substrates. The supernatant of the Temer09484 *A. niger* shake flask was dosed at 10 mg/g to three different polymeric xylan substrates. From all three substrates xylose was released (Table 4) while no xylooligomers were formed. This shows that Temer09484 also has beta-xylosidase activity on polymeric substrates next to small oligomers as shown in Example 6.

Table 4: Effect of *Rasamsonia emersonii* Temer09484 on release of xylose from several xylan substrates after incubation for 24h at pH 4.5 and 60 °C at a dosage of 10 mg/g DM.

	ug/mL*
Substrate (2 mg/mL)	xylose
Beech wood xylan	320
Birch wood xylan	250
Oat arabinoxylan	334
* All substrates contain < 3.0 ug/mL xylose when no enzyme was added	

Example 8. Improvement of two different cellulose mixtures by addition of Temer09484 for the hydrolysis of lignocellulosic feedstocks

[0482] The supernatant of the Temer09484 *A. niger* shake flask fermentation was concentrated and spiked on a mild acid pretreated corn stover feedstock as described above. The enzyme showed significant xylose release from this feedstock in a wide range of temperatures (50, 65 and 75 °C) and pH values (3.5 - 4.5 - 5.0) used during the 72 hours of incubation as shown in Table 5. This shows that Temer09484 is important for the hydrolysis of lignocellulosic feedstocks.

Table 5: Effect of *Rasamsonia emersonii* Temer09484 on release of xylose (g/L) from mildly acid pretreated corn stover feedstock after 72h incubation at different temperature/pH conditions.

Protein ID	pH 5.0-50°C	pH 3.5-65°C	pH 4.5-65°C	pH 4.5-75°C
Feedstock only- no enzyme	0.14	0.14	0.14	0.13
Temer09484	0.29	0.22	0.23	0.19

[0483] The supernatant of the Temer09484 *A. niger* shake flask fermentation was also tested in combination with 2 different cellulose mixtures: TEC-210 and Celluclast, both with additional BG added. The xylose release from mildly acid pretreated corn stover was improved for both cellulose mixes by the addition of Temer09484 in a wide range of temperatures (50, 65 and 75 °C) and pH values (3.5 - 4.5 - 5.0) used during the 72 hours of incubation as shown in Table 6. This shows that Temer09484 can be used to improve cellulose mixes in a wide range of temperatures and pH values used for the hydrolysis of lignocellulosic feedstocks.

Table 6: Effect of *Rasamsonia emersonii* Temer09484 when spiked to two different cellulose mixes on release of xylose (g/L) from mildly acid pretreated corn stover feedstock after 72h incubation at different temperature/pH conditions.

Protein ID	pH 5.0-50°C	pH 3.5-65°C	pH 4.5-65°C	pH 4.5-75°C
Feedstock only- no enzyme	0.14	0.14	0.14	0.13
TEC-210 +8% BG	0.51	0.45	0.57	0.22

Protein ID	pH 5.0-50°C	pH 3.5-65°C	pH 4.5-65°C	pH 4.5-75°C
TEC-210 + 8% BG + Temer09484	0.63	0.53	0.63	0.33
Celluclast + 8% BG	0.49	0.23	0.27	0.19
Celluclast + 8% BG + Temer09484	0.61	0.24	0.32	0.24

Example 9: Identification of thermophilic *Rasamsonia emersonii* Temer00088 beta-xylosidase activity on xylobiose

[0484] The beta-xylosidase activity of *Rasamsonia emersonii* Temer00088 was analysed as described above. The supernatant of the Temer00088 *A. niger* shake flask fermentation was concentrated and assayed in two dosages for xylose release from xylobiose after incubation for 24 hours at pH 4,5 and 62°C. The enzyme showed significant xylose release from xylobiose as shown in Table 7. This shows that Temer00088 has beta-xylosidase activity.

Table 7: Effect of *Rasamsonia emersonii* Temer00088 on release of xylose from xylobiose (100 ug/mL) after 24h incubation at pH 4.5 and 62 °C.

Protein ID	Dosage (mg/g DM)	Product xylose (ug/mL)
No enzyme	0	0
Temer00088	1	76
Temer00088	5	99

Example 10: Identification of thermophilic *Rasamsonia emersonii* Temer00088 beta-xylosidase activity on polymeric xylan substrates

[0485] As a second experiment the activity of the beta-xylosidase activity of *Rasamsonia emersonii* Temer00088 was also analysed on polymeric xylan substrates. The supernatant of the Temer00088 *A. niger* shake flask was dosed at 10 mg/g to three different polymeric xylan substrates. From all three substrates xylose was released (Table 8) while no xylooligomers were formed. This shows that Temer00088 also has beta-xylosidase activity on polymeric substrates next to small oligomers as shown in Example 9.

Table 8: Effect of *Rasamsonia emersonii* Temer00088 on release of xylose from several xylan substrates after incubation for 20h at pH 4.5 and 60 °C at a dosage of 10 mg/g DM.

	ug/mL*
Substrate (2 mg/mL)	xylose
Beech wood xylan	373
Birch wood xylan	469

	ug/mL*
Substrate (2 mg/mL)	xylose
Oat arabinoxylan	298
* All substrates contain < 3.0 ug/mL xylose when no enzyme was added	

Example 11. Improvement of two different cellulose mixtures by addition of Temer00088 for the hydrolysis of lignocellulosic feedstocks

[0486] The supernatant of the Temer00088 *A. niger* shake flask fermentation was concentrated and spiked on a mild acid pretreated corn stover feedstock as described above. The enzyme showed significant xylose release from this feedstock in a wide range of temperatures (50, 65 and 75 °C) and pH values (3.5 - 4.5 - 5.0) used during the 72 hours of incubation as shown in Table 3. This shows that Temer00088 is important for the hydrolysis of lignocellulosic feedstocks.

Table 9: Effect of *Rasamsonia emersonii* Temer00088 on release of xylose (g/L) from mildly acid pretreated corn stover feedstock after 72h incubation at different temperature/pH conditions.

Protein ID	pH 5.0-50°C	pH 3.5-65°C	pH 4.5-65°C	pH 4.5-75°C
Feedstock only- no enzyme	0.14	0.14	0.14	0.13
Temer00088	0.29	0.26	0.27	0.22

[0487] The supernatant of the Temer00088 *A. niger* shake flask fermentation was also tested in combination with 2 different cellulose mixtures: TEC-210 and Celluclast, both with additional BG added. The xylose release from mildly acid pretreated corn stover was improved for both cellulose mixes by the addition of Temer00088 in a wide range of temperatures (50, 65 and 75 °C) and pH values (3.5 - 4.5 - 5.0) used during the 72 hours of incubation as shown in Table 10. This shows that Temer00088 can be used to improve cellulose mixes in a wide range of temperatures and pH values used for the hydrolysis of lignocellulosic feedstocks.

Table 10 Effect of *Rasamsonia emersonii* Temer00088 when spiked to two different cellulose mixes on release of xylose (g/L) from mildly acid pretreated corn stover feedstock after 72h incubation at different temperature/pH conditions.

Protein ID	pH 5.0-50°C	pH 3.5-65°C	pH 4.5-65°C	pH 4.5-75°C
Feedstock only- no enzyme	0.14	0.14	0.14	0.13
TEC-210 + 8% BG	0.51	0.45	0.57	0.22
TEC-210 + 8% BG + Temer09484	0.62	0.59	0.67	0.39

Protein ID	pH 5.0-50°C	pH 3.5-65°C	pH 4.5-65°C	pH 4.5-75°C
Celluclast + 8% BG	0.49	0.23	0.27	0.19
Celluclast + 8% BG + Temer09484	0.66	0.29	0.35	0.27

Example 12: Identification of thermophilic *Rasamsonia emersonii* xyloglucan specific endoglucanase

[0488] The xyloglucanase activity of *Rasamsonia emersonii* Temer04790 was analysed as described above. The supernatant of the Temer04790 *A. niger* shake flask fermentation was concentrated, added to the substrate xyloglucan and incubated for 24 hours at pH 4.5 and 60°C. The enzyme was able to release several oligomers as shown in Figure 6. This shows that Temer04790 is active on xyloglucan and releases similar oligomers as the commercial cellulase mix Celluclast from *Trichoderma reesei*.

[0489] To quantify the amount of oligomers formed reducing ends were measured after incubation of both Temer04790 and the cellulase mix. Carboxymethylcellulose was also used as substrate to determine the specificity of the enzymes and a higher temperature, 75 °C was used next to 60°C. Temer04790 is specific towards xyloglucan as hardly any activity on CMC was seen in contrast to the cellulase mixture (Table 11). Furthermore, Temer04790 was still active at 75°C while the cellulase mixture was almost inactive on xyloglucan at 75°C.

Table 11: Effect of *Rasamsonia emersonii* Temer04790 on the hydrolysis of xyloglucan (tamarind) and carboxymethylcellulose (CMC) (Sigma) measured by the formation of reducing ends expressed as glucose equivalents (ug/mL) after 24h incubation at pH 4.5 at 60 °C and 75°C.

	60°C pH 4.5		75°C pH 4.5	
	xyloglucan	CMC	xyloglucan	CMC
no enzyme	-17	-18	-18	-18
Temer04790	92	8	69	-9
cellulase mix*	64	132	5	47
* Celluclast from <i>Trichoderma reesei</i> (Sigma)				

Example 13: Identification of thermophilic *Rasamsonia emersonii* arabinofuranosidase activity

[0490] The arabinofuranosidase activity of *Rasamsonia emersonii* Temer05249 was analysed as described above. The supernatant of the Temer05249 *A. niger* shake flask fermentation

was concentrated and added to arabinoxylooligomers at 10 mg/g followed by incubation for 24 hours at pH 4,5 and 65°C. The enzyme showed significant arabinose release from arabinoxylooligomers as shown in Table 12. This shows that Temer05249 has arabinofuranosidase activity.

Table 12: Effect of *Rasamsonia emersonii* Temer05249 on the release of arabinose from wheat arabinoxylan, which was pre-incubated with an endo-xylanase, after incubation for 24h at pH 4.5 and 65 °C at a dosage of 10 mg/g DM.

Protein ID	Arabinose (ug/mL)
No enzyme	4
Temer05249	111

Example 14: Identification of thermophilic *Rasamsonia emersonii* endo-xylanase activity

[0491] The endo-xylanase activity of *Rasamsonia emersonii* Temer03124 was analysed as described above. The supernatant of the Temer03124 *A. niger* shake flask fermentation was concentrated and added to several xylan substrates at 10 mg/g followed by incubation for 20 hours at pH 4,5 and 60°C. The enzyme showed significant release of xylose and a range of xylooligomers as shown in Table 13. This shows that Temer03124 has endo-xylanase activity.

Table 13: Effect of *Rasamsonia emersonii* Temer03124 on release of xylose and xylose oligomers from several xylan substrates after incubation for 20h at pH 4.5 and 60 °C at a dosage of 10 mg/g DM.

Substrate (2 mg/mL)	ug/mL*			
	xylose	xylobiose	xylotriose	xylotetraose
Beech wood xylan	34.3	12.6	10.4	11.4
Birch wood xylan	30.6	17.8	16.1	16.1
Oat arabinoxylan	27.3	17.2	12.5	10.9
Wheat arabinoxylan	33.4	36.9	15.0	5.2
* All substrates contain < 3.5 ug/mL of each product measured if no enzyme is added				

Example 15: Identification of thermophilic *Rasamsonia emersonii* endo-xylanase activity

[0492] The endo-xylanase activity of *Rasamsonia emersonii* Temer08570 was analysed as described above. The supernatant of the Temer08570 *A. niger* shake flask fermentation was concentrated and added to several xylan substrates at 10 mg/g followed by incubation for 20 hours at pH 4,5 and 60°C. The enzyme showed significant release of xylose and a range of xylooligomers as shown in Table 14. This shows that Temer08570 has endo-xylanase with xylobiose, xylotriose and xylotetraose as main products.

Table 14: Effect of *Rasamsonia emersonii* Temer08570 on release of xylose and xylose oligomers from several xylan substrates after incubation for 20h at pH 4.5 and 60 °C at a dosage of 10 mg/g DM.

	ug/mL*			
Substrate (2 mg/mL)	xylose	xylobiose	xylotriose	xylotetraose
Beech wood xylan	5	19	25	25
Birch wood xylan	4	14	17	17
Oat arabinoxylan	0	16	18	15
* All substrates contain < 3.5 ug/mL of each product measured if no enzyme is added				

Example 16: Identification of thermophilic *Rasamsonia emersonii* endo-xylanase activity

[0493] The endo-xylanase activity of *Rasamsonia emersonii* Temer08163 was analysed as described above. The supernatant of the Temer08163 *A. niger* shake flask fermentation was concentrated and added to several xylan substrates at 10 mg/g followed by incubation for 20 hours at pH 4,5 and 60°C. The enzyme showed significant release of xylbiose and xylose as shown in Table 15. This shows that Temer08570 has endo-xylanase activity with xylobiose as main product which was 12 - 25 times higher than the amount of xylose released.

Table 15: Effect of *Rasamsonia emersonii* Temer08163 on release of xylose and xylose oligomers from several xylan substrates after incubation for 20h at pH 4.5 and 60 °C at a dosage of 10 mg/g DM.

	ug/mL*			
Substrate (2 mg/mL)	xylose	xylobiose	xylotriose	xylotetraose
Beech wood xylan	22.4	581.4	0	0
Birch wood xylan	30.9	527.3	0	0
Oat arabinoxylan	13.6	205.1	0	0
Wheat arabinoxylan	5.4	65.9	0	0

	ug/mL*			
Substrate (2 mg/mL)	xylose	xylobiose	xylotriose	xylotetraose
* All substrates contain < 3.5 ug/mL of each product measured.				

Example 17: Identification of thermophilic *Rasamsonia emersonii* alpha-glucuronidase activity

[0494] The alpha-glucuronidase activity of *Rasamsonia emersonii* Temer07305 was analysed as described above. The supernatant of the Temer07305 *A. niger* shake flask fermentation was concentrated and added to aldouronic acids both 1 and 10 mg/g followed by incubation for 24 hours at pH 4,5 and 60°C. The enzyme was able to remove 4-O-methylglucuronic acid from the xylooligomers resulting in the simultaneous release of xylose, xylobiose, xylotriose and xylotetraose as shown in Table 16. This shows that Temer07305 has alpha-glucuronidase activity.

Table 16: The release of xylose and xylose oligomers by *Rasamsonia emersonii* Temer07305 from aldouronic acids as a result of the hydrolysis of 4-O-methylglucuronic acid from these xylooligomers, after incubation for 24h at pH 4.5 and 60 °C at a dosage of 1 and 10 mg/g DM.

Protein ID	Dosage (mg/g DM)	Area/ (mg/mL) substrate			
		xylose	xylobiose	xylotriose	xylotetraose
No enzyme	x	25	6	0	0
Temer07305	1	45	180	58	19
Temer07305	10	120	180	55	9

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Ala Asn Phe Ser His Ser Gly Glu Tyr Ser Trp Ala Thr Ser Phe Pro
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aatggagtcc caagctgtgc caactccttc ttctccaga cgcttctccg agaaaacttt 900
gacttcgttg acgacgggta cgtctcgtcg gattgcgacg ccgtctacaa cgtcttcaac 960
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ccacacggtt acgcccttaa ccagtcggga gccgctcggg actcgtcctt agcaggtacc      1020
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ctggaagccg ccaaggccag tgggttcacg gtcaactatg cattcggtag caacatctcg      1440
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gaccttttct ccacctctca tccgggatac gactacatcg agcaggttcc gttcatcaac      2040
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ctgccgacga tccagccggg cgagactgcc aagttgacga tcccggtgcc gttgggcgcg      2220
attgcgcggg cggacgagaa cggcaacaag gtggtcttcc cgggcaacta cgaattggca      2280
ctgaacaatg agcgatcggt agtgggtgctg ttcacgctga cgggcgatgc ggcgactcta      2340
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<210> 11

<211> 1473

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1473)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 11

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gttggtgctc tcgacaacgg tcttgccatc actcccaga tgggctggaa cacctggaac      120
tcgttcggct gctcgtgaa cgaaaccgtc atcctggatg ctgctgagaa gcttgtgctg      180
ctaggattca aggacctagg atacgagtac gtggtgctgg atgactgctg gtccgctggc      240

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cgtaacgcct ctggetacct ggttcctgac cctgccaaagt tccccaacgg cattgatggt      300
cttgccgaga agatccacgc tcttggcctc aagatcggta tctactcttc tgctggtacc      360
atgacctgcg ctcgttacgc tggctctctt ggatacaggg agaaggatgc cgccctctgg      420
gcctcctggg gtatcgacta cctcaagtac gacaactgct acaaccaggg tcaagagggt      480
actcccaagc tcagctacga ccgctacaac gccatggggc aggctctgaa caagaccggc      540
cgtcccatte tctactccct ctgcaactgg ggtgttgacg gcccctggaa cttcgctccc      600
accattgcca acagctggcg cacctccggt gacctgctca acacctggga ccgtgatgat      660
gccaaactgcc cctgctctga gctcgaaggc ttggactgca agacccccgg ctacaagtgc      720
tcgatcctga acgtcatcaa caaggccgtc tactaccctt ccaaggcctt ccctggtgcc      780
tggaacgacc ttgacatgct ccaggctcgc aacggtggat tgaccgacga tgaggccgtt      840
gctcacatga gcctctgggc tgctttcaag tctcctctcc tcatgaccaa cgtcctcagc      900
aacattgacc ctcccacct gtccatcctg cagaaccccg ccgttctagc ggtgtctcag      960
gaccccgctg gtcctccgt caaccgtatc tggcgctact acgtggatga tgtcgacgcc     1020
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ctccttctga acgctggcag caaggaccgt accatgaacg ccacctgga ggacatcttc     1140
tggaagatg gacctggtgg tactgcctcc caggctcagc agtcctggga tgtctacgat     1200
ctctgggcca accgcatgag caacgagact gctgctgcca tcatcaacgc cgccaacagc     1260
actggaagcg ctgctcctgc tgctcccatc aacatgactg ctcttggtgg tgccaagcac     1320
gtctactctc aggttctctc ctccgactcc aaggctctga tgggtaccaa ggtcggctcc     1380
gtccagccct ccggcacctg caaggctttc gtcaaggccc acggtgttgc catgctccgc     1440
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<210> 12

<211> 468

<212> PRT

<213> Rasamsonia emersonii

<400> 12

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

Glu Lys Leu Val Ser Leu Gly Phe Lys Asp Leu Gly Tyr Glu Tyr Val
35           40           45

Val Leu Asp Asp Cys Trp Ser Ala Gly Arg Asn Ala Ser Gly Tyr Leu
50           55           60

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

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Lys Ile His Ala Leu Gly Leu Lys Ile Gly Ile Tyr Ser Ser Ala Gly
 85 90 95

Thr Met Thr Cys Ala Arg Tyr Ala Gly Ser Leu Gly Tyr Glu Glu Lys
 100 105 110

Asp Ala Ala Leu Trp Ala Ser Trp Gly Ile Asp Tyr Leu Lys Tyr Asp
 115 120 125

Asn Cys Tyr Asn Gln Gly Gln Glu Gly Thr Pro Lys Leu Ser Tyr Asp
 130 135 140

Arg Tyr Asn Ala Met Gly Gln Ala Leu Asn Lys Thr Gly Arg Pro Ile
 145 150 155 160

Leu Tyr Ser Leu Cys Asn Trp Gly Val Asp Gly Pro Trp Asn Phe Ala
 165 170 175

Ser Thr Ile Ala Asn Ser Trp Arg Thr Ser Gly Asp Leu Leu Asn Thr
 180 185 190

Trp Asp Arg Asp Asp Ala Asn Cys Pro Cys Ser Glu Leu Glu Gly Leu
 195 200 205

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

Lys Ala Val Tyr Tyr Pro Ser Lys Ala Phe Pro Gly Ala Trp Asn Asp
 225 230 235 240

Leu Asp Met Leu Gln Val Gly Asn Gly Gly Leu Thr Asp Asp Glu Ala
 245 250 255

Val Ala His Met Ser Leu Trp Ala Ala Phe Lys Ser Pro Leu Leu Met
 260 265 270

Thr Asn Val Leu Ser Asn Ile Asp Pro Pro Thr Leu Ser Ile Leu Gln
 275 280 285

Asn Pro Ala Val Leu Ala Val Ser Gln Asp Pro Val Gly Ser Ser Val
 290 295 300

Asn Arg Ile Trp Arg Tyr Tyr Val Asp Asp Val Asp Ala Asn Gly Tyr
 305 310 315 320

Gly Glu Ile Gln Leu Phe Ser Gly Gly Leu Ala Gly Gly Asp Gln Leu
 325 330 335

Val Leu Leu Leu Asn Ala Gly Ser Lys Asp Arg Thr Met Asn Ala Thr
 340 345 350

Leu Glu Asp Ile Phe Trp Glu Asp Gly Pro Gly Gly Thr Ala Ser Gln
 355 360 365

Val Gln Gln Ser Trp Asp Val Tyr Asp Leu Trp Ala Asn Arg Met Ser
 370 375 380

Asn Glu Thr Ala Ala Ala Ile Ile Asn Ala Ala Asn Ser Thr Gly Ser
385 390 395 400

Ala Ala Pro Ala Ala Pro Ile Asn Met Thr Ala Leu Gly Gly Ala Lys
405 410 415

His Val Tyr Ser Gln Val Pro Pro Ser Asp Ser Lys Ala Leu Met Gly
420 425 430

Thr Lys Val Gly Ser Val Gln Pro Ser Gly Thr Val Lys Ala Phe Val
435 440 445

Lys Ala His Gly Val Ala Met Leu Arg Leu Arg Gln Gln Ser Gln Lys
450 455 460

Lys Asp Glu Leu
465

<210> 13

<211> 23

<212> PRT

<213> *Rasamsonia emersonii*

<400> 13

Met Gly Arg Arg Ile Ala Thr Ala Ala Leu Leu Leu Phe Gly Leu Asn
1 5 10 15

Ala Leu Lys Gly Val Val Ala
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<210> 14

<211> 1670

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1670)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 14

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ccaattgaat ggccaaactt gaaagttgca attggaattt gaataatcct gctcatgcat	180
aagtcaacag aacacatgga actccttcg atgctcgcta aacgagaccg tcatcctaga	240
cgcggccgaa aagctcgtct cgctcggatt caaggatctc ggctatgagt acgtcgtcct	300
ggacgactgc tggcttgccg gccggaacgc gtctggctat ctggtgccgg atccagccaa	360
gtttcccaat ggcatcgatg gcctggcgga gaagatccat gcgctgggct tgaagattgg	420
catttattcc agtgcgggaa ccatgacttg cgcccgtat gctgggtcgt tgggatatga	480

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agagaaggat gcagcgcttt gggctagttg gggggtaagt acgcctaaag ggcataaaac      540
ctgcaaagaa aatacttaaa aaaaaacgta aatagatcga ctacctcaa tacgacaact      600
gctacaacca aggccaaagaa ggcacgcccc agctctcgtg cgaccgctac aacgccatgg      660
gccaaagccct caacaagaca ggcgccccga ttctctactc gctctgcaac tggggcgctcg      720
acggcccgctg gaactttgcc tcgaccatcg ccaactcgtg gcgcacgtcg ggcgatctgc      780
tcaacacgtg ggaccgcgac gacgcaaact gtccgtgcag tgagctcgag ggctcgcact      840
gcaagactcc cgggtacaag tggtcgatcc tgaacgtcat caacaaggcg gtgtattatc      900
cgtctaaggc gttccctggg gcgtggaatg acctggacat gctacgtatg tctccatcta      960
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ccaacgtcct gagcaacatc gaccctccta cgctgtccat cctgcagaac ccggccgtgc     1140
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acgacgtgga cgccaacggg tacggcgaga tccagctgtt cagcggcggc ctggcaggag     1260
gcgaccagct ggtgctgctg ctgaacgcgg ggtcgaagga ccgcaccatg aacgcgacgc     1320
tgaggagcat cttctgggaa gacgggcccg gtggcacggc cagccaggta cagcagagct     1380
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ggggtgcaa gcacgtgtac tcgcagggtc cgccgtccga ctcgaaggcg ttgatgggca     1560
ccaaggttgg gagegtccag ccgagtggga cggtaaggc gtttgtcaag gcgcacggcg     1620
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<210> 15

<211> 1476

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1476)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 15

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tccttcggat gctcgctaaa cgagaccgtc atcctagacg cggccgaaaa gctcgtctcg     180
ctcgattca aggatctcgg ctatgagtac gtcgtcctgg acgactgctg gtctgccggc     240
cggaacgcgt ctggctatct ggtgccggat ccagccaagt ttcccaatgg catcgatggc     300
ctggcggaga agatccatgc gctgggcttg aagattggca ttattccag tgccggaacc     360
atgacttgcg cccgctatgc tgggtcgttg ggatatgaag agaaggatgc agcgctttgg     420
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acgcccgaagc tctcgtacga ccgctacaac gccatgggcc aagccctcaa caagacaggc      540
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accatcgcca actcgtggcg cacgtcgggc gatctgctca acacgtggga ccgcgacgac      660
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tcgatcctga acgtcatcaa caaggcgggtg tattatccgt ctaaggcggt ccctggggcg      780
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gtgtactcgc aggtgccgcc gtccgactcg aaggcggtga tgggcaccaa ggttgggagc     1380
gtccagccga gtgggacggt caaggcgttt gtcaaggcgc acggcggtgg gatgttgccg     1440
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<210> 16

<211> 2046

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1) .. (2046)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 16

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cagtccaacg ccaaggcctt ggttgacttc ggtctggaca ccctaggata ccgctacgtc     240
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ctcaagtacg acaactgcta ctcggtatgct gctgctggct accccgatgc cgactacact     540
cctagcacct ccccgagctt ccgttacgcc aacatgacca aggccttgc ctccgttgac     600
cgcaagatcc tcttccagat ctgcgactgg ggtgttgact tccccgccct ctgggctcct     660

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tctctgggaa acacctggcg catctccaac gacattatct ctgcctggcg caccatcttc 720
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ctcgacatgc ttgaggttgg caacaacgtg ttcacccatcc ccgaggagca gaccacttc 840
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gagagccaga tctccgtcaa catctccctg tctgctggca gctccaacac catcaccatc 1500

tctcccagcc ccatcatctc ctacatcaac gtcacctcgc ctacggttac ctactacccc 1560
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ctgcccgctg gctccaagat tggttacatc tccccaccg gcaacgccag catcaccatt 1680
cccgccaccg tcgtcagcgg ctccggtgac aacaccactg ccgccaccac caccgctggc 1740
aagtacctcg aaattgatta catcaacaac gacatcgctt tctccacctc ctggaccact 1800
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gttctctttt ctggcaagca cagcgaactc ttccggtcctg gtcgtggctg gtgggattct 1920
gccaccttcg gtgtgcttgt tgacggctgg cgcaacggtg agaacactgt tgtcattggc 1980
aaccagggtg gtgacgaggg tgtgcagccc tacggtgccg acttcgtcgg tctgctctg 2040
tacgac 2046

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<210> 17

<211> 657

<212> PRT

<213> Rasamsonia emersonii

<400> 17

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Ser Thr Arg Leu Glu Pro Arg Leu Asp Asn Gly Leu Ala Ile Thr Pro
1           5           10           15

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Pro Met Gly Trp Asn Ser Tyr Asn His Tyr Ser Cys Ser Pro Asn Glu
20           25           30

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Ser Ile Ile Gln Ser Asn Ala Lys Ala Leu Val Asp Phe Gly Leu Asp
35           40           45

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Thr Leu Gly Tyr Arg Tyr Val Thr Thr Asp Cys Gly Trp Thr Val Pro
50           55           60

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Tyr Arg Leu Pro Asn Gly Ser Leu Thr Trp Asn Glu Thr Leu Phe Pro
 65 70 75 80

Ser Gly Phe Pro Ala Leu Gly Gln Tyr Ile His Asp Leu Gly Leu Leu
 85 90 95

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

Asp Gln Val Gly Ser Leu Phe His Glu Gln Gln Asp Ala Glu Thr Phe
 115 120 125

Ala Ala Trp Lys Ala Asp Ala Leu Lys Tyr Asp Asn Cys Tyr Ser Asp
 130 135 140

Ala Ala Ala Gly Tyr Pro Asp Ala Asp Tyr Thr Pro Ser Thr Ser Pro
 145 150 155 160

Ser Phe Arg Tyr Ala Asn Met Thr Lys Ala Leu Ala Ser Val Asp Arg
 165 170 175

Lys Ile Leu Phe Gln Ile Cys Asp Trp Gly Val Asp Phe Pro Ala Leu
 180 185 190

Trp Ala Pro Ser Leu Gly Asn Thr Trp Arg Ile Ser Asn Asp Ile Ile
 195 200 205

Pro Ala Trp Arg Thr Ile Phe Arg Ile Leu Asn Gln Ala Val Pro Gln
 210 215 220

Thr Ser Phe Ala Gly Pro Gly His Trp Pro Asp Leu Asp Met Leu Glu
 225 230 235 240

Val Gly Asn Asn Val Phe Thr Ile Pro Glu Glu Gln Thr His Phe Ser
 245 250 255

Leu Trp Ala Ile Leu Lys Ser Pro Leu Thr Ile Gly Ala Ala Leu Asn
 260 265 270

Asp Thr Leu Thr Thr Ile Arg Asp Ala Ser Leu Gln Ile Leu Lys Gln
 275 280 285

Lys Asp Val Ile Ser Tyr Asn Gln Asp Pro Leu Gly Val Ser Ala Ser
 290 295 300

Leu Lys Arg Arg Trp Thr Glu Glu Gly Phe Glu Val Trp Ser Gly Pro
 305 310 315 320

Ile Ser Gly Gly Lys Thr Val Ala Ala Leu Ile Asn Trp Ala Asp Glu
 325 330 335

Ser Arg Asn Leu Thr Leu Asp Leu Pro Val Val Gly Leu Gln His Ala
 340 345 350

Gln Thr Leu Arg Asn Ile Trp Asp Glu Ser Ala Ala Thr Asn Val Arg
 355 360 365

Thr Ser Tyr Thr Ala Asn Val Ala Ala His Gly Thr Met Leu Val Glu
 370 375 380
 Leu Ala Gly Thr Thr Glu Ala Gly Lys Tyr Pro Ala Asp Ile Phe Ala
 385 390 395 400
 Thr Ser Asp Gly His Ser Thr Thr Phe Glu Asn Ile Tyr Ala Glu Thr
 405 410 415
 Thr Ser Ser Gln Tyr Gln Leu Thr Ile Ala Phe Ala Pro Gly Ser Ser
 420 425 430
 His Ser Ser Glu Ile Thr Ile Arg Thr Ser Leu Gly Gly Phe Lys Thr
 435 440 445
 Ser Ala Lys Val Gln Pro Thr Glu Ser Gln Ile Ser Val Asn Ile Ser
 450 455 460
 Leu Ser Ala Gly Ser Ser Asn Thr Ile Thr Ile Ser Pro Ser Pro Ile
 465 470 475 480
 Ile Ser Tyr Ile Asn Val Thr Ser Pro Ser Gly Thr Tyr Tyr Pro Cys
 485 490 495
 Thr Ser Phe Thr Pro Val Gly Ser Ala Lys Pro Glu Thr Cys Asp Ala
 500 505 510
 Gly Phe Cys Leu Pro Val Gly Ser Lys Ile Gly Tyr Ile Ser Pro Thr
 515 520 525
 Gly Asn Ala Ser Ile Thr Ile Pro Ala Thr Val Val Ser Gly Ser Gly
 530 535 540
 Asp Asn Thr Thr Ala Ala Thr Thr Thr Ala Gly Lys Tyr Leu Glu Ile
 545 550 555 560
 Asp Tyr Ile Asn Asn Asp Ile Ala Phe Ser Thr Ser Trp Thr Thr Gly
 565 570 575
 Ser Asn Ser Arg Asn Leu Thr Ile Ser Val Asn Gly Gly Pro Pro Thr
 580 585 590
 Arg Ile Glu Val Pro Leu Ser Gly Lys His Ser Glu Leu Phe Gly Pro
 595 600 605
 Gly Arg Gly Trp Trp Asp Ser Ala Thr Phe Gly Val Leu Val Asp Gly
 610 615 620
 Trp Arg Asn Gly Glu Asn Thr Val Val Ile Gly Asn Gln Gly Gly Asp
 625 630 635 640
 Glu Gly Val Gln Pro Tyr Gly Ala Asp Phe Val Gly Leu Arg Leu Tyr
 645 650 655

Asp

<210> 18

<211> 25

<212> PRT

<213> *Rasamsonia emersonii*

<400> 18

Met	Thr	Arg	Tyr	Pro	Ser	Leu	Ser	Tyr	Tyr	Ala	Leu	Ser	Ser	Tyr	Leu
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Leu	Phe	Thr	Ser	Cys	Gly	Ala	Leu	Ala
			20				25	

<210> 19

<211> 2315

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1) .. (2315)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 19

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cctccaatgg ggtaagtctc gtcttgtgaa gagttattat tattattatt ctagctagat	180
acagcttggc tcattcatat atgaaccgtg aagatggaac tcctacaacc actactcatg	240
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<210> 20

<211> 2049

<212> DNA

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<220>

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<211> 1821

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<210> 22

<211> 586

<212> PRT

<213> Rasamsonia emersonii

<400> 22

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<212> PRT

<213> Rasamsonia emersonii

<400> 23

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<210> 24

<211> 1824

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<211> 1824

<212> DNA

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<210> 26

<211> 756

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(756)

<223> /organism="*Rasamsonia emersonii*" /mol_type="unassigned DNA"

<400> 26

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<210> 27

<211> 233

<212> PRT

<213> *Rasamsonia emersonii*

<400> 27

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35 40 45

Ser Leu Asn Gly Asn Thr Leu Ala Trp His Thr Ser Trp Thr Trp Glu
50 55 60

Gly Gly Ala Ser Ser Val Lys Ser Phe Ala Asn Ala Ala Tyr Ala Phe
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Thr Ala Thr Gln Leu Ser Gln Ile Ser Ser Ile Pro Thr Thr Trp Gln
85 90 95

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

Phe Thr Ser Ser Ser Pro Ser Gly Ser Asn Glu Tyr Glu Val Met Ile
115 120 125

Trp Leu Ala Ala Leu Gly Gly Ala Phe Pro Ile Ser Ser Thr Gly Thr
130 135 140

Thr Pro Ile Ala Thr Pro Thr Ile Gly Gly Ile Ser Trp Asn Leu Tyr
145 150 155 160

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

Glu Gln Thr Asp Phe Ser Gly Asp Ile Asn Asp Phe Leu Thr Tyr Leu
180 185 190

Gln Gln Asn Glu Gly Leu Ser Ser Ser Gln Tyr Leu Leu Ser Ile Gln
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Ala Gly Thr Glu Pro Phe Thr Gly Glu Asn Ala Glu Leu Lys Thr Thr
210 215 220

Ala Tyr Ser Val Ser Val Ser Thr Ser
225 230

<210> 28

<211> 19

<212> PRT

<213> *Rasamsonia emersonii*

<400> 28

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<210> 29

<211> 819

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(819)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

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<210> 30

<211> 759

<212> DNA

<213> *Rasamsonia emersonii*

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<210> 31

<211> 1923

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1923)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 31

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gag 1923

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<210> 32

<211> 615

<212> PRT

<213> Rasamsonia emersonii

<400> 32

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Ile His Ser Gln Leu Leu Gln Asn Asn Gly Phe Gln Gly Ala Asn Pro
35          40          45

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

Thr Glu Asn Pro Leu Ser Ser Ala Ile Thr Arg Ser Leu Lys Val Thr
65          70          75          80

Val Pro Pro Asn Ala Ser Gly Lys Val Gly Phe Ser Asn Ser Gly Tyr
85          90          95

Trp Gly Ile Pro Val Asn Glu Ala Asn Tyr Thr Asn Ser Phe Tyr Ile
100         105         110

Lys Gly Asp Tyr Asn Gly Asp Val Thr Leu Arg Leu Ala Gly Ala Ser
115         120         125

Ser Gly Ser Leu Tyr Ala Ser Gln Thr Ile Ser Val Lys Ser Asn Ser
130         135         140

Ser Ser Tyr Thr Tyr Val Glu Thr Gln Tyr Pro Val Lys Gln Ala Pro
145         150         155         160

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

His Asp Arg Pro Asn Gly Leu Lys Pro Glu Ile Ala Asn Val Leu Val
 195 200 205

Asp Met Lys Gly Ser Phe Leu Arg Phe Pro Gly Gly Asn Asn Leu Glu
 210 215 220

Gly Leu Thr Pro Ala Thr Arg Trp Lys Trp Asn Glu Thr Ile Gly Pro
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Leu Thr Ser Arg Pro Gly Arg Gln Gly Asn Trp Gly Tyr Pro Asn Thr
 245 250 255

Asp Ala Leu Gly Leu Asn Glu Tyr Phe Leu Trp Ile Gln Asp Met Gly
 260 265 270

Leu Thr Ala Val Leu Gly Val Trp Asp Gly Leu Thr Ile Gly Gly Pro
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Ser Pro Gln Val Ile Thr Gly Asp Ala Leu Lys Pro Tyr Ile Asp Asp
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Val Leu Asn Glu Leu Glu Tyr Ile Leu Gly Asp Lys Asp Thr Thr Tyr
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Gly Lys Leu Arg Ala Ser His Gly Phe Pro Asp Pro Trp Pro Leu Gln
 325 330 335

Tyr Val Glu Ile Gly Asn Glu Asp Asn Leu Asn Gly Gly Gly Pro Ser
 340 345 350

Tyr Ala Glu Arg Phe Thr Ala Phe His Asp Ala Ile Lys Ala Lys Tyr
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Pro His Leu Thr Ile Ile Ser Ser Thr Asp Gln Tyr Leu Pro Asn Pro
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Lys Pro Lys Gly Ile Trp Met Asp Trp His Thr Tyr Ser Pro Ala Gly
 385 390 395 400

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 405 410 415

Pro Tyr Phe Val Gly Glu Tyr Ala Cys Ile Ser Leu Asp Asn Gly Thr
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Glu Leu Ala Gln Pro Ile Met Gln Gly Ser Val Ala Glu Ala Val Phe
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Met Ile Gly Met Glu Arg Asn Ser Asp Val Val Lys Met Ala Ala Tyr
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Ala Pro Leu Leu Gln Gln Tyr Gly Gly Tyr Thr Trp Asn Asp His Val
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Pro Asn Leu Ile Met Phe Asn Asn Asn Pro Asn Gly Ile Val Arg Ser
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Thr Ser Tyr Tyr Val Gln Gln Met Phe Ser Val Asn Arg Gly Ser Thr
500 505 510

Ile Leu Pro Val Glu Ser Asp Gly Ser Phe Gly Pro Val Tyr Tyr Val
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Ala Ser Lys Thr Ser Asp Asn Lys Thr Tyr Tyr Val Lys Phe Ala Asn
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Tyr Gly Pro Thr Pro Gln Pro Val Thr Val Asn Ile Pro Lys Thr Glu
545 550 555 560

Thr Gly Arg Leu Thr Thr Leu Ser Gly Ala Ala Thr Ala Ala Asn Thr
565 570 575

Trp Ser Ser Pro Asn Ala Val Thr Pro Lys Thr Ser Asn Val Ser Ser
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Val Ala Val Leu Ala Val Glu
610 615

<210> 33

<211> 26

<212> PRT

<213> *Rasamsonia emersonii*

<400> 33

Met Ser Leu Ala Ser Lys Asn Leu Leu Ala Cys Gly Leu Phe Leu Ala
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20 25

<210> 34

<211> 2381

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1) .. (2381)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

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<210> 35

<211> 1926

<212> DNA

<213> *Rasamsonia emersonii*

<220>

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<222> (1)..(1926)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

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<210> 36

<211> 2235

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1) .. (2235)

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<400> 36

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<211> 722

<212> PRT

<213> *Rasamsonia emersonii*

<400> 37

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25

30

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

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Met	Glu	Pro	Val	Leu	Ala	Val	Tyr	Ala	Gly	Phe	Ser	Leu	Asp	Ile	Trp
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Gly	Gln	Glu	Gly	Thr	Ser	Tyr	Pro	Glu	Asp	Arg	Met	Asp	Glu	Ile	Val
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Pro Ser Phe Phe Leu Glu Asn Phe Asn Tyr Phe Asp Asn Trp Gln Ala
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Ala Thr Asn Asn Thr Asp Val Lys Ile Phe Val Gly Glu Tyr Ser Val
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Tyr Gln Ile Asp Thr Pro Asp Gly Tyr Val Asn Phe Ser Asn Pro Glu
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Gly Ile His Met Phe Phe Pro Glu Leu Val Ser Ala Ile Ala Glu Ala
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Val Tyr Leu Leu Gly Ala Glu Arg Asn Pro Asn Thr Val Thr Met Thr
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Ser Tyr Ala Pro Ser Phe Gln Asn Leu Asn Trp Tyr Asn Trp Ser Pro
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Lys Gly Val Asn Gly Thr Ile Leu Val Arg Arg Arg Ile Cys Leu Gln
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Leu His Ile Tyr Thr Val Pro Asp Glu Leu Thr Ile Ala Phe Leu Gln
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Thr His Pro Asn Leu Tyr Gly Phe Asn Tyr Leu Asn Asn Gln Thr Ala
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<210> 38

<211> 23

<212> PRT

<213> Rasamsonia emersonii

<400> 38

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Leu Thr Ser Leu Val Asp Ala
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<211> 2483

<212> DNA

<213> Rasamsonia emersonii

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<211> 506

<212> PRT

<213> *Rasamsonia emersonii*

<400> 42

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Asn Phe Thr Ala Thr Tyr His Trp Leu Asp Gly Val Gly Pro Lys Asp
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100 105 110

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

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Pro Leu Ala Ala Glu Arg Ala Ile Glu Ile Thr Ser Ser Leu Ile Asp
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<211> 2005

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gctgctgaga tggaaggcag agtga	2005

<210> 45

<211> 1521

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1521)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 45

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tgcattctacg gaggcatata tgatcccga aatcctctgt cggacgagaa tggctttcga	180
aaggatgttc tggaggctct gaaggagctc aatatccctg tggttcgcta tcccggcggg	240
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aacctgcgga ggaagaatgg tcgggagaag ccctacaatg ttaaatactg ggctctgggt	540
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gcgtatcaat gggccaaagc tctcaagctg ctcgatccga atataattct cattctttgc	660
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gacgtcagcg cggccttggg tgacgatggc tttgtcaacg tagttgtcgt caacatccat	1320
gaaactaagg actttaagac caacgtcaag ggcgtcagt gaggtcctgt cactgtctac	1380

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acggtcaccg gagccgatgt gtctgctact aacatgaagg ggaagcaaga ggtgggagtt      1440
caggagagta catgggacgg caaaggcagt tatgtgttcc cgaagcattc tctgacgctg      1500
ctgagatgga aggcagagtg a                                     1521

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<210> 46

<211> 966

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(966)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 46

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tccgctgagc ctgtccgtgt tctcgacacc gacttcctctg acccttgctt gatctccacc      120

aacggcaagt actacgcttt cgccaccact ggcaacggtg tcaacgtcca gattgcccag      180
tcggatgact tcgtcacctg ggagcgtctt gctggctactg atgcccttcc tgggtcccttc      240
cccagctggg ttgcctcctc ccccaactgtc tgggctcccc atgtcatcca gcgtctggac      300
ggtacctacg tcatgtacta ctctgctctt tcttccaccg accccagcaa gcactgcttc      360
ggtgctgcca cctcgacctc catcaccggt ccctacaagc ccgaggacaa ctacattgcc      420
tgccccctcg accaggggtg tgccatcgac cccgatggat tcatcgatga tgacggcacc      480
atgtacgtgg tctacaaggt tgacggcagc aacctggatg gagatggcac catccacccc      540
actcccatca tgctccaggc tctggagcct gacggcatca ccccaactgg tgaccccatc      600
aagctcctcg accgtgatgc ctccgacggc atcttgattg aggctccctc cctcgtccgc      660
tccgttgttt ccggcaccta ctctctgagc tactcttctc actactacgc ctccctgcac      720
tacgacgttg gatacgccac tggccctgcc gtcaagggtc ccttcaccaa ggcccaggct      780
cctcttctcg tcaccggtga caacaccacc aacgcoggtc ctctgggtgg tcccggtggt      840
gccgacttct ccgtcgacgg cactcgtatc gtgttccacg ctttcgagaa cggccgcaac      900
ctgaccaacg gccgtgctct ctacaccagc ggtatcgtcc tcgagggtga tgtcattcgc      960
ctagtt                                     966

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<210> 47

<211> 300

<212> PRT

<213> *Rasamsonia emersonii*

<400> 47

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Glu Pro Val Arg Val Leu Asp Thr Asp Phe Pro Asp Pro Cys Leu Ile
1           5           10          15

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Ser Thr Asn Gly Lys Tyr Tyr Ala Phe Ala Thr Thr Gly Asn Gly Val

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

<210> 48

<211> 22

<212> PRT

<213> Rasamsonia emersonii

<400> 48

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1				5					10					15	

Ser Ala Ala Ala Ser Ala

20

<210> 49

<211> 1026

<212> DNA

<213> Rasamsonia emersonii

<220>

<221> source

<222> (1)..(1026)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 49

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aacggcaagt	actatgcctt	tgcgacgacg	ggcaatggcg	tcaacgtgca	aatcgcccag	180
toggacgact	tcgtcaacctg	ggagcgtctg	gctggcaactg	atgccctgcc	gggaccgttt	240
ccctcgtggg	tggcgtcttc	gccgactgta	tgggcgccgg	acgtgattca	acgggtgcgt	300
ttaaactata	cataggattt	ttcatcgtca	tatctaacga	ggtgcatcta	gctcgatggc	360
acgtacgtga	tgtactactc	gcacctctcg	agcacggacc	cgccaagca	ctgctttggc	420
gccgccacct	cgacctccat	cacaggccct	tacaagcccg	aagacaacta	catcgccctgt	480
cogctggacc	agggcggcgc	catcgaccca	gacggcttca	tcgacgacga	cggcaccatg	540
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actaatggca	gggcgctgta	tacgtcgggg	attgtccttg	agggggacgt	catacggttg	1020
gtgtag						1026

<210> 50

<211> 969

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(969)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 50

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aacggcaagt actatgcctt tgcgacgacg ggcaatggcg tcaacgtgca aatcgcccag	180
toggacgact tcgtcacctg ggagcgtctg gctggcactg atgccctgcc gggaccgttt	240
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ggcgcgcgcca cctcgacctc catcacaggc ccttacaagc ccgaagacaa ctacatcgcc	420
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gcagactttt ccgtcgacgg gacgaggatt gtctttcatg cgtttgagaa tggaaggaat	900
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<210> 51

<211> 1998

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1998)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 51

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gacaactccg tccagcgtca ccaccgctct ccttccggcc gtcccgccga tcttccatt	240
actaccagct actccacctc caacggcact cagactgcca cgttcaccaa cggacagccc	300

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ggatccagct acccaccat caccgcaat cagatcgca cggcaccac cggatccgct 300
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atcctcacco gcaacatt

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<210> 52

<211> 647

<212> PRT

<213> *Rasamsonia emersonii*

<400> 52

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Lys Thr Glu Asn Ser Thr Ala Asn Thr Pro Gly Ile Arg Leu Ile Asn
1           5           10           15

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Gly His Glu His Val Leu Ile Gln Pro Trp Gly Ala Asp Gly Phe Arg
20 25 30

Val Arg Ala Thr Leu Asn Arg Phe Pro Asp Asn Ser Val Gln Arg His
35 40 45

His Arg Ser Pro Ser Gly Arg Pro Ala Asp Leu Pro Ile Gly Thr Ser
50 55 60

Tyr Ser Thr Ile Asn Ala Thr Gln Thr Ala Thr Val Thr Asn Gly His
65 70 75 80

Ala Ser Val Val Val Asp Lys Gly Gln Leu Ser Phe Tyr Arg Val Asn
85 90 95

Gly Asn Asn Ser Lys Thr Leu Val Leu Gln Glu Leu Trp Leu Gln Thr
100 105 110

Pro Gly Phe Pro Ala Arg Trp Tyr Gln Lys Arg Asp Ala Arg Arg Gly
115 120 125

Phe Arg Ala Gln Phe Ser Phe Val Ala Pro Asp Ser Pro Thr Glu Arg
130 135 140

Leu Phe Gly Thr Gly Gln Asp Leu Thr Gly Ser Leu Ile Lys Lys Asn
145 150 155 160

Gln Thr Ile Asp Leu Val Lys Phe Asn Thr Leu Asn Pro Ile Pro Thr
165 170 175

Ile Val Ser Asp Arg Gly Tyr Leu Phe Phe Trp Asn Val Pro Ser Leu
180 185 190

Gly Gln Met Glu Leu Ser Pro Thr Arg Thr Ser Phe Leu Ser Asp His
195 200 205

Thr Ser Val Val Asp Tyr Tyr Ile Ala Ile Arg Pro Glu Ala Asp Tyr
210 215 220

Asp Gly Leu Leu Gln Arg Tyr Thr Ser Val Thr Gly Arg Ser Pro Met
225 230 235 240

Ile Pro Asp Phe Gly Thr Gly Tyr Trp Gln Cys Lys Leu Arg Tyr Ala
245 250 255

Thr Gln Glu Glu Leu Leu Asn Val Thr Met Gly Phe Ala Glu Arg Lys
260 265 270

Ile Pro Val Ser Met Phe Ile Ile Asn Tyr Leu Ser Trp Ser His Glu
275 280 285

Gly Asp Trp Ala Leu Asn Ala Ser Ala Trp Pro Asp Pro Ala Lys Met
290 295 300

Ala Ala Glu Ala Glu Leu Met Ala Ser Val Trp Pro Ser Ile Glu Asp
305 310 315 320

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305              310              315              320
Ala Ser Pro Asn Trp Ala Glu Met Gln Ser Leu Gly Phe Ala Ala Gln
              325              330              335

Thr Phe Asp Pro Leu Asp Ile Ala Gly Tyr Trp Gln Asn Lys Tyr Gln
              340              345              350

Asn Gly Ile Arg Asn Phe Trp Leu Asp Glu Asp Glu Gly Gly Gln Val
              355              360              365

Ala Leu Asp Val Tyr Pro Trp Thr Asp Tyr Tyr Leu Gly Pro Gly Asp
              370              375              380

Gln Tyr Ala Met Leu Phe Pro Tyr Phe His Gln Met Gly Val Phe Glu
              385              390              395              400

Gly Gln Met Lys Thr Val Gly Ser Asn Asn Val Ser Ala Val Ser Leu
              405              410              415

Ser Arg Ser Ser Ala Asn Trp Asp Ser Met Lys Met Met Ile Ser Ala
              420              425              430

Gly Gln Ser Met Ala Met Ser Gly Gln Gly Trp Trp Thr Leu Asp Ile
              435              440              445

Gly Gly Phe Lys Thr Asp Gly Gln Ser Asn Ser Ala Asn Ile Ser Asp
              450              455              460

Pro Glu Tyr Gln Glu Leu Phe Val Arg Trp Leu Gln Trp Gly Thr Phe
              465              470              475              480

Leu Pro Ile Met Arg Asn His Gly Met Arg Thr Cys Leu Pro Ser Ala
              485              490              495

Gln Glu Gly Phe Leu Thr Cys Pro Ser Glu Pro Trp Ser Tyr Gly Pro
              500              505              510

Asp Asn Leu Pro Ile Ile Val Ser Tyr Ile Asn Leu Arg Tyr Lys Leu
              515              520              525

Gln Pro Tyr Ile Lys Ala Leu Phe Arg Met Leu Ser Glu Ser Gly Arg
              530              535              540

Ala Met Met Arg Pro Leu Phe Met Asp Phe Ser Leu Ser Asp Pro Tyr
              545              550              555              560

Thr Leu Glu Ala Thr Glu Asp Leu Lys Leu Gln Tyr Met Phe Gly Pro
              565              570              575

Arg Leu Leu Val Ser Pro Val Thr Thr Tyr Arg Ala Thr Asn Ala Thr
              580              585              590

Val Tyr Leu Pro Lys Leu Pro Ser Asp Ala Pro Asp Thr Lys Trp Thr
              595              600              605

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Tyr Trp Trp Thr Asn Glu Ser Phe Asp Gly Gly Gln Trp Val Thr Val
610 615 620

Pro Ala Asn Lys Ser Ile Ile Pro Leu Phe Arg Leu Gly Ser Glu Ala
625 630 635 640

Asp Ile Leu Thr Arg Asn Ile
645

<210> 53

<211> 19

<212> PRT

<213> Rasamsonia emersonii

<400> 53

Met Leu Ser Ala Phe Leu Phe Ser Ser Pro Thr Leu Ser Ser Pro Gln
1 5 10 15

Ser Ala Ser

<210> 54

<211> 2684

<212> DNA

<213> Rasamsonia emersonii

<220>

<221> source

<222> (1)..(2684)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 54

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gacagtgcgt agccacggaa aacgcattct gtctcatctga ctaatttctt acctgctgat    240
tgacactctg tagatgaagc gtacagcgtc atcatagatc cccctctgga cggcccgag    300
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<210> 55

<211> 2001

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(2001)

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<210> 56

<211> 840

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(840)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 56

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<210> 57

<211> 233

<212> PRT

<213> *Rasamsonia emersonii*

<400> 57

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Met Ala Thr Leu Cys Met Ser Thr Tyr Leu Asn Asp Leu Cys Ile Val
20             25             30

Pro Gly Gly Met Thr Lys Ile Ser Asp Ile Thr Asn Ser Thr Thr Asp
35             40             45

Val His Gly Trp Ile Leu Arg Asp Asp Gly Ala Arg Glu Ile Leu Ala
50             55             60

Val Phe Arg Gly Thr Glu Ser Leu Gln Asn Tyr Ala Thr Asp Thr Asn
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Tyr Thr Leu Ala Pro Phe Asp Ile Phe Pro Gln Cys Glu Gly Cys Glu

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[illegible]

<210> 58

$\langle 211 \rangle$ 20

<212> PRT

<213> *Rasamsonia emersonii*

<400> 58

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Ala Ile Ile Lys
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<210> 59

$\langle 211 \rangle$ 1100

<212> DNA

<213> *Rasamsonia emersonii*

$\langle 220 \rangle$

<221> source

$\langle 222 \rangle$ (1)..(1100)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 59

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<210> 60

<211> 843

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(843)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

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<210> 61

<211> 1374

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1374)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

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<210> 62

<211> 442

<212> PRT

<213> Rasamsonia emersonii

<400> 62

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 20 25 30

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 35 40 45

Gly Arg Ala Gly Gly Ala Gln Leu Gly Ala Pro Ala Arg Gly Trp Ile
 50 55 60

Trp Gly Ile Asp Glu Tyr Gln Gly Arg Leu Asn Ser Thr Leu Ser Asn
 65 70 75 80

Tyr Arg Thr Cys Arg Gln Tyr Gly Ala Asp Phe Ile Ile Leu Pro His
 85 90 95

Asp Ile Trp Gly Thr Asp His Ala Asn Asp Ser Thr Ile Trp Pro Gly
 100 105 110

Asp Asn Gly Asp Trp Thr Asp Tyr Asp Asn Phe Ile Arg Arg Leu Met
 115 120 125

Ala Asp Leu Lys Ala Asn Asn Ala Leu Asp Gly Leu Val Trp Asp Val
 130 135 140

Trp Asn Glu Pro Asp Ile Ser Ile Phe Trp Thr Arg Ser Gln Gln Gln
 145 150 155 160

Trp Ile Asp Leu Tyr Ile Arg Thr His Lys Leu Leu Arg Gln Asp Pro
 165 170 175

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

Phe Pro Asn Asn Thr Trp Trp Thr Asn Trp Leu Asp Gln Ile Ala Gly
 195 200 205

Asn Gln Thr Ile Pro Asp Gln Tyr Ala Tyr His Leu Glu Gly Asp Pro
 210 215 220

Ser Ser Pro Asp Asp Asp Leu Gln Asn Thr Asn Ala Ser Leu Ala Ala
 225 230 235 240

Met Leu Gln Thr Tyr Arg Leu Pro Ser Arg Gln Ile Asn Ile Asn Glu

245					250					255					
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	290					295					300				
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Tyr	Pro	Val	Tyr	Arg	Tyr	Tyr	Tyr	Arg	Asn	Met	Thr	Gly	Gln	Arg	Val
				325					330					335	
Gln	Thr	Thr	Gly	Ser	Glu	Asp	Arg	Leu	Leu	Asp	Val	Tyr	Ala	Thr	Val
			340					345					350		
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	370					375					380				
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385					390					395					400
Trp	Glu	Glu	Val	Asp	Arg	Pro	Glu	Asp	Leu	Gly	Val	Thr	Ala	His	Thr
				405					410					415	
Tyr	Ser	Gly	Asp	Ser	Val	Thr	Phe	Pro	Ile	Tyr	Gln	Thr	Asp	Asn	His
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<210> 63

<211> 16

<212> PRT

<213> *Rasamsonia emersonii*

<400> 63

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<210> 64

<211> 1377

<212> DNA

<213> *Rasamsonia emersonii*

$\langle 220 \rangle$

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<400> 64

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<210> 65

<211> 1377

<212> DNA

<213> Rasamsonia emersonii

<220>

<221> source

<222> (1)..(1377)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 65

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ggcttccgat acggccgcgc aggcgggtgcg cagctagggg cccccgcgcg aggctggatc      240
tggggcatcg acgagtacca gggcgtctc aactcgaccg tgtcgaatta cgcacctgt      300
cgtcagtacg ggcgcgactt tatcatcttg ccgcacgaca tctggggcac cgaccacgcc      360
aacgactcaa caatctggcc cggcgacaac ggcgactgga ccgactacga caacttcac      420
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<210> 66

<211> 1425

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1425)

<223> /organism="Rasamsonia emersonii"/mol_type="unassigned DNA"

<400> 66

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ttcagcgaag cgttccagcg tgetgaggat atctacggca aggacgggtct ttctcctgag      180
aaccgtaccc gtgtcctcga cctcctcttc tccgacaccc acggtgctgg tctgaccatt      240
gtccgcaacg gcatctggcg cagcaacagc agcatcaagg acttcatgaa ctocattgag      300
cccttctccc ccggctcccc ctctgctcct cctcactacg tgtgggaccg caacgactct      360
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<210> 67

<211> 459

<212> PRT

<213> Rasamsonia emersonii

<400> 67

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 20 25 30

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 35 40 45

Val Leu Asp Leu Leu Phe Ser Asp Thr His Gly Ala Gly Leu Thr Ile
 50 55 60

Val Arg Asn Gly Ile Gly Ser Ser Asn Ser Ser Ile Lys Asp Phe Met
 65 70 75 80

Asn Ser Ile Glu Pro Phe Ser Pro Gly Ser Pro Ser Ala Pro Pro His
 85 90 95

Tyr Val Trp Asp Arg Asn Asp Ser Gly Gln Val Trp Leu Ser His Glu
 100 105 110

Ala Ala Ser Tyr Gly Val Asn Thr Phe Tyr Ala Asp Ala Trp Ser Ala

115						120						125			
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Cys	Gly	Val	Thr	Asn	Thr	Ser	Cys	Ala	Ser	Gly	Asp	Trp	Lys	Gln	Ala
145					150					155					160
Tyr	Ala	Asn	Tyr	Leu	Val	Gln	Tyr	Val	Arg	Phe	Tyr	Gln	Gln	Val	Gly
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Thr	Tyr	Ala	Ser	Met	Leu	Ser	Asp	Gly	Thr	Gln	Ala	Ala	Asp	Phe	Ile
	195						200					205			
Lys	Val	Leu	Ala	Pro	Thr	Val	Lys	Ala	Ala	Gly	Leu	Asp	Val	Lys	Leu
	210					215					220				
Thr	Cys	Cys	Asp	Gly	Val	Gly	Trp	Glu	Glu	Gln	Arg	Ala	Met	Leu	Pro
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Gly	Leu	Gln	Ala	Gly	Gly	Pro	Glu	His	Ser	Ala	Glu	Ser	Tyr	Leu	Ser
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Val	Ile	Thr	Ala	His	Gly	Tyr	Asn	Ser	Pro	Pro	Thr	Thr	Pro	Leu	Glu
			260					265					270		
Thr	Ser	Leu	Pro	Val	Trp	Met	Thr	Glu	Trp	Ala	Asp	Leu	Asn	Gly	Asn
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Tyr	Thr	Ala	Ala	Trp	Tyr	Glu	Asn	Gly	Ala	Ala	Gly	Glu	Gly	Leu	Thr
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Trp	Ala	Asn	Arg	Ile	Gln	Asp	Ala	Phe	Thr	Arg	Ser	Asn	Val	Ser	Ala
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Phe	Leu	His	Trp	Ile	Gly	Ala	Glu	Asn	Gly	Thr	Ser	Asn	Ser	Pro	Leu
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Ile	Asn	Leu	Asn	Gly	Asp	Ser	Tyr	Val	Ala	Thr	Lys	Arg	Leu	Trp	Ala
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Phe	Gly	Gln	Phe	Ser	Arg	Phe	Val	Arg	Pro	Gly	Ala	Val	Arg	Ile	Asp
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Ala	Val	Ser	Ser	Asp	Ser	Leu	Val	Thr	Val	Ser	Ala	Phe	Gln	Asn	Lys
	370					375					380				
Asp	Asn	Gly	Val	Val	Ala	Thr	Gln	Ala	Ile	Asn	Asn	Ala	Asp	Thr	Asp
385					390					395					400
Tyr	Glu	Val	Glu	Val	Glu	Leu	Thr	Gly	Tyr	Gly	Pro	Val	Ser	Val	Ile
				405					410					415	

Gln Pro Tyr Leu Thr Asn Asn Glu Asn Asp Leu Glu Ala Ser Lys Pro
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Pro Ala Arg Ser Leu Val Ser Phe Val Ser Lys
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<210> 68

<211> 16

<212> PRT

<213> Rasamsonia emersonii

<400> 68

Met Ile Ser Leu Leu Ala Leu Ala Ala Val Pro Ile Pro Val Leu Ser
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<210> 69

<211> 1428

<212> DNA

<213> Rasamsonia emersonii

<220>

<221> source

<222> (1)..(1428)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

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aaccgcacca gagtgtctga tctcctgttc agcgacaccc atggcgccgg cctgaccatc	240
gtccgcaatg gcatcggtct cagcaatagc tccatcaagg acttcatgaa ctccatcgag	300
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ggccaggtgt ggctgtccca cgaagcggcc tcgtatggcg tcaacacgtt ctatgccgac	420
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gccgacttca tcaaagttct agcaccaccc gtcaaggcgg caggactcga cgtcaagctc	720
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tccccgccca caacgcctct tgagacctcg ttgccagtgt ggatgaccga gtgggccgat	900
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gtcgcgacca agcggctgtg ggcgttcggc cagttcagtc gattcgtccg gccgggtgcc      1140
gtccgcatcg acgcggtcag ttccggactcc ttgggtcacgg tgagcgcggt ccagaacaag      1200
gataacggcg tgggtggccac gcaggccatc aacaatgccg acacagacta tgaggtcgag      1260

gtggagttga cgggttatgg acccgtgtcc gttatccagc cgtatctgac gaacaatgaa      1320
aacgacctgg aagcctccaa gccgatcatc gcgcttctgt ttggggcagc aaccaagttc      1380
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<210> 70

<211> 1428

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(1428)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 70

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aacgacctgg	aagcctccaa	gccgatcatc	gcgcttgctg	ttggggcagc	aaccaagttc	1380
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<210> 71

<211> 3036

<212> DNA

<213> *Rasamsonia emersonii*

<220>

<221> source

<222> (1)..(3036)

<223> /organism="Rasamsonia emersonii" /mol_type="unassigned DNA"

<400> 71

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<210> 72

<211> 991

<212> PRT

<213> Rasamsonia emersonii

<400> 72

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20 25 30

Trp Pro Ala Val Leu Arg Ala Ala Gly Asp Leu Ala Val Asp Phe Gly

35					40					45					
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50					55					60					
Thr	Ser	Ser	Gly	Leu	Ala	Ala	Val	Ser	Asn	Lys	Gly	Pro	Val	Ile	Ile
65				70					75					80	
Ala	Gly	Thr	Ile	Gly	Asn	Ser	Ser	Leu	Ile	Asn	Ala	Leu	Ala	Gln	Ser
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Gly	Lys	Ile	Asp	Val	Ser	Ala	Thr	Glu	Gly	Arg	Trp	Glu	Ala	Phe	Gln
			100					105					110		
Thr	Glu	Ile	Val	Asp	Asn	Pro	Phe	Pro	Gly	Ile	Ser	Arg	Ala	Leu	Val
		115					120					125			
Val	Ser	Gly	Ser	Asp	Arg	Arg	Gly	Thr	Val	Tyr	Gly	Leu	Tyr	Asp	Ile
	130					135					140				
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		195				200						205			
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935

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<213> *Rasamsonia emersonii*

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301

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Patentkrav

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5 aminosyresekvens, der kodes af nukleotidsekvensen ifølge SEQ ID NO: 36, SEQ ID NO: 39, eller et variant polypeptid eller et variant polynukleotid deraf, hvor det variante polypeptid har mindst 85 % sekvensidentitet med sekvensen ifølge SEQ ID NO: 37, eller det variante polynukleotid koder for et polypeptid, der
10 har mindst 85 % sekvensidentitet med sekvensen ifølge SEQ ID NO: 37, hvor polypeptidet eller det variante polypeptid har alfa-arabinofuranosidaseaktivitet.
2. Isoleret nukleinsyresekvens, der koder for en
15 hemicellulase, hvor nukleinsyresekvensen er valgt fra gruppen, der består af:
- (a) en nukleinsyresekvens, der har mindst 70 % identitet med nukleinsyresekvensen ifølge SEQ ID NO: 36, SEQ ID NO: 39 eller SEQ ID NO: 40;
- 20 (b) en nukleinsyresekvens, der koder for (i) aminosyresekvensen ifølge SEQ ID NO: 37, (ii) en aminosyresekvens, der har mindst 85 % identitet med aminosyresekvensen ifølge SEQ ID NO: 37, eller (iii) en aminosyresekvens, der adskiller sig i 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 eller 12 aminosyrer fra
25 aminosyresekvensen ifølge SEQ ID NO: 37; eller
- (c) en nukleinsyresekvens, som er det reverse komplement til en nukleinsyresekvens som defineret i (a) eller (b), hvor hemicellulasen har alfa-arabinofuranosidaseaktivitet.
- 30 3. Nukleinsyrekonstruktion eller vektor, der omfatter nukleinsyresekvensen ifølge krav 2.
4. Rekombinant celle, der omfatter et polypeptid ifølge krav 1, en nukleinsyresekvens ifølge krav 2 eller en
35 nukleinsyrekonstruktion eller vektor ifølge krav 3, hvor cellen fortrinsvis er en svampecelle, fortrinsvis en svampecelle valgt fra gruppen, der består af slægterne Acremonium, Agaricus, Aspergillus, Aureobasidium, Chrysosporium, Coprinus,

Cryptococcus, Filibasidium, Fusarium, Humicola, Magnaporthe, Mucor, Myceliophthora, Neocallimastix, Neurospora, Paecilomyces, Penicillium, Piromyces, Panerochaete, Pleurotus, Schizophyllum, Talaromyces, Rasamsonia, Thermoascus, Thielavia,
5 Tolypocladium og Trichoderma.

5. Celle ifølge krav 4, hvor et eller flere gener er deleteret, knockoutet eller ødelagt fuldstændigt eller delvist, hvor eventuelt genet koder for en protease.

10

6. Fremgangsmåde til fremstilling af et polypeptid ifølge krav 1, der har hemicellulaseaktivitet, hvilken fremgangsmåde omfatter dyrkning af en celle ifølge krav 4 eller 5 under betingelser, der åbner mulighed for ekspression af polypeptidet,
15 og eventuelt indvinding af det udtrykte polypeptid.

7. Sammensætning, der omfatter: (i) et polypeptid ifølge krav 1 og; (ii) en cellulase og/eller en yderligere hemicellulase og/eller en pectinase.

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8. Sammensætning ifølge krav 7, hvor cellulasen er en GH61, cellobiohydrolase I, cellobiohydrolase II, endo- β -1,4-glucanase, β -glucosidase eller β -(1,3)(1,4)-glucanase, og/eller hvor den yderligere hemicellulase er en endoxylanase, β -xylosidase, α -L-arabinofuranosidase, α -D-glucuronidase, feruloylsterase, coumaroylsterase, α -galactosidase, β -galactosidase, β -mannanase eller β -mannosidase.

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9. Sammensætning ifølge krav 7 eller 8, hvor sammensætningen er en rå cellemassefermenteringssuppe.

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10. Fremgangsmåde til behandling af et substrat, der omfatter hemicellulose, eventuelt et plantemateriale, hvilken fremgangsmåde omfatter etablering af kontakt mellem substratet og et polypeptid ifølge krav 1 og/eller en sammensætning ifølge et hvilket som helst af kravene 7 til 9.

35

11. Fremgangsmåde ifølge krav 10, hvor substratet før enzymatisk behandling forbehandles med varme, mekanisk og/eller kemisk modifikation eller en hvilken som helst kombination af sådanne fremgangsmåder.

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12. Fremgangsmåde til fremstilling af et fermenteringsprodukt, hvilken fremgangsmåde omfatter fremstilling af et fermenterbart sukker ved etablering af kontakt mellem lignocellulosemateriale og et polypeptid ifølge krav 1 og/eller en sammensætning ifølge et hvilket som helst af kravene 7 til 9 og fermentering af det resulterende fermenterbare sukker til derved fremstilling af fermenteringsproduktet.

13. Anvendelse af et polypeptid ifølge krav 1 og/eller en sammensætning ifølge et hvilket som helst af kravene 7 til 9 til fremstilling af sukker fra et lignocellulosemateriale.

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DRAWINGS

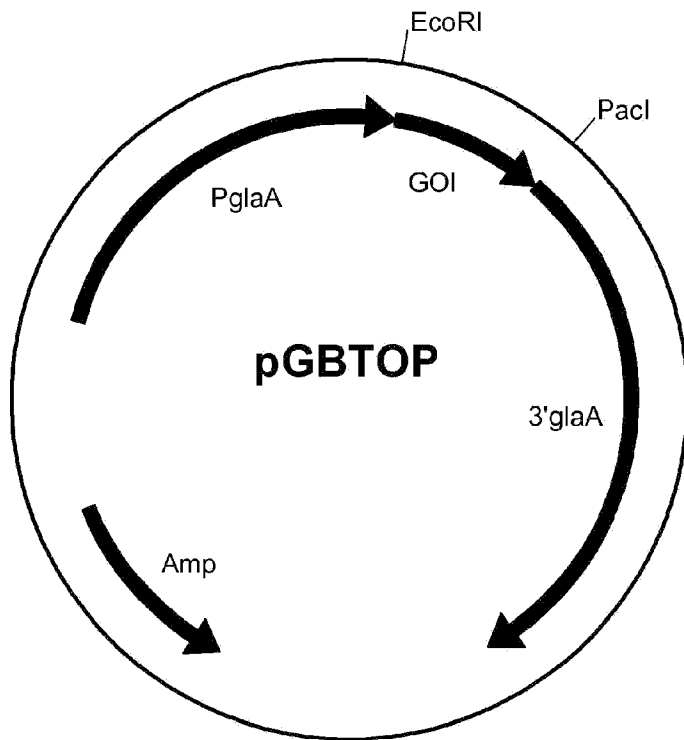


Fig. 1

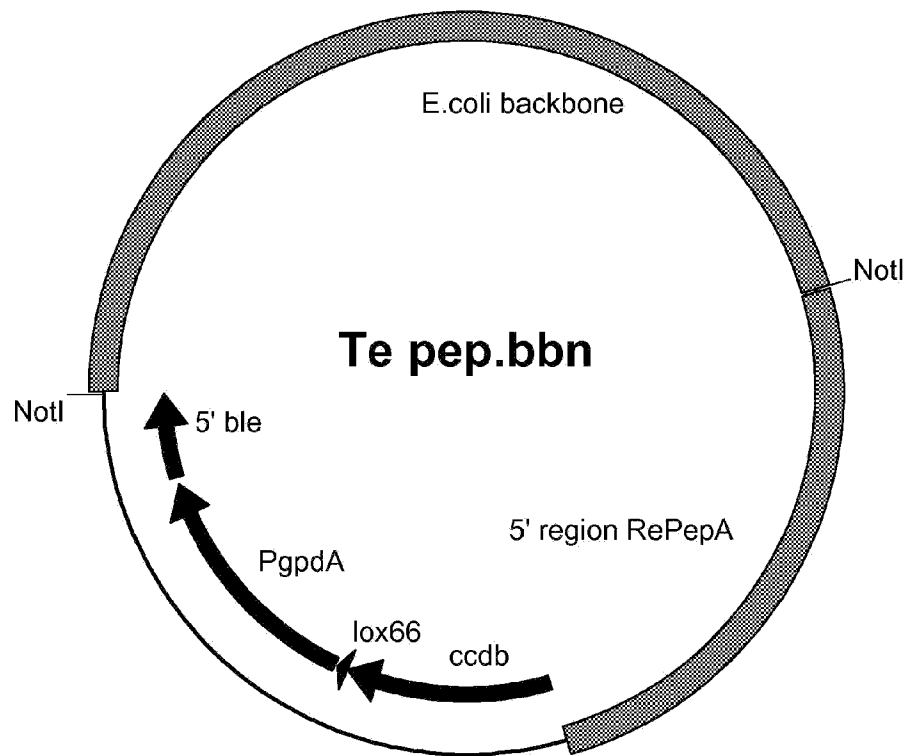


Fig. 2

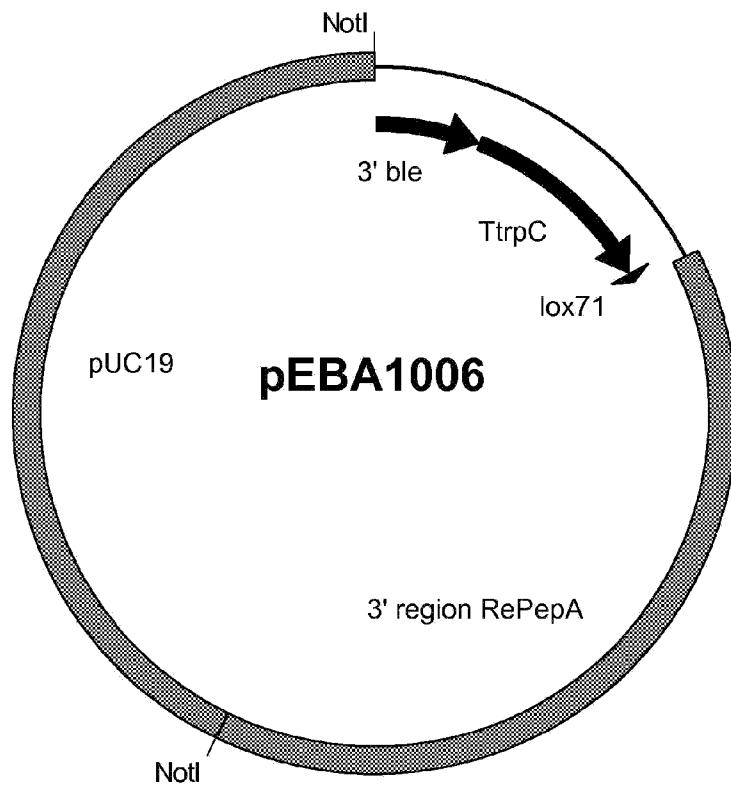


Fig. 3

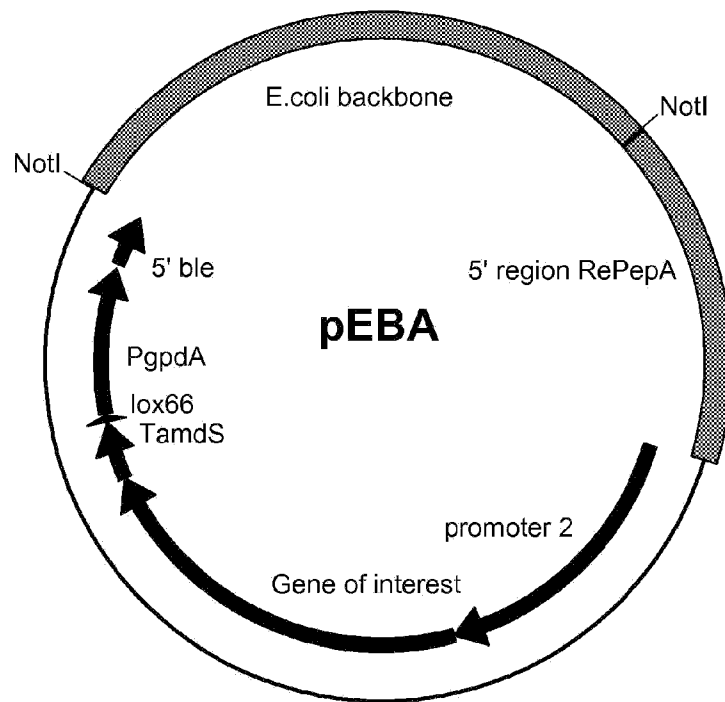


Fig. 4

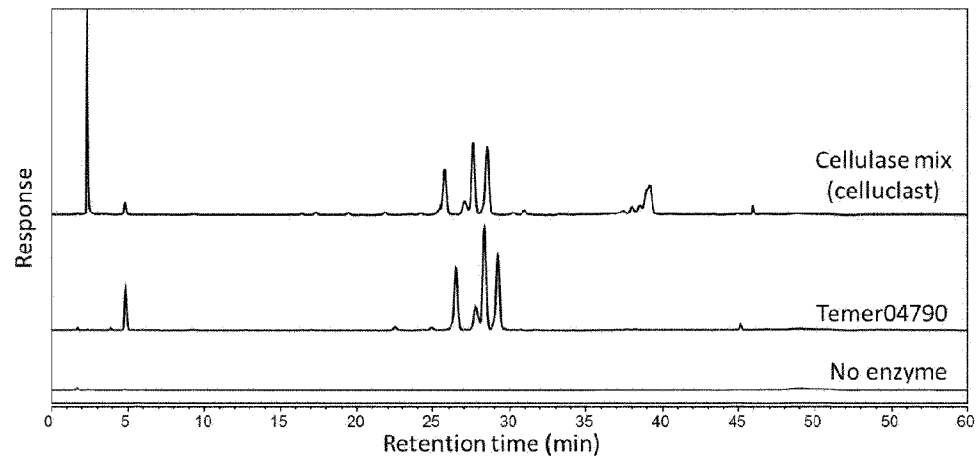


Fig. 5