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Primer Name	Seq ID No.	Primer sequence (5'→3')	Description
MH290	27	caaGGCGCGCCaagtATAACTTCGTATAATGTATGCTATACGAAGTTATCGGCCGGCGTATTGGGTGTTACG	hph reverse primer AscI loxP site
MH292	28	GAAGCGCGCCACAGATAAATTCGTATAGCATACATTATACGAAGTTATcctggcctgigactggtccgag	hph forward primer full promoter AscI loxP site
MH375	29	ccatgtcaactgtcttgaacac	BxlI 5' forward
MH376	30	caaggcgcGCCATCTCTTTTCGATCTCAACAG	BxlI 5' reverse AscI
MH377	31	gatgctgatcgcctctcaaacgttttcaacc	BxlI 3' forward AsiSI AclI
MH378	32	GGTCCAACCTTGAATGTAACAGC	BxlI 3' reverse primer
MH379	33	gltgctgtaacataaaggtctc	BxlI deletion nested forward primer
MH380	34	CCTCATTCTTCCAACAAGCC	BxlI deletion nested reverse primer

TABLE 4

(57) Abstract: The present disclosure is directed, in a first aspect, to the use of inverting beta-xylosidase enzymes to reduce byproduct formation and increase the yield of fermentation products, as well as, in a second aspect, to the use of retaining beta-xylosidase enzymes to improve production of alkyl-beta-xylopyranoside compounds, in a simultaneous saccharification and fermentation reactions.

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METHODS FOR IMPROVING THE EFFICIENCY OF SIMULTANEOUS SACCHARIFICATION AND FERMENTATION REACTIONS

1. CROSS-REFERENCE TO RELATED APPLICATION

This application claims the benefit of U.S. Provisional Application No. 61/289,917,
5 filed December 23, 2010, which is incorporated by reference in its entirety.

2. FIELD OF THE DISCLOSURE

The present disclosure is generally directed to methods and compositions for
improving product yield from simultaneous saccharification and fermentation reactions.

3. BACKGROUND

10 Bioconversion of renewable lignocellulosic biomass to a fermentable sugar that is
subsequently fermented to produce an alcohol {e.g., ethanol or "bioethanol"}, which can
serve as an alternative to liquid fuels, has attracted intensive attention of researchers
since the 1970s, when the oil crisis occurred because OPEC decreased the output of
petroleum (Bungay, "Energy: the biomass options". NY: Wiley; 1981 ; Olsson and Hahn-
15 Hagerdal, 1996, Enzyme Microb. Technol. 18:31 2-31 ; Zaldivar *et ai*, 2001 , Appl.
Microbiol. Biotechnol. 56:17-34; Galbe and Zacchi, 2002, Appl. Microbiol. Biotechnol.
59:618-28). 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. The importance of fuel bioethanol
will increase in parallel with skyrocketing prices for oil and gradual depletion of its
20 sources.

Lignocellulosic biomass is predicted to be a low-cost renewable resource that can
support the sustainable production of biofuels {e.g., bioethanol} on a large enough scale
to significantly address the world's increasing energy needs. Lignocellulosic materials
include, without limitation, corn stover (the corn plant minus the kernels and the roots),
25 forestry residues such as sawdust and paper, yard waste from municipal solid waste,
herbaceous plants such as switchgrass, and woody plants such as poplar trees.
Lignocellulosic biomass has three major components: hemicellulose, cellulose, and
lignin. Hemicellulose is an amorphous, branched polymer that is usually composed
primarily of five sugars (arabinose, galactose, glucose, mannose, and xylose). Cellulose
30 is a large, linear polymer of glucose molecules typically joined together in a highly
crystalline structure due to hydrogen bonding between parallel chains. Lignin is a
complex phenyl-propane polymer.

The biological processing of lignocellulosic biomass involves using cellulases and
hemicellulases to release sugars from hemicellulose and cellulose, respectively, typically

by hydrolysis reactions. The resulting sugars are then fermented into biofuels such as bioethanol using suitable fermenting microorganisms.

The glucose released when cellulose is broken down by cellulases can often be a potent inhibitor of this class of enzymes. To reduce glucose accumulation during cellulose breakdown (or "saccharification" herein), a fermenting microorganism can be added to convert the released sugars into bioethanol at the same time the sugars are revealed from saccharification. This configuration is called simultaneous saccharification and fermentation ("SSF"). Generally, SSF offers better/higher rates, yields, and concentrations of ethanol produced than a separate hydrolysis and fermentation ("SHF") configuration, despite operating at lower temperatures than are optimal for most enzymes involved in these fermentation processes. Nonetheless, the typical SSF reaction can be exceedingly lengthy, lasting, for example, several days in order to achieve modest ethanol concentrations (see, *e.g.*, Kadam *et al.*, 2004, *Biotechnol. Progr.* 20(3):705).

Accordingly, there exists a need in the art to identify methods and compositions related thereto for improving the efficiency of SSF reactions and increasing the yield of biofuels such as bioethanol.

4. SUMMARY

The instant disclosure is based on the discovery that the presence of certain β -xylosidases in simultaneous saccharification and fermentation ("SSF") reactions results in a rapid accumulation of alkyl- β -xylopyranoside byproducts. In particular, it is discovered that certain β -xylosidases with a retaining mechanism of action, when used in SSF reactions, can result in rapid accumulation of alkyl- β -xylopyranoside byproducts that would lead to a reduced yield of fermentation products. The present disclosure is further based on the discovery that the presence of certain other β -xylosidases with an inverting mechanism of action in SSF reactions can reduce or minimize the accumulation of alkyl- β -xylopyranoside byproducts. The inclusion of β -xylosidases with an inverting mechanism of action in SSF reactions has been found to improve the yield of fermentation products.

For the purpose of this disclosure, a β -xylosidase with an inverting mechanism of action is also referred to as "an enzyme with inverting β -xylosidase activity," "an inverting β -xylosidase," or "an inverting β -xylosidase polypeptide." Conversely, a β -xylosidase with a retaining mechanism of action is also referred to as "an enzyme with retaining β -xylosidase activity," "a retaining β -xylosidase," or "a retaining β -xylosidase polypeptide."

Accordingly, provided herein are improved methods for conducting SSF reactions that entail reducing the amount of retaining β -xylosidases. Provided herein are also improved methods for conducting SSF reactions that entail increasing the amount of inverting β -xylosidases. Provided further herein are improved methods for conducting
5 SSF reaction that entail decreased amount of retaining β -xylosidases and increased amount of inverting β -xylosidases. Compositions related to the above-described improved methods and other methods described herein are also contemplated.

In certain aspects, the present invention provides SSF methods comprising culturing a complete fermentation medium, said complete fermentation medium
10 comprising at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and at least one enzyme with inverting β -xylosidase activity, for a period and under conditions suitable for formation of a fermentation product.

In the present disclosure, the one or more enzymes (or alternatively and
15 interchangeably stated as "at least one enzyme" herein) with inverting β -xylosidase activity can be present in said complete fermentation medium in an amount effective to reduce short chain alkyl-xylopyranoside ("AXP") (e.g., methyl-xylopyranoside ("MXP"), ethyl-xylopyranoside ("EXP"), propyl-xylopyranoside ("PXP"), or butyl- β -xylopyranoside ("BXP")) formation, as compared to a control fermentation medium
20 lacking said one or more enzymes with inverting β -xylosidase activity. For example, such enzyme(s) are present in an amount effective to (a) reduce the amount of AXP formation by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80%, and/or (b) to increase the yield (e.g., by at least 0.1%, at least 0.5%, at least 0.7%, at least 1%, at least 2%, at least 3%, at least
25 5%, at least 7.5%, or at least 10%) of the fermentation product (e.g., an alcohol, such as, but not limited to, methanol, ethanol, propanol, propane-1,3-diol, or butanol), as compared to that of a control fermentation medium lacking said one or more enzymes with inverting β -xylosidase activity. In certain embodiments, such enzyme(s) are present
30 in an amount effective to reduce the amount of AXP formation to a level that is within 50%, within 40%, within 30%, within 20%, or within 10% above the level of AXP at the reaction equilibrium, as compared to that of a control fermentation medium lacking said one or more enzymes with inverting β -xylosidase activity.

In certain aspects, the fermenting microorganism is capable of producing an alcohol, for example, methanol, ethanol, propanol, propane-1,3-diol, or butanol, from at
35 least one fermentable carbon source. In certain aspects, the fermenting microorganism

is a bacterium such as a *Zymomonas mobilis* or a fungus such as a yeast or a filamentous fungus.

In certain aspects, the at least one inverting β -xylosidase is a GH43 family enzyme. In certain embodiments, the inverting β -xylosidase is selected from an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide. Specifically, the Fv43D polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:2, or to residues 21 to 350 of SEQ ID NO:2. The Pf43A polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:8, or to residues 21 to 445 of SEQ ID NO:8. The Fv43E polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:10 or to residues 19 to 530 of SEQ ID NO:10. The Fv43B polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:12, or to residues 17 to 574 of SEQ ID NO:12. The Af43A polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:14 or to residues 15-558 of SEQ ID NO:14. The Fo43A polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:24, or to residues 21 to 348 of SEQ ID NO:24. The Gz43A polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at

least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:22, or to residues 19 to 340 of SEQ ID NO:22. The XynB3 polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least
5 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:25.

In certain aspects, the amount of inverting β -xylosidase polypeptides in said complete medium is at least about 0.2 mg, at least about 0.3 mg, at least about 0.4 mg,
10 at least about 0.5 mg, at least about 0.7 mg, at least about 1 mg, at least about 2 mg, or at least about 3 mg per gram of xylan in said xylan-containing biomass, which is also a component of the complete fermentation medium. In other aspects, the amount of inverting β -xylosidase polypeptides is about 3 mg or less, about 2 mg or less, about 1.5 mg or less, about 1.0 mg or less, about 0.7 mg or less, about 0.5 mg or less, about 0.4
15 mg or less, about 0.3 mg or less, or about 0.2 mg or less per gram of xylan in said xylan-containing biomass. In certain aspects, the amount of inverting β -xylosidase polypeptides in said complete medium ranges from, for example, (a) 0.4 mg to 10 mg, (b) 0.5 mg to 2 mg, (c) 0.4 mg to 5 mg, (d) 0.5 mg to 1.5 mg, (e) 1 mg to 2 mg, (f) 0.3 mg to 3 mg, (g) 0.2 mg to 5 mg, (h) 0.3 mg to 5 mg, or (i) 0.3 mg to 10 mg, per gram of xylan
20 in said xylan-containing biomass, or the amount is within a range whose upper and lower limits are each independently selected from the foregoing values.

In certain aspects, the amount of inverting β -xylosidase polypeptide(s) in said complete fermentation medium exceeds the amount of retaining β -xylosidase polypeptide(s), on a mole basis, on a molecular weight basis, or on both a mole basis
25 and a molecular weight basis. In specific embodiments, the ratio of inverting β -xylosidase polypeptide(s) to retaining β -xylosidase polypeptide(s) is at least 2:1, at least 3:1, at least 4:1, at least 5:1, at least 10:1, or at least 50:1, on a mole basis, on a molecular weight basis, or on both a mole basis and a molecular weight basis. In specific embodiments, enzyme(s) with retaining β -xylosidase activity are absent from or
30 undetectable in the complete fermentation medium. In certain embodiments, there is no detectable retaining β -xylosidase activity in the complete fermentation medium.

According to the methods described herein, the culturing of the complete fermentation medium is conducted under continuous, batch, or fed-batch conditions. For example, the culturing of the complete fermentation medium of the invention is a
35 continuous SSF reaction, a batch-type SSF reaction, or a fed-batch type SSF reaction.

The methods of the present disclosure, in certain aspects, further encompass the formation of the complete fermentation medium prior to the culturing step. For example, the complete fermentation medium can be formed by combining (a) at least one fermenting microorganisms, (b) at least one xylan-containing biomass, (c) at least one cellulase, (d) at least one hemicellulase, (e) at least one inverting β -xylosidase, and (f) a medium lacking one or more of the components (a) to (e). In specific embodiments, the at least one cellulase can be present in the form of a cellulase preparation. For example the cellulase preparation can be a whole cellulase preparation, which can optionally also include the at least one hemicellulase. In specific embodiments, the cellulase preparation is a culture broth from a filamentous fungal culture, e.g., a *T. reesei* culture prepared using a *T. reesei* cell. In a certain aspect, the *T. reesei* cell has been engineered such that the native β -xylosidase gene is inactivated or deleted. It should be noted that a "*T. reesei* cell [that] has been engineered such that the native β -xylosidase gene is inactivated or deleted" includes not only the original or parental cell, in which the inactivation first took place, but also progeny of that cell wherein the native β -xylosidase gene is inactivated or deleted.

In certain aspects, the methods of the present disclosure pertain to culturing a fermentation broth comprising at least one xylan-containing biomass. In certain aspects, the xylan-containing biomass is, for example, corn stover, bagasse, sorghum, giant reed, elephant grass, miscanthus, Japanese cedar, wheat straw, switchgrass, hardwood pulp, or softwood pulp. For example, the xylan-containing biomass can suitably be added to the SSF reaction in the form of a slurry. For example, the xylan-containing biomass can be added to the SSF reaction in the form of a solid. Accordingly, the xylan-containing biomass can suitably be added to the SSF reaction in either a liquid form (which can be, for example, a solution, a suspension, or a mixture of solids and liquid) or in a solid form. In certain embodiments, the xylan-containing biomass has been subject to pre-treatment.

After the SSF reaction has taken place, optionally to completion, a recovery step can follow, wherein the fermentation product (e.g., ethanol, methanol, propanol, propane-1,3-diol, or butanol) is recovered.

The present disclosure further provides a complete fermentation medium suitable for use in the present methods, for example as described hereinabove and hereinbelow with respect to cellulase, hemicellulase, β -xylosidase and fermenting microorganism components.

The present disclosure also provides a *T. reesei* cell that has been engineered such that the native β -xylosidase gene is inactivated or deleted. The *T. reesei* cell can

be engineered to recombinantly express an enzyme of the GH43 family, for example, an enzyme selected from an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide. For example, the Fv43D polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:2 or to residues 21 to 350 of SEQ ID NO:2. The Pf43A polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:8, or to residues 21 to 445 of SEQ ID NO:8. The Fv43E polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:10, or to residues 19 to 530 of SEQ ID NO:10. The Fv43B polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:12 or to residues 17 to 574 of SEQ ID NO:12. The Af43A polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:14, or to residues 15-558 of SEQ ID NO:14. The Fo43A polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:24 or to residues 21 to 348 of SEQ ID NO:24. The Gz43A polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:22, or to residues 19 to 340 of SEQ ID NO:22. The XynB3 polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%,

at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:25.

The present disclosure further provides methods for producing cellulase polypeptides, comprising (a) culturing such a *T. reesei* cell, such as one described herein
5 above and/or herein below, under conditions that allow the production of one or more cellulase polypeptides, and (b) recovering the cellulase polypeptides, for example, by recovering a culture broth comprising the cellulase polypeptides. The present disclosure further provides a culture broth produced by the *T. reesei* cell, and its use in saccharification reactions, including, for example, SSF reactions.

10 In certain aspects, the present disclosure provides a complete fermentation medium composition, comprising, at least one inverting β -xylosidase, at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and a fermentation medium. The inverting β -xylosidase is, for example, a GH43 family enzyme. The inverting β -xylosidase can, in certain aspects,
15 be one selected from an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide. The fermenting microorganism is suitably one that is capable of fermenting a suitable carbon source such as a xylan-containing biomass, or sugars, such as glucose, xylose, arabinose, mannose, galactose, or oligosaccharides, directly or indirectly into a desired fermentation product, including, for example, methanol
20 ("MeOH"), ethanol ("EtOH"), propanol, propane-1,3-diol, or butanol. The fermenting microorganism can be selected from a fungus, such as, for example, a yeast or a filamentous fungus, a bacterium, such as a *Zymomonas mobilis* or a *Clostridium thermocellum*. Suitable carbon sources or substrates include, for example, xylan-containing biomass substrates, selected from, for example, lignocellulosic substrates or
25 other carbohydrate-containing raw materials. Certain of the lignocellulosic substrates can, for example, comprise cellulose, hemicellulose, and/or lignin.

The cellulase is, for example, a β -glucosidase, an endoglucanase, or a cellobiohydrolase polypeptide. Enzymes are referred to herein either by their names, or by the enzyme families to which they belong {e.g., the GH43 family enzyme; or enzyme
30 classified in or under EC 3.2.1.91 }; when they are referred to by their names, they can also be referred to interchangeably as a "[name] polypeptide {e.g., a β -glucosidase can also be referred to, interchangeably, as a β -glucosidase polypeptide). The cellulase can also be, for example, in the form of a whole cellulase preparation. The hemicellulase is, for example, a xylanase, a β -xylosidase, an L-a-arabinofuranosidase, or an accessory

protein. The whole cellulase preparation can comprise one or more of the hemicellulase polypeptides in certain embodiments.

The fermentation medium can be one that results from a partial saccharification process, or one that comprises certain amounts of the products of saccharification. Such
5 a composition can be suitably used in a saccharification reaction, including, for example, an SSF reaction, under conditions that allow production of the fermentation product(s) of interest.

In certain aspects, the one or more cellulases and/or the one or more hemicellulases are produced by a genetically engineered microorganism wherein the
10 gene encoding the one or more (if more than one native β -xylosidase is present) native β -xylosidases have been deleted or there is no detectable native β -xylosidase activity. In certain embodiments, the microorganism engineered to produce the one or more cellulases and/or one or more hemicellulases does not comprise a retaining β -xylosidase or has no detectable retaining β -xylosidase activity.

In some aspects, the instant disclosure pertains to an improved method for
15 conducting an SSF reaction on a xylan-containing biomass, in order to obtain a bioethanol fermentation product, wherein the method comprises culturing a fermentation medium comprising at least one cellulase, at least one hemicellulase, and at least one fermenting microorganism, wherein the improvement comprises the use of an enzyme
20 with inverting β -xylosidase activity.

In related aspects, the instant disclosure also provides methods of improving
production of alkyl¹-xylopyranosides, which are known to be useful and valuable for a number of industrial applications, in situations where such production is desirable. For example, alkyl¹-xylopyranoside can suitably be used as chemical intermediates in the
25 synthesis of alkyl-glucosides, which is useful as biodegradable surfactants and emulsifiers (see, e.g., K. Schmid & H. Tesmann, 2001, Alkyl Polyglucosides, in Detergency of Specialty Surfactants, Surfactant science series, vol. 98; (F.E. Fried ed.); Marcel Dekker Inc., NY, pp.1-70). These compounds are also inducers themselves or can be used to prepare inducers of xylanase production in a number of microorganisms
30 (see, e.g., M. Marui *et al.*, 1985, Agric. Biol. Chem. 49(12):3399-3407; H. Shinoyama *et al.*, 1988, Agric. Biol. Chem. 52(9):2197-2202). Various alkyl-pyranosides can, in addition, be used as primers for chondroitin sulphate and stimulants of the biosynthesis of proteoglycans (see, e.g., H. Shinoyama *et al.*, 1988, Agric. Biol. Chem. 52(9):2197-2202). The inclusion or increased production of β -xylosidases with a retaining

mechanism of action in SSF reactions can be used to improve the yield of these useful alkyl- β -xylopyranosides in another aspect of the present invention .

Accordingly, in certain embodiments, the method of the disclosure comprises increasing an amount of retaining β -xylosidases. Provided herein are also improved
5 methods of conducting SSF reactions that entail increasing the amount of retaining β -xylosidases. In a further example, an improved method of conducting SSF reactions that entails increasing the amount of retaining β -xylosidases while decreasing the amount of inverting β -xylosidases is contemplated.

In other aspects, the present invention provides SSF methods comprising
10 culturing a complete fermentation medium, said complete fermentation medium comprising at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and at least one enzyme with retaining β -xylosidase activity, for a period and under conditions suitable for formation of
of alkyl[^]-xylopyranoside, such as, for example, methyl[^]-xylopyranoside ("MXP"), ethyl-
15 β -xylopyranoside ("EXP"), propyl[^]-xylopyranoside ("PXP"), or butyl[^]-xylopyranoside ("BXP").

In certain aspects, the at least one enzyme with retaining β -xylosidase activity can be present in said complete fermentation medium in an amount effective to increase short chain alkyl[^]-xylopyranoside ("AXP") {e.g., methyl[^]-xylopyranoside ("MXP"), ethyl-
20 β -xylopyranoside ("EXP"), propyl[^]-xylopyranoside ("PXP"), or butyl[^]-xylopyranoside ("BXP")} formation, as compared to a control fermentation medium lacking or having lesser amount of said enzymes with retaining β -xylosidase activity. For example, such enzyme(s) are present in an amount effective to increase the amount of AXP formation
by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at
25 least 70%, or by at least 80%, as compared to that of a control fermentation medium lacking or having a lesser amount of said one or more enzymes with retaining β -xylosidase activity.

In certain aspects, the fermenting microorganism is capable of producing a number of short chain alkyl[^]-xylopyranoside ("AXP") compounds, including, without
30 limitation, methyl[^]-xylopyranoside ("MXP"), ethyl[^]-xylopyranoside ("EXP"), propyl- β -xylopyranoside ("PXP"), or butyl[^]-xylopyranoside ("BXP") compounds. In some aspects the fermenting microorganism is a bacterium such as a *Zymomonas mobilis* or a fungus such as a yeast or a filamentous fungus.

In certain aspects, the at least one retaining β -xylosidase is a GH3, GH30, GH31, ,
35 GH39, GH52, GH54, or GH16 family enzyme. In certain embodiments, the retaining

β -xylosidase is selected from a XInD, an Fv30A, an Fv30B, an Fv39A, an Fv39B, a XynB, a XylA, or a Xyl1 polypeptide. Specifically, the XInD polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:40, or to residues 18-804 of SEQ ID NO:40. The Fv30A polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:42, or to residues 20-537 of SEQ ID NO:42. The Fv30B polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:44 or to residues 25-485 of SEQ ID NO:44. The Fv39A polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:46, or to residues 20-439 of SEQ ID NO:46. The Fv39B polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:48 or to residues 19-456 of SEQ ID NO:48. The XynB polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:50. The XylA, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:52. The Xyl1 polypeptide, if present in the complete fermentation medium, is a polypeptide comprising at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at

least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:54, or to residues 22-500 of SEQ ID NO:54.

In certain aspects, the amount of retaining β -xylosidase polypeptides in said complete medium is at least about 0.2 mg, at least about 0.5 mg, at least about 0.7 mg, at least about 1 mg, at least about 2 mg, or at least about 5 mg per gram of xylan in said xylan-containing biomass, which is also a component of the complete fermentation medium. In other aspects, the amount of inverting β -xylosidase polypeptide(s) is about 10 mg or less, about 5 mg or less, about 2 mg or less, about 1 mg or less, about 0.7 mg or less, about 0.5 mg or less, or about 0.2 mg or less per gram of xylan in said xylan-containing biomass. In certain aspects, the amount of retaining β -xylosidase polypeptides in said complete medium ranges from, for example, (a) 0.2 mg to 10 mg, (b) 0.2 mg to 5 mg, (c) 0.5 mg to 5 mg, (d) 1 mg to 10 mg, (e) 2 mg to 10 mg, (f) 0.2 to 5 mg, (g) 0.2 mg to 2 mg, or (h) 0.5 mg to 10 mg, per gram of xylan in said xylan-containing biomass, or the amount is within a range whose upper and lower limits are each independently selected from the foregoing values.

In certain aspects, the amount of retaining β -xylosidase polypeptide(s) in said complete fermentation medium exceeds the amount of inverting β -xylosidase polypeptide(s), on a mole basis, on a molecular weight basis, or on both a mole basis and a molecular weight basis. In specific embodiments, the ratio of retaining β -xylosidase polypeptides to inverting β -xylosidase polypeptides is at least 2:1, at least 3:1, at least 4:1, at least 5:1, at least 10:1, or at least 50:1, on a mole basis, on a molecular weight basis, or on both a mole basis and a molecular weight basis. In specific embodiments, enzymes with inverting β -xylosidase activity are absent from or undetectable in the complete fermentation medium. In certain embodiments, there is no detectable inverting β -xylosidase activity in the complete fermentation medium.

According to the method describe herein, the culturing of the complete fermentation medium is conducted under continuous, batch, or fed-batch conditions. For example, the culturing of the complete fermentation medium of the invention is a continuous SSF reaction, a batch-type SSF reaction, or a fed-batch type SSF reaction.

The methods of the present disclosure, in certain aspects, further encompass the formation of the complete fermentation medium prior to the culturing step. For example, the complete fermentation medium can be formed by combining (a) at least one fermenting microorganisms, (b) at least one xylan-containing biomass, (c) at least one cellulase, (d) at least one hemicellulase, (e) at least one retaining β -xylosidase, and (f) a

medium lacking one or more of the components (a) to (e). In specific embodiments, the at least one cellulase can be present in the form of a cellulase preparation. For example the cellulase preparation can be a whole cellulase preparation, which can optionally also include the at least one hemicellulase. In specific embodiments, the cellulase
5 preparation is a culture broth from a filamentous fungal culture, e.g., a *T. reesei* culture prepared using a *T. reesei* cell. In a certain aspect, the *T. reesei* cell has been engineered such that either the native retaining β -xylosidase gene is overexpressed or that a foreign retaining β -xylosidase gene is introduced and expressed therein. It should be noted that a "*T. reesei* cell [that] has been engineered such that either the native
10 retaining β -xylosidase gene is overexpressed or that a foreign retaining β -xylosidase gene is introduced and expressed therein" includes not only the original or parental cell, in which the inactivation first took place, but also progeny of that cell.

In certain aspects, the methods of the present disclosure pertain to culturing a fermentation broth comprising at least one xylan-containing biomass. In certain aspects,
15 the xylan-containing biomass is, for example, corn stover, bagasse, sorghum, giant reed, elephant grass, miscanthus, Japanese cedar, wheat straw, switchgrass, hardwood pulp, or softwood pulp. For example, the xylan-containing biomass can suitably be added to the SSF reaction in the form of a slurry. For example, the xylan-containing biomass can be added to the SSF reaction in the form of a solid. Accordingly, the xylan-containing
20 biomass can suitably be added to the SSF reaction in either a liquid form (which can be, for example, a solution, a suspension, or a mixture of solids and liquid) or in a solid form. In certain embodiments, the xylan-containing biomass has been subject to pre-treatment.

After the SSF reaction has taken place, optionally to completion, a recovery step can follow, wherein the AXP product {e.g., MXP, EXP, PXP, or BXP} is recovered.

25 The present disclosure further provides a complete fermentation medium suitable for use in the present methods, for example as described hereinabove and hereinbelow with respect to cellulase, hemicellulase, β -xylosidase and fermenting microorganism components.

The present disclosure also provides a *T. reesei* cell that has been engineered
30 such that the native retaining β -xylosidase gene is overexpressed, or that a foreign retaining β -xylosidase gene is expressed therein. The *T. reesei* cell can be engineered to recombinantly express an enzyme of the GH3, GH30, GH31, GH39, GH52, GH54, or GH16 family, for example, one selected from a XlnD, an Fv30A, an Fv30B, an Fv39A, an Fv39B, a XynB, a XylA, or a Xyl1 polypeptide. For example, the XlnD polypeptide
35 has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at

least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:40 or to residues 18-804 of SEQ ID NO:40. The Fv30A polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at
5 least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:42, or to residues 20-537 of SEQ ID NO:42. The Fv30B polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at
10 least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:44, or to residues 25-485 of SEQ ID NO:44. The Fv39A polypeptide has at least 65%, at least 70%, at least 75%, at
15 least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:46 or to
residues 20-439 of SEQ ID NO:46. The Fv39B polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%,
20 at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID NO:48, or to residues 19-456 of SEQ ID NO:48. The XynB polypeptide has at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%,
at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence
corresponding to SEQ ID NO:50. The XylA polypeptide has at least 65%, at least 70%,
25 at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence corresponding to SEQ ID
NO:52, or to residues 19-705 of SEQ ID NO:52. The Xyl1 polypeptide has at least 65%,
30 at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the amino acid sequence
corresponding to SEQ ID NO:54, or to residues 22-500 of SEQ ID NO:54.

The present disclosure further provides methods for producing cellulase polypeptides, comprising (a) culturing such a *T. reesei* cell, such as one described herein
35 above and/or herein below, under conditions that allow the production of one or more

cellulase polypeptides and (b) recovering the cellulase polypeptides, for example, by recovering a culture broth comprising the cellulase polypeptides. The present disclosure further provides a culture broth produced by the *T. reesei* cell, and its use in saccharification reactions, including, for example, SSF reactions.

5 In certain aspects, the present disclosure provides a complete fermentation medium composition, comprising, at least one retaining β -xylosidase, at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and a fermentation medium. The retaining β -xylosidase is, for example, either a native retaining β -xylosidase that is overexpressed or a foreign β -
10 xylosidase that is introduced into a suitable host cell. The retaining β -xylosidase is, for example, a GH3, GH30, GH31, GH39, GH52, GH54, or GH 116 family enzyme. The retaining β -xylosidase can, in certain aspects, be one selected from a XInD, an Fv30A, an Fv30B, an Fv39A, an Fv39B, a XynB, a XylA, or a Xyl1 polypeptide. The fermenting microorganism is suitably one that is capable of fermenting a suitable carbon source
15 such as a xylan-containing biomass, or sugars, such as glucose, xylose, arabinose, mannose, galactose, or oligosaccharides, directly or indirectly into a desired fermentation product, including, for example, methanol, ethanol, propanol, propane-1,3-diol, or butanol. The fermenting microorganism can be a fungus, such as, for example, a yeast or a filamentous fungus, or a bacterium, such as a *Zymomonas mobilis* or a *Clostridium*
20 *thermocellum*. Suitable carbon sources or substrates can be, for example, xylan-containing biomass substrates, selected from, for example, lignocellulosic substrates or other carbohydrate-containing raw materials. Certain of the lignocellulosic substrates can, for example, comprise cellulose, hemicellulose, and/or lignin.

The cellulase is, for example, a β -glucosidase, an endoglucanase, or a
25 cellobiohydrolase polypeptide. The cellulase can also be, for example, in the form of a whole cellulase preparation. The hemicellulase is, for example, a xylanase, a β -xylosidase, an L-a-arabinofuranosidase, or an accessory protein. The whole cellulase preparation can comprise one or more hemicellulase polypeptides in certain embodiments.

30 The fermentation medium can be one that results from a partial saccharification process, or one that comprises certain amounts of the products of saccharification. Such a composition can be suitably used in a saccharification reaction, including, for example, an SSF reaction, under conditions that allow production of the AXP compounds, including, for example, MXP, EXP, PXP, or BXP.

In certain aspects, the one or more cellulases or the one or more hemicellulases are produced by a genetically engineered microorganism wherein the gene encoding the one or more (if more than one native β -xylosidase is present) native β -xylosidases have been overexpressed or a gene encoding a foreign β -xylosidase has been introduced
5 and/or expressed. In certain embodiments, the microorganism engineered to produce one or more cellulases and/or one or more hemicellulases has an increased expression of retaining β -xylosidase activity over a control microorganism which did not undergo the same genetic engineering. In certain embodiments, the microorganism engineered to produce one or more cellulases and/or one or more hemicellulases does not comprises
10 an inverting β -xylosidase or has no detectable inverting β -xylosidase activity.

In certain related aspects, the instant disclosure pertains to an improved method for conducting an SSF reaction on a xylan-containing biomass, in order to obtain an AXP product wherein the method comprises culturing a fermentation medium comprising at least one cellulase, at least one hemicellulase, and at least one fermenting
15 microorganism, wherein the improvement comprises the use of a cellulase preparation made from a *T. reesei* cell, which has been engineered to overexpress the native β -xylosidase gene, or to express a foreign β -xylosidase. In some embodiments, the native β -xylosidase gene that is overexpressed or the foreign β -xylosidase gene that is expressed is a gene encoding a retaining β -xylosidase.

20 All publications, patents, patent applications, GenBank sequences and ATCC deposits cited herein are hereby expressly incorporated by reference for all purposes.

5. BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Table 1: EXP formation with recombinant *Zymomonas mobilis* under the SSF
25 conditions from cob and glucose/xylose.

Table 2: EXP formation using various types of biomass substrates.

Table 3: Time course of EXP and/or xylose formation (expressed as RI area, proportional to mg/mL) from xylobiose (20 mg/mL) in 50 mM NaCitrate, pH 4.7 plus 0.9 M EtOH at 46 °C in the presence of Multifect® Xylanase ("MF," 560 μ g/mL) and purified
30 Fv43D (36 μ g/mL) or Fv3A (54 μ g/mL).

Table 4: Primer sequences for construction of *bx11* deletion cassette.

Table 5: Primer sequences for construction of *F. verticillioides* β -xylosidase Fv43D expression cassette.

Table 6: provides a summary of the sequence identifiers for certain enzymes used in SSF reactions.

Figure 1: HPLC chromatograms of samples taken after 48 hrs of incubation at 46 °C of xylose (10 mg/mL) in 50 mM sodium citrate, pH 4.6, Multifect® Xylanase (1.35 mg/mL) and with no alcohol, with ethanol ("EtOH"), with methanol ("MeOH"), or with n-propanol ("n-PrOH"), each at 0.72 M. HPLC conditions: column HPX-87H at 60 °C, 0.60 mL/min in 0.01 N H₂SO₄, RI detector.

Figure 2: Time course following the appearance/formation of alkyl-xylopyranosides ("AXP") under the the same conditions as those described in the experiments of Figure 1. The amounts of fermentation products formed are expressed as ratios of the areas of the product peaks compared to those of the xylose peaks.

Figure 3: NMR spectrum indicating the presence of ethyl-β-xylopyranoside.

Figure 4: EXP formation with yeast and wild-type *Zymomonas mobilis* under SSF conditions.

Figure 5: EXP formation under the yeast SSF conditions with and without the addition of *T. reesei* Bxl1 .

Figure 6: EXP dose response following addition of *T. reesei* Bxl1 to the enzyme complex produced from integrated *T. reesei* strain #229 under the recombinant *Zymomonas* SSF conditions.

Figure 7: EXP formation during an SSF reaction with the following enzyme configurations/mixtures for saccharification : Accellerase™ 1500 ("A1 500")+Multifect® Xylanase, Accellerase™ 1500 ("A1 500") +XlnA, and an enzyme complex produced from the integrated *T. reesei* strain #229 with the addition of a hemicellulase (Fv3A, Fv51 A, or Bxl1).

Figure 8: EXP formation during an SSF reaction using various purified cellulase enzymes and XynB3 for saccharification.

Figure 9: EXP formation during an SSF reaction using an enzyme complex produced from the integrated *T. reesei* strain #229 in the presence of *T. reesei* Bxl1 , or in the presence of certain other GH43 family β-xylosidase enzymes.

Figure 10: Reduced EXP formation observed from the addition of Fv43D under the recombinant *Zymomonas* SSF conditons.

Figure 11: Reduced EXP formation observed from the addition of Fv43D under the yeast SSF conditons.

Figure 12: Reduced EXP formation observed after the addition of Fv43D to Accellerase™ 1500+Multifect® Xylanase, to Accellerase™ 1500+XlnA, and to an

enzyme complex produced from the integrated *T. reesei* strain #229 under the recombinant *Zymomonas* SSF conditions.

Figure 13: Reduced EXP formation observed from the addition of Fv43D to purified cellulase enzymes and XynB3.

5 **Figures 14A-14B:** Figure 14A shows EXP reduction dose response from the addition of Fv43D to the enzyme composition or blend produced from the *T. reesei* integrated strain #229 + *T. reesei* Bx11 under the recombinant *Zymomonas* SSF conditions. Figure 14B shows EXP reduction from the addition of Fo43A or Gz43A to the enzyme complex produced from the integrated *T. reesei* strain #229 + *T. reesei* Bx11
10 under the recombinant *Zymomonas* SSF conditions.

Figure 15: Time course of xylose and EXP formation (expressed as RI area, which is proportional to mg/mL) from xylobiose (20 mg/mL) in 50 mM sodium citrate, pH 4.7 plus 0.9 M ethanol at 46 °C in the presence of Multifect® Xylanase (560 µg/mL) and purified Fv43D (36 µg/mL) and Fv3A (54 µg/mL).

15 **Figure 16:** Time course of formation of xylose and EXP from xylobiose (20 mg/mL, left) or xylose oligomers (20 mg/mL, right), in 50 mM sodium citrate, pH 4.7 plus 0.9 M ethanol at 46 °C in the presence of Multifect® Xylanase (560 µg/mL), Fv43D (36 µg/mL), or Fv3A (54 µg/mL). The results are expressed as ratios of the amount of EXP to the amount of xylose formed.

20 **Figure 17:** Plasmid map of pCR-Blunt II-TOPO, *bx11* deletion, *hph-loxP*.

Figure 18: Plasmid map of TOPO Blunt/Peg11 -Fv43D.

Figures 19A-19B: Figure 19A: Fv43D nucleotide sequence (SEQ ID NO:1).
Figure 19B: Fv43D amino acid sequence (SEQ ID NO:2). SEQ ID NO:2 is the sequence of the immature Fv43D. Fv43D has a predicted signal sequence
25 corresponding to residues 1 to 20 of SEQ ID NO:2 (underlined); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 21 to 350 of SEQ ID NO:2. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>). The predicted conserved domain residues are in boldface type. Domain predictions were made based on the Pfam,
30 SMART, or NCBI databases.

Figures 20A-20B: Figure 20A: *T. reesei* Bx11 nucleotide sequence (SEQ ID NO:3). Figure 20B: *T. reesei* Bx11 amino acid sequence (SEQ ID NO:4). The signal sequence is underlined. The predicted conserved domain residues are in bold face type. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figures 21A-21 B: Figure 21A: Fv3A nucleotide sequence (SEQ ID NO:5).

Figure 21B: Fv3A amino acid sequence (SEQ ID NO:6). SEQ ID NO:6 is the sequence of the immature Fv3A. Fv3A has a predicted signal sequence corresponding to residues 1 to 23 of SEQ ID NO:6 (underlined); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 24 to 766 of SEQ ID NO:6. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>). The predicted conserved domain residues are in boldface type. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figures 22A-22B: Figure 22A: Pf43A nucleotide sequence (SEQ ID NO:7).

Figure 22B: Pf43A amino acid sequence (SEQ ID NO:8). SEQ ID NO:8 is the sequence of the immature Pf43A. Pf43A has a predicted signal sequence corresponding to residues 1 to 20 of SEQ ID NO:8 (underlined); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 21 to 445 of SEQ ID NO:8. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>). The predicted conserved domain residues are in boldface type, the predicted carbohydrate binding module ("CBM") residues are in uppercase type, and the predicted linker separating the CD and CBM is in italics. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figures 23A-23B: Figure 23A: Fv43E nucleotide sequence (SEQ ID NO:9).

Figure 23B: Fv43E amino acid sequence (SEQ ID NO:10). SEQ ID NO:10 is the sequence of the immature Fv43E. Fv43E has a predicted signal sequence corresponding to residues 1 to 18 of SEQ ID NO:10 (underlined); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 19 to 530 of SEQ ID NO:10. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>). The predicted conserved domain residues are in boldface type. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figures 24A-24B: Figure 24A: Fv43B nucleotide sequence (SEQ ID NO:11).

Figure 24B: Fv43B amino acid sequence (SEQ ID NO:12). SEQ ID NO:12 is the sequence of the immature Fv43B. Fv43B has a predicted signal sequence corresponding to residues 1 to 16 of SEQ ID NO:12 (underlined); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 17 to 574 of SEQ ID NO:12. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>). The predicted conserved domain

residues are in boldface type. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figures 25A-25B : Figure 25A: Af43A nucleotide sequence (SEQ ID NO:1 3).
Figure 25B: Af43A amino acid sequence (SEQ ID NO:1 4). SEQ ID NO:1 4 is the
5 sequence of the immature Af43A. Af43A does not have a predicted signal sequence,
which can be derived using the SignalP algorithm (available at: <http://www.cbs.dtu.dk>) .
The predicted conserved domain residues are in boldface type. Domain predictions
were made based on the Pfam, SMART, or NCBI databases.

Figures 26A-26B : Figure 26A: Fv51 A nucleotide sequence (SEQ ID NO:1 5).
10 Figure 26B: Fv51 A amino acid sequence (SEQ ID NO:1 6). SEQ ID NO:1 6 is the
sequence of the immature Fv51 A. Fv51 A has a predicted signal sequence
corresponding to residues 1 to 19 of SEQ ID NO:1 6 (underlined) ; cleavage of the signal
sequence is predicted to yield a mature protein having a sequence corresponding to
residues 20 to 660 of SEQ ID NO:1 6. Signal sequence predictions were made with the
15 SignalP algorithm (available at: <http://www.cbs.dtu.dk>) . The predicted L-a-
arabinofuranosidase conserved domain residues are in boldface type. Domain predictions
were made based on the Pfam, SMART, or NCBI databases.

Figures 27A-27B : Figure 27A: *T. reesei*/ Xyn3 nucleotide sequence (SEQ ID
NO:1 7). Figure 27B: *T. reesei*/ Xyn3 amino acid sequence (SEQ ID NO:1 8). SEQ ID
20 NO:1 8 is the sequence of the immature *T. reesei*/ Xyn3. *T. reesei*/Xyn3 has a predicted
signal sequence corresponding to residues 1 to 16 of SEQ ID NO:1 8 (underlined) ;
cleavage of the signal sequence is predicted to yield a mature protein having a sequence
corresponding to residues 17 to 347 of SEQ ID NO:1 8. Signal sequence predictions
were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>) . The
25 predicted conserved domain residues are in bold face type. Domain predictions were
made based on the Pfam, SMART, or NCBI databases.

Figures 28A-28B : Figure 28A: XlnA nucleotide sequence (SEQ ID NO:1 9).
Figure 28B: XlnA amino acid sequence (SEQ ID NO:20) . SEQ ID NO:20 is the
30 sequence of the immature XlnA protein. XlnA has a predicted signal sequence
corresponding to residues 1 to 27 of SEQ ID NO:20 (underlined) ; cleavage of the signal
sequence is predicted to yield a mature protein having a sequence corresponding to
residues 28 to 211 of SEQ ID NO:20. Signal sequence predictions were made with the
SignalP algorithm (available at: <http://www.cbs.dtu.dk>) . SEQ ID NO:1 9 is the genomic
35 sequence of XlnA; the initiation and termination codon residues are shown in bold face
type in Figure 28A, and intron A of the XlnA gene is underlined in Figure 28A.

Figure 29: Figure 29 shows the "α" and "β" anomer configurations of glucose. Anomers are identified as "α" or "β" based on the relation between the stereochemistry of the exocyclic oxygen atom at the anomeric carbon and the oxygen attached to the configurational atom (defining the sugar as D or L), which is often the furthest chiral center in the ring. The α anomer is the one in which these two positions have the same configuration ; they are the opposite in the β anomer. Thus the structure of α-D-glucose has the same stereochemistry at both C1 and C5 whereas β-D-glucose has opposite stereochemistry at C1 compared to C5.

Figures 30A-30B : Figure 30A: Gz43A nucleotide sequence (SEQ ID NO:21). Figure 30B: Gz43A amino acid sequence (SEQ ID NO:22). SEQ ID NO:22 is the sequence of the immature Gz43A. Gz43A has a predicted signal sequence corresponding to residues 1 to 18 of SEQ ID NO:22 (underlined) ; cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 19 to 340 of SEQ ID NO:22. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>) . The predicted conserved domain residues are in boldface type. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figures 31A-31 B: Figure 31A: Fo43A nucleotide sequence (SEQ ID NO:23). Figure 31B: Fo43A amino acid sequence (SEQ ID NO:24). SEQ ID NO:24 is the sequence of the immature Fo43A. Fo43A has a predicted signal sequence corresponding to residues 1 to 20 of SEQ ID NO:24 (underlined) ; cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 21 to 348 of SEQ ID NO:24. Signal sequence predictions were made with the SignalP algorithm (available at: <http://www.cbs.dtu.dk>) . The predicted conserved domain residues are in boldface type. Domain predictions were made based on the Pfam, SMART, or NCBI databases.

Figure 32-1 to 32-2: Alignment of GH43 family hydrolases. Amino acid residues that are highly conserved among members of the family are shown in bold and underline type.

Figure 33: XynB3 amino acid sequence (SEQ ID NO:25).

Figure 34: *T. reesei* Bgl1 amino acid sequence (SEQ ID NO:45) . The signal sequence is underlined. The predicted conserved domain residues are in bold face type. The coding sequence is described in Barnett *et al.*, 1991 , Bio-Technology 9(6) :562-567.

Figures 35A-35B : Figure 35A: XlnD nucleotide sequence (SEQ ID NO:39). Figure 35B: XlnD amino acid sequence (SEQ ID NO:40). SEQ ID NO:40 is the

sequence of the immature XInD. XInD has a predicted signal sequence corresponding to residues 1 to 17 of SEQ ID NO:40 (underlined) ; cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 18 to 804 of SEQ ID NO:40. Signal sequence predictions were made with the SignalP
5 algorithm (available at: <http://www.cbs.dtu.dk>).

Figures 36A-36B : Figure 36A: Fv30A nucleotide sequence (SEQ ID NO:41) .
Figure 36B: Fv30A amino acid sequence (SEQ ID NO:42) . SEQ ID NO:42 is the
sequence of the immature Fv30A. Fv30A has a predicted signal sequence
10 corresponding to residues 1 to 19 of SEQ ID NO:42(underlined) ; cleavage of the signal
sequence is predicted to yield a mature protein having a sequence corresponding to
residues 20 to 537 of SEQ ID NO:42. Signal sequence predictions were made with the
SignalP algorithm (available at: <http://www.cbs.dtu.dk>) .

Figures 37A-37B : Figure 37A: Fv30B nucleotide sequence (SEQ ID NO:43) .
Figure 37B: Fv30B amino acid sequence (SEQ ID NO:44) . SEQ ID NO:44 is the
15 sequence of the immature Fv30B. Fv30B has a predicted signal sequence
corresponding to residues 1 to 24 of SEQ ID NO:44 (underlined) ; cleavage of the signal
sequence is predicted to yield a mature protein having a sequence corresponding to
residues 25 to 485 of SEQ ID NO:44. Signal sequence predictions were made with the
SignalP algorithm (available at: <http://www.cbs.dtu.dk>) .

Figures 38A-38B : Figure 38A: Fv39A nucleotide sequence (SEQ ID NO:45) .
Figure 38B: Fv39A amino acid sequence (SEQ ID NO:46) . SEQ ID NO:46 is the
20 sequence of the immature Fv39A. Fv39A has a predicted signal sequence
corresponding to residues 1 to 19 of SEQ ID NO:46 (underlined) ; cleavage of the signal
sequence is predicted to yield a mature protein having a sequence corresponding to
25 residues 20 to 439 of SEQ ID NO:46. Signal sequence predictions were made with the
SignalP algorithm (available at: <http://www.cbs.dtu.dk>) .

Figures 39A-39B : Figure 39A: Fv39B nucleotide sequence (SEQ ID NO:47) .
Figure 39B: Fv39B amino acid sequence (SEQ ID NO:48) . SEQ ID NO:48 is the
30 sequence of the immature Fv39B. Fv39B has a predicted signal sequence
corresponding to residues 1 to 18 of SEQ ID NO:48 (underlined) ; cleavage of the signal
sequence is predicted to yield a mature protein having a sequence corresponding to
residues 19 to 456 of SEQ ID NO:48. Signal sequence predictions were made with the
SignalP algorithm (available at: <http://www.cbs.dtu.dk>) .

Figures 40A-40B : Figure 40A: XynB nucleotide sequence (SEQ ID NO:49).
35 Figure 40B: XynB amino acid sequence (SEQ ID NO:50) . XynB does not have a

predicted signal sequence from the SignalP algorithm (available at: <http://www.cbs.dtu.dk>) .

Figures 41A-41 B: Figure 41A: XylA nucleotide sequence (SEQ ID NO:51).
 Figure 41B: XylA amino acid sequence (SEQ ID NO:52). XylA does not have a
 5 predicted signal sequence from the SignalP algorithm (available at:
<http://www.cbs.dtu.dk>) , but has a signal sequence predicted from the Uniprot algorithm
 (available at: <http://www.uniprot.org/uniprot>) that corresponds to residues 1 to 18 of SEQ
 ID NO:52 (underlined) ; cleavage of the signal sequence is predicted to yield a mature
 protein having a sequence corresponding to residues 19-705 of SEQ ID NO:52.

Figures 42A-42B : Figure 42A: Xyl1 nucleotide sequence (SEQ ID NO:53) .
 Figure 42B: Xyl1 amino acid sequence (SEQ ID NO:54) . SEQ ID NO:54 is the sequence
 of the immature Xyl1 . Xyl1 has a predicted signal sequence corresponding to residues 1
 to 21 of SEQ ID NO:54 (underlined) ; cleavage of the signal sequence is predicted to
 yield a mature protein having a sequence corresponding to residues 22 to 500 of SEQ ID
 15 NO:54. Signal sequence predictions were made with the SignalP algorithm (available at:
<http://www.cbs.dtu.dk>) .

Figures 43A-43B : Figure 43A: EXP and ethanol concentrations measured on
 Day 1 from an SSF reaction employing the *bx11⁻ T. reesei* strain #229, where 0.5 or 1.5
 mg/g xylan of purified *T. reesei* Bx1 was added to the SSF reaction or where 1 mg/g
 20 xylan of purified Fv43D was added ; Figure 43B: EXP and ethanol concentrations
 measured on Day 3 from an SSF reaction employing the *bx11⁻ T. reesei* #229, where 0.5
 or 1.0 mg/g xylan or purified *T. reesei* Bx1 was added to the SSF reaction or where 1
 mg/g xylan of purified Fv43D was added. Conditions of the SSF reaction(s) are
 described below in Example 6.

25 6. DETAILED DESCRIPTION

The meanings of abbreviations used herein are listed below: "min" means minute,
 "mins" means minutes; "hr" means hour, "hrs" means hours, "d" means day(s), "μL"
 means microliter(s), "mL" means milliliter(s) , "L" means liter(s) , "nm" means to
 nanometer(s) , "mm" means millimeter(s), "cm" means centimeter(s) , "μm" means
 30 micrometer(s), "mM" means millimolar(s), "M" means molar(s), "mmol" means
 millimole(s), "μmol" means micromole(s) , "g" means gram(s) , "μg" means
 microgram(s) , "mg" means to milligram(s) , "kg" means kilogram(s) , , "RPM" or "rpm"
 means revolutions per minute, "vol.%" means volume % , "wt.%" means weight % , and
 "RPS" means revolutions per second.

6.1. Common Definitions

Unless otherwise noted, all U.S. Patents and U.S. Patent Applications cited to herein are incorporated by reference in their entirety. Moreover, when an amount, concentration, or other value or parameter is given as a range, a preferred range, or a list of upper preferable value, or lower preferable values, it should be understood as specifically disclosing all ranges or numbers along the continuum formed in those ranges. When a range of numerical values is recited herein, unless otherwise noted, the range is intended to encompass the endpoints of that range, and all intergers and fractions within the range. It is not intended that the scope of the invention be limited to the specific values recited when defining a range.

As used herein, the articles "a", "an", and "the" preceding an element or component of the invention are intended to be nonrestrictive regarding the number of instances (e.g., occurrences) of the element or component. Thus "a", "an", and "the" should be read to include one or at least one, and the singular word form of the element or component also includes the plural unless the number is obviously meant to be singular.

As used herein, the term "comprising" means the presence of the stated features, integers, steps, or components as referred to in the claims, but that it does not preclude the presence or addition of one or more other features, integers, steps, components or groups thereof. The term "comprising" is intended to include embodiments encompassed by the term "consisting essentially of" and "consisting of." Similarly, the term "consisting essentially of" is intended to include embodiments encompassed by the term "consisting of."

As used herein, the term "about" modifying the quantity of an ingredient or reactant, or the quantity of a parameter of the invention, refers to variation in the numerical quantity that can occur, for example, through typical measuring and liquid handling procedures used for making concentrates or solutions in the real world, through inadvertent errors in these procedures, through differences in the manufacture, source, or purity of the ingredients employed to make the compositions or carry out the methods; and the like. The term "about" also encompasses amounts that differ due to different equilibrium conditions for a composition resulting from a particular initial mixture. Whether or not modified by the term "about" the claims include equivalents to the quantities they recite.

The term "simultaneous saccharification and fermentation" or "SSF" refers to a process or reaction configuration wherein biomass is saccharified and the fermentable

sugars produced from the saccharification are used by an enzyme and/or by a fermenting microorganism to produce a product all at the same time, typically in the same reaction vessel.

5 The term "hybrid saccharification and fermentation" or "HSF" refers to a process or reaction configuration wherein biomass is saccharified to a limited extent (incomplete or partial saccharification), followed by continued saccharification and fermentation occurring simultaneously.

10 The terms "separate saccharification and fermentation," "separate hydrolysis and fermentation," and "SHF" are used interchangeably herein. They refer to a process or reaction configuration wherein biomass is saccharified or hydrolyzed to substantial completion {e.g., about 60% or more complete, about 70% or more complete, about 80% or more complete, about 90% or more complete, or about 95% or more complete} or to completion {e.g., about 99% or more complete, or about 100% complete, such that all fermentable sugars that would be released from a given saccharification reaction are
15 released), followed by a separate and distinct fermentation step, wherein the fermentation sugars produced by the saccharification or hydrolysis step is fermented to produce a fermentation product.

The term "fermentable sugar" refers to oligosaccharides and monosaccharides that can be used as a carbon source by a microorganism in a fermentation process.

20 The term "partial saccharification" refers to limited saccharification of biomass where the fermentable sugars released are less than the total of fermentable sugars that would be released if saccharification is run to completion.

The term "cellulosic" refers to a composition comprising cellulose and additional components, including, for example, hemicellulose.

25 The term "saccharification" refers to the production of fermentable sugars from polysaccharides or polysaccharide-containing materials.

30 The term "biomass" refers to any cellulosic or lignocellulosic material and includes materials comprising cellulose, and optionally further comprising hemicellulose, lignin, starch, oligosaccharides, and/or monosaccharides. Biomass can also comprise additional components, such as proteins and/or lipids. Biomass can be derived from a single source, or biomass can comprise a mixture derived from more than one source. For example, biomass can comprise a mixture of corn cobs and corn stover, or a mixture of grass and leaves. Biomass includes, but is not limited to, bioenergy crops, agricultural residues, municipal solid waste, industrial solid waste, sludge from paper manufacture,
35 yard waste, wood and forestry waste. Examples of biomass include, without limitation,

corn cobs, crop residues such as corn husks, corn stover, grasses, wheat, wheat straw, barley straw, hay, rice straw, switchgrass, wasted paper, sugar cane bagasse, sorghum, giant reed, elephant grass, miscanthus, Japanese cedar, components obtained from milling of grains, tress, branches, roots, leaves, wood chips, sawdust, shrubs and bushes, vegetables, fruits, flowers and animal manure.

The term "saccharification enzyme" refers to an enzyme that can catalyze conversion of a component of biomass to fermentable sugars. It is often the case that the enzyme is more effective at producing fermentable sugars when the biomass is pretreated.

6.2. Detailed Description

Production of a substance or fermentation product from cellulosic material typically involves three major steps. These three steps are (1) pretreatment or pre-hydrolysis, (2) enzymatic hydrolysis or saccharification, and (3) fermentation, after which the substance or fermentation product can be recovered. Exemplified below is a process for producing ethanol, but it will be understood that similar processes can be used to produce other substances.

Pretreatment. In the pretreatment or pre-hydrolysis step, the cellulosic material (including, for example, a lignocellulosic material) is heated to break down the lignin and carbohydrate structure, to solubilize most of the hemicellulose, and to make the cellulose fraction accessible to cellulolytic enzymes. The heating step is performed either directly using steam or in a slurry or mixture where a catalyst may optionally be added to the material to accelerate the reactions. Suitable catalysts include, for example, strong acids, such as sulfuric acid and SO_2 , or strong bases, such as sodium hydroxide. The pretreatment step facilitates the penetration of the enzymes and microorganisms. Cellulosic biomass may also be subject to a hydrothermal steam explosion pre-treatment {see, e.g., U.S. Patent Publication No. 2002/01 64730}.

Saccharification. In the enzymatic hydrolysis step, also known as the saccharification step, enzymes as described herein are added to the pretreated material to convert the cellulose fraction to glucose and/or other sugars. The saccharification step is generally performed in stirred-tank reactors or fermentors under controlled pH, temperature, and mixing conditions. A saccharification step may, in certain cases, last up to 200 hrs. Saccharification can be carried out at temperatures from about 30 °C to about 65 °C, in particular about 50 °C, and at a pH of between about 4 and about 5, in particular at about pH 4.5. To produce glucose that can be metabolized by a fermenting microorganism such as a fungus (e.g., a yeast or a filamentous fungus) or a bacterium

(e.g., a *Zymomonas mobilis* or a *Clostridium thermocellum*) the enzymatic hydrolysis step is typically performed in the presence of a β -glucosidase.

Fermentation. In the fermentation step, sugars, released from the cellulosic material as a result of the pretreatment and enzymatic hydrolysis steps, are fermented to ethanol (or other substances) by a fermenting organism, such as a fungus (e.g., a yeast or a filamentous fungus) or a bacterium (e.g., a *Zymomonas mobilis* or a *Clostridium thermocellum*).

SSF. The present disclosure provides methods and compositions for improving the yield of reactions in which the fermentation step is carried out, rather than in a distinct or separate step following the enzymatic hydrolysis step, simultaneously with the enzymatic hydrolysis step in the same vessel, preferably under controlled pH, temperature, and mixing conditions. In certain aspects, the saccharification and fermentation are performed simultaneously in the same vessel, and as such is a simultaneous saccharification and fermentation, or "SSF." This process, as described herein, encompasses, also processes that are carried out using a "hybrid saccharification and fermentation" or "HSF" configuration. In certain aspects, an SSF reaction is initiated {e.g., by the addition of fermenting microorganism to a saccharification reaction, or by instituting a set of conditions to favor fermentation) when no more than 30%, no more than 25%, no more than 20%, no more than 15%, no more than 10%, or no more than 5% of the biomass is saccharified. As used herein, the term "SSF" also encompasses the co-fermentation of multiple sugars (Sheehan and Himmel, 1999, *Enzymes, energy and the environment: A strategic perspective on the U.S. Department of Energy's research and development activities for bioethanol*, *Biotechnol. Prog.* 15: 817-827).

25 **6.3 Enzymatic Hydrolysis**

The cell walls of higher plants are comprised of a variety of carbohydrate polymer (CP) components. These CP components interact through covalent and non-covalent means, providing the structural integrity plants require to form rigid cell walls and to resist turgor pressure. The major CP found in plants is cellulose, which forms the structural backbone of the plant cell walls. During cellulose biosynthesis, chains of poly- β -1,4-D-glucose self associate through hydrogen bonding and hydrophobic interactions to form cellulose microfibrils, which further self-associate to form larger fibrils. Cellulose microfibrils are somewhat irregular and contain regions of varying crystallinity. The degree of crystallinity of cellulose fibrils depends on how tightly ordered the hydrogen bonding is between any two component cellulose chains. Areas with less-ordered

bonding, and therefore more accessible glucose chains, are referred to as amorphous regions.

The general model for converting or depolymerizing cellulose into glucose involves three enzymatic activities. Endoglucanases cleave cellulose chains internally to generate shorter chains and increase the number of accessible ends, which are then acted upon by exoglucanases. Exoglucanases are specific for either the reducing ends or the non-reducing ends of the shorter chains, and are capable of liberating cellobiose, the dimer of glucose. Examples of exoglucanases include, without limitation, various cellobiohydrolases. The accumulating cellobiose is then cleaved to form glucose by cellobiases. Examples of cellobiases include, without limitation, various β -1,4-glucosidases.

Hemicellulose contains a set of different sugar monomers from those of cellulose, which contains anhydro-glucose. For instance, aside from glucose, sugar monomers in hemicellulose can include xylose, mannose, galactose, rhamnose, and arabinose. Hemicelluloses contain mostly D-pentose sugars and occasionally small amounts of L-sugars as well. Xylose is the sugar monomer present in the largest amount, but mannuronic acid and galacturonic acid also tend to be present. Hemicelluloses include, for example, xylan, glucuronoxylan, arabinoxylan, glucomannan, and xyloglucan.

Enzymes and multi-enzyme compositions of the present disclosure are useful for saccharification of hemicellulose materials, *e.g.*, xylan, arabinoxylan and xylan- or arabinoxylan-containing substrates. Arabinoxylan is a polysaccharide composed of xylose and arabinose, wherein L-a -arabinofuranose residues are attached as branch-points to a β -(1,4)-linked xylose polymeric backbone.

Due to the complexity of most biomass sources, which can contain cellulose, hemicellulose, pectin, lignin, protein, and ash, among other components, in certain aspects the enzyme blends of the disclosure can contain enzymes with a range of substrate specificities that work together to degrade biomass into fermentable sugars in an efficient manner. One example of a multi-enzyme complex for lignocellulose saccharification comprises a mixture of cellobiohydrolase(s), xylanase(s), endoglucanase(s), β -glucosidase(s), β -xylosidase(s), and, optionally, various accessory proteins.

Accordingly, the present disclosure contemplates the use of one or more enzymes that are capable, individually or collectively, of producing a carbohydrate that can be used as an energy-source by the fermenting organism(s) in an SSF reaction for producing a fermentation product, such as ethanol.

In certain aspects, multi-enzyme compositions are used in an SSF reaction for hydrolysis of carbohydrates or carbohydrate-containing biomass substrates to produce sugars that are fermented in the same reaction by a fermenting microorganism . The multi-enzyme compositions (including products of manufacture, enzyme ensembles, or
5 "blends") comprise a mixture (or "blend") of enzymes that, in certain aspects, is non-naturally occurring. As used herein, the term "blend" refers to:

- (1) a composition made by combining component enzymes, whether in the form of a fermentation broth or in the form of partially or completely isolated or purified polypeptides;
- 10 (2) a composition produced by an organism modified to express one or more component enzymes; optionally, the organism can be modified to delete one or more genes or inactivate one or more gene products, wherein the genes encode proteins that affect xylan hydrolysis, hemicellulose hydrolysis and/or cellulose hydrolysis;
- 15 (3) a composition made by combining component enzymes simultaneously, separately, or sequentially during an SSF reaction ; and
- (4) an enzyme mixture produced *in situ*, e.g., during an SSF reaction ;
- (5) a combination of any or all of (1)-(4) above.

It is also to be understood that any of the enzymes described specifically herein
20 can be combined with any one or more of the enzymes described herein or with any other available and suitable enzymes, to produce a multi-enzyme composition. The disclosure is not restricted or limited to the specific exemplary combinations listed or exemplified herein.

In the methods of the present disclosure, any of the enzyme(s) described herein
25 can be added prior to or during the SSF reaction, including during or after the propagation of the fermenting microorganism(s) . The enzymes can be added individually, as an enzyme blend, or as a fermentation broth, *etc.*

The enzymes referenced herein can be derived or obtained from any suitable origins, including, for example, from bacterial, fungal, yeast, or mammalian origins. The
30 term "obtained" is meant that the enzyme can be isolated from an organism , which naturally produces the enzyme as a native enzyme, or that the enzyme can be produced recombinantly in a host organism , wherein the recombinantly produced enzyme is either native or foreign to the host organism , has a modified amino acid sequence, e.g., having one or more amino acids, which are deleted, inserted and/or substituted, or is an enzyme
35 produced by nucleic acid shuffling processes known in the art. For example, the

recombinantly produced enzyme can be one that is a mutant and/or a fragment of a native amino acid sequence. By "a native enzyme" it is meant to encompass the product of a gene in its natural location in the genome of an organism, and also to encompass natural variants; by a "foreign enzyme" it is meant to encompass the product of a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer, or gene inserted into a non-native organism, or chimeric genes, which includes enzymes that are obtained recombinantly, such as by site-directed mutagenesis or shuffling.

The enzymes can, in certain aspects, be purified. The term "purified," as used herein to modify substances like enzymes, proteins, polypeptides, polynucleotides, and other components, refers to enzymes free or substantially free from other components of the organisms from which they are derived. In certain aspects, the term "purified" also encompasses situations wherein the enzymes are free or substantially free from components of the native organisms from which they are obtained. Enzymes can be deemed "purified," but remain associated or in the presence of minor amounts of other proteins. The term "other proteins," as used herein, refers, in particular, to other enzymes. The term "purified" as used herein also refers to the removal of other components, particularly the removal of other proteins and more particularly other enzymes present in the originating cells of the enzymes of the disclosure. Accordingly, an enzyme can be, for example, a "substantially pure polypeptide," which is substantially free from other components. The organism in which a given enzyme is produced can be, for example, a host organism suitable for recombinantly produced enzymes. For example, a substantially pure polypeptide can refer to a polypeptide present at a level of 50 wt.% or more, 60 wt.% or more, 70 wt.% or more, 80 wt.% or more, 90 wt.% or more, 95 wt.% or more, 98% or more, or 99% or more in a mixture to which it is a part. A polypeptide substantially free of other components is one that is in a mixture that contains less than 40 wt.%, less than 30 wt.%, less than 20 wt.%, less than 10 wt.%, less than 5 wt.%, less than 2 wt.%, or less than 1 wt.% of other components.

6.3.1. Cellulases

Enzyme blends of the disclosure can comprise one or more cellulases. Cellulases are enzymes that hydrolyze cellulose (β -1,4-glucan or β -D-glucosidic linkages) to form glucose, cellobiose, cellooligosaccharides, and the like. Cellulases are traditionally divided into three major classes: endoglucanases (EC 3.2.1.4) ("EG"), exoglucanases or cellobiohydrolases (EC 3.2.1.91) ("CBH") and β -glucosidases (β -D-glucoside glucohydrolase; EC 3.2.1.21) ("BG") (Knowles *et al.*, 1987, Trends in Biotechnol.

5(9) :255-261 , and Schulein, 1988, Methods of Enzymology 160:234-242) .

Endoglucanases act mainly on the amorphous parts of the cellulose fiber, whereas cellobiohydrolases are capable of degrading crystalline cellulose.

Cellulases for use in accordance with the methods and compositions of the disclosure can be obtained from, *inter alia*, one or more of the following organisms:

5 *Crinipellis scapella*, *Macrophomina phaseolina*, *Myceliophthora thermophila*, *Sordaria fimicola*, *Volutella colletotrichoides*, *Thielavia terrestris*, *Acremonium sp.*, *Exidia glandulosa*, *Fomes fomentarius*, *Spongipellis sp.*, *Rhizophlyctis rosea*, *Rhizomucor pusillus*, *Phycomyces niteus*, *Chaetostylum fresenii*, *Diplodia gossypina*, *Ulospora*

10 *bilgramii*, *Saccobolus dilutellus*, *Penicillium verruculosum*, *Penicillium chrysogenum*, *Thermomyces verrucosus*, *Diaporthe syngenesia*, *Colletotrichum lagenarium*, *Nigrospora sp.*, *Xylaria hypoxylon*, *Nectria pinea*, *Sordaria macrospora*, *Thielavia thermophila*, *Chaetomium mororum*, *Chaetomium virscens*, *Chaetomium brasiliensis*, *Chaetomium cunicolorum*, *Syspastospora boninensis*, *Cladorrhinum foecundissimum*, *Scytalidium*

15 *thermophila*, *Gliocladium catenulatum*, *Fusarium oxysporum ssp. lycopersici*, *Fusarium oxysporum ssp. passiflora*, *Fusarium solani*, *Fusarium anguioides*, *Fusarium poae*, *Humicola nigrescens*, *Humicola grisea*, *Panaeolus retirugis*, *Trametes sanguinea*, *Schizophyllum commune*, *Trichothecium roseum*, *Microsphaeropsis sp.*, *Acsobolus stictoideus spej.*, *Pomonia punctata*, *Nodulisporum sp.*, *Trichoderma sp.* {e.g.,

20 *Trichoderma reesei*) and *Cylindrocarpon sp.*

In specific embodiments, a cellulase for use in the composition of the disclosure is capable of achieving at least 0.1, at least 0.2, at least 0.3, at least 0.4, or at least 0.5 fraction product as determined by a calcofluor assay as described in the following subsection. In some embodiments, a cellulase for use in the composition of the

25 disclosure is a whole cellulase and/or is capable of achieving at least 0.1, at least 0.2, at least 0.3, at least 0.4, or at least 0.5 fraction product as determined by a calcofluor assay as described in the following subsection. In some embodiments, a cellulase for use in the composition of the disclosure is a whole cellulase and/or is capable of achieving about

30 0.1 to about 0.5, or about 0.1 to about 0.4, or about 0.2 to about 0.4, or about 0.3 to about 0.4, or about 0.2 to about 0.5, or about 0.3 to about 0.5 fraction product as determined by a calcofluor assay.

6.3.1.1. Cellulase Activity Assay Using Calcofluor White

Phosphoric acid swollen cellulose (PASC) is prepared from Avicel PH-101 using an adapted protocol of Walseth, 1971, TAPPI 35:228, and of Wood, 1971, Biochem. J.

35 121:353-362. In short, in an exemplary method, Avicel is solubilized in concentrated

phosphoric acid then precipitated using cold deionized water. After the cellulose is collected and washed with water to achieve neutral pH, it is diluted to 1% solids in 50 mM sodium acetate buffer, at pH 5.0.

All enzyme dilutions are made with a 50 mM sodium acetate buffer, pH 5.0.

- 5 GC220 Cellulase (Danisco US Inc., Genencor) is diluted to 2.5, 5, 10, and 15 mg protein/g PASC, to produce a linear calibration curve. Samples to be tested are diluted to fall within the range of the calibration curve, *i.e.*, to obtain a response of 0.1 to 0.4 fraction product. One hundred and fifty (150) μL of cold 1% PASC is added to each 20 μL of enzyme solution in suitable vessels, for example, 96-well microtiter plates. The
- 10 plates are covered and incubated for 2 hrs at 50 °C, spun at 200 rpm, in an incubator/shaker. The reactions are then quenched using 100 μL of 50 $\mu\text{g/mL}$ Calcofluor in 100 mM Glycine, pH 10. Fluorescence is read on a fluorescence microplate reader at excitation wavelength $E_x = 365$ nm and emission wavelength $E_m = 435$ nm. The result is expressed as the fraction product according to the equation :
- 15
$$FP = 1 - (FI_{\text{sample}} - FI_{\text{buffer with cellobiose}}) / (FI_{\text{zero enzyme}} - FI_{\text{buffer with cellobiose}})$$
, wherein "FP" is fraction product and "FI" is fluorescence units.

6.3.1.2. β -Glucosidase

The enzyme blends of the disclosure optionally comprise one or more β -glucosidases. The term " β -glucosidase" as used herein refers to a β -D-glucoside

20 glucohydrolase classified in or under EC 3.2.1.21, and/or to an enzyme that is a member of certain glycosyl hydrolase ("GH") families, including, without limitation, GH families 1, 3, 9 or 48. In certain aspects, the term refers to an enzyme that is capable of catalyzing the hydrolysis of cellobiose to release β -D-glucose.

β -glucosidases can be obtained from any suitable microorganisms. They can be

25 obtained or produced by recombinant means, or can be obtained from commercial sources. Suitable β -glucosidases can, for example, be obtained from microorganisms such as bacteria and fungi. For example, a suitable β -glucosidase can be obtained from a filamentous fungus.

In certain aspects, a suitable β -glucosidase can be obtained from *Aspergillus*

30 *aculeatus* (Kawaguchi *et al.*, 1996, Gene 173: 287-288), *Aspergillus kawachi* (Iwashita *et al.*, 1999, Appl. Environ. Microbiol. 65: 5546-5553), *Aspergillus oryzae* (PCT patent application publication WO 2002/09501 4), *Cellulomonas biazotea* (Wong *et al.*, 1998, Gene 207:79-86), *Penicillium funiculosum* (PCT patent application publication WO 20047891 9), *Saccharomycopsis fibuligera* (Machida *et al.*, 1988, Appl. Environ. Microbiol. 54: 3147-3155), *Schizosaccharomyces pombe* (Wood *et al.*, 2002, Nature

35

4 15: 871 -880), or *Trichoderma reesei*. For example, suitable β -glucosidases from *Trichoderma reesei* can include β -glucosidase 1 (U.S. Patent No. 6,022,725), *Trichoderma reesei* β -glucosidase 3 (U.S. Patent No. 6,982,159), *Trichoderma reesei* β -glucosidase 4 (U.S. Patent No. 7,045,332), *Trichoderma reesei* β -glucosidase 5 (US
5 Patent No. 7,005,289), *Trichoderma reesei* β -glucosidase 6 (U.S. Patent Application Publication 20060258554), or *Trichoderma reesei* β -glucosidase 7 (U.S. Patent Application Publication 20060258554).

In some embodiments, suitable β -glucosidases can be produced by expressing genes encoding β -glucosidases. For example, a suitable β -glucosidase can be secreted
10 into the extracellular space e.g., by certain Gram-positive organism, (such as *Bacillus* or *Actinomycetes*), or by a eukaryotic host {e.g., *Trichoderma*, *Aspergillus*, *Saccharomyces*, or *Pichia*).

Suitable β -glucosidases can also be obtained from commercial sources. Examples of commercial β -glucosidase preparation suitable for use in the methods,
15 compositions and other embodiments of the present disclosure include, without limitation, *Trichoderma reesei* β -glucosidase in Accellerase™ BG (Danisco US Inc., Genencor); NOVOZYM™ 188 (a β -glucosidase from *Aspergillus niger*); *Agrobacterium* sp. β -glucosidase, and *Thermatoga maritima* β -glucosidase available from Megazyme (Megazyme International Ireland Ltd., Bray Business Park, Bray, Co. Wicklow, Ireland).

20 In certain aspects, a suitable β -glucosidase can be a component of a whole cellulase, as described in Section 6.3.1.5 below.

β -glucosidase activity can be determined by means that are known in the art. For example, the assay described by Chen *et al.*, 1992, in *Biochimica et Biophysica Acta* 121:54-60 can be used. In that assay, one unit pNPG denotes 1 μ mol of Nitrophenol
25 liberated from para-nitrophenyl-B-D-glucopyranoside in 10 mins at 50 °C (or 122 °F) and pH 4.8.

6.3.1 .3. Endoglucanases

The enzyme blends of the disclosure optionally comprise one or more endoglucanase. The term "endoglucanase" refers to any polypeptides classified in EC
30 3.2.1 .4..

In some aspects, a *Trichoderma reesei* EG1 (Penttila *et al.*, 1986, Gene 63:1 03-112) and/or *T. reesei* EGII (Saloheimo *et al.*, 1988, Gene 63:1 1-21) are used in the methods and compositions of the present disclosure. In other aspects, the endoglucanase can be a *T. reesei* endoglucanase VI (see, e.g., U.S. Patent No.

7,351,568), endoglucanase VII (see, e.g., U.S. Patent No. 7,449,319), or endoglucanase VIII (see, e.g., U.S. Patent No. 7,049,125).

In specific embodiments, a suitable endoglucanase can be a *Thielavia terrestris* thermostable endoglucanase (Kvesitadze *et al.*, 1995, Appl. Biochem. Biotechnol. 50:137-143); *Trichoderma reesei* EGIII (Okada *et al.*, 1988, Appl. Environ. Microbiol. 64:555-563), EGIV (Saloheimo *et al.*, 1997, Eur. J. Biochem. 249:584-591), EG5 (Saloheimo *et al.*, 1994, Mol. Microbiol. 13:219-228), EGVI (U.S. Patent Application Publication No. 20070213249), or EGVII (U.S. Patent Application Publication No. 20090170181); *Acidothermus cellulolyticus* EI endoglucanase (U.S. Patent No. 5,536,655); *Humicola insolens* endoglucanase V (EGV) (Protein Data Bank entry 4ENG); *Staphylotrichum coccosporum* endoglucanase (U.S. Patent Application Publication No. 20070111278); *Aspergillus aculeatus* endoglucanase F1-CMC (Ooi *et al.*, 1990, Nucleic Acid Res. 18:5884); *Aspergillus kawachii* IFO 4308 endoglucanase CMCCase-1 (Sakamoto *et al.*, 1995, Curr. Genet. 27:435-439); or *Erwinia carotovora* (Saarilahti *et al.*, 1990, Gene 90:9-14); *Acremonium thermophilum* ALK04245 endoglucanase (U.S. Patent Publication No. 20070148732).

Suitable endoglucanases for use in the methods and compositions of the present disclosure can also be those described in, e.g., PCT patent application publications WO 91/17243, WO 91/17244, WO 91/10732, or U.S. Patent No. 6,001,639.

20 6.3.1.4. Cellobiohydrolases

The term "cellobiohydrolase" as used herein refers to any cellobiohydrolases that are classified in EC 3.2.1.91. The methods and compositions of the present disclosure can suitably comprise one or more cellobiohydrolases ("CBH").

In some aspects, a *Trichoderma reesei* CBHI (Shoemaker *et al.*, 1983, Bio/Technology 1:691-696) and/or CBHII (Teeri *et al.*, 1983, Bio/Technology 1:696-699) can be used in the methods and compositions of the present disclosure.

In some aspects, a suitable CBH can be an *Agaricus bisporus* CBH1 (Swiss Prot Accession no. Q92400); *Aspergillus aculeatus* CBH1 (Swiss Prot Accession No. 059843); *Aspergillus nidulans* CBHA (GenBank Accession No. AF420019); *Aspergillus nidulans* CBHB (GenBank Accession No. AF420020); *Aspergillus niger* CBHA (GenBank Accession No. AF156268); *Aspergillus niger* CBHB (GenBank Accession No. AF156269); *Claviceps purpurea* CBH1 (Swiss Prot Accession No. 000082); *Cochliobolus carbonarum* CBH1 (Swiss Prot Accession No. Q00328); *Cryphonectria parasitica* CBH1 (Swiss Prot Accession No. Q00548); *Fusarium oxysporum* CBW (Cel7A) (Swiss Prot Accession No. P46238); *Humicola grisea* cbhl.2 (GenBank

Accession No. U50594); *Humicola grisea* var. *thermoidea* CBH1 (GenBank Accession No. D6351 5); *Humicola grisea* var. *thermoidea* CBHI.2 (GenBank Accession No. AF1 23441); *Humicola grisea* var. *thermoidea* exol (GenBank Accession No. AB0031 05); *Melanocarpus albomyces* Cel7B (GenBank Accession No. AJ51 5705), *Neurospora* 5 *crassa* CBH1 (GenBank Accession No. X77778); *Penicillium funiculosum* CBH1 (Cel7A) (U.S. Patent Publication No. 200701 48730); *Penicillium janthinellum* CBH1 (GenBank Accession No. S561 78); *Phanerochaete chrysosporium* CBH (GenBank Accession No. M22220); *Phanerochaete chrysosporium* CBHI-2 (Cel7D) (GenBank Accession No. L22656); *Talaromyces emersonii* Cbh1 A (GenBank Accession No. AF439935); 10 *Trichoderma viride* CBH1 (GenBank Accession No. X53931), or *Volvariella volvacea* V 14 Cbh1 (GenBank Accession No. AF1 56693).

6.3.1 .5. Whole Cellulases

In certain aspects, an enzyme blend of the disclosure comprises a whole cellulase. As used herein, a "whole cellulase" refers to both naturally occurring and non- 15 naturally occurring cellulase-containing compositions comprising: (1) an endoglucanase, which cleaves internal β -1,4 linkages of a cellulose, resulting in shorter glucooligosaccharides, (2) a cellobiohydrolase, which acts in an "exo" manner to release cellobiose units from the shorter glucooligosaccharides; examples of cellobiose units 20 include β -1,4 glucose-glucose disaccharide, and (3) a β -glucosidase, which catalyzes the release of glucose monomers from short cellooligosaccharides or cellobioses, which are glucose dimers. .

A "naturally occurring cellulase-containing" composition is one produced by a naturally occurring source, which comprises one or more cellobiohydrolase-type, one or more endoglucanase- type, and one or more β -glucosidase-type components or 25 activities, wherein each of these components or activities is found at the ratios and levels produced in nature, untouched by the human hand. Accordingly, a naturally occurring cellulase-containing composition is, for example, one that is produced by an organism unmodified with respect to the cellulolytic enzymes such that the ratios or levels of the component enzymes are unaltered from that produced by the native organism in nature. 30 A "non-naturally occurring cellulase-containing composition" refers to a composition produced by: (1) combining component cellulolytic enzymes either in a naturally occurring ratio or a non-naturally occurring, *i.e.*, altered, ratio; or (2) modifying an organism to overexpress or underexpress one or more cellulolytic enzymes; or (3) modifying an organism such that at least one cellulolytic enzyme is deleted. A "non- 35 naturally occurring cellulase containing" composition can also refer to a composition

resulting from adjusting the culture conditions for a naturally-occurring organism, such that the naturally-occurring organism grows under a non-native condition, and produces an altered level or ratio of enzymes. Accordingly, in some embodiments, the whole cellulase preparation of the present disclosure can have one or more EGs and/or CBHs and/or β -glucosidases deleted and/or overexpressed. In the present disclosure, a whole cellulase preparation can be from any microorganism that is capable of hydrolyzing a cellulosic material. In some embodiments, the whole cellulase preparation is a filamentous fungal whole cellulase. For example, the whole cellulase preparation can be from an *Acremonium*, *Aspergillus*, *Emericella*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Scytalidium*, *Thielavia*, *Tolyocladium*, or *Trichoderma* species. The whole cellulase preparation is, for example, an *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, or *Aspergillus oryzae* whole cellulase. Moreover, the whole cellulase preparation can be a *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, or *Fusarium venenatum* whole cellulase preparation. The whole cellulase preparation can also be a *Chrysosporium lucknowense*, *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Penicillium funiculosum*, *Scytalidium thermophilum*, or *Thielavia terrestris* whole cellulase preparation. Moreover, the whole cellulase preparation can be a *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei* (e.g., RL-P37 (Sheir-Neiss G *et al.* Appl. Microbiol. Biotechnol. 1984, 20, pp.46-53), QM941 4 (ATCC No. 26921), NRRL 15709, ATCC 13631, 56764, 56466, 56767), or a *Trichoderma viride* (e.g., ATCC 32098 and 32086) whole cellulase preparation.

The whole cellulase preparation can, in particular, suitably be a *Trichoderma reesei* RutC30 whole cellulase preparation, which is available from the American Type Culture Collection as *Trichoderma reesei* ATCC 56765. For example, the whole cellulase preparation can also suitably be a whole cellulase of *Penicillium funiculosum*, which is available from the American Type Culture Collection as *Penicillium funiculosum* ATCC Number: 10446.

The whole cellulase preparation can also be obtained from commercial sources. Examples of commercial cellulase preparations suitable for use in the methods and compositions of the present disclosure include, for example, CELLUCLAST™ and Cellic™ (Novozymes A/S) and LAMINEX™ BG, IndiAge™ 44L, Primafast™ 100, 5 Primafast™ 200, Spezyme™ CP, Accellerase™ 1000, and Accellerase™ 1500 (Danisco US. Inc., Genencor) .

Suitable whole cellulase preparations can be made using any microorganism cultivation methods known in the art, especially fermentation, resulting in the expression of enzymes capable of hydrolyzing a cellulosic material. As used herein, "fermentation" 10 refers to shake flask cultivation, small- or large-scale fermentation, such as continuous, batch, fed-batch, or solid state fermentations in laboratory or industrial fermenters performed in a suitable medium and under conditions that allow the cellulase and/or enzymes of interest to be expressed and/or isolated.

Generally, the microorganism is cultivated in a cell culture medium suitable for 15 production of enzymes capable of hydrolyzing a cellulosic material. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures and variations known in the art. Suitable culture media, temperature ranges and other conditions for growth and cellulase production are known in the art. As a non-limiting example, a typical temperature range for the 20 production of cellulases by *Trichoderma reesei* is 24 °C to 28 °C

The whole cellulase preparation can be used as it is produced by fermentation with no or minimal recovery and/or purification. For example, once cellulases are secreted into the cell culture medium, the cell culture medium containing the cellulases can be used directly. The whole cellulase preparation can comprise the unfractionated 25 contents of fermentation material, including the spent cell culture medium, extracellular enzymes and cells. On the other hand, the whole cellulase preparation can also be subject to further processing in a number of routine steps, e.g., precipitation, centrifugation, affinity chromatography, filtration, or the like. For example, the whole cellulase preparation can be concentrated, and then used without further purification. 30 The whole cellulase preparation can, for example, be formulated to comprise certain chemical agents that decrease cell viability or kill the cells after fermentation. The cells can, for example, be lysed or permeabilized using methods known in the art.

The endoglucanase activity of the whole cellulase preparation can be determined using carboxymethyl cellulose (CMC) as a substrate. A suitable assay 35 measures the production of reducing ends created by the enzyme mixture acting on

CMC wherein 1 unit is the amount of enzyme that liberates 1 μmole of product/min (Ghose, T. K., Pure & Appl. Chem. 1987, 59, pp. 257-268).

The whole cellulase can be a β -glucosidase-enriched cellulase. The β -glucosidase-enriched whole cellulase generally comprises a β -glucosidase and a whole cellulase preparation. The β -glucosidase-enriched whole cellulase compositions can be produced by recombinant means. For example, such a whole cellulase preparation can be achieved by expressing a β -glucosidase in a microorganism capable of producing a whole cellulase. The β -glucosidase-enriched whole cellulase composition can also, for example, comprise a whole cellulase preparation and a β -glucosidase. For instance, the β -glucosidase-enriched whole cellulase composition can suitably comprise at least 5 wt.%, 7 wt.%, 10 wt.%, 15 wt.% or 20 wt.%, and up to 25 wt.%, 30 wt.%, 35 wt.%, 40 wt.%, or 50 wt.% β -glucosidase based on the total weight of proteins in that blend/composition.

In certain aspects, a suitable whole cellulase can be obtained from a microorganism that is or has been genetically engineered to reduce or eliminate retaining β -xylosidase activity. In other aspects, a suitable whole cellulase can be obtained from a microorganism that is or has been genetically engineered to increase inverting β -xylosidase activity. In yet further aspects, a suitable whole cellulase can be obtained from a microorganism that is or has been genetically engineered to not only have reduced or eliminated retaining β -xylosidase activity, but also have increased inverting β -xylosidase activity. For example, a whole cellulase can suitably be obtained from *Trichoderma reesei* that has been engineered such that the native *bx11* gene is deleted. In another example, a whole cellulase can suitably be obtained from *Trichoderma reesei* that has been engineered to recombinantly express an enzyme with inverting β -xylosidase activity. In yet another example, a whole cellulase can suitably be obtained from *Trichoderma reesei* that has been engineered such that its native *bx11* gene is deleted and that it recombinantly expresses an enzyme with inverting β -xylosidase activity. Examples of enzymes with inverting β -xylosidase activity include, without limitation, Fv43D and others described herein in Section 6.4.

β -xylosidase activity can be determined by measuring the level of hydrolysis of an artificial substrate p-nitrophenyl β -xylopyranoside. The hydrolysis reaction can be followed using $^1\text{H-NMR}$ analysis during the course of the reaction. The anomeric proton of the residue contributing the reducing end of a glycosidic bond has a distinct chemical shift depending upon its axial or equatorial orientation as does the anomeric proton of the newly formed reducing sugar after hydrolysis. Mutarotation of the newly formed

reducing sugar anomeric proton to the equilibrium mixture of axial and equatorial forms is slower in comparison to the hydrolysis reaction. Thus the $^1\text{H-NMR}$ determination of the orientation of the first formed reducing end anomeric proton in comparison to the form present in the substrate is an assay for mechanisms that retain configuration versus those that invert configuration. The experimental methods are described in, e.g., Pauly
5 *et al*, 1999, *Glycobiology* 9:93-100.

Alternatively, the level of hydrolysis can be determined by distinguishing transglycosylase activity of the retaining enzymes, which is absent in inverting enzymes. An example of such an assay is shown in Figure 16. Xylobiose or xylose oligomers, in
10 the presence of a retaining enzyme (e.g., Multifect® Xylanase or Fv3A), show a rapid rise in EXP/xylose to 7-8 times the equilibrium ratio in the presence of EtOH after which EXP/xylose falls toward the equilibrium ratio. In the case of the inverting enzymes (e.g., Fv43D), under the same conditions, EXP/xylose increases monotonically toward the equilibrium ratio.

15 6.3.2. Hemicellulases

A wide variety of fungi and bacteria are capable of enzymatically hydrolyzing hemicelluloses. Similar to cellulose degradation, hemicellulose hydrolysis involves coordinated actions of a number of enzymes. Hemicellulases are often grouped into three general categories: the endo-acting enzymes that attack internal bonds within
20 polysaccharide chains, the exo-acting enzymes that act processively from either the reducing or the nonreducing end of the polysaccharide chain, and the accessory enzymes, acetyl esterases, and/or esterases that hydrolyze lignin glycoside bonds. Examples of esterases can include coumaric acid esterase and ferulic acid esterase (Wong *et al*, 1988, *Microbiol. Rev.* 52:305-317; Tenkanen and Poutanen, 1992,
25 Significance of esterases in the degradation of xylans, in *Xylans and Xylanases*, Visser *et al*, eds., Elsevier, New York, N.Y., pp. 203-212; Coughlan and Hazlewood, 1993, *Hemicellulose and hemicellulases*, Portland, London, UK; Brigham *et al*, 1996, *Hemicellulases: Diversity and applications*, in *Handbook on Bioethanol: Production and Utilization*, Wyman, ed., Taylor & Francis, Washington, D.C., pp. 119-141).

30 Suitable hemicellulases for use with the compositions and/or methods of the present disclosure include, for example, xylanases, arabinofuranosidases, acetyl xylan esterase, glucuronidases, endo-galactanase, mannanases, endo or exo arabinases, exo-galactanases, and mixtures thereof. Examples of endo-acting hemicellulases and ancillary enzymes include, without limitation, endoarabinanase,
35 endoarabinogalactanase, endoglucanase, endomannanase, endoxylanase, and feraxan

endoxyylanase. Examples of exo-acting hemicellulases and ancillary enzymes include, without limitation, α -L-arabinosidase, β -L-arabinosidase, α -1,2-L-fucosidase, α -D-galactosidase, β -D-galactosidase, β -D-glucosidase, β -D-glucuronidase, β -D-mannosidase, β -D-xylosidase, exoglucosidase, exocellobiohydrolase, exomannobiohydrolase, exomannanase, exoxyylanase, xylan α -glucuronidase, and coniferin β -glucosidase. Examples of esterases include, without limitation, acetyl esterases (acetylgalactan esterase, acetylmannan esterase, and acetylxylan esterase) and aryl esterases (coumaric acid esterase and ferulic acid esterase).

In certain aspects, the hemicellulase is an exo-acting hemicellulase. Preferably, the exo-acting hemicellulase has the ability to hydrolyze hemicellulose under acidic conditions, for example, at or below pH 7.

In certain aspects, the hemicellulase is added in an effective amount. For example, the hemicellulase is added to the multienzyme blends of the present disclosure in an amount of about 0.001 wt.% or more, about 0.002 wt.% or more, about 0.0025 wt.% or more, about 0.005 wt.% or more, or about 0.01 wt.% or more relative to the weight of solids in the complete fermentation medium. In another example, the hemicellulase is added to the multienzyme blends of the present disclosure in an amount of about 0.001 wt.% to about 5.0 wt.%, for example, about 0.025 wt.% to about 4.0 wt.%, about 0.005 wt.% to about 2.0 wt.% relative to the weight of solids in the complete fermentation medium.

6.3.2.1 . Xylanases

The enzyme blends of the disclosure optionally comprise one or more xylanases. The term "xylanase" as used herein refers to any xylanase classified in or under EC 3.2.1.8. Suitable xylanases include, for example, a *Caldocellum saccharolyticum* xylanase (Luthi *et al.*, 1990, Appl. Environ. Microbiol. 56(9):2677-2683), a *Thermatoga maritima* xylanase (Winterhalter & Liebel, 1995, Appl. Environ. Microbiol. 61(5):1810-1815), a *Thermatoga Sp.* Strain FJSS-B.1 xylanase (Simpson *et al.*, 1991, Biochem. J. 277, 413-417), a *Bacillus circulans* xylanase (BcX) (U.S. Patent No. 5,405,769), an *Aspergillus niger* xylanase (Kinoshita *et al.*, 1995, J. Ferment. Bioeng. 79(5):422-428); a *Streptomyces lividans* xylanase (Shareck *et al.*, 1991, Gene 107:75-82; Morosoli *et al.*, 1986, Biochem. J. 239:587-592; Kluepfel *et al.*, 1990, Biochem. J. 287:45-50); *Bacillus subtilis* xylanase (Bernier *et al.*, 1983, Gene 26(1):59-65); a *Cellulomonas fimi* xylanase (Clarke *et al.*, 1996, FEMS Microbiol. Lett. 139:27-35), a *Pseudomonas fluorescens* xylanase (Gilbert *et al.*, 1988, J. Gen. Microbiol. 134:3239-3247); a *Clostridium thermocellum* xylanase (Dominguez *et al.*, 1995, Nat. Struct. Biol. 2(7):569-76); a *Bacillus*

pumilus xylanase (Nuyens *et al.*, 2001, Appl. Microbiol. Biotech. 56:431-434; Yang *et al.*, 1988, Nucleic Acids Res. 16(14B):7187); a *Clostridium acetobutylicum* P262 xylanase (Zappe *et al.*, 1990, Nucleic Acids Res. 18(8):2179) or a *Trichoderma harzianum* xylanase (Rose *et al.*, 1987, J. Mol. Biol. 194(4):755-756).

5 Xylanases can suitably be obtained from a number of sources, including, for example, fungal and bacterial organisms, such as *Aspergillus*, *Disporotrichum*, *Penicillium*, *Neurospora*, *Fusarium*, *Trichoderma*, *Humicola*, *Thermomyces*, and *Bacillus*. Certain commercially available preparations comprising xylanase(s) can also be used in the compositions and methods of the present disclosure; those include Multifect®
 10 xylanase, Laminex® BG and Spezyme® CP (Danisco US, Genencor), and Celluclast® and Viscozyme® (Novozymes A/S).

In certain aspects, the xylanase does not have retaining β -xylosidase activity and/or inverting β -xylosidase activity. An enzyme can be tested for retaining vs. inverting activity as described in Section 6.3.1 .5 above.

15 6.3.2.2. β -Xylosidases

The enzyme blends of the disclosure optionally comprise one or more β -xylosidases.

As used herein, the term " β -xylosidase" refers to any β -xylosidase classified in or under EC 3.2.1 .37. Suitable β -xylosidases include, for example *Talaromyces emersonii*
 20 Bxl1 (Reen *et al.*, 2003, Biochem. Biophys. Res. Commun. 305(3) :579-85); as well as β -xylosidases obtained from *Geobacillus stearothermophilus* (Shallom *et al.*, 2005, Biochem. 44:387-397); *Scytalidium thermophilum* (Zanoelo *et al.*, 2004, J. Ind. Microbiol. Biotechnol. 31:170-176); *Trichoderma lignorum* (Schmidt, 1988, Methods Enzymol. 160:662-671); *Aspergillus awamori* (Kurakake *et al.*, 2005, Biochim. Biophys. Acta
 25 1726:272-279); *Aspergillus versicolor* (Andrade *et al.*, Process Biochem. 39:1931-1938); *Streptomyces sp.* (Pinphanichakarn *et al.*, 2004, World J. Microbiol. Biotechnol. 20:727-733); *Thermotoga maritima* (Xue and Shao, 2004, Biotechnol. Lett. 26:151 1-1515); *Trichoderma sp.* SY (Kim *et al.*, 2004, J. Microbiol. Biotechnol. 14:643-645); *Aspergillus niger* (Oguntimein and Reilly, 1980, Biotechnol. Bioeng. 22:1 143-1 154); or *Penicillium wortmanni* (Matsuo *et al.*, 1987, Agric. Biol. Chem. 51:2367-2379).
 30

In certain aspects, the β -xylosidase does not have retaining β -xylosidase activity. In other aspects, the β -xylosidase has inverting β -xylosidase activity. In yet further aspects, the β -xylosidase has no retaining β -xylosidase activity but has inverting β -xylosidase activity. An enzyme can be tested for retaining vs. inverting activity as
 35 described in Section 6.3.1 .5 above.

6.3.2.3. L-g-Arabinofuranosidases

The enzyme blends of the disclosure optionally comprise one or more L- α -arabinofuranosidases.

As used herein, the term "L-arabinofuranosidase" refers to any enzyme
 5 classified in or under EC 3.2.1.55. Suitable L-a-arabinofuranosidase can be obtained
 from, for example, *Aspergillus oryzae* (Numan & Bhosle, 2006, J. Ind. Microbiol.
 Biotechnol. 33:247-260) ; *Aspergillus sojae* (Oshima *et al.*, 2005, J. Appl. Glycosci .
 52:261 -265) ; *Bacillus brevis* (Numan & Bhosle, 2006, J. Ind. Microbiol. Biotechnol.
 33:247-260) ; *Bacillus stearothermophilus* (Kim *et al.*, 2004, J. Microbiol. Biotechnol.
 10 14:474-482) ; *Bifidobacterium breve* (Shin *et al.*, 2003, Appl. Environ. Microbiol. 69:71 16-
 7 123) ; *Bifidobacterium longum* (Margolles *et al.*, 2003, Appl. Environ. Microbiol. 69:5096-
 5 103) ; *Clostridium thermocellum* (Taylor *et al.*, 2006, Biochem . J. 395:31 -37) ; *Fusarium*
oxysporum (Panagiotou *et al.*, 2003, Can. J. Microbiol. 49:639-644) ; *Fusarium*
oxysporum f. sp. dianthi (Numan & Bhosle, 2006, J. Ind. Microbiol. Biotechnol. 33 :247-
 15 260) ; *Geobacillus stearothermophilus* T-6 (Shallom *et al.*, 2002, J. Biol. Chem .
 277:43667-43673) ; *Hordeum vulgare* (Lee *et al.*, 2003, J. Biol. Chem . 278:5377-5387) ;
Penicillium chrysogenum (Sakamoto *et al.*, 2003, Biophys. Acta 1621 :204-21 0) ;
Penicillium sp. (Rahman *et al.*, 2003, Can. J. Microbiol. 49:58-64) ;
Pseudomonas cellulosa (Numan & Bhosle, 2006, J. Ind. Microbiol. Biotechnol. 33 :247-
 20 260) ; *Rhizomucor pusillus* (Rahman *et al.*, 2003, Carbohydr. Res. 338:1 469-1 476) ;
Streptomyces chartreusis (Numan & Bhosle, 2006, J. Ind. Microbiol. Biotechnol. 33:247-
 260) ; *Streptomyces thermoviolacus* (Numan & Bhosle, 2006, J. Ind. Microbiol.
 Biotechnol. 33:247-260) ; *Thermoanaerobacter ethanolicus* (Numan & Bhosle, 2006, J.
 Ind. Microbiol. Biotechnol. 33:247-260) ; *Thermobacillus xylanilyticus* (Numan & Bhosle,
 25 2006, J. Ind. Microbiol. Biotechnol. 33:247-260) ; *Thermomonospora fusca* (Tuncer and
 Ball, 2003, Folia Microbiol. (Praha) 48:1 68-1 72) ; *Thermotoga maritima* (Miyazaki, 2005,
 Extremophiles 9:399-406) ; *Trichoderma sp.* SY (Jung *et al.*, 2005, Agric. Chem .
 Biotechnol. 48:7-1 0) ; *Aspergillus kawachii* (Koseki *et al.*, 2006, Biochim . Biophys. Acta
 1760:1 458-1 464) ; *Fusarium oxysporum f. sp. dianthi* (Chacon-Martinez *et al.*, 2004,
 30 Physiol. Mol. Plant Pathol. 64:201 -208) ; *Thermobacillus xylanilyticus* (Debeche *et al.*,
 2002, Protein Eng. 15:21 -28) ; *Humicola insolens* (Sorensen *et al.*, 2007, Biotechnol.
 Prog. 23:1 00-1 07) ; *Meripilus giganteus* (Sorensen *et al.*, 2007, Biotechnol. Prog. 23:1 00-
 107) ; or *Raphanus sativus* (Kotake *et al.*, 2006, J. Exp. Bot. 57:2353-2362).

In certain aspects, the L-a-arabinofuranosidase does not have retaining β -
 35 xylosidase activity. In other aspects, the L-a-arabinofuranosidase has inverting β -

xylosidase activity. In yet further aspects, the L-a-arabinofuranosidase has no retaining β -xylosidase but has inverting β -xylosidase activity. An enzyme can be tested for retaining vs. inverting activity as described in Section 6.3.1.5 above.

6.3.3. Accessory proteins

5 A number of polypeptides having cellulolytic enhancing activity can also be used in conjunction with the above-noted enzymes and/or cellulolytic proteins to further degrade the cellulose component of the biomass substrate, (see, *e.g.*, Brigham *et al.*, 1995, in Handbook on Bioethanol (Charles E. Wyman, ed.), pp. 119-141, Taylor & Francis, Washington D.C.; Lee, 1997, J. Biotechnol. 56: 1-24).

10 The optimum amounts of such a polypeptide having cellulolytic enhancing activity and of cellulolytic proteins depend on a number of factors including, without limitation, the specific mixture of component cellulolytic proteins, the cellulosic substrate, the concentration of cellulosic substrate, the pretreatment(s) of the cellulosic substrate, the temperature, time, and pH, and the nature of the fermenting organism.

15 The enzyme blends/compositions of the disclosure can, for example, suitably further comprise one or more accessory proteins. Examples of accessory proteins include, without limitation, mannanases (*e.g.*, endomannanases, exomannanases, and β -mannosidases), galactanases (*e.g.*, endo- and exo-galactanases), arabinases (*e.g.*, endo-arabinases and exo-arabinases), ligninases, amylases, glucuronidases, proteases, 20 esterases (*e.g.*, ferulic acid esterases, acetyl xylan esterases, coumaric acid esterases or pectin methyl esterases), lipases, glycoside hydrolase Family 61 polypeptides, xyloglucanases, CIP1, CIP2, swollenin, expansins, and cellulose disrupting proteins. Examples of accessory proteins can also include CIP1-like proteins, CIP2-like proteins, cellobiose dehydrogenases and manganese peroxidases. In particular embodiments, 25 the cellulose disrupting proteins are cellulose binding modules.

6.4 Enzymes with Inverting β -xylosidase Activity

According to the present disclosure, an enzyme with inverting β -xylosidase activity is used to reduce AXP (*e.g.*, EXP) formation in SSF reactions. Thus, the present disclosure pertains, in one aspect, to a composition comprising at least one inverting β - 30 xylosidase polypeptide. In another aspect, the present disclosure pertains to a method of producing a desired fermentation product in an SSF reaction comprising culturing a complete fermentation medium, said complete fermentation medium comprises at least one inverting β -xylosidase polypeptide.

Suitable inverting β -xylosidase polypeptides can be selected from those that are 35 members of the glycoside hydrolase family 43 ("GH43"). GH43 family enzymes have a

number of known activities. For example, a GH43 family enzyme can be one that is classified under EC 3.2.1.55 and can have L-a-arabinofuranosidase activity. In another example, a GH43 family enzyme can be one that is classified under EC 3.2.1.99, and can have endo-arabinanase activity. In yet another example, a GH43 family enzyme can be classified under EC 3.2.1.145, and can have galactan 1,3- β -galactosidase activity. In other examples, GH43 family of enzymes can be classified under EC 3.2.1.37 and can have β -xylosidase activity. Whilst GH43 family of β -xylosidases, such as those described above, often can only perform inverting hydrolysis, various β -xylosidases from the GH3, -39, -52, and -54 families, in contrast, have been reported to have retaining activities and to be able to perform both hydrolysis and transglycosylation reactions. (Smaali *et al*, 2006, Appl. Microbiol. Biotechnol. 73:582-590).

GH43 family enzymes typically display a five-bladed β -propeller three-dimensional conformation. The "propeller" part of the structure is based upon a five-fold repeat of "blade"-like conformation that comprises four-stranded β -sheets. The catalytic general base, an aspartate, the catalytic general acid, a glutamate, and an aspartate residue that modulates the pKa of the general base have been identified through the crystal structure of *Cellvibrio japonicus* CjArb43A, and have been confirmed by site-directed mutagenesis (see Nurizzo *et al*, 2002, Nat. Struct. Biol. 9(9) 665-8). The catalytic residues are arranged in three conserved blocks, which spread widely throughout the amino acid sequence (Pons *et al*, 2004, Proteins: Structure, Function and Bioinformatics 54:424-432). For GH43 family of β -xylosidase enzymes, the predicted catalytic residues are shown as the bold and underlined type face fonts in the sequences of Figure 32. The crystal structure of *Geobacillus stearothermophilus* xylosidase (Brux *et al* 2006, J. Mol. Bio. 359:97-109) suggests several additional residues that might be important for substrate binding in that enzyme.

As described in Section 6.3.1.5 above, inverting β -xylosidase activity can be determined by suitable assays.

Accordingly, in certain aspects, the enzyme with inverting β -xylosidase activity herein is a GH43 family member. For example, the enzyme is an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide. Such polypeptides are described below.

6.4.1 . Fv43D Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is an Fv43D polypeptide. The amino acid sequence of Fv43D (SEQ ID NO:2) is shown in Figure 19B and on the first line of Figure 32. SEQ ID NO:2 is the sequence of the

immature Fv43D. Fv43D has a predicted signal sequence corresponding to residues 1 to 20 of SEQ ID NO:2 (underlined in Figure 19B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 21 to 350 of SEQ ID NO:2. The predicted conserved domain residues are in boldface type in Figure 19B. Fv43D was shown to have β -xylosidase activity in an assay using *p*-nitrophenyl- β -xylopyranoside, xylobiose, or mixed, linear xylo-oligomers as substrates. The predicted catalytic residues are: either D37 or D71; D155; and E251.

As used herein, "an Fv43D polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, or 320 contiguous amino acid residues among residues 21 to 350 of SEQ ID NO:2. An Fv43D polypeptide preferably is unaltered as compared to native Fv43D in residues D37 or D71; D155, and E251. An Fv43D polypeptide is preferably unaltered in at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fo43A, Gz43A, Pf43A, Fv43A, Fv43B, Af43A, Pf43B, and Fv43E, as shown in the alignment of Figure 32. An Fv43D polypeptide suitably comprises the entire predicted conserved domain of native Fv43D as shown in Figure 19B. An exemplary Fv43D polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv43D sequence as shown in Figure 19B. The Fv43D polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv43D polypeptide of the invention has inverting β -xylosidase activity.

6.4.2. Pf43A Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is a Pf43A polypeptide. The amino acid sequence of Pf43A (SEQ ID NO:8) is shown in Figure 22B and on the fourth line of Figure 32. SEQ ID NO:8 is the sequence of the immature Pf43A. Pf43A has a predicted signal sequence corresponding to residues 1 to 20 of SEQ ID NO:8 (underlined in Figure 22B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 21 to 445 of SEQ ID NO:8. The predicted catalytic domain residues are in boldface type, the predicted carbohydrate binding domain residues are in uppercase type, and the predicted linker residues separating the catalytic domain and carbohydrate binding

domain are in italics in Figure 22B. Pf43A was shown to have β -xylosidase activity in an assay using p-nitrophenyl α -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates. The predicted catalytic residues are: either D32 or D60; D145; and E196.

As used herein, "a Pf43A polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 contiguous amino acid residues among residues 21 to 445 of SEQ ID NO:8. A Pf43A polypeptide preferably is unaltered as compared to native Pf43A in residues D32 or D60; D145, and E196. A Pf43A polypeptide is preferably unaltered in at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fv43A, Gz43A, Pf43A, Fv43A, Fv43B, Af43A, Pf43B, and Fv43E, as shown in the alignment of Figure 32. A Pf43A polypeptide suitably comprises the entire predicted conserved domain of native Pf43A as shown in Figure 22B. An exemplary Pf43A polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Pf43A sequence as shown in Figure 22B. The Pf43A polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Pf43A polypeptide of the invention has inverting β -xylosidase activity.

6.4.3. Fv43E Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is an Fv43E polypeptide. The amino acid sequence of Fv43E (SEQ ID NO:10) is shown in Figure 23B and on the ninth line of Figure 32. SEQ ID NO:10 is the sequence of the immature Fv43E. Fv43E has a predicted signal sequence corresponding to residues 1 to 18 of SEQ ID NO:10 (underlined in Figure 23B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 19 to 530 of SEQ ID NO:10. The predicted catalytic domain residues are in boldface type in Figure 23B. Fv43E was shown to have β -xylosidase activity in an assay using p-nitrophenyl α -xylopyranoside, xylobiose and mixed, linear xylo-oligomers as substrates. The predicted catalytic residues are: either D40 or D71; D155; and E242.

As used herein, "an Fv43E polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence

identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, or 500 contiguous amino acid residues among residues 19 to 530 of SEQ ID NO:10. An Fv43E polypeptide preferably is unaltered as compared to native Fv43E in residues D40 or D71; D155; and E242. An Fv43E polypeptide is preferably unaltered in at least 70%,
5 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fo43A, Gz43A, Pf43A, Fv43A, Fv43B, Af43A, Pf43B, and Fv43E, as shown in the alignment of Figure 32. An Fv43E polypeptide suitably comprises the entire predicted conserved domain of native Fv43E as shown in
10 Figure 23B. An exemplary Fv43E polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv43E sequence as shown in Figure 23B. The Fv43E polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv43E polypeptide of the invention has inverting β -xylosidase
15 activity.

6.4.4. Fv43B Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is an Fv43B polypeptide. The amino acid sequence of Fv43B (SEQ ID NO:12) is shown in Figure 24B and on the sixth line of Figure 32. SEQ ID NO:12 is the sequence of the
20 immature Fv43B. Fv43B has a predicted signal sequence corresponding to residues 1 to 16 of SEQ ID NO:12 (underlined in Figure 24B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 17 to 574 of SEQ ID NO:12. The predicted catalytic domain residues are in boldface type in Figure 24B. Fv43B was shown to have both β -xylosidase and L-arabinofuranosidase
25 activity in assays using p-nitrophenyl α -xylopyranoside and/or p-nitrophenyl- α -L-arabinofuranoside as substrates. It was shown to release arabinose from branched arabino-xylooligomers and to increase xylose release from oligomer mixtures in the presence of other xylosidase enzymes. The predicted catalytic residues are: either D38 or D68; D151; and E236.

30 As used herein, "an Fv43B polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, or 550 contiguous amino acid residues among residues 17 to 472 of SEQ ID
35 NO:12. An Fv43B polypeptide preferably is unaltered as compared to native Fv43B in

residues D38 or D68; D151; and E236. An Fv43B polypeptide is preferably unaltered in at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fo43A, Gz43A, Pf43A, Fv43A, 5 Fv43B, Af43A, Pf43B, and Fv43E, as shown in the alignment of Figure 32. An Fv43B polypeptide suitably comprises the entire predicted conserved domain of native Fv43B as shown in Figure 24B. An exemplary Fv43B polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv43B sequence as shown in 10 Figure 24B. The Fv43B polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv43B polypeptide of the invention has inverting β -xylosidase activity.

6.4.5. Af43A Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is an 15 Af43A polypeptide. The amino acid sequence of Af43A (SEQ ID NO:14) is shown in Figure 25B and on the seventh line of Figure 32. SEQ ID NO:14 is the sequence of the immature Af43A. The predicted conserved domain residues are in boldface type in Figure 25B. Af43A was shown to have L-arabinofuranosidase activity in an assay using p-nitrophenyl- α -L-arabinofuranoside and by the release of arabinose from 20 converting the set of oligomers produced *via* the action of an endoxylanase. The predicted catalytic residues are: either D26 or D58; D139; and E227.

As used herein, "an Af43A polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence 25 identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, or 300 contiguous amino acid residues of SEQ ID NO:14. An Af43A polypeptide preferably is unaltered as compared to native Af43A in residues D26 or D58; D139; and E227. An Af43A polypeptide is preferably unaltered in at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, 30 four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fo43A, Gz43A, Pf43A, Fv43A, Fv43B, Af43A, Pf43B, and Fv43E, as shown in the alignment of Figure 32. An Af43A polypeptide suitably comprises the entire predicted conserved domain of native Af43A as shown in Figure 25B. An exemplary Fv43B polypeptide of the invention comprises a sequence having at least 85%, 86%, 35 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%

identity to the mature Af43A sequence as shown in Figure 25B. The Af43A polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Af43A polypeptide of the invention has inverting β -xylosidase activity.

6.4.6. Fo43A Polypeptides

5 In certain embodiments, the enzyme with inverting β -xylosidase activity is an Fo43A polypeptide. The amino acid sequence of Fo43A (SEQ ID NO:24) is shown in Figure 31B and on the second line of Figure 32. SEQ ID NO:24 is the sequence of the immature Fo43A. Fo43A has a predicted signal sequence corresponding to residues 1 to 17 of SEQ ID NO:24 (underlined in Figure 31B); cleavage of the signal sequence is
10 predicted to yield a mature protein having a sequence corresponding to residues 21 to 348 of SEQ ID NO:24. The predicted conserved domain residues are in boldface type in Figure 31B. Fo43A was shown to have β -xylosidase activity in an assay using p-nitrophenyl α -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates. The predicted catalytic residues are: either D37 or D72; D159; and E251.

15 As used herein, "an Fo43A polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, 300, or 320 contiguous amino acid residues among residues 21 to 348 of SEQ ID NO:24. An Fo43A
20 polypeptide preferably is unaltered as compared to native Fo43A in residues D37 or D72; D159; and E251. An Fo43A polypeptide is preferably unaltered in at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fo43A, Gz43A, Pf43A, Fv43A, Fv43B, Af43A,
25 Pf43B, and Fv43E, as shown in the alignment of Figure 32. An Fo43A polypeptide suitably comprises the entire predicted conserved domain of native Fo43A as shown in Figure 31B. An exemplary Fo43A polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fo43A sequence as shown in Figure
30 31B. The Fo43A polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fo43A polypeptide of the invention has inverting β -xylosidase activity.

6.4.7. Gz43A Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is a
35 Gz43A polypeptide. The amino acid sequence of Gz43A (SEQ ID NO:22) is shown in

Figure 30B and on the third line of Figure 32. SEQ ID NO:22 is the sequence of the immature Gz43A. Gz43A has a predicted signal sequence corresponding to residues 1 to 18 of SEQ ID NO:22 (underlined in Figure 30B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 19 to 340 of SEQ ID NO:22. The predicted conserved domain residues are in boldface type in Figure 30B. Gz43A was shown to have β -xylosidase activity in an assay using p-nitrophenyl- β -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates. The predicted catalytic residues are: either D33 or D68; D154; and E243.

As used herein, "a Gz43A polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, or 300 contiguous amino acid residues among residues 19 to 340 of SEQ ID NO:22. A Gz43A polypeptide preferably is unaltered as compared to native Gz43A in residues either D33 or D68; D154; and E243. A Gz43A polypeptide is preferably unaltered in at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the amino acid residues that are conserved among two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, or all nine of Fv43D, Fo43A, Gz43A, Pf43A, Fv43A, Fv43B, Af43A, Pf43B, and Fv43E, as shown in the alignment of Figure 32. A Gz43A polypeptide suitably comprises the entire predicted conserved domain of native Gz43A as shown in Figure 30B. An exemplary Gz43A polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fo43A sequence as shown in Figure 30B. The Gz43A polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Gz43A polypeptide of the invention has inverting β -xylosidase activity.

6.4.8. *G. stearothermophilus* XynB3 Polypeptides

In other aspects, the enzyme with inverting β -xylosidase activity is a *G. stearothermophilus* XynB3 polypeptide. The sequence of *G. stearothermophilus* XynB3 is presented as SEQ ID NO:25. *G. stearothermophilus* XynB3 is a 535-amino-acid GH43 family enzyme from *Geobacillus stearothermophilus* T-6. The enzyme cleaves single xylose units from the non-reducing end of xylooligomers; the three catalytic residues D15, D128, and E187 were found to be essential for its activity (Shallom *et al.*, 2005, *Biochemistry*, 44:387-397).

As used herein, "a *G. stearothermophilus* XynB3 polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, or 500 contiguous amino acid residues of SEQ ID NO:25. A *G. stearothermophilus* XynB3 polypeptide preferably is unaltered as compared to native XynB3 in residues D15, D128, and E187. The *G. stearothermophilus* XynB3 polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the *G. stearothermophilus* XynB3 polypeptide of the invention has inverting β -xylosidase activity.

6.4.9. *Vibrio* sp. XloA Polypeptides

In certain embodiments, the enzyme with inverting β -xylosidase activity is a *Vibrio* sp. XloA polypeptide. *Vibrio* sp. XloA is a β -1,3-xylosidase from *Vibrio* sp. strain XY-214.

As used herein, "a *Vibrio* sp. XloA polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 contiguous amino acid residues of β -1,3-Xylosidase from *Vibrio* sp. Strain XY-214 (Umamoto *et al.*, 2008, Appl. Environ. Microbiol. 74(1):305-308; Genbank Accession No. AB300564). The *Vibrio* sp. XloA polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the *Vibrio* sp. XloA polypeptide of the invention has inverting β -xylosidase activity.

6.5 Enzymes with Retaining β -xylosidase Activity

According to the present disclosure, an enzyme with retaining β -xylosidase activity is used to improve or increase AXP (e.g., EXP) production in SSF reactions. Thus, the present disclosure pertains, in one aspect, to a composition comprising at least one retaining β -xylosidase polypeptide. In another aspect, the present disclosure pertains to a method of producing a desired AXP compound or an improved or increased amount of an AXP product in an SSF reaction comprising culturing a complete fermentation medium, said complete fermentation medium comprises at least one retaining β -xylosidase polypeptide.

Suitable inverting β -xylosidase polypeptides can be selected from those that are members of the glycoside hydrolase family 3 ("GH3"), GH30, GH31, GH39, GH52, GH54, or GH16 family enzymes.

As described in Section 6.3.1.5 above, retaining β -xylosidase activity can be determined by suitable assays.

Accordingly, in certain aspects, the enzyme with retaining β -xylosidase activity herein is a GH3, GH30, GH31, GH39, GH52, GH54, or GH116 family member. For example, the enzyme is an *Aspergillus japonicus* XInD, a *Fusarium verticillioides* Fv30A, a *Fusarium verticillioides* Fv30B, a *Fusarium verticillioides* Fv39A, a *Fusarium verticillioides* Fv39B, a *Thermoanaerobacter saccharolyticum* XynB, a *Geobacillus stearothermophilus* XylA, or a *Trichoderma koningii* (*Hypocrea koningii*) Xyl1 polypeptide. Such polypeptides are described below.

10 **6.5.1. *Aspergillus japonicus* XInD Polypeptides**

In certain embodiments, the enzyme with retaining β -xylosidase activity is a XInD polypeptide. The amino acid sequence of XInD (SEQ ID NO:40) is shown in Figure 35B. SEQ ID NO:40 is the sequence of the immature XInD. XInD has a predicted signal sequence corresponding to residues 1 to 17 of SEQ ID NO:40 (underlined in Figure 15 35B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 18 to 804 of SEQ ID NO:40.

As used herein, "a XInD polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 20 600, 650, 700, or 750 contiguous amino acid residues among residues 18-804 of SEQ ID NO:40. An exemplary XInD polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature XInD sequence as shown in Figure 35B. The XInB 25 polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the XInB polypeptide of the invention has retaining β -xylosidase activity.

6.5.2. *Fusarium verticillioides* Fv30A Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is an Fv30A polypeptide. The amino acid sequence of XInD (SEQ ID NO:42) is shown in 30 Figure 36B. SEQ ID NO:42 is the sequence of the immature Fv30A. XInD has a predicted signal sequence corresponding to residues 1 to 19 of SEQ ID NO:42 (underlined in Figure 36B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 20 to 537 of SEQ ID NO:42.

As used herein, "an Fv30A polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, or 500 contiguous amino acid residues among residues 20 to 537 of SEQ ID NO:42. An exemplary Fv30A polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv30A sequence as shown in Figure 36B. The Fv30A polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv30A polypeptide of the invention has retaining β -xylosidase activity.

6.5.3. *Fusarium verticillioides* Fv30B Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is an Fv30B polypeptide. The amino acid sequence of Fv30B (SEQ ID NO:44) is shown in Figure 37B. SEQ ID NO:44 is the sequence of the immature Fv30B. Fv30B has a predicted signal sequence corresponding to residues 1 to 24 of SEQ ID NO:44 (underlined in Figure 37B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 25 to 485 of SEQ ID NO:44.

As used herein, "an Fv30B polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, or 450 contiguous amino acid residues among residues 25-485 of SEQ ID NO:44. An exemplary Fv30B polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv30B sequence as shown in Figure 37B. The Fv30B polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv30B polypeptide of the invention has retaining β -xylosidase activity.

6.5.4. *Fusarium verticillioides* Fv39A Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is an Fv39A polypeptide. The amino acid sequence of Fv39A (SEQ ID NO:46) is shown in Figure 38B. SEQ ID NO:46 is the sequence of the immature Fv39A. Fv39A has a predicted signal sequence corresponding to residues 1 to 19 of SEQ ID NO:46 (underlined in Figure 38B); cleavage of the signal sequence is predicted to yield a

mature protein having a sequence corresponding to residues 20 to 439 of SEQ ID NO:46.

As used herein, "an Fv39A polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 contiguous amino acid residues among residues 20-439 of SEQ ID NO:46. An exemplary Fv39A polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv39A sequence as shown in Figure 38B. The Fv39A polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv39A polypeptide of the invention has retaining β -xylosidase activity.

6.5.5. *Fusarium verticillioides* Fv39B Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is an Fv39B polypeptide. The amino acid sequence of Fv39B (SEQ ID NO:48) is shown in Figure 39B. SEQ ID NO:48 is the sequence of the immature Fv39B. Fv39B has a predicted signal sequence corresponding to residues 1 to 18 of SEQ ID NO:48 (underlined in Figure 39B); cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 19 to 456 of SEQ ID NO:48.

As used herein, "an Fv39B polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, or 350 contiguous amino acid residues among residues 19-456 of SEQ ID NO:48. An exemplary Fv39B polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Fv39B sequence as shown in Figure 39B. The Fv39B polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the Fv39B polypeptide of the invention has retaining β -xylosidase activity.

6.5.6. *Thermoanaerobacter saccharolyticum* XynB Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is a XynB polypeptide. The amino acid sequence of XynB (SEQ ID NO:50) is shown in Figure 40B. XynB does not have a predicted signal sequence from the SignalP algorithm (available at: <http://www.cbs.dtu.dk>).

As used herein, "a XynB polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, or 450 contiguous amino acid residues of SEQ ID NO:50 . An exemplary XynB polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to XynB sequence as shown in Figure 40B. The XynB polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the XynB polypeptide of the invention has retaining β -xylosidase activity.

6.5.7. *Geobacillus stearothermophilus* XylA Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is a XylA polypeptide. The amino acid sequence of XylA (SEQ ID NO:52) is shown in Figure 41B. XylA does not have a predicted signal sequence from the SignalP algorithm (available at: <http://www.cbs.dtu.dk>) , but has a signal sequence predicted from the Uniprot algorithm (available at: <http://www.uniprot.org/uniprot>) that corresponds to residues 1 to 18 of SEQ ID NO:52 (underlined) ; cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 19-705 of SEQ ID NO:52.

As used herein, "a XylA polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, e.g., at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, e.g., at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, or 650 contiguous amino acid residues of SEQ ID NO:52, or to residues 19-705 of SEQ ID NO:52. An exemplary XylA polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature XylA sequence as shown in Figure 41B. The XylA polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments, the XylA polypeptide of the invention has retaining β -xylosidase activity.

6.5.8. *Trichoderma koningii* (*Hypocrea koningii*) Xyl1 Polypeptides

In certain embodiments, the enzyme with retaining β -xylosidase activity is a Xyl1 polypeptide. The amino acid sequence of Xyl1 (SEQ ID NO:54) is shown in Figure 42B. SEQ ID NO:54 is the sequence of the immature Xyl1 . Xyl1 has a predicted signal sequence corresponding to residues 1 to 21 of SEQ ID NO:54 (underlined in Figure 42B) ; cleavage of the signal sequence is predicted to yield a mature protein having a sequence corresponding to residues 22 to 500 of SEQ ID NO:54.

As used herein, "a Xyl1 polypeptide" refers to a polypeptide and/or to a variant thereof comprising a sequence having at least 85%, *e.g.*, at least 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to at least 50, *e.g.*, at least 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, or 450
5 contiguous amino acid residues among residues 22-500 of SEQ ID NO:54. An exemplary Xyl1 polypeptide of the invention comprises a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the mature Xyl1 sequence as shown in Figure 42B. The Xyl1 polypeptide of the invention suitably has β -xylosidase activity. In certain embodiments,
10 the Xyl1 polypeptide of the invention has retaining β -xylosidase activity.

6.6 Recombinant Methods for Production of Enzymes for Use In SSF

6.6.1 . Nucleic Acids and Expression Vectors

Natural or synthetic polynucleotide fragments encoding an enzyme for use in SSF ("SSF enzyme"), including an inverting β -xylosidase polypeptide or other saccharifying
15 enzyme(s) (*e.g.*, a cellulase or a hemicellulase), can be incorporated into heterologous nucleic acid constructs or vectors. Those vectors can then be introduced into, or replicated in a suitable host cell, including, for example, a filamentous fungal, yeast, or bacterial cell. The vectors and methods disclosed herein can be used to express one or more SSF enzyme(s). Any vector can be used as long as it is replicable and viable in
20 the cells into which it is introduced. Many suitable vectors and promoters are known to those of skill in the art, among which a large number are commercially available. Cloning and expression vectors have been extensively described in the literature, for example, in Sambrook *et al.*, 2001, Molecular Cloning: A Laboratory Manual (CSHL Press) and in Ausubel *et al.*, 2002, Short Protocols in Molecular Biology (Current
25 Protocols), the content of each concerning expression vectors is expressly incorporated by reference herein. Other exemplary expression vectors that are suitable for fungal host cells are described in van den Hondel *et al.*, 1991, Bennett and Lasure (eds.) More Gene Manipulations in Fungi. Academic Press, pp. 396-428.

It is known in the art that various DNA sequences of interest can be inserted into
30 plasmids or vectors (collectively referred to herein as "vectors") using a number of standard procedures. Typically, for example, the DNA sequence of interest is inserted into an appropriate restriction endonuclease site using standard procedures and under standard conditions. Such procedures and related sub-cloning procedures are within the scope of knowledge of those ordinarily skilled in the art.

Recombinant filamentous fungi comprising the coding sequence for an SSF enzyme can be produced by introducing a heterologous nucleic acid construct comprising the SSF enzyme coding DNA sequence into the genetic material of the filamentous fungi host cells.

5 Once the desired form of nucleic acid sequence encoding the SSF enzyme is obtained, it can optionally be modified in a variety of ways. Where the sequence involves non-coding flanking regions, the flanking regions can be subjected to resection, mutagenesis, *etc.* Thus, transitions, transversions, deletions, and/or insertions can be performed on the naturally occurring sequence.

10 A selected SSF enzyme coding sequence can be inserted into a suitable vector according to well-known recombinant techniques, which can then be used to transform a filamentous fungal host cell capable of expressing the SSF enzyme. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence can be used to clone and
15 express the SSF enzyme.

 The present disclosure also includes recombinant nucleic acid constructs comprising one or more of the SSF enzyme-encoding nucleic acid sequences as described above. The constructs each suitably comprises a vector, such as a plasmid or a viral vector, into which a sequence of the disclosure has been inserted, in a forward or
20 reverse orientation.

 A heterologous nucleic acid construct can suitably include the coding sequence of an SSF enzyme: (i) in isolation; (ii) in combination with additional coding sequences, such as, for example, fusion protein or signal peptide coding sequences, where the desired SSF enzyme coding sequence is the dominant coding sequence; (iii) in
25 combination with one or more non-coding sequences, such as, for example, introns and control elements, such as, for example, promoter and terminator elements, or 5' and/or 3' untranslated regions, effective for expression of the coding sequence in a suitable host; and/or (iv) in a vector or host environment in which the SSF enzyme coding sequence is heterologous relative to the host cell.

30 In certain aspects, a heterologous nucleic acid construct is employed to transfer an SSF enzyme-encoding nucleic acid sequence into a cell *in vitro*, for example, a cell of an established filamentous fungal or yeast lines. For long-term production of an SSF enzyme, stable expression is preferred. It follows that any method effective to generate stable transformants can suitably be used to practice the invention disclosed herein.

Appropriate vectors are typically equipped with a selectable marker-encoding nucleic acid sequence, insertion sites, and suitable control elements, such as, for example, promoter and termination sequences. The vectors may comprise regulatory sequences, including, for example, non-coding sequences, such as introns and control elements that are operably linked to the coding sequences, and that are effective for expression of the coding sequence in the host cells. Suitable control elements include, for example, promoter and terminator elements, or 5' and/or 3' untranslated regions. A number of vectors and promoters are known to those of skill in the art, and among which, many are commercially available. Suitable vectors and promoters are also described in the literature, for example, in Sambrook, *et al.*, 2001, *Molecular Cloning: A Laboratory Manual* (CSHL Press).

Exemplary promoters include, for example, constitutive promoters and inducible promoters, such as, without limitation, a CMV promoter, an SV40 early promoter, an RSV promoter, an EF-1 α promoter, a promoter containing the tet responsive element (TRE) in the tet-on or tet-off system [see, e.g., ClonTech's description of its Tet-On $^{\circledR}$ and Tet-Off $^{\circledR}$ Advanced Inducible Gene Expression System], or the β actin promoter and the metallothionine promoter that can upregulated by addition of certain metal salts. A promoter sequence is a DNA sequence which is recognized by the particular filamentous fungal host cell for expression purposes. It is operably linked to DNA sequence encoding the SSF enzyme of interest. Such a linkage positions the promoter with respect to the initiation codon of the DNA sequence encoding the SSF enzyme of interest in the expression vector. The promoter sequence contains transcription and/or translation control sequences, which mediate the expression of the SSF enzyme of interest. Examples include promoters from the *Aspergillus niger*, *A. awamori*, or *A. oryzae* glucoamylase, α -amylase, or α -glucosidase encoding genes; the *A. nidulans* *gpdA* or *trpC* genes; the *Neurospora crassa* *cbh1* or *trp1* genes; the *A. niger* or *Rhizomucor miehei* aspartic proteinase encoding genes; the *H. jecorina* *cbh1*, *cbh2*, *egl1*, *egl2*, or other cellulase encoding genes.

The choice of selectable marker will depend on the host cell, and appropriate selectable markers suitable for use in different host cells are known in the art. Exemplary selectable marker genes include *argB* from *A. nidulans* or *H. jecorina*, *amdS* from *A. nidulans*, *pyr4* from *Neurospora crassa* or *H. jecorina*, *pyrG* from *Aspergillus niger* or *A. nidulans*. Other suitable selectable markers include, for example, *trpc*, *trp1*, *oliC31*, *niaD* or *leu2*, which are included in heterologous nucleic acid constructs used to transform a mutant strain such as a *trp* $^{-}$, *pyr* $^{-}$, or *leu* $^{-}$ mutant strain, or the like.

Such selectable markers can confer, to the transformants, the ability to utilize a metabolite that is otherwise not metabolized by the host cell. For example, the *amdS* gene from *H. jeconna*, which encodes the enzyme acetamidase, allows the transformant cells to grow on acetamide as a nitrogen source. In a further example, selectable marker
5 {e.g., *pyrG*) can restore the ability of an auxotrophic mutant strain to grow on a selective minimal medium. In yet another example, selectable marker {e.g., *olic31*) can confer, to the transformants, the ability to grow in the presence of an inhibitory drug or an antibiotic.

The selectable marker coding sequence is suitably cloned into a plasmid using methods and techniques known in the art. Exemplary plasmids include, without
10 limitation, pUC18, pBR322, pRAX, and pUC100. For example, the pRAX plasmid contains AMAL sequences from *A. nidulans*, making it possible to replicate in *A. niger*.

The practice of the present disclosure will employ, unless otherwise specifically indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the ordinary skill in the art. Such techniques are
15 described extensively in the literature. See, e.g., Sambrook *et al.*, 2001, Molecular Cloning: A Laboratory Manual (CSHL Press); Ausubel *et al.*, 2002, Short Protocols in Molecular Biology (Current Protocols); Freshney, 2005, Culture of Animal Cells: A Manual of Basic Technique (Wiley-Liss); and Dunn *et al.*, 2003, Short Protocols in Protein Science (Wiley). All patents, patent applications, articles and publications
20 mentioned herein, are hereby incorporated by reference.

6.6.2. Host Organisms and Protein Expression

Provided by this disclosure are host cells that are engineered to express an SSF protein of interest for use in the methods described herein. Suitable host cells include any microorganism {e.g., a bacterium, a protist, an alga, a fungus {e.g., a yeast, or a
25 filamentous fungus}, or any other microbe). Suitable host cell is preferably a bacterium, a yeast, or a filamentous fungus cell.

Suitable bacterial genera include, but are not limited to, *Escherichia*, *Bacillus*, *Lactobacillus*, *Pseudomonas* and *Streptomyces*. Suitable bacterial species include, but are not limited to, *Escherichia coli*, *Bacillus subtilis*, *Bacillus licheniformis*, *Lactobacillus
30 brevis*, *Pseudomonas aeruginosa* and *Streptomyces lividans*.

Suitable genera of yeast include, but are not limited to, *Saccharomyces*, *Schizosaccharomyces*, *Candida*, *Hansenula*, *Pichia*, *Kluyveromyces*, and *Phaffia*. Suitable yeast species include, but are not limited to, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, *Hansenula polymorpha*, *Pichia
35 pastoris*, *P. canadensis*, *Kluyveromyces marxianus* and *Phaffia rhodozyma*.

Suitable filamentous fungi include all filamentous forms of the subdivision Eumycotina. Suitable filamentous fungal genera include, but are not limited to, *Acremonium*, *Aspergillus*, *Aureobasidium*, *Bjerkandera*, *Ceriporiopsis*, *Chrysosporium*, *Coprinus*, *Coriolus*, *Corynascus*, *Chaetomium*, *Cryptococcus*, *Filobasidium*, *Fusarium*,
 5 *Gibberella*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Mucor*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Phlebia*, *Piromyces*, *Pleurotus*, *Scytalidium*, *Schizophyllum*, *Sporotrichum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trametes*, and *Trichoderma*.

Suitable filamentous fungal species include, but are not limited to, *Aspergillus*
 10 *awamori*, *Aspergillus fumigatus*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Chrysosporium lucknowense*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium*
 15 *sambucinum*, *Fusarium sarcochromum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Bjerkandera adusta*, *Ceriporiopsis aneirina*, *Ceriporiopsis aneirina*, *Ceriporiopsis caregiea*, *Ceriporiopsis gilvescens*, *Ceriporiopsis pannocinta*, *Ceriporiopsis rivulosa*, *Ceriporiopsis subrufa*, *Ceriporiopsis subvermispora*, *Coprinus cinereus*, *Coriolus hirsutus*, *Humicola*
 20 *insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Neurospora intermedia*, *Penicillium purpurogenum*, *Penicillium canescens*, *Penicillium solitum*, *Penicillium funiculosum*, *Phanerochaete chrysosporium*, *Phlebia radiata*, *Pleurotus eryngii*, *Talaromyces flavus*, *Thielavia terrestris*, *Trametes villosa*, *Trametes versicolor*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma*
 25 *longibrachiatum*, *Trichoderma reesei*, and *Trichoderma viride*.

Once a recombinant SSF enzyme expression construct has been generated, for example, in accordance with the methods described herein, the construct can be transformed into a suitable host cell using routine methodology.

6.6.3. Methods of Enzyme Isolation and/or Purification

30 In certain aspects, a recombinant SSF enzyme is engineered with a signal sequence such that the recombinant SSF enzyme is secreted into the culture medium of the host cell. In certain aspects, the SSF enzyme of interest is recovered in the form of fermentation broth. The term "fermentation broth," as used herein, refers to an enzyme preparation produced by fermentation that then undergoes no or minimal recovery and/or
 35 purification thereafter. For example, microbial cultures are grown to saturation,

incubated under carbon-limiting conditions to allow protein synthesis (e.g., expression of enzymes), and once the enzyme is secreted into the cell culture medium, the fermentation broth is one from which an SSF enzyme of interest can be recovered. The fermentation broth can, for example, contain the unfractionated or fractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the fermentation broth is unfractionated and comprises the spent culture medium and cell debris present after the microbial cells (e.g., filamentous fungal cells) are removed, e.g., by centrifugation. In certain embodiments, the fermentation broth contains the spent cell culture medium, extracellular enzymes, and either live or killed microbial cells. In some embodiments, the fermentation broth is fractionated to remove the microbial cells, and as such comprises the spent cell culture medium and extracellular enzymes.

In some aspects, partial or complete purification of an SSF enzyme may be desirable. In certain embodiments, an SSF enzyme is purified to at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 95%, at least 98%, or at least 99% homogeneity.

However, in certain other aspects, an SSF enzyme of interest can be produced in a cellular form (i.e., partially or entirely not secreted), which then may require recovery from a cell lysate. In such cases, the SSF enzyme is purified from the cells in which it was produced using techniques routinely employed in the art. Examples of such techniques include, without limitation, affinity chromatography (see, e.g., van Tilbeurgh *et al.*, 1984, FEBS Lett. 169:21 5-21 8), ion-exchange chromatographic methods (see, e.g., Goyal *et al.*, 1991, Bioresource Technol. 36:37-50; Fliess *et al.*, 1983, Eur. J. Appl. Microbiol. Biotechnol. 17:31 4-31 8; Bhikhabhai *et al.*, 1984, J. Appl. Biochem. 6:336-345; Ellouz *et al.*, 1987, J. Chromatography 396:307-31 7), ion-exchange chromatographic methods employing materials that have high resolution power (see, e.g., Medve *et al.*, 1998, J. Chromatography A 808:1 53-1 65), hydrophobic interaction chromatography (see, e.g., Tomaz and Queiroz, 1999, J. Chromatography A 865:1 23-1 28), and two-phase partitioning (see, e.g., Brumbauer, *et al.*, 1999, Bioseparation 7:287-295).

Suitably, the SSF enzyme is fractionated to segregate proteins having pre-identified properties, such as binding affinity to particular binding agents or media, e.g., antibodies or receptors; a certain molecular weight range; or a certain isoelectric point range.

Once expression of a given SSF enzyme is achieved, the SSF enzyme thereby produced can be purified from the cells or from the cell culture. Exemplary procedures suitable for such purification include, without limitation, antibody-affinity column

chromatography; ion exchange chromatography; ethanol precipitation ; reverse phase HPLC ; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing ; SDS-PAGE; ammonium sulfate precipitation ; and gel filtration using, e.g., Sephadex G-75. A number of methods of protein purification can be employed and these methods are known in the art and described extensively in the literature. For example, protein purification methods are described in Deutscher, 1990, Methods in Enzymology, 182(57) :779; and Scopes, 1982, Methods in Enzymology 90: 479-91 .

Often time, the selection of purification step(s) or methods depends, e.g., on the nature of the production process, and the particular proteins that are produced.

6.6.4. Fermenting Microorganisms

The SSF methods of the disclosure employ a "fermenting microorganism" to generate a fermentation product {e.g., ethanol) from the sugars produced in an attendant saccharification reaction and/or added to the system . Fermenting microorganisms capable of producing ethanol are sometimes referred to as ethanologens.

The term "fermenting microorganism," as used herein, refers to any microorganism suitable for use in a desired fermentation process. Suitable fermenting microorganisms according to the instant disclosure are able to ferment, i.e., convert, sugars, such as, for example, glucose, xylose, arabinose, mannose, galactose, or oligosaccharides, directly or indirectly into the desired fermentation product.

Examples of suitable fermenting microorganisms include, without limitation, fungal organisms, such as yeast. Specifically, a suitable yeast can be selected from strains of the *Saccharomyces spp.*, and in particular, *Saccharomyces cerevisiae*. Various types of yeast are commercially available, among which, for example, ETHANOL RED™ yeast (available from Fermentis/Lesaffre, USA), FALI (available from Fleischmann's Yeast, USA), SUPERSTART™ and THERMOSACC® fresh yeast (available from Ethanol Technology, WI, USA), BIOFERM AFT and XR (available from NABC-North American Bioproducts Corporation, GA, USA), GERT STRAND (available from Gert Strand AB, Sweden), or FERMIOL (available from DSM Specialties) can be employed in performing the methods of the invention described herein.

In other aspects, the yeast is a *Saccharomyces distaticus* or a *Saccharomyces uvarum*. In yet other aspects, the yeast is a *Kluyveromyces*. Non-limiting examples of *Kluyveromyces* include *Kluyveromyces marxianus* or *Kluyveromyces fragilis*. In yet other aspects, the yeast is a *Candida*. Non-limiting examples of *Candida* include *Candida pseudotropicalis* and *Candida brassicae*. In yet other aspects, the yeast is a *Clavispora*.

Non-limiting examples of *Clavispora* include *Clavispora lusitaniae* and *Clavispora*

opuntiae. In another aspect, the yeast is a *Pachysolen*, e.g., a *Pachysolen tannophilus*. In another aspect, the yeast is a *Bretannomyces*, e.g., a *Bretannomyces clausenii*. Yeast fermentation has been described in the literature. See, e.g., Philippidis, 1996, Cellulose bioconversion technology, in Handbook on Bioethanol: Production and Utilization
5 (Wyman, ed., Taylor & Francis, Washington, D.C., 179-212).

Bacteria that can efficiently ferment glucose to ethanol include, for example, *Zymomonas mobilis* and *Clostridium thermocellum* {see, e.g., Philippidis, 1996, supra}.

The cloning of heterologous genes in a *Saccharomyces cerevisiae* {see, e.g., Chen and Ho, 1993, Appl. Biochem. Biotechnol. 39-40:135-147; Ho et al., 1998, Appl.
10 Environ. Microbiol. 64:1852-1859}, or in a bacterium such as an *Escherichia coli* {see, e.g., Beall et al., 1991, Biotech. Bioeng. 38:296-303}, a *Klebsiella oxytoca* {see, e.g., Ingram, et al., 1998, Biotechnol. Bioeng. 58:204-214}, or a *Zymomonas mobilis* {see, e.g., Zhang et al., 1995, Science 267:240-243; Deanda et al., 1996, Appl. Environ. Microbiol. 62:4465-4470}, has led to the construction of organisms capable of converting
15 hexoses and pentoses to ethanol (cofermentation). Such microorganisms can advantageously be used in the methods of the present disclosure.

In certain embodiments, the fermenting microorganism is a *Zymomonas mobilis* with improved tolerance for acetate {see, e.g., U.S. Patent Publication US
2009/0221078}.

20 In certain embodiments, the fermenting microorganism is a *Zymomonas mobilis* with improved utilization of xylose {see, e.g., U.S. Patent Publication US 2009/0246846}.

In certain embodiment, the fermenting microorganism is a *Zymomonas mobilis* with the ability to ferment pentoses into ethanol {see, e.g., U.S. Patent Publication US
2003/0162271}.

25 **6.6.5. Fermentation Media**

In some aspects, the SSF reactions or methods of the disclosure are performed in a fermentation medium or a complete fermentation medium. The term "fermentation medium," as used herein, refers to a medium before all of the components necessary for the SSF reaction to take place are present. A fermentation medium can thus be, for
30 example, a medium resulting from a partial saccharification process. A fermentation medium can, in other embodiments, be a medium containing all the components necessary for the SSF reaction to take place. In that case, the fermentation medium is also termed "a complete fermentation medium." Moreover, a fermentation medium can, in yet other embodiments, be a medium wherein an SSF reaction is in progress or under
35 way, and as such may contain certain products of saccharification.

A complete fermentation medium includes enzymes capable of hydrolyzing carbohydrate-based cellulosic or other substrates, a fermenting organism, and a carbohydrate-based cellulosic or other substrate (*e.g.*, as described in Section 6.7.2 below). Over the course of culturing the complete fermentation medium, fermentable
5 sugars are formed through enzymatic hydrolysis, which are in turn metabolized by the fermenting organism to produce a fermentation product.

6.7. Simultaneous Saccharification and Fermentation Processes

In certain aspects, an SSF reaction of the present disclosure is performed at a temperature of between 25 °C and 50 °C. For example, the SSF reaction takes place at
10 a temperature of 25 °C or above, 28 °C or above, 30 °C or above, 32 °C or above, 35 °C or above, or 38 °C or above. For example, the SSF reaction takes place at a temperature of 50 °C or below, 45 °C or below, 40 °C or below, 38 °C or below, 35 °C or below, or 30 °C or below. For example, the SSF reaction takes place in a temperature range of from 28 °C to 45 °C, such as from 30 °C to 40 °C, from 32 °C to 38 °C. In an
15 exemplary embodiment, the SSF reaction is carried out at a temperature of from 32 °C to 35 °C. In another embodiment, the SSF reaction is carried out at a temperature of about 32 °C. The temperature at which the SSF reaction is carried out can, for example, be adjusted up or down during the reaction.

In SSF, the enzymatic hydrolysis of cellulose and the fermentation of glucose to
20 ethanol are combined in one step (see, *e.g.*, Philippidis, 1996, Cellulose bioconversion technology, Handbook on Bioethanol: Production and Utilization, Wyman, ed., Taylor & Francis, Washington, D.C., pp. 179-212).

SSF processes are usually carried out as batch fermentation processes, wherein the fermentation is conducted from start to finish in a single tank. Alternatively, SSF
25 processes can be carried out as continuous fermentation processes which are steady-state fermentation systems that operate without interruption, and wherein each stage of the fermentation occurs in a separate section of a given fermentation system, and flow rates are set to correspond to required residence times. In other words, the individual steps in a fermentation process of the disclosure can be performed batch-wise or
30 continuously. Processes where all steps are performed batch-wise, or processes where all steps are performed continuously, or processes where one or more steps are performed batch-wise and one or more steps are performed continuously are contemplated herein.

In certain embodiments, a fed-batch SSF process may be desirable. A fed-batch
35 process entails a batch phase and a feeding phase. The culture medium of the batch

phase and the culture medium added during the feeding phase are chemically defined, and the culture medium of the feeding phase is added, at least for a fraction of the feeding phase, at a feeding rate that follows a pre-defined exponential function, thereby maintaining the specific growth rate at a pre-defined value.

5 An SSF reaction of the present disclosure can suitably proceed for a period of 3 to 7 d. For example, an SSF reaction of the disclosure can proceed for up 3 d, 4 d, 5 d, 6 d, or 7 d.

The SSF fermentation processes of the disclosure include, without limitation, fermentation processes used to produce fermentation products including alcohols {e.g., ethanol, methanol, butanol, 1,3-propanediol}; organic acids {e.g., citric acid, acetic acid, itaconic acid, lactic acid, gluconic acid, gluconate, lactic acid, succinic acid, 2,5 diketo-D-gluconic acid}; ketones {e.g., acetone}; amino acids {e.g., glutamic acid}; gases {e.g., H₂ and CO₂}, and more complex compounds, including, for example, antibiotics {e.g., penicillin and tetracycline}; enzymes; vitamins {e.g., riboflavin, B₁₂, β-carotene};
10 hormones, and other compounds.
15

In certain aspects, the present disclosure provides a set of SSF conditions that are specifically suitable for use with a recombinant fermenting bacteria such as a *Zymomonas* {i.e., also termed "recombinant *Zymomonas* SSF conditions" herein}. For example, these conditions include carrying out the SSF flask runs anaerobically under
20 suitable recombinant *Zymomonas mobilis*, using pretreated substrates such as, for example, corn cob, bagasse, Kraft pulp substrate, and carrying out the reaction at about 33 °C, pH 5.8, and about 10 wt.% to 25 wt.% solids loading, dependent upon the particular substrates and pretreatment. These conditions also include, for example, commencing the fermentation by the addition of 10% of a suitable *Zymomonas mobilis*
25 strain, for example, strains ZW705 (recombinant) or ZW1 (wild-type) inoculum (5 g), into the reaction mixture without any additional nutrients.

In certain aspects, the present disclosure provides a set of SSF conditions that are specifically suitable for use with a fermenting microorganism that is a fungus, for example, a *S. cerevisiae* yeast (i.e., also termed "yeast SSF conditions" herein). For
30 example, these conditions include carrying out the reaction with a suitable yeast strain, for example the THERMOSACC® DRY yeast, at 38 °C and pH 5.0, inoculation at 0.1 wt% without any additional nutrients, carrying out the SSF runs anaerobically by, for example CO₂ outgassing, using a reaction mixture comprising pretreated substrate, water, sulfuric acid, saccharification enzyme(s) and the yeast strain, as well as agitating

the reaction vessel at an appropriate speed, for example, at 100 RPM, for a suitable period of time, for example, 3 d.

6.7.1 . Recovery of SSF Products

The fermentation product can be any substance that is produced by the
5 fermenting organism . In a specific aspect, the substance is an alcohol. It will be understood that the term "alcohol" encompasses a substance that contains one or more hydroxyl moieties. In a specific aspect, the alcohol is arabinitol. In another aspect, the alcohol is butanol. In another aspect, the alcohol is ethanol. In another aspect, the alcohol is glycerol. In another aspect, the alcohol is methanol. In another aspect, the
10 alcohol is 1,3-propanediol. In yet another aspect, the alcohol is sorbitol. In another more aspect, the alcohol is xylitol. See, e.g., Gong *et al.*, 1999, Ethanol production from renewable resources, in *Advances in Biochemical Engineering/Biotechnology*, Scheper, ed., Springer-Verlag Berlin Heidelberg, Germany, 65: 207-241 ; Silveira and Jonas 2002, *Appl. Microbiol. Biotechnol.* 59: 400-408; Nigam, and Singh, 1995, *Process Biochem.* 30
15 (2) : 117-1 24; Ezeji *et al.*, 2003, *World J. Microbiol. Biotechnol.* 19 (6) : 595-603.

Distillation can be performed on the fermentation broth from the fermentation step to recover the fermentation products such as, for example, ethanol. The fermentation and distillation steps can be carried out simultaneously or separately/sequentially. In some aspects, after distillation, two products are recovered : an alcohol, such as, for
20 example, ethanol, and a fermentation rest or residual product (whole stillage) . The alcohol, being an azeotropic mixture with water, is further purified in the separation step by a standard process such as, for example, molecular sieving. For example, ethanol with a purity of up to about 96 vol.% can be obtained, which can be used as, for example, fuel ethanol, drinking ethanol, *i.e.*, potable neutral spirits, or industrial ethanol.

25 For other substances or fermentation products, any method known in the art can be used for recovery, including, but not limited to, chromatography {e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures {e.g., preparative isoelectric focusing) , differential solubility {e.g., ammonium sulfate precipitation) , SDS-PAGE, distillation, or extraction.

6.7.2. Sources of Carbohydrates or Feedstocks

30 Any suitable cellulosic substrates or raw materials can be used in practicing the SSF processes of the present disclosure. The substrate can be selected based on the desired fermentation product, *i.e.*, the substance to be obtained from the fermentation, and the process employed, as is well known in the art.

Examples of substrates suitable for use in the methods of present disclosure, include cellulose-containing materials, such as wood or plant residues, or low molecular sugars DP1-3 obtained from processed cellulosic materials that can then be metabolized by the fermenting microorganism, and/or which can be supplied by direct addition to the fermentation medium.

The biomass can include any composition comprising cellulose and/or hemicellulose (lignocellulosic biomass can also comprise lignin), e.g., seeds, grains, tubers, plant waste or byproducts of food processing or industrial processing {e.g., stalks}, corn (including cobs, stover, and the like), grasses {e.g., Indian grass, such as *Sorghastrum nutans*; or, switch grass, e.g., *Panicum* species, such as *Panicum virgatum*}, wood (including wood chips, processing waste), paper, pulp, recycled paper {e.g., newspaper}. Other biomass materials include, but are not limited to, potatoes, soybean (rapeseed), barley, rye, oats, wheat, beets or sugar cane bagasse.

6.8. Pretreatment of Biomass

Prior to an SSF reaction, biomass {e.g., lignocellulosic material} is preferably subject to a pretreatment step in order to render xylan, hemicellulose, cellulose and/or lignin material more accessible to enzymes, and thus more amenable to saccharification and fermentation by the methods of the disclosure.

In one aspect, the pretreatment entails subjecting dried biomass material in a suitable vessel, such as for example, a reactor, to a catalyst comprised of a dilute solution of a strong acid and a metal salt; this can lower the activation energy, or the temperature, of cellulose hydrolysis to obtain higher sugar yields; see, e.g., U.S. Patent Nos. 6,660,506; 6,423,145.

Another exemplary pretreatment method entails hydrolyzing biomass by subjecting the material to a first stage hydrolysis step in an aqueous medium at a temperature and a pressure level chosen to effectuate primarily depolymerization of hemicellulose without major depolymerization of cellulose to glucose. This step results in a slurry, in which the liquid aqueous phase contains dissolved monosaccharides resulting from depolymerization of hemicellulose, and the solid phase contains cellulose and lignin. A second hydrolysis step can involve conditions under which at least a major portion of the cellulose is depolymerized, resulting in a liquid aqueous phase containing dissolved/soluble depolymerization products of cellulose. See, e.g., U.S. Patent No. 5,536,325.

Another exemplary method comprises processing a biomass material by one or more stages of dilute acid hydrolysis using about 0.4% to 2% of a strong acid; and

treating an unreacted solid lignocellulosic component of the acid-hydrolyzed biomass material by alkaline delignification. See, e.g., U.S. Patent No. 6,409,841 .

Another exemplary pretreatment method comprises prehydrolyzing biomass {e.g., lignocellulosic materials) in a prehydrolysis vessel, for example, a reactor; adding an
5 acidic liquid to the solid lignocellulosic material to make a mixture; heating the mixture to a suitable reaction temperature; maintaining the reaction temperature for a time period sufficient to fractionate the lignocellulosic material into a solubilized portion containing at least about 20% of the lignin from the lignocellulosic material and a solid fraction
10 containing cellulose; removing a solubilized portion from the solid fraction while maintaining the mixture at or near the reaction temperature, wherein the cellulose in the solid fraction is rendered more amenable to enzymatic digestion ; and recovering a solubilized portion. See, e.g., U.S. Patent No. 5,705,369.

In another exemplary method, the pretreatment method uses hydrogen peroxide H₂O₂. See, e.g., Gould, 1984, Biotech. Bioengr. 26:46-52.

15 In yet another exemplary method, pretreatment comprises contacting biomass with stoichiometric amounts of sodium hydroxide and ammonium hydroxide at very low biomass concentration. See, e.g., Teixeira *et al.*, 1999, Appl. Biochem .Biotech. 77-79:19-34.

In another embodiment, pretreatment comprises contacting the lignocellulose
20 with a chemical {e.g., a base, such as sodium carbonate or potassium hydroxide) at a pH of about 9 to about 14 at moderate temperature, pressure and pH. See, e.g., PCT patent application publication WO2004/081 185.

In another exemplary method, the pretreatment uses ammonia. For example, the pretreatment method comprises subjecting the biomass to low ammonia concentration
25 under conditions of high solids. See, e.g., U.S. Patent Publication No. 20070031 918, PCT patent application publication WO 2006/1 1901 .

The invention is further illustrated by the following examples. The examples are provided for illustrative purposes only. They are not to be construed as limiting the scope or content of the invention in any way.

30 7. Example 1: analysis of Exp formation in SSF reactions

7.1. Materials & Methods

7.1.1. Substrates

Below is a list of substrates used in this work. The cellulose, xylan, and lignin compositions of the pretreated substrates are listed as well. Compositional analyses
35 were performed using the standard assays detailed in the NREL protocols for Standard

Biomass Analytical Procedures (available at: <http://www.nrel.gov/biomass/pdfs/42618.pdf>) :

5 **Dilute ammonia pretreated corn cob.** Corn cob was pretreated prior to enzymatic hydrolysis according to the methods and processing ranges described in, for example, US Patent Application Publications 2007-0031 918-A1 , US-2007-0031 919-A1 , US-2007-0031 953-A1 , US-2007-0037259-A1 , and PCT patent application publication WO06/1 10901 A2 (unless otherwise noted). The composition of the substrate comprises : 34.8% cellulose, 29.2% xylan , 12.8% lignin .

10 **Dilute sulfuric acid pretreated sugar cane bagasse.** This substrate was produced and provided by NREL, as detailed in Schell *et al*, 2003, (App. Biochem . Biotechnol. Vol. 105-1 08, 69-85) . The bagasse was pretreated at a solids concentration of 20% (w/w) , temperature of 165 °C, 1.44% (w/w) acid and an approximate residence time of 8 min. The composition of the substrate
15 comprises : 55.0% cellulose, 3.1% xylan , 31.2% lignin .

Mixed hardwood industrial unbleached pulp substrate. This substrate was produced using the Kraft process and oxygen delignification (Kappa Number = 13) . (Research funded by l'Agence Nationale de la Recherche (ANR-05-BIOE-007) through l'Agence de l'Environnement et de la Maitrise de l'Energie (ADEME
20 0501 C0099) . The composition of the substrate comprises: 74.6% cellulose, 20.7% xylan, 2.6% lignin .

Softwood industrial unbleached pulp substrate. This substrate was produced using the Kraft process and oxygen delignification (Kappa Number = 14) . (Research funded by l'Agence Nationale de la Recherche (ANR-05-BIOE-007)
25 through l'Agence de l'Environnement et de la Maitrise de l'Energie (ADEME 0501 C0099) . The composition of the substrate comprises: 81.9% cellulose, 8.0% xylan, 1.9% lignin .

7.1.2. Enzymes

Below is a list of enzymes and enzyme mixtures used in this work.

30 **Accellerase™ 1500** (Danisco U.S. Inc. , Genencor) is a high β -glucosidase activity cellulase enzyme complex produced by a genetically modified *Trichoderma reesei* . It contains multiple enzyme activities a majority of which are exoglucanase, endoglucanase, β -glucosidase, and hemi-cellulase activities.

35 **Multifect® Xylanase** (Danisco U.S. Inc. , Genencor) , also produced by a *Trichoderma reesei* , is a hemicellulase enzyme complex designed to work as an

accessory product to supplement whole cellulase with xylanase activity, and to work synergistically to enhance various polysaccharide conversions in the lignocellulosic biomass processing industry. The predominant xylanase activity in Multifect® Xylanase is that of *T. reesei* Xyn2 (see, LaGrange *et al.*, 1996, Appl. Environ. Microbiol. 62:1 036-1 044).

Bxl1 : is a β -xylosidase from *Trichoderma reesei*. The amino acid sequence of Bxl1 is provided herewith as SEQ ID NO:4. Bxl1 has been shown to have β -xylosidase activity in an assay using p-nitrophenyl β -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates.

Xyn3: is a GH10 family xylanase from *Trichoderma reesei*. The amino acid sequence of Xyn3 is provided herewith as SEQ ID NO:18. Xyn3 was shown to have endoxylanase activity using birchwood azo-xylan (Megazyme, Wicklow, Ireland), and indirectly by its ability to increase xylose monomer production in the presence of xylobiosidase when Xyn3 in combination with xylobiosidase act on pretreated biomass or on isolated hemicellulose.

Fv3A: is a GH3 family enzyme from *Fusarium verticillioides*. The amino acid sequence of Fv3A is provided herewith as SEQ ID NO:6. Fv3A was shown to have β -xylosidase activity in an assay using p-nitrophenyl β -xylopyranoside, xylobiose and mixed, linear xylo-oligomers (Figures 15 and 16) and branched arabinoxylan oligomers from hemicellulose as substrates.

Fv51A is a GH51 family enzyme from *Fusarium verticillioides*. The amino acid sequence of Fv51A is provided herein as SEQ ID NO:16. Fv51A was shown to have L-arabinofuranosidase activity in an assay using p-nitrophenyl- α -L-arabinofuranoside and by the release of arabinose from the set of oligomers released from hemicellulose by the action of endoxylanase.

Fv43D: is a GH43 family enzyme from *Fusarium verticillioides*. The amino acid sequence of Fv43D is provided herein as SEQ ID NO:2. Fv43D was shown to have β -xylosidase activity in an assay using p-nitrophenyl β -xylopyranoside, xylobiose, or mixed, linear xylo-oligomers as substrates. (Figures 15 and 16).

Fv43B: is a GH43 family enzyme from *Fusarium verticillioides*. The amino acid sequence of Fv43B is provided herein as SEQ ID NO:12. Fv43E was shown to have β -xylosidase activity in an assay using p-nitrophenyl β -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates.

Pf43A : is a GH43 family enzyme from *Penicillium funiculosum*. The amino acid sequence of Pf43A is provided herein as SEQ ID NO:8. Pf43A was shown to

have β -xylosidase activity in an assay using p-nitrophenyl β -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates.

Fv43E: is a GH43 family enzyme from *Fusarium verticillioides*. The amino acid sequence of Fv43E is provided herein as SEQ ID NO:10. Fv43E was shown to have β -xylosidase activity in an assay using p-nitrophenyl β -xylopyranoside, xylobiose or mixed, linear xylo-oligomers as substrates.

Af43A: is a GH43 family enzyme from *Aspergillus fumigatus*. The amino acid sequence of Af43A is provided herein as SEQ ID NO:14. Af43A was shown to have L-a-arabinofuranosidase activity in an assay using p-nitrophenyl- α -L-arabinofuranoside and by the release of arabinose from the set of oligomers released from hemicellulose by the action of endoxylanase.

XlnA: XlnA is a xylanase from *Aspergillus tubengensis*. The amino acid sequence of XlnA is provided herein as SEQ ID NO:20. The XlnA protein used in the present examples was unpurified, in the form of an enzyme preparation whose main constituent was XlnA.

Bgl1: Bgl1 is *T. reesei* β -glucosidase 1 (SEQ ID NO:26). The Bgl1 gene has been described, for example, in Barnett *et al.*, 1991, Bio-Technology 9(6):562-567.

7.1.3. Strains

Strain #229: A *Trichoderma reesei* strain, derived from RL-P37 (Sheir-Neiss and Montenecourt, 1984, Appl. Microbiol. Biotechnol. 20:46-53) through mutagenesis and selection for high cellulase production titer, was co-transformed with the β -glucosidase expression cassette (which comprised a *cbh1* promoter, *T. reesei* β -glucosidase gene, a *cbh1* terminator, and an *amdS* marker (*A. nidulans* acetamidase)), and the endoxylanase expression cassette (which comprised a *cbh1* promoter, *T. reesei xyn3*, and a *cbh1* terminator) using PEG mediated transformation (see, e.g., Penttila *et al.*, 1987, Gene 61(2):155-64). Numerous transformants were isolated and examined for β -glucosidase and endoxylanase production. One transformant, referred to as *T. reesei* strain #229, was used in certain studies described herein.

Strain H3A: *T. reesei* strain #229 was co-transformed with the β -xylosidase Fv3A expression cassette (which comprised a *cbh1* promoter, an *fv3A* gene, a *cbh1* terminator, and an *alsR* marker (chlorimuron ethyl resistant mutant of the native *T. reesei* acetolactate synthase)), the β -xylosidase Fv43D expression cassette (which comprised an *egl1* promoter, an *fv43D* gene, a native *fv43D* terminator), and the Fv51A α -arabinofuranosidase expression cassette (which comprised an *egl1* promoter, an *fv51A*

gene, a native *fv51A* terminator) using electroporation (see, e.g., PCT patent application publication WO2008/1 5371 2 A2). Transformants were selected on Vogels agar plates containing chlorimuron ethyl. Numerous transformants were isolated and examined for β -xylosidase and L-a-arabinofuranosidase production. *T. reesei* integrated expression strain H3A, which recombinantly expresses *T. reesei* β -glucosidase 1, *T. reesei* xyn3, Fv3A, Fv51 A, and Fv43D, was isolated, and used in certain studies described herein.

7.1 .4. Organisms and inoculum preparation

7.1 .4.1 . *Zymomonas mobilis*

Background: *Zymomonas mobilis* strain ZW1 is a wild type strain similar to strain ZM4 from American Type Culture Collection (ATCC 31821 , Manassas, VA). Recombinant *Zymomonas mobilis* strain ZW705 was produced from strain ZW801 -4 as summarized below. Cultures of *Z. mobilis* strain ZW801 -4 were grown under conditions of stress as follows. ZW801 -4 is a recombinant xylose-utilizing strain of *Z. mobilis* that was described in U.S. Patent Application Publication 2008/0286870. Strain ZW801 -4 was derived from strain ZW800, which was, in turn, derived from strain ZW658, all as was described in U.S. Patent Application Publication 2008/0286870. ZW658 was constructed by integrating two operons, P_{gap} *xyIAB* and P_{gap} *taltkt*, containing four xylose-utilizing genes encoding xylose isomerase, xylulokinase, transaldolase, and transketolase, into the genome of ZW1 (ATCC #31 821) via sequential transposition events, and followed by adaptation steps conducted on selective media containing xylose. ZW658 was deposited as ATCC #PTA-7858. In ZW658, the gene encoding glucose-fructose oxidoreductase was insertionally-inactivated using host-mediated, double-crossover, homologous recombination and spectinomycin resistance as a selectable marker to create ZW800. The spectinomycin resistance marker, which was bounded by loxP sites, was removed by site specific recombination using Cre recombinase to create ZW801 -4.

A continuous culture of ZW801 -4 was grown in a 250 ml_ stirred, pH- and temperature-controlled fermentors (Sixfors; Bottmingen, Switzerland). The basal medium for fermentation was 5 g/L yeast extract, 15 mM ammonium phosphate, 1 g/L magnesium sulfate, 10 mM sorbitol, 50 g/L xylose, and 50 g/L glucose. Adaptation to growth in the presence of high concentrations of acetate and ammonia was achieved by gradually increasing the concentration of ammonium acetate in the above continuous culture media while maintaining an established growth rate as measured by the specific dilution rate over a period of 97 d to a concentration of 160 mM. Further increases in ammonium ion concentration were achieved by incremental additions of ammonium

phosphate, to a final total ammonium ion concentration of 210 mM by the end of 139 d of continuous culture. Strain ZW705 was isolated from the adapted population by plating, PCR amplification, and/or other conventional well-known methods.

7.1 .4.2. Growth of seed cultures for SSF

5 *Zymomonas mobilis* strains ZW705 and ZW1 were maintained as 20% glycerol stocks, frozen at -80 °C. To make a seed culture, a 2 mL of this frozen stock was thawed and used to inoculate 45 mL of a medium containing 5 g/L of yeast extract, 4 g/L of potassium hydrogen phosphate, 1 g/L of magnesium sulfate, and 100 g/L of glucose at pH 5.8. The starting OD 600 nm was 0.4. The culture was grown at 32 °C in a
10 capped 50 mL tube to an OD 600 nm of about 2.5, and it was then used to inoculate a final seed culture containing 200 g/L glucose, 4 g/L potassium hydrogen phosphate, 2 g/L magnesium sulfate, and 20 g/L yeast extract, at pH 5.8. That culture was grown at 32 °C in a pH-controlled and stirred fermenter to an OD 600 nm of about 10, and a remaining glucose concentration of about 80 g/L. A volume of this seed culture (having
15 an OD 600 nm of about 10) equivalent to 10% of the SSF fermentation volume was used to start the SSF.

7.1 .4.3. Yeast

The yeast ethanologen used was the THERMOSACC® DRY yeast (Ethanol Technology, Milwaukee, WI) which is only capable of fermenting C6 (*i.e.*, glucose)
20 carbon sugars into ethanol (EtOH). The dry yeast was hydrated with sterile deionized water for 2-3 hrs prior to inoculation.

7.1 .5. Fermentation using sugars

Zymomonas mobilis fermentation using synthetic sugars was carried out for 3 d in the 500 mL Sixfors bioreactor, using a batch and fed-batch process. The synthetic
25 sugars consisted of glucose and xylose. For the batch process, the sugars were initially loaded at a concentration of about 80 g/L glucose and 70 g/L xylose. For the fed-batch process, a concentrated stock sugar solution was prepared first, which was then fed into the bioreactor using a syringe pump (PHD2000, Harvard Apparatus, Holliston, MA). The flow rate was set and controlled such that it gave a final equivalent sugar loading of
30 about 80 g/L glucose and 70 g/L xylose at day 3. For the batch or the fed-batch processes, the *Zymomonas* inoculum was loaded into the reaction mixture in the beginning at 10 wt.% and the fermentations were carried out anaerobically at 33 °C and pH 5.5.

7.1 .6. Simultaneous saccharification and fermentation (SSF)

SSF flask runs were carried out anaerobically under suitable recombinant *Zymomonas mobilis* and yeast fermentation conditions. Unless otherwise stated, the recombinant *Zymomonas* SSF experiments using dilute ammonia pretreated corn cob, bagasse, or Kraft pulp substrate were carried out at 33 °C, pH 5.8, and 25 wt.%, 20 wt.%, 10 wt.% solids loading, respectively. 25 wt.% solids (12.5 g dry weight), 20 wt.% solids (10.0 g dry weight), or 10 wt.% solids (5.0 g dry weight) of the respective substrates were each loaded first into a 125 mL Erlenmeyer flask, followed by the addition of deionized water pre-mixed with the required amount of 6N sulfuric acid, in order to titrate the substrate pH to 5.8. The cellulase and hemicellulase enzymes, described above, were added in an amount based on mg cellulase protein/g cellulose and mg hemicellulase protein/g xylan in the biomass substrate, respectively. Fermentation was initiated by the addition of 10 wt.% *Zymomonas mobilis* strains ZW705 (recombinant) or ZW1 (wild-type) inoculum (5 g) into the reaction mixture without any additional nutrients. For the THERMOSACC® DRY yeast SSF, the reactions were carried out at 38 °C and pH 5.0. The level of yeast inoculation was at 0.1 % w/w without any additional nutrients. The anaerobic environment and CO₂ outgassing were maintained by a 23 Gauge needle protruding from a rubber stopper that was used to cap the flask. At the start of fermentation, all SSF runs had an initial 50 g total reaction weight in a flask and the reaction mixture consisted of pretreated substrate, water, sulfuric acid, enzyme, and either *Zymomonas* or yeast cells. The flasks were agitated inside a shaker incubator (New Brunswick Scientific, Innova 44, Edison, New Jersey) at 100 RPM for 3 d.

7.1 .7. Separate hydrolysis and fermentation (SHF)

The SHF runs involved a saccharification stage that was followed by a fermentation stage. The saccharification conditions were based on the NREL Laboratory Analytical Procedure (see, Selig *et al.*, 2008, Enzymatic Saccharification of Lignocellulosic Biomass Laboratory Analytical Procedure (LAP), Technical Report NREL/TP-51 0-42629) except for certain modifications of the enzyme types and/or levels, cellulose loading, and pH. 25 wt.% solids (12.5 g dry weight) of dilute ammonia pretreated corn cob or 10 wt.% solids (5.0 g dry weight) of the mixed hardwood pulp was loaded into a 125 mL Erlenmeyer flask. This was then followed by the addition of deionized water pre-mixed with the required amount of 6N sulfuric acid so as to titrate the substrate pH to 5.3. The saccharification step was commenced by the addition of cellulase and hemicellulase enzymes in an amount based the total mg protein/g cellulose

and the total mg protein/g xylan in the biomass substrate, respectively. For all *Zymomonas* SHF runs, a temperature of 50 °C and a pH of 5.30 were used for the saccharification at a duration of 3 d, followed by the fermentation step using similar conditions as those described in the SSF process (above). Sodium hydroxide was used
5 to raise the pH from 5.3 to 5.8. This was followed by the addition of 10 wt.% of *Zymomonas* inoculum to commence fermentation.

7.1.8. Fed-batch SSF

The fed-batch SSF studies were carried out under similar conditions as described in the SSF process (above) except that the dilute ammonia pretreated corn cob substrate
10 (required to achieve a final 25 wt.% solids) was divided evenly into 8 batches, and fed batch-wise into the bioreactor, with the final batch loaded at the 30th hr.

7.1.9. HPLC analysis and EXP quantification

Fermentation samples were taken at timed intervals and analyzed for ethanol, residual sugars, ethyl- β -xylopyranoside (EXP), and other metabolic products, such as,
15 for example, acetic acid and glycerol, using a Waters HPLC system (Alliance system, Waters Corp., Milford, MA). The HPLC column was purchased from BioRad (Aminex HPX-87H, BioRad Inc., Hercules, CA). The EXP quantification under refractive index detection followed a set of procedures that were similar to those described in by Zhang
20 *et al.* (in 2009, Enzyme and Microbial Technology 44:1 96-202). Another metabolic co-product, succinic acid, was found to co-elute with the EXP and to have potentially inflated the EXP quantification. It was determined that, for the yeast and *Zymomonas* fermentations, the concentrations of succinic acid generated at the conditions tested were no more than 1-2 g/L, as measured using both an UV detector at 220 nm and an enzymatic assay kit (K-SUCC, Megazyme, Co. Wicklow, Ireland).

7.2. Results

7.2.1. EXP formation and identification

7.2.1.1. EXP formation in SSF with recombinant

Zymomonas mobilis

Formation of a byproduct was observed under the SSF fermentation conditions
30 described above, using a recombinant *Zymomonas mobilis* strain that is capable of co-fermenting glucose and xylose into ethanol. The substrate used in this study was dilute ammonia pretreated corn cob, which has a high xylan content, treated with commercial cellulase/hemi-cellulase enzyme preparations (Accellerase™ 1500 at 20 mg/g cellulose) and Multifect® Xylanase (5 mg/g xylan), both derived from *Trichoderma reesei* {*T.*
35 *reesei*). Under the conditions tested, the highest amount of formation of the byproduct

was found under fed-batch SSF, and the second highest in SSF (Table 1). SHF using dilute ammonia pretreated corn cob, batch, and fed-batch fermentation processes using sugars (80 g/L glucose + 70 g/L xylose) formed little of this byproduct.

The byproduct generated under the SSF conditions, using dilute ammonia pretreated corn cob and the *Zymomonas mobilis* strain as described above had an elution time on an HPLC HPX-87H column of approximately 11.75 mins (at a flow rate of 0.6 mL/min), close to that of succinic acid. Figure 1 panel 2 shows a peak eluting at 11.61 min, following incubation of xylose and Multifect® Xylanase with ethanol. That particular peak was absent when no alcohol was present in the incubation. It was observed that the position of the byproduct generated in the presence of alcohol during incubation shifted to an extent and in a direction that tracked the alcohol added. The elution times of the byproduct produced after incubation with methanol (MeOH) at 9.46 min, and the byproduct produced after incubation with n-PrOH at 27.65 min were shorter and longer, respectively, when compared to the byproduct produced after incubation with ethanol (EtOH), at 21.99 min. The elution times of the products produced by incubation of xylose with Multifect® Xylanase and 0.72 M alcohol shift, relative to the ethanol-induced product (at 11.61 min), to shorter elution times with MeOH (at 11.03 min) and longer elution times with n-PrOH (at 13.60 min). These results were consistent with the conclusion that the mobile peaks in question were xylose-alcohol adducts (alkyl-xylopyranosides) formed by reverse hydrolysis from xylose and alcohol, with the components eluting at 11.03, 11.61 and 13.60 corresponding to the methyl-, ethyl- and n-propyl-xylopyranosides, respectively.

7.2.1.2. Time Course

The time course for the appearance of the methyl-, ethyl- and n-propyl xylopyranosides is shown in Figure 2. The relative amounts of the products formed after 100 hrs were as follows: methyl->ethyl->n-propyl-xyloside (Figure 2), consistent with the order reported by Drouet *et al.* (in 1994, Biotech. & Bioeng. 43:1 075-1 080) for the formation of the alkyl-p-D-xylopyranosides by reverse hydrolysis in the presence of MeOH, EtOH, and n-PrOH. The coincidence of the elution times of the ethyl xylopyranoside (EXP) with those observed under the SSF conditions, the dependencies of the elution time on the presence and nature of the alcohol, and the relative reactivities of these alcohols, all suggested that the EXP was the byproduct generated under the SSF conditions.

7.2.1 .3. Identification of ethyl-B-glycosides in an EXP sample by ¹H NMR analysis

Preparation of ethyl b-D-xylopyranoside standard : A sample of ethyl xylosides was prepared by dissolving 50 mg of D-xylose in 3 mL of ethanol and heating the resulting solution in the presence of Amberlyst 15 H⁺ resin (100 mg) at 70 °C for 3 hrs. The resin was filtered and the ethanol solvent removed under reduced pressure, yielding a colorless oil. Analysis by ¹H NMR revealed a mixture of ethyl xylosides, with a-D-xylopyranoside predominating, along with amounts of ethyl β-xylopyranoside and ethyl α/β-xylofuranoside.

¹H NMR of EXP Sample : A lyophilized EXP sample purified and fractionated (using HPLC) from a dilute ammonia pretreated corn cob SSF fermentation broth sample was reconstituted into 750 μL of D₂O and transferred to a PP-528 glass NMR tube. A proton NMR spectrum was acquired on a Varian 500 MHz VNMRs NMR system using a basic s2pul pulse sequence for over 8 pulses. The ¹H NMR spectrum (500 MHz, D₂O), referenced to the HOD signal at *d* 4.80, indicated the presence of at least 4 distinct ethyl glycosides, based on the appearance of several triplet signals in the *d* 1.20-1.26 region. The spectrum also contained 5 distinct doublets at *d* 4.43, 4.49, 4.53, and 4.66 with coupling constants of 7.8 Hz indicative of *b*-glycosidic linkages. The signal at *d* 4.43 was the most intense and matches the chemical shift reported in the literature (Drouet *et al.*, 1994, Biotech. & Bioeng. 43:1 075-1 080), Zhang *et al.* (2009, Enzyme and Microbial Technology 44:196-202) for ethyl ^α-D-xylopyranoside. Overall the signals observed in the ¹H NMR spectrum (Figure 3) indicated the presence of the β-anomer, β-D-ethylxylopyranoside, along with 3-4 additional ethyl β-glycosides.

7.2.2. EXP formation with yeast and wild-type *Zymomonas mobilis*

Co-fermentation of C5/C6 sugars using the ethanologen *Zymomonas mobilis* under SSF and fed-batch SSF conditions with a dilute ammonia pretreated corn cob substrate resulted in high levels of EXP. A new experiment was designed to determine whether EXP is formed when SSF is performed using wild-type yeast and *Zymomonas mobilis*, which are organisms that are only capable of fermenting C6 sugars. The results (Figure 4) indicated that the EXP was produced at high levels in the SSF reactions wherein the yeast (5.5 g/L) or wild-type *Zymomonas mobilis* (9.1 g/L) did the fermenting. Thus, the EXP formation is not specific to the recombinant *Zymomonas mobilis*, as it was also detected during SSF by a *Saccharomyces cerevisiae* yeast and a wild-type *Zymomonas mobilis*.

7.2.3. EXP formation from other sources of biomass

Additional experiments were designed to determine if EXP could be formed using substrates other than the dilute ammonia pretreated corn cob. From the results shown in Table 2, the formation of EXP appears to be linked to the fermentation of any high xylan-containing substrates under the SSF conditions with the *T. reesei* cellulase/hemicellulase preparations. For example, as much as 16.1 g/L EXP was formed under the recombinant *Zymomonas* SSF conditions using a mixed hardwood industrial Kraft pulp with high xylan content. On the other hand, the lower xylan-containing substrates, such as the pretreated bagasse and the softwood pulp, produced lower amounts of EXP (0.91 and 4.75 g/L, respectively) under similar conditions. Furthermore, it was again demonstrated that, only under the SSF processes as described herein would large amounts of EXP be generated. Formation of EXP was much decreased under the SHF process conditions, (3.52 g/L), even when a higher xylan-containing substrate was used.

7.2.4. EXP formation with different permutations of enzymes used in SSF

7.2.4.1. EXP formation with Bxl1

According to Drouet *et al.* (in 1994, Biotech. & Bioeng. 43:1 075-1 080), EXP formation was catalyzed by *T. reesei* Bxl1 via both a transxylosylation and a reverse hydrolysis reaction. Figure 5 shows that the EXP formation under the yeast SSF conditions described above was enhanced in the presence of *T. reesei* Bxl1. With the addition of 5 mg/g Bxl1, the EXP production was increased from 5.5 g/L to 18.8 g/L.

EXP formation under recombinant *Zymomonas mobilis* SSF conditions with 25 wt.% solids of dilute ammonia pretreated corn cob substrate was also enhanced in the presence of *T. reesei* Bxl1, as shown in Figure 6. EXP plateaued at a concentration of 25.6 g/L, with the addition of 6 mg/g *T. reesei* Bxl1. A cellulase/hemi-cellulase enzyme complex from *T. reesei* integrated strain #229 (which overexpresses xylanase, *T. reesei* Xyn3) was used in this experiment in place of Accellerase™ 1500 + Multifect® Xylanase. The ability of *T. reesei* Bxl1 to catalyze EXP formation is surprisingly strong, because only 1 mg/g of it was added but an over 2-fold increase of EXP as compared to the control sample (enzyme complex from *T. reesei* integrated strain #229 alone) was clearly observed.

The effect of *Fusarium verticillioides* hemi-cellulase addition on EXP formation was investigated. Accellerase™ 1500 + Multifect® Xylanase, Accellerase™ 1500 + XlnA, and enzyme complex from the integrated *T. reesei* strain #229, with the addition of

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B χ I1, and *Fusarium verticillioides* hemi-cellulases (Fv3A, and Fv51 A L- α -arabinofuranosidase) were used. This study was conducted under recombinant *Zymomonas* SSF conditions. The substrate used was a 25 wt.% solids dilute ammonia pre-treated corn cob. Results were shown in Figure 7, which indicated that the addition of XlnA and Accellerase™ 1500 produced more EXP (31.5 vs. 19.5) than the addition of Multifect® Xylanase and Accellerase™ 1500. The enzyme complex from the integrated *T. reesei* strain #229 alone produced the least amount of EXP (9.1 g/L) among all three enzyme configurations. This is possibly due to the fact that Bxl1 represented a smaller fraction of the total amount of proteins in the enzyme complex in the *T. reesei* strain #229 enzyme complex, which also produced a relatively large amount of accumulated xylobiose, as compared to other two enzyme configurations. For Accellerase™ 1500 + Multifect® Xylanase and Accellerase™ 1500 + XlnA, the addition of Fv3A or Fv51 A did not result in substantial increases in EXP formation. With the enzyme complex from integrated *T. reesei* strain #229, however, the addition of Fv3A alone gave a 2-fold increase in EXP formation while the addition of Fv51 A increased EXP formation by 1.4 fold, as compared to a 3-fold increase in EXP when *T. reesei* Bxl1 was added to the enzyme complex produced from the integrated *T. reesei* strain #229.

7.2A.2. EXP formation using purified enzymes

The results discussed above indicated that the EXP formation was strongly affected and effectively catalyzed by *T. reesei* Bxl1 and that *T. reesei* Bxl1 is remarkably and particularly effective at making EXP under the SSF conditions using certain high xylan-containing biomass substrates. However, all of the enzymes tested so far (and discussed above) were not purified and might contain background enzyme activities similar to that of the *T. reesei* Bxl1, capable of making EXP. To investigate the effect of background enzyme activities, the effect of purified enzymes on EXP formation was also studied. A cellulase mixture of purified *T. reesei* cellobiohydrolases, CBH1 and CBH2; *T. reesei* endoglucanase, EG2; and *T. reesei* β -glucosidase, Bgl1, was used as a substitute for Accellerase™ 1500, while purified *T. reesei* Xyn3 was used as a substitute for Multifect™ Xylanase. It is clear from the results depicted in Figure 8 that the cellulase alone does not produce EXP. The addition of unpurified *T. reesei* Xyn3 produced large amounts of EXP, for example, about 13.1 g/L. This large increase is potentially due to a larger background *T. reesei* Bxl1 that exists within the unpurified *T. reesei* Xyn3 sample.

7.2A.3. EXP formation using GH43 class Bxl enzymes

Bxl1, which is a GH3 family hydrolase, has been shown to be active and effective at catalyzing the formation of EXP under the SSF conditions (above). A

question remains as to whether other GH family β -xylosidases can also catalyze the formation of EXP under similar conditions. A number of β -xylosidases from the GH43 family, including Fv43B, Pf43A, Fv43E, and Af43A, were tested under the recombinant *Zymomonas* SSF conditions using a 25 wt.% solids dilute ammonia pretreated corn cob substrate. Pf43A, Fv43E, and Af43A were found to increase EXP formation slightly, as compared to the control sample made from a protein preparation of strain #229. On the other hand, Fv43B gave a greater increase of EXP formation by 1.5-fold (Figure 9). Because all of these GH43 family enzymes were expressed in *T. reesei*, and because they were all unpurified protein preparations in this study, it could be postulated that the increase in EXP formation may be attributed to the presence of native Bxl1 in the protein preparations.

8. EXAMPLE 2: REDUCTION IN EXP BY HEMICELLULASES

The following examples show that EXP is reduced by addition of certain hemicellulases to SSF reactions.

8.1. Reduction in EXP by Fv43D in SSF by *Zymomonas*

EXP formation typically consumes both xylose (directly, or from xylobiose or other xylo-oligomers) and ethanol on an equal molar basis. This consumption mechanism directly results in a substantial decrease in yield for ethanol, because many microorganisms, including *Zymomonas*, are incapable of degrading and fermenting, or otherwise utilizing EXP. One (1) g of EXP is calculated to be equivalent to a 0.688 g loss of ethanol that would have been produced (assuming xylose is fermented into ethanol at a rate of 0.51 g/g xylose). Thus preventing the formation of EXP can lead to an attendant increase in ethanol yield. It was found, as shown in Figure 10, that the addition of the *Fusarium verticillioides* β -xylosidase, Fv43D, at only 1 mg/g xylan, greatly reduced (~4-fold) the amount of EXP formed under the recombinant *Zymomonas* SSF conditions.

8.2 Reduction in EXP by Fv43D in SSF by yeast

Similar to the results obtained from the C5/C6-fermenting recombinant *Zymomonas*, the supplementation of Accellerase™ 1500+Multifect® Xylanase with Fv43D in an SSF reaction using yeast as a C6-fermenting microorganism also resulted in a reduction in EXP formation. Specifically the addition of Fv43D at 1 mg/g xylan resulted in a 2 to 3-fold reduction in EXP (Figure 11).

8.3 Reduction in EXP by Fv43D in SSF with Multifect xylanase, with XlnA and with enzyme complex from *T. reesei* integrated strain #229

The reduction in EXP by the addition of Fv43D to three enzyme configurations, Accellerase™ 1500+Multifect® Xylanase, Accellerase™ 1500+A *niger*xylanase, and the enzyme complex produced from the integrated *T. reesei* strain #229, under the recombinant *Zymomonas* SSF conditions was investigated. The substrate used was a 25 wt.% solids dilute ammonia pretreated corn cob.

Figure 12 shows that the addition of only 1 mg/g xylan of Fv43D to Accellerase™ 1500+Multifect® Xylanase, and to Accellerase™ 1500+XlnA, resulted in an over 4-fold reduction in EXP formation, and the same addition to the enzyme complex produced from the integrated *T. reesei* strain #229 resulted in a 1.36-fold reduction of EXP formation. At the same time, a corresponding increase in ethanol was observed with all three enzyme configurations, confirming the benefit of Fv43D in terms of reducing EXP formation and preventing ethanol yield loss.

8.4 Reduction in EXP formation in SSF with purified enzymes

To insure that the reduction of EXP from Fv43D was not due to background enzyme activities, purified enzymes including a purified Fv43D were used to test for reductions of EXP formation. A *T. reesei* cellulase mixture of purified CBH1, CBH2, EG2 and Bgl1 was used to substitute for Accellerase™ 1500, and a purified *T. reesei* Xyn3 was used as a substitute for Multifect® Xylanase. The results as depicted in Figure 13 showed a slight reduction in EXP formation and an attendant slight increase in ethanol titer, when purified and unpurified Fv43D were added. The relatively small reduction in EXP formation is likely due to the lack of background *T. reesei* Bxl1 in the purified enzymes (e.g., the cellulases and Xyn3). It is also noted that only a small amount of EXP (5.7 g/L) was formed by the control sample, due to the action of *T. reesei* Xyn3. Further addition of Fv43D thus does not substantially reduce EXP formation. To investigate this further, another study with results shown in Figure 14A was performed to investigate the effect of EXP reduction by Fv43D addition in the presence of a large amount of Bxl1.

8.5 EXP reduction dose response from the addition of Fv43D to SSF

EXP formation in the presence of Bxl1 was substantial where more than 20 g/L of EXP was consistently detected, although the exact amount varies by the SSF conditions used. A dose response study was performed to assess reduction of EXP formation in relation to the amount of Fv43D added. Figure 14A shows the results for EXP reduction from the addition of increasing amounts of Fv43D to the enzyme complex produced from

the *T. reesei* integrated strain #229 and *T. reesei* Bx11 . Similar to the results shown previously, 1 mg/g of Fv43D was found to be effective at reducing EXP formation by nearly 3-fold and at the same time resulted in an increase in ethanol titer. However, addition of increasing amounts of Fv43D at 3, 6, and 9 mg/g did not greatly reduce EXP formation, although a significant increase in ethanol titer was observed. It appeared that even with addition of a large amount of Fv43D (at 9 mg/g), the EXP concentration could not be reduced to below 6.6 g/L, a level at which the amount of EXP may have reached equilibrium for the specific conditions that were used for testing. Under these particular experimental conditions, further additions of Fv43D beyond, for example, 1 mg/g xylan, no longer had an effect on reducing EXP formation.

These observations can potentially be explained by the mechanism of EXP formation and reduction under SSF conditions.

The proposed mechanism, which is based on the observations made from this work and is consistent with the data reported in the literature (see, e.g., Drouet *et al.*, 1994, *Biotech. & Bioeng.* 43:1 075-1 080 and Zhang *et al.*, 2009, *Enzyme and Microbial Technology* 44:196-202), is described in detail in Example 3 below.

8.6 EXP reduction by the addition of Fo43A and Gz43A to SSF

Fo43A and Gz43A, which are inverting GH43 family β -xylosidases, were also tested for efficacy in reducing EXP formation under the SSF conditions described herein. Based on the results shown in Figure 14B, these two enzymes were each able to reduce EXP formation by nearly 4-fold, when they are added to a enzyme blend comprising a protein complex produced from the *T. reesei* integrated strain #229, *T. reesei* Bx11, a dilute ammonia pretreated corn cob substrate, and a recombinant *Zymomonas*, and at 3 mg/g xylan. Similar to what was observed with the addition of Fv43D (above), a reduction in EXP formation and a corresponding increase (by about 10 g/L) in ethanol titer was observed.

9. EXAMPLE 3: MECHANISM OF EXP FORMATION

Observations that the yield of EXP was approximately four times higher under the SSF conditions (Figures 10 and 11) in the presence of *Fusarium verticillioides* β -xylosidase Fv3A as compared to the yield of EXP in the presence of *Fusarium verticillioides* β -xylosidase Fv43D led to an effort to understand the mechanism of EXP formation.

Potentially there are two possible routes for the formation of EXP: (1) by transglycosylation; or (2) by reverse hydrolysis. Each of these routes are depicted as follows:

1) *Transglycosylation*: $X-O-X + EtOH \rightarrow X-O-Et + X$

2) *Reverse Hydrolysis*: $X + EtOH \leftrightarrow X-O-Et + H_2O$

According to Drouet *et al.* (in 1994, *Biotech. & Bioeng.* 43:1 075-1 080), the transglycosylation mechanism is the more rapid of the two. The fact that only the β anomer (see Figure 29) is formed in a transglycosylation reaction implies that the reaction is catalyzed by enzymes that operate with retention of anomeric configuration on the substrates, wherein the sugars are linked by β -glycosyl linkages. On the other hand, formation of the β anomer of EXP by reverse hydrolysis would suggest that the starting substrate is either α - or β -xylose, depending on whether EXP is formed, respectively, by inversion or retention of anomeric configuration.

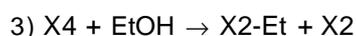
The β -xylosidases, Fv3A (a member of the GH3 family) and Fv43D (a member of the GH43 family), operate with retention and inversion of configuration, respectively. To distinguish and identify which of the two potential mechanisms described above is the true mechanism, an experiment was performed in which Multifect® Xylanase (which is an enzyme preparation characterized by the retaining activity of *T. reesei* Xyn2) and purified Fv43D and Fv3A were incubated at 46 °C with xylobiose and ethanol. The kinetics of EXP formation in these samples was examined by HPLC.

As shown in Figure 15 and Table 3, after a short period of time Multifect® Xylanase with Fv3A produced a substantial amount of EXP, which appeared to correspond with xylose formation (e.g., having a constant ratio of EXP formation to xylose formation with time). When Fv43D was used with Multifect® Xylanase, on the other hand, EXP appeared with a substantial lag relative to xylose formation. It can be postulated that Multifect® Xylanase and Fv3A produced EXP rapidly through transglycosylation. A xylose-enzyme ester adduct would have been formed first with C1 anomeric inversion, followed by a second inversion by ethanol doing an S_N2 displacement, at the C1 carbon of the attached xylose, of the active site carboxyl group. The double inversion gives retention of configuration in the product. On the other hand, Fv43D did not appear to catalyze a transglycosylation reaction; instead it produced EXP much more slowly through reverse hydrolysis. As Fv43D operates with inversion of anomeric configuration, EXP was likely formed from α -D-xylose, which in turn was formed from xylobiose by Fv43D, but also by inversion at C1 of β -D-xylose in an aqueous solution. Figure 15 indicates that EXP can also be formed by reverse hydrolysis from xylose, catalyzed by Multifect® Xylanase. Because the β -xylosidase

mechanism in this case was retaining, the likely substrate of this reaction was β -D-xylose.

9.1 Equilibrium equation for EXP formation

Under the SSF conditions, Multifect® Xylanase and Fv3A would encounter not only xylobiose but larger xylose oligomers as well. Hydrolysis of such oligomers could result in an increased formation of EXP, if upon scission, one of the oligomer products is transglycosylated to produce an ethyl glycosyl adduct. Further scission, by transglycosylation, could then form an additional ethyl adduct such that the ratio of EXP formation to xylose formation would be greater than that observed when only xylobiose is transglycosylated. For example:



It is noted that if only xylobiose is transglycosylated, the only EXP formation is from the reaction of line 5).

These possibilities were examined by comparing hydrolysis of xylose oligomers (average molecular weight = 539) with that of xylobiose using each of the same three enzymes: Fv3A, Fv43D, and Multifect® Xylanase. The results are depicted in Figure 16.

Plotted in Figure 16 (left panel) and Figure 16 (right panel) are the ratios of EXP to Xylose RI peak areas generated following incubation of xylobiose (20 mg/mL) (Figure 16 (left)) or xylose oligomer (20 mg/mL) (Figure 16 (right)) in the presence of 0.9 M EtOH at 46 °C in the presence of Multifect® Xylanase (560 $\mu\text{g}/\text{mL}$), Fv43D (36 $\mu\text{g}/\text{mL}$), or Fv3A (54 $\mu\text{g}/\text{mL}$), at concentrations that would give rates of xylose formation that were within a factor of two of each other. The EXP formation rates were nearly the same for xylobiose and xylose oligomers in the presence of Multifect® Xylanase and Fv43D. However, in the case of Fv3A, the EXP yield was about 1/3 higher in the presence of the xylose oligomers as compared to in the presence of xylobiose. As outlined above, this observation suggests that, at least for Fv3A, transglycosylation can occur with ethanol upon scission of oligomers larger than a xylobiose. Such transglycosylation of $>\text{dp}3$ oligomers does not appear to occur as prevalently in the cases of Multifect® Xylanase, although the EXP yield did appear to be higher than that was observed for Fv3A in both the xylobiose and xylose oligomer cases. This higher yield is likely an indication of a higher rate of transglycosylation with ethanol for Multifect® Xylanase than for Fv3A. The

fact that for both Multifect® Xylanase and Fv3A, EXP is formed for every 2.5 to 3.5 scission reactions is remarkable, considering that the molarity of ethanol is 0.9 M as compared to 55 M for H₂O. The selectivity for ethanol likely indicates a greater affinity for ethanol over water at or near the active site of the particular enzyme, with that affinity being higher for Multifect® Xylanase relative to that for Fv3A. The ratio of EXP to xylose is the same for Fv43D with xylobiose or xylose oligomer as substrate, which can be explained by the fact that, in this the case of Fv43D, EXP is formed by reverse hydrolysis from xylose, which was the product of hydrolysis from both xylobiose and xylose oligomer substrates.

In the case of Multifect® Xylanase and Fv3A, the maximum yield of EXP is attained after 3.5 hrs of incubation. The EXP yield at this point of incubation using Multifect® Xylanase was about 7 to 8 times that of the EXP yield obtained using Fv43D. After 3.5 hours the yield of EXP decreased in the Multifect® Xylanase reaction and the Fv3A reaction with a $t_{1/2}$ of 40-60 h. The reaction involving Fv3A was likely the enzyme-catalyzed hydrolysis of EXP from the high value formed in the transglycosylation reaction toward the equilibrium value of EXP/xylose formed upon reverse hydrolysis. In SSF reactions, the speediness of EXP formation and the sluggishness of the subsequent EXP hydrolysis in the presence of β -xylosidases having retaining activities suggests that the concentration of EXP is likely to remain substantially higher throughout the duration of an SSF reaction when a retaining β -xylosidase is present than when an inverting β -xylosidase is present. This further suggests that replacing retaining β -xylosidases with inverting β -xylosidases in SSF reactions would be beneficial for product yield. It is noted that all of the above mentioned reactions are enzyme catalyzed. Control samples/reactions, in the absence of enzyme, showed no formation of EXP upon incubation of xylobiose, of xylose oligomer, or of xylose in the presence of 0.9M ethanol at 46 °C.

9.2 Calculation of equilibrium constant

It has been suggested by Drouet *et al.* (in 1994, Biotech. & Bioeng. 43:1 075-1080) that the extent of formation of the alkyl-xylopyranoside (AXP), for example, EXP, upon reverse hydrolysis can be determined by the equilibrium established between the alcohol, xylose and the alkyl-xylopyranoside product.

The dissociation constant for ethyl-xylopyranoside (EXP) would be:

$$K_d = \frac{[\text{xylose}][\text{EtOH}]}{[\text{EXP}]}$$

Using this formula, a K_d of 27 M can be calculated from the data of Figure 2 as the equilibrium constant when Multifect® Xylanase was present in the SSF reaction. Also using this formula, a K_d of about 9.4 M can be calculated from the data of Figure 16 as the equilibrium constant when Fv43D was present in the SSF reaction. From Drouet *et al.* (1994, Biotech. Bioeng. 43:1 075-1 080), used *T. reesei* β -xylosidase and calculated a K_d of 40 M, although it did not appear that the EXP concentration had reached the equilibrium constant even after 160 hrs of incubation. The equilibrium constant calculations above were all made from SSF reactions started with xylose and ethanol, with the exception of the results depicted in Figure 16 of the disclosure, where the xylobiose and xylose oligomers were completely hydrolyzed by Fv43D in 20 hrs but the SSF reaction was allowed to proceed for a total of 145 hrs. Thus it is postulated that the K_d falls in the range of between about 10 and about 40M and is probably closer to the lower value, because the inverting β -xylosidase Fv43D produces a significant amount of EXP by the reverse reaction at equilibrium .

10. EXAMPLE 4: DELETION OF *BXL 1* GENE FROM *T. REESEI*

10.1 Construction of the *bxl1* deletion cassette

To construct the *bxl1* deletion cassette, 5' and 3' flanking sequences of the *bxl1* gene (Margolles-Clark *et al.*, 1996, App. Environ. Microbiol. 62(10):3840-6) from *Trichoderma reesei* genomic-DNA were amplified by PCR with primer pairs MH375/MH376 and MH377/MH378 respectively (shown in Table 4), using PfuUltra II Fusion HS DNA Polymerase (Stratagene). The 3'-flanking sequence contained part of the *Bxl1* coding sequence to avoid the nearby *bgl1* gene. Primer MH376 was phosphorylated at the 5'-end. One (1) μ L of T4 DNA Ligase at a concentration of 5 U/ μ L (Roche Applied Bioscience), 1 μ L of 10X ligation buffer (Roche) and approximately 20 ng of the PCR fragments were incubated for 10 mins at room temperature in a total volume of 10 μ L. The ligation reaction mixture was used as a template for a PCR reaction with primer pair MH379/MH380 and PfuUltra II Fusion HS DNA Polymerase (Stratagene).

The resulting 4.0 kb fragment was cloned into pCR-Blunt II-TOPO according to manufacturer's specifications (Invitrogen). The plasmid was transformed into *E. coli One Shot® TOP10* Chemically Competent cells (Invitrogen). A colony, which contained the 4.0 kb *bxl1* 5'+3' PCR fusion product cloned into the TOPO vector, was isolated. The plasmid was extracted by QiaPrep plasmid purification (Qiagen) and its sequence confirmed (Sequetech, Mountain View, CA). The resulting plasmid was digested with *AcI*

and *Ascl* (NEB) to allow for subsequent cloning with the fragment containing the hygromycin-resistance gene.

The hygromycin resistance gene was amplified with primers MH292/MH290 from a vector containing the *Aspergillus nidulans oliC* promoter, the hygromycin resistance gene (*E. coli*, hygromycin phosphotransferase, *hph*), and the *Aspergillus nidulans trpC* terminator, using PfuUltra II Fusion HS DNA Polymerase (Stratagene). The PCR-amplified fragment was cloned into pCR-blunt II-TOPO (Invitrogen) and transformed into *E. coli One Shot® TOP10* Chemically Competent cells (Invitrogen). A colony was isolated and sequencing confirmed that the extracted plasmid displayed a mutated 5' *Ascl* restriction site, which was replaced with a *NaA* site (GGCGCGCC[^]GGCGCCC). The construct was then digested with *NaA* (Roche), *Ascl* (NEB) and *DraI* (Roche), and the resulting 2.5 kb fragment was isolated using the QiaQuick Gel Extraction kit in accordance with the manufacturer's protocol (Qiagen) in preparation for cloning subsequently into the *Bxl1*-deletion plasmid.

Ligation of the two isolated fragments as described above was performed with 1 μ L 10X Ligation Buffer (Roche), 1 μ L 5 U/ml T4 DNA Ligase (Roche), and 50 ng of each fragment in a reaction volume of 10 μ L. The ligation mixture was cloned into *E. coli One Shot® TOP10* Chemically Competent cells and a single colony was isolated. The *bxl1*-deletion vector (Figure 17, pCR-BluntII-TOPO, *bxl1* deletion, *hph-loxP*) containing the *loxP*-flanked hygromycin resistance gene was extracted from the *E. coli* and the appropriate ligations were verified by restriction digest using *Bmt1*, resulting in 4 fragments of 4754, 2195, 1899, and 1182 base pairs.

The *bxl1*-deletion cassette was generated by amplifying the fragment from plasmid pCR-BluntII-TOPO, *bxl1* deletion, *hph-loxP* using primers MH379/ MH380 in a total volume of 10 mL and PfuUltra II Fusion HS DNA Polymerase (Stratagene). The PCR product was cleaned and concentrated using a QiaexII kit (Qiagen). The DNA was further concentrated by SpeedVac to a concentration of about 1.5 mg/mL.

10.2 Transformation of *bxl1* deletion plasmid into *T. reesei*

The DNA from the *bxl1*-deletion cassette was transformed into *T. reesei* strain #229, which overexpressed *T. reesei* Bgl1 and *T. reesei* Xyn3 as previously described herein. Transformants were selected on a medium containing 100 ppm Hygromycin B (Invitrogen). A transformant containing the *bxl1* deletion was selected by PCR. A *bxl1*-deficient *T. reesei* strain is referred to herein as a "*bxl1*⁻" strain.

11. EXAMPLE 5: EXPRESSION OF FV43D BY *T. REESEI* STRAIN

The following example shows how *Trichoderma reesei* was engineered to express Fv43D. A *T. reesei* strain engineered to express Fv43D is referred to herein as a "Fv43D+" strain

5 11.1 Construction of expression cassette

A *F. verticillioides* β -xylosidase Fv43D expression cassette was constructed by PCR amplification of the Fv43D gene from *F. verticillioides* genomic DNA sample using the primers SK1 322/SK1 297 (Table 5). A region of the promoter of the endoglucanase gene *egl1* was amplified by PCR from a *T. reesei* genomic DNA sample extracted from
10 an engineered *T. reesei* strain RL-P37 [see, e.g., Sheir-Neiss G. and B.S. Montenecourt, Appl. Microbiol. Biotechnology, 20 (1984) pp. 46-53], using the primers SK1 236/SK1 321. These two amplified fragments were subsequently fused together in a fusion PCR reaction using the primers SK1 236/SK1 297. The resulting fusion PCR fragment was cloned into pCR-Blunt II-TOPO vector (Invitrogen) to yield plasmid TOPO Blunt/Pegh -
15 Fv43D (Figure 18), which was in turn used to transform *E. coli One Shot® TOP10* chemically competent cells (Invitrogen). Plasmid DNA was extracted from several *E. coli* clones and confirmed by restriction digests.

The expression cassette from TOPO Blunt/Pegh1 -Fv43D was amplified by PCR using primers SK1 236/SK1 297 (Table 5) to generate a DNA product for transformation of
20 *T. reesei*. The expression cassette was co-transformed with an existing selection marker cassette containing the *als* gene (acetolactate synthase).

11.2 Transformation of *frx/f*-deficient *T. reesei* with Fv43D expression cassette

The *bx1/7*-deletion *T. reesei* host strain is transformed with the *Fv43D* expression
25 cassette (comprising an *egl1* promoter, an Fv43D open reading frame, and a native terminator of Fv43D) and an existing selection marker cassette containing the native *als* gene, using a standard transformation method such as, for example, electroporation [see, e.g., PCT patent application publication WO 08/1 5371 2]. Transformants are selected on minimal media agar plates containing chlorimuron ethyl. These
30 transformants are *bx1⁻Fv43D⁺ T. reesei*.

11.3 Transformation of *frx/7*-expressing *T. reesei* with Fv43D expression cassette

A *T. reesei* host strain having a wild type *bx1/1* gene [see, PCT patent application publication WO 2005/001 036 A2] was transformed with the *Fv43D* expression cassette

(comprising an *eg1* promoter, an Fv43D open reading frame, and a native Fv43D terminator) and an existing selection marker cassette containing the native *als* gene, using standard transformation methods such as, for example, electroporation (see, e.g., PCT patent application publication WO 08/1 5371 2). Transformants were selected on
5 minimal media agar plates containing chlorimuron ethyl. These transformants are Fv43D+ *T. reesei*.

12. EXAMPLE 6: USE OF CELLULASE PRODUCED ENGINEERED *T. REESEI* STRAINS IN SSF

The transformants *bxl1*-Fv43D+ *T. reesei*, and Fv43D+ *T. reesei* are used to
10 produce cellulase-containing culture broths. These culture broths are then used in SSF reactions in continuous, batch, or fed-batch configurations, as described herein to reduce the production of AXP and reduce the sugar yield loss by the production of a trans-xylosication of reverse hydrolysis product.

In a particular example, the transformant of a *bxl1*-*T. reesei* strain #229 ("229 Bxl del") was cultured to produce a cellulase-containing culture broth, which was then
15 supplemented with either a purified *T. reesei* Bxl1 (at 0.5 mg/g or 1 mg/g of xylan) or a purified FV43D, at 1 mg/g of xylan. The concentration of the EXP and ethanol at days 1 and 3 were plotted in Figures 43A (Day 1) and 43B (Day 3), respectively. The reactions were carried out under the recombinant *Zymomonas* SSF conditions using a 25 wt.%
20 solids loading of dilute ammonia pretreated corn cob substrate.

CLAIMS**WHAT IS CLAIMED IS:**

1. A method for simultaneous saccharification and fermentation (SSF) comprising culturing a complete fermentation medium, said complete fermentation medium comprising at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and at least one inverting β -xylosidase, for a period and under conditions suitable for producing a fermentation product.
2. The method of claim 1, wherein the complete fermentation medium comprises an effective amount of the inverting β -xylosidase such that the complete fermentation medium produces less short chain alkyl-p-xylopyranoside ("AXP") than does a control fermentation medium lacking the inverting β -xylosidase.
3. The method of claim 1 or 2, wherein the complete fermentation medium comprises an effective amount of the inverting β -xylosidase such that the complete fermentation medium produces at least 40% less AXP than does a control fermentation medium lacking the inverting β -xylosidase.
4. The method of claim 3, wherein the complete fermentation medium comprises an effective amount of the inverting β -xylosidase such that the complete fermentation medium produces at least 50% less AXP than does a control fermentation medium lacking the inverting β -xylosidase.
5. The method of claim 4, wherein the complete fermentation medium comprises an effective amount of the inverting β -xylosidase such that the complete fermentation medium produces at least 60% less AXP than does a control fermentation medium lacking the inverting β -xylosidase.
6. The method of claim 5, wherein the complete fermentation medium comprises an effective amount of the inverting β -xylosidase such that the complete fermentation medium produces at least 70% less AXP than does a control fermentation medium lacking the inverting β -xylosidase.
7. The method of any one of claims 1-6, wherein the AXP is a methyl- β -xylopyranoside (MXP), an ethyl- β -xylopyranoside (EXP), a propyl- β -xylopyranoside (PXP), or a butyl- β -xylopyranoside (BXP).
8. The method of any one of claims 1-7, wherein the complete fermentation medium comprises an effective amount of the inverting β -xylosidase to increase the yield

- of the fermentation product, as compared to the yield of the fermentation product from culturing a control fermentation medium lacking the inverting β -xylosidase.
9. The method of claim 8, wherein the yield of the fermentation product is increased by at least 1%.
- 5 10. The method of claim 9, wherein the yield of fermentation product is increased by at least 2%.
11. The method of claim 10, wherein the yield of fermentation product is increased by at least 3%.
12. The method of claim 11, wherein the yield of fermentation product is increased by at least 5%.
- 10 13. The method of claim 12, wherein the yield of fermentation product is increased by at least 7.5%.
14. The method of claim 13, wherein the yield of fermentation product is increased by at least 10%.
- 15 15. The method of any one of claims 1-14, wherein the fermentation product is an alcohol.
16. The method of claim 15, wherein the alcohol is methanol, ethanol, propanol, propane-1,3-diol, or butanol.
17. The method of any one of claims 1-16, wherein the inverting β -xylosidase is a GH43 family enzyme.
- 20 18. The method of claim 17, wherein the inverting β -xylosidase is an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide.
19. The method of claim 18, wherein the Fv43D polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:2, or to residues 21 to 350 of SEQ ID NO:2.
- 25 20. The method of claim 18, wherein the Pf43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:8, or to residues 21 to 445 of SEQ ID NO:8.
21. The method of claim 18, wherein the Fv43E polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:10, or to residues 19 to 530 of SEQ ID NO:10.
- 30 22. The method of claim 18, wherein the Fv43B polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:12, or to residues 17 to 574 of SEQ ID NO:12.

23. The method of claim 18, wherein the Af43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:14, or to residues 15-558 of SEQ ID NO:14.
24. The method of claim 18, wherein the Fo43A polypeptide has at least 90%
5 sequence identity to an amino acid sequence corresponding to SEQ ID NO:24, or to residues 21-348 of SEQ ID NO:24.
25. The method of claim 18, wherein the Gz43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:22, or to residues 19-340 of SEQ ID NO:22.
- 10 26. The method of claim 18, wherein the XynB3 polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:25.
27. The method of any one of claims 17-26, wherein the inverting β -xylosidase is present in the complete fermentation medium at a concentration of 0.3 mg to 10 mg per gram of xylan in the xylan-containing biomass.
- 15 28. The method of claim 27, wherein the inverting β -xylosidase is present at a concentration of 0.4 mg to 10 mg per gram of xylan in the xylan-containing biomass.
29. The method of claim 27, wherein the inverting β -xylosidase is present at a concentration of 0.3 mg to 3 mg per gram of xylan in the xylan-containing
20 biomass.
30. The method of any one of claims 1-29, which is performed as a continuous, a batch, or a fed-batch SSF process.
31. The method of any one of claims 1-30, further comprising a step of forming the complete fermentation medium.
- 25 32. The method of claim 31, wherein the step of forming the complete fermentation medium comprises combining (a) the fermenting microorganism, (b) the xylan-containing biomass, (c) the cellulase, (d) the hemicellulase, (e) the inverting β -xylosidase, and (f) a medium lacking one or more or all of (a)-(e).
33. The method of claim 32, wherein the cellulase is present in the form of a whole
30 cellulase preparation.
34. The method of claim 33, wherein the whole cellulase preparation comprises a hemicellulase.
35. The method of claim 33 or 34, wherein the whole cellulase preparation is a culture broth obtained from culturing a filamentous fungus.

36. The method of claim 35, wherein the filamentous fungus is a *T. reesei*.
37. The method of claim 36, wherein the *T. reesei* has been engineered such that the native β -xylosidase gene has been deleted or inactivated.
38. The method of any one of claims 1-37, wherein the fermenting microorganism is a fungus.
39. The method of claim 38, wherein the fungus is a *Saccharomyces cerevisiae* yeast.
40. The method of any one of claims 1-37, wherein the fermenting microorganism is a bacterium.
41. The method of claim 40, wherein the bacterium is a *Zymomonas mobilis*.
42. The method of any one of claims 1-41, wherein the xylan-containing biomass is corn stover, bagasses, sorghum, giant reed, elephant grass, miscanthus, Japanese cedar, wheat straw, switchgrass, hardwood pulp, or softwood pulp.
43. The method of claim 42, wherein the xylan-containing biomass is in a slurry.
44. The method of claim 42 or 43, wherein the xylan-containing biomass has been pretreated.
45. The method of any one of claims 1-44, further comprising the step of recovering the fermentation product.
46. The method of any one of claims 1-45, wherein the complete fermentation medium comprise a greater amount of inverting β -xylosidases than that of retaining β -xylosidases on a mole basis, molecular weight basis, or on both a mole basis and a molecular weight basis.
47. The method of claim 46, wherein the ratio of inverting β -xylosidases to retaining β -xylosidases in the complete fermentation medium is at least 2:1, on a mole basis, molecular weight basis, or on both a mole basis and molecular weight basis.
48. A *T. reesei* cell, which has been engineered such that the native β -xylosidase gene has been deleted or that it has no detectable β -xylosidase activity.
49. The *T. reesei* cell of claim 48, which is engineered to recombinantly express a GH43 family enzyme.
50. The *T. reesei* cell of claim 48, which is engineered to recombinantly express an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide.

51. The *T. reesei* cell of claims 49-50, wherein the Fv43D polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:2, or to residues 21 to 350 of SEQ ID NO:2.
52. The *T. reesei* cell of claim 51, wherein the Pf43A polypeptide has at least 90%
5 sequence identity to an amino acid sequence corresponding to SEQ ID NO:8, or to residues 21 to 445 of SEQ ID NO:8.
53. The *T. reesei* cell of claim 51, wherein the Fv43E polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:10, or to residues 19 to 530 of SEQ ID NO:10.
- 10 54. The *T. reesei* cell of claim 51, wherein the Fv43B polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:12, or to residues 17 to 574 of SEQ ID NO:12.
55. The *T. reesei* cell of claim 51, wherein the Af43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:14, or
15 to residues 15-558 of SEQ ID NO:14.
56. The *T. reesei* cell of claim 51, wherein the Fo43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:24, or to residues 21-348 of SEQ ID NO:24.
57. The *T. reesei* cell of claim 51, wherein the Gz43A polypeptide has at least 90%
20 sequence identity to an amino acid sequence corresponding to SEQ ID NO:22, or to residues 19-340 of SEQ ID NO:22.
58. The *T. reesei* cell of claim 51, wherein the XynB3 polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:25.
59. A method for producing a cellulase preparation, comprising culturing the *T. reesei*
25 cell of any one of claims 49-58 under conditions that result in the production of the cellulase preparation.
60. The method of claim 59, further comprising recovering the cellulase preparation.
61. A cellulase preparation obtained from performing the method of claims 59 or 60.
62. A culture broth produced by culturing the *T. reesei* cell of any one of claims 49-
30 58.
63. A method of biomass saccharification comprising contacting the biomass with the cellulase preparation of claim 61.
64. A method of biomass saccharification comprising contacting the biomass with the culture broth of claim 62.

65. A composition comprising at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and at least one inverting β -xylosidase.
- 5 66. The composition of claim 65, wherein the inverting β -xylosidase is a GH43 family enzyme.
67. The composition of claim 65, wherein the inverting β -xylosidase is an Fv43D, a Pf43A, an Fv43E, an Fv43B, an Af43A, an Fo43A, a Gz43A, or a XynB3 polypeptide.
- 10 68. The composition of claim 66 or 67, wherein, if present, the Fv43D polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:2, or to residues 21 to 350 of SEQ ID NO:2.
69. The composition of claim 66 or 67, wherein, if present, the Pf43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:8, or to residues 21 to 445 of SEQ ID NO:8.
- 15 70. The composition of claim 66 or 67, wherein, if present, the Fv43E polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:10, or to residues 19 to 530 of SEQ ID NO:10.
71. The composition of claim 66 or 67, wherein, if present, the Fv43B polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:12, or to residues 17 to 574 of SEQ ID NO:12.
- 20 72. The composition of claim 66 or 67, wherein, if present, the Af43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:14, or to residues 15-558 of SEQ ID NO:14.
73. The composition of claim 66 or 67, wherein, if present, the Fo43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:24, or to residues 21-348 of SEQ ID NO:24.
- 25 74. The composition of claim 66 or 67, wherein, if present, the Gz43A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:22, or to residues 19-340 of SEQ ID NO:22.
- 30 75. The composition of claim 66 or 67, wherein, if present, the XynB3 polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:25.
76. The composition of any one of claims 65-75, wherein the xylan-containing biomass is corn stover, bagasses, sorghum, giant reed, elephant grass,

- miscanthus, Japanese cedar, wheat straw, switchgrass, hardwood pulp, or softwood pulp.
77. The composition of any one of claims 65-76, wherein the fermenting microorganism is a fungus or a bacterium .
- 5 78. The composition of claim 77, wherein the fungus is a *Saccharomyces cerevisiae* yeast.
79. The composition of claim 77, wherein the bacterium is a *Zymomonas mobilis*.
80. The composition of any one of claims 65-79, wherein the cellulase is present in the form of a whole cellulase preparation.
- 10 81. The composition of claim 80, wherein the cellulase preparation comprises a hemicellulase.
82. The composition of any one of claims 65-81 , wherein the composition is substantially free of retaining β -xylosidase or has no detectable retaining β -xylosidase activity.
- 15 83. A method of producing a fermentation product comprising culturing the composition of any one of claims 65-82 for a period of time.
84. The method of claim 83, wherein the fermentation product is an alcohol.
85. The method of claim 84, wherein the alcohol is methanol, ethanol, propanol, propane-1 ,3-diol, or butanol.
- 20 86. A method for simultaneous saccharification and fermentation (SSF) comprising culturing a complete fermentation medium , said complete fermentation medium comprising at least one fermenting microorganism , at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and at least one retaining β -xylosidase, for a period and under conditions suitable for producing a
- 25 alkyl[^]-xylopyranoside ("AXP") .
87. The method of claim 86, wherein the complete fermentation medium comprises an effective amount of retaining β -xylosidase such that the complete fermentation medium produces more AXP than does a control fermentation medium lacking the retaining β -xylosidase or having a lower amount of the retaining β -xylosidase.
- 30 88. The method of claim 86 or 87, wherein the AXP is a methyl[^]-xylopyranoside (MXP) , an ethyl[^]-xylopyranoside (EXP) , a propyl[^]-xylopyranoside (PXP) , or a butyl[^]-xylopyranoside (BXP).
89. The method of any one of claims 86-88, wherein the retaining β -xylosidase is a GH3, GH30, GH31 , GH39, GH52, GH54, or GH16 family enzyme.

90. The method of any one of claims 86-89, wherein the retaining β -xylosidase is a XlnD, an Fv30A, an Fv30B, an Fv39A, an Fv39B, or a XynB polypeptide.
91. The method of claim 90, wherein the XlnD polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:40, or
5 to residues 18-804 of SEQ ID NO:40.
92. The method of claim 90, wherein the Fv30A polypeptide has at least 90% sequence identity an amino acid sequence corresponding to SEQ ID NO:42, or to residues 20-537 of SEQ ID NO:42.
93. The method of claim 90, wherein the Fv30B polypeptide has at least 90%
10 sequence identity to an amino acid sequence corresponding to SEQ ID NO:44, or to residues 25-485 of SEQ ID NO:44.
94. The method of claim 90, wherein the Fv39A polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:46, or to residues 20-439 of SEQ ID NO:46.
95. The method of claim 90, wherein the Fv39B polypeptide has at least 90%
15 sequence identity to an amino acid sequence corresponding to SEQ ID NO:48, or to residues 19-456 of SEQ ID NO:48.
96. The method of claim 90, wherein the XynB polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:50.
97. The method of claim 90, wherein the XylA polypeptide has at least 90%
20 sequence identity to an amino acid sequence corresponding to SEQ ID NO:52 or to residues 19-705 of SEQ ID NO:52.
98. The method of claim 90, wherein the Xyl1 polypeptide has at least 90% sequence identity to an amino acid sequence corresponding to SEQ ID NO:54.
99. The method of any one of claims 86-98, which is performed as a continuous, a
25 batch, or a fed-batch SSF process.
100. The method of any one of claims 86-99, further comprising a step of forming the complete fermentation medium .
101. The method of claim 100, wherein the step of forming the complete
30 fermentation medium comprises combining (a) the fermenting microorganism , (b) the xylan-containing biomass, (c) the cellulase, (d) the hemicellulase, (e) the retaining β -xylosidase, and (f) a medium lacking one or more or all of (a)-(e).
102. The method of claim 101, wherein the cellulase is present in the form of a whole cellulase preparation.

103. The method of claim 102, wherein the whole cellulase preparation comprises a hemicellulase.
104. The method of claim 102 or 103, wherein the whole cellulase preparation is a culture broth obtained from culturing a filamentous fungus.
- 5 105. The method of claim 104, wherein the filamentous fungus is a *T. reesei*.
106. The method of claim 105, wherein the *T. reesei* has been engineered to overexpress a native retaining β -xylosidase gene or to express a foreign retaining β -xylosidase gene.
107. The method of any one of claims 86-1 06, wherein the fermenting
10 microorganism is a fungus or a bacterium .
108. The method of any one of claims 86-1 07, wherein the xylan-containing biomass is corn stover, bagasses, sorghum , giant reed, elephant grass, miscanthus, Japanese cedar, wheat straw, switchgrass, hardwood pulp, or softwood pulp.
- 15 109. The method of claim 108, wherein the xylan-containing biomass has been pretreated.
110. The method of any one of claims 86-1 08, further comprising the step of recovering the AXP compound.
111. The method of any one of claims 86-1 10, wherein the complete
20 fermentation medium comprise a greater amount of retaining β -xylosidases than inverting β -xylosidases on a mole basis, molecular weight basis, or on both a mole basis and a molecular weight basis.
112. A *T. reesei* cell, which has been engineered such that its native β -xylosidase gene has been overexpressed or that it expresses a foreign β -xylosidase gene.
25
113. The *T. reesei* cell of claim 112, which is engineered to recombinantly express a GH3, GH30, GH31 , GH39, GH52, GH54, or GH1 6 family enzyme.
114. The *T. reesei* cell of claim 112, which is engineered to recombinantly express a XlnD, an Fv30A, an Fv30B, an Fv39A, an Fv39B, a XynB, a XylA, or a
30 Xyl1 polypeptide.
115. A method for producing a cellulase preparation, comprising culturing the *T. reesei* cell of any one of claims 112-1 14 under conditions that result in the production of the cellulase preparation.

116. The method of claim 115, further comprising recovering the cellulase preparation.
117. A cellulase preparation obtained from performing the method of claim 115 or 116.
- 5 118. A culture broth produced by culturing the *T. reesei* cell of any one of claims 112-114.
119. A method of biomass saccharification comprising contacting the biomass with the cellulase preparation of claim 117.
- 10 120. A method of biomass saccharification comprising contacting the biomass with the culture broth of claim 118.
121. A composition comprising at least one fermenting microorganism, at least one xylan-containing biomass, at least one cellulase, at least one hemicellulase, and at least one retaining β -xylosidase.
122. The composition of claim 121, wherein the retaining β -xylosidase is a
15 GH3, GH30, GH31, GH39, GH52, GH54, or GH16 family enzyme.
123. The composition of claim 121, wherein the inverting β -xylosidase is a XlnD, an Fv30A, an Fv30B, an Fv39A, an Fv39B, a XynB, a XylA, or a XylI polypeptide.
124. The composition of any one of claims 121-123, wherein the xylan-
20 containing biomass is corn stover, bagasses, sorghum, giant reed, elephant grass, miscanthus, Japanese cedar, wheat straw, switchgrass, hardwood pulp, or softwood pulp.
125. The composition of any one of claims 121-124, wherein the fermenting microorganism is a fungus or a bacterium.
- 25 126. The composition of any one of claims 121-125, wherein the cellulase is present in the form of a whole cellulase preparation.
127. The composition of claim 126, wherein the cellulase preparation comprises a hemicellulase.
128. The composition of any one of claims 121-127, wherein the composition is
30 substantially free of inverting β -xylosidase or has no detectable inverting β -xylosidase activity.
129. A method of producing an AXP compound comprising culturing the composition of any one of claims 121-128 for a period of time.

Process	Substrate	Solids loading	Enzymes used	EtOH at day 3 of fermentation (g/L)	EXP at day 3 of fermentation (g/L)
Batch	Glucose+xylose (80 g/L+70 g/L)	~	No enzyme added	77.6	1.53
Fed-batch	Glucose+xylose (80 g/L+70 g/L)	~	No enzyme added	78.0	0.99
SHF	Corn cob	25%	A1500+MF (20+5 mg/g)	32.1	1.11
SSF	Corn cob	25%	A1500+MF (20+5 mg/g)	37.5	6.10
Fed-batch SSF	Corn cob	25%	A1500+MF (20+5 mg/g)	48.0	14.3

TABLE 1

Process	Substrate	Substrate's xylan composition	Solids loading	Enzymes used	EtOH at day 3 of fermentation (g/L)	EXP at day 3 of fermentation (g/L)
SSF	Bagasse	3.1%	20%	A1500+MF (20+5 mg/g)	20.9	0.91
SSF	Softwood pulp	8.0%	10%	A1500+MF (20+5 mg/g)	48.6	4.75
SHF	Mixed hardwood pulp	20.7%	10%	A1500+MF (20+5 mg/g)	41.6	3.52
SSF	Mixed hardwood pulp	20.7%	10%	A1500+MF (20+5 mg/g)	43.7	10.7
SSF	Mixed hardwood pulp	20.7%	12%	A1500+MF (20+5 mg/g)	60.2	16.1

TABLE 2

Time (h)	MF EXP	MF Xylose	Fv43D Exp	Fv43D Xylose	Fv3A EXP	Fv3A Xylose
0	2778	12043	0	7046	3991	11900
0.5	47400	91600	3056	59800	44000	114000
1	72000	125000	4563	84200	62500	147500
2	98300	151000	9534	117800	81420	178000
3.5	98800	153000	8359	118000	82100	180000
20	140000	220000	32800	326000	94100	264000
	Refractive Index Area					

TABLE 3

Primer sequences for the construction of <i>bx11</i> deletion cassette			
Primer Name	Seq ID No.	Primer sequence (5'→3')	Description
MH290	27	caaGGCGCGCCaagtATAACTTCGTATAAT GTATGCTATACGAAGTTATCGGCCGGCG TATTGGGTGTTACG	hph reverse primer Ascl loxP site
MH292	28	GAAGGCGCGCCACAGATAACTTCGTATA GCATACATTATACGAAGTTATcctgggcttg actggtcgcgag	hph forward primer full promoter Ascl loxP site
MH375	29	ccatgtcacctgtcttgaacac	Bxl1 5' forward
MH376	30	caaggcgc GCCATCTCTTTTCGATCTCAACA G	Bxl1 5' reverse Ascl
MH377	31	gattgcatcgccgtctacaacgtttcaacc	Bxl1 3' forward AsiSI AclI
MH378	32	GGTCCAACCTTGAATGTAACAGC	Bxl1 3' reverse primer
MH379	33	gtgctgctgaacataaggtctc	Bxl1 deletion nested forward primer
MH380	34	CCTCCATTCTTCCAACAAGCC	Bxl1 deletion nested reverse primer

TABLE 4

Primer sequences for the construction of <i>F. verticillioides</i> β-xylosidase Fv43D expression cassette		
Primer Name	Primer sequence (5'→3')	SEQ ID NO.
Forward Primer (SK1322)	CACCATGCAGCTCAAGTTTCTGTC	35
Reverse Primer (SK1297)	GGTTACTAGTCAACTGCCCGTTCTGTAGCGAG	36
Forward Primer (SK1236)	CATGCGATCGCGACGTTTTGGTCAGGTCG	37
Reverse Primer (SK1321)	GACAGAAACTTGAGCTGCATGGTGTGGGACAACAAGAAGG	38

TABLE 5

SEQ ID NO:	Nucleotide or amino acid	Description
1.	Nucleotide	Nucleotide sequence for Fv43D, a GH43 family enzyme from <i>Fusarium verticillioides</i>
2.	Amino acid	Protein sequence of Fv43D
3.	Nucleotide	Nucleotide sequence of Bxl1, a GH3 β -xylosidase from <i>Trichoderma reesei</i>
4.	Amino acid	Protein sequence of Bxl1
5.	Nucleotide	Nucleotide sequence for Fv3A, a GH3 family enzyme from <i>Fusarium verticillioides</i>
6.	Amino acid	Protein sequence of Fv3A
7.	Nucleotide	Nucleotide sequence for Pf43A, a GH43 family enzyme from <i>Penicillium funiculosum</i>
8.	Amino acid	Protein sequence of Pf43A
9.	Nucleotide	Nucleotide sequence for Fv43E, a GH43 family enzyme from <i>Fusarium verticillioides</i>
10.	Amino acid	Protein sequence of Fv43E
11.	Nucleotide	Nucleotide sequence for Fv43B, a GH43 family enzyme from <i>Fusarium verticillioides</i>
12.	Amino acid	Protein sequence of Fv43B
13.	Nucleotide	Nucleotide sequence for Af43A, a GH43 family enzyme from <i>Aspergillus fumigatus</i>
14.	Amino acid	Protein sequence of Af43A
15.	Nucleotide	Nucleotide sequence for Fv51A, a GH51 family enzyme from <i>Fusarium verticillioides</i>
16.	Amino acid	Protein sequence of Fv51A
17.	Nucleotide	Nucleotide sequence for Xyn3, a GH10 family xylanase from <i>Trichoderma reesei</i>
18.	Amino acid	Protein sequence of Xyn3
19.	Nucleotide	Nucleotide sequence for xlnA, an <i>Aspergillus tubingensis</i> xylanase
20.	Amino acid	xlnA protein sequence
21.	Nucleotide	Nucleotide sequence for Gz3A, a GH43 family enzyme from <i>Gibberella zeae</i>
22.	Amino acid	Protein sequence of Gz3A
23.	Nucleotide	Nucleotide sequence for Fo43A, a GH43 family enzyme from <i>Fusarium oxysporum</i>
24.	Amino acid	Protein sequence of Fo43A
25.	Amino acid	Protein sequence of XynB3, a GH43 family enzyme from <i>Geobacillus stearothermophilus</i> T-6
26.	Amino acid	Protein sequence of Bgl1, a GH3 family enzyme from <i>T. reesei</i>
39.	Nucleotide	Nucleotide sequence for XlnD, a GH3 family enzyme from <i>A. japonicus</i>
40.	Amino acid	Protein sequence of XlnD
41.	Nucleotide	Nucleotide sequence of Fv30A, a GH30 family enzyme from <i>F. verticillioides</i>
42.	Amino acid	Protein sequence of Fv30A
43.	Nucleotide	Nucleotide sequence of Fv30B, a GH30 family enzyme

		from <i>F. verticillioides</i>
44.	Amino acid	Protein sequence of Fv30B
45.	Nucleotide	Nucleotide sequence of Fv39A, a GH39 family enzyme from <i>F. verticillioides</i>
46.	Amino acid	Protein sequence of Fv39A
47.	Nucleotide	Nucleotide sequence of Fv39B, a GH39 family enzyme from <i>F. verticillioides</i>
48.	Amino acid	Protein sequence of Fv39B
49.	Nucleotide	Nucleotide sequence of XynB, a GH39 family enzyme from <i>T. saccharolyticum</i>
50.	Amino acid	Protein sequence of XynB
51.	Nucleotide	Nucleotide sequence of XylA, a GH52 family enzyme from <i>G. stearothermophilus</i>
52.	Amino acid	Protein sequence of XylA
53.	Nucleotide	Nucleotide sequence of Xyl1, a GH54 family enzyme from <i>T. koningii</i> (<i>H. Koningii</i>)
54.	Amino acid	Protein sequence of Xyl1

TABLE 6

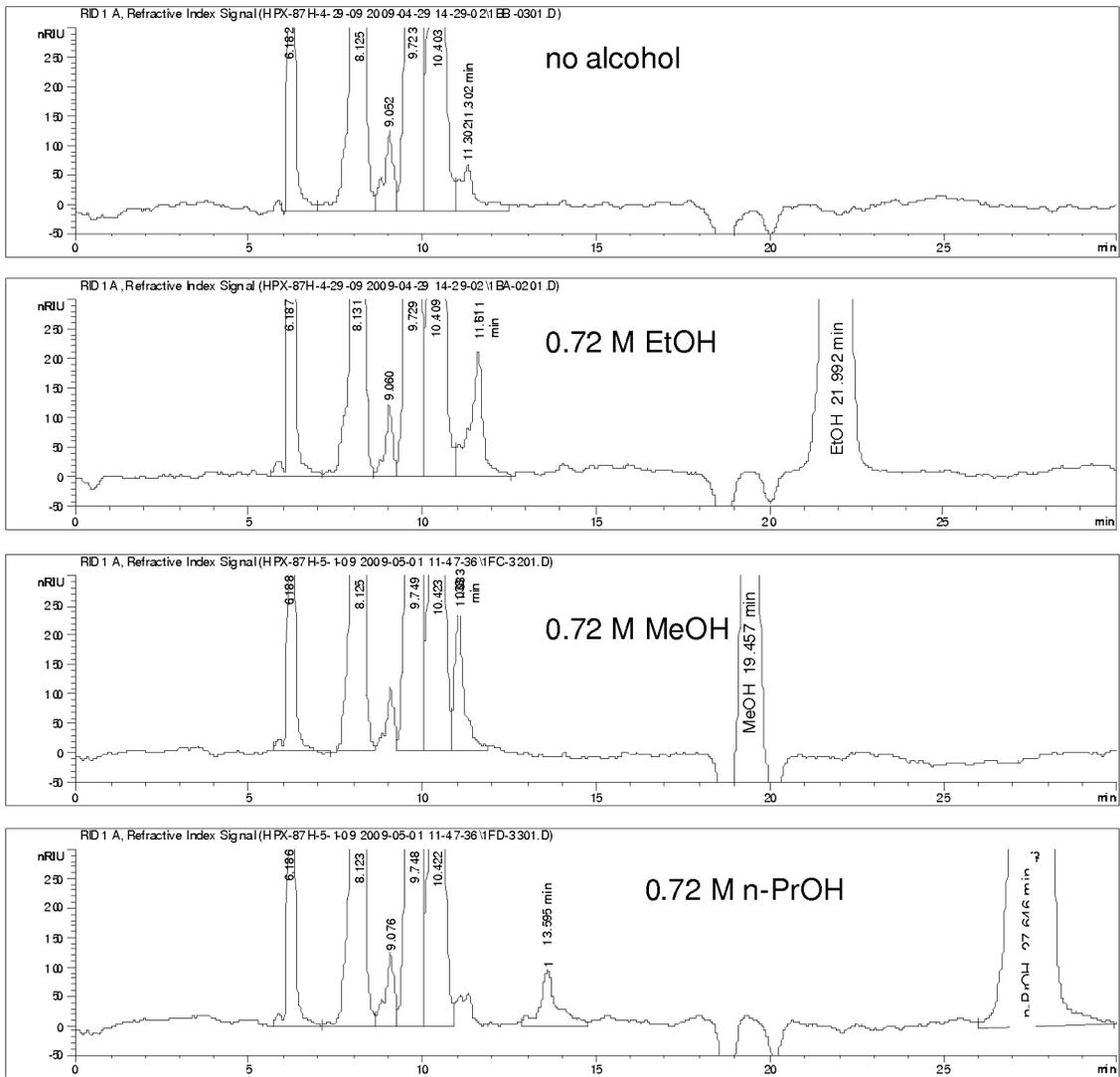


FIGURE 1

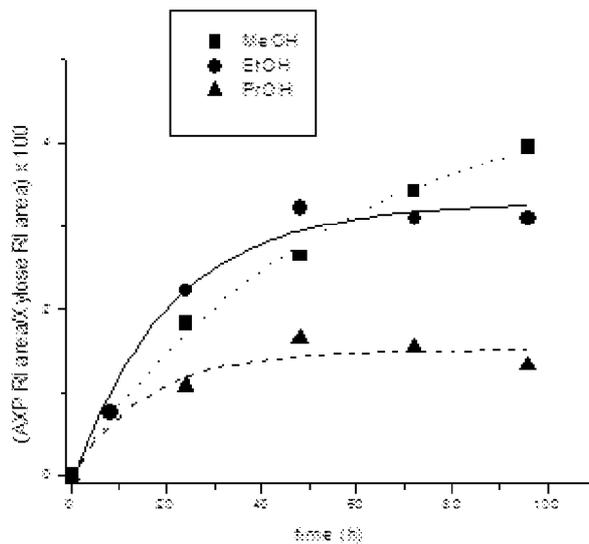


FIGURE 2

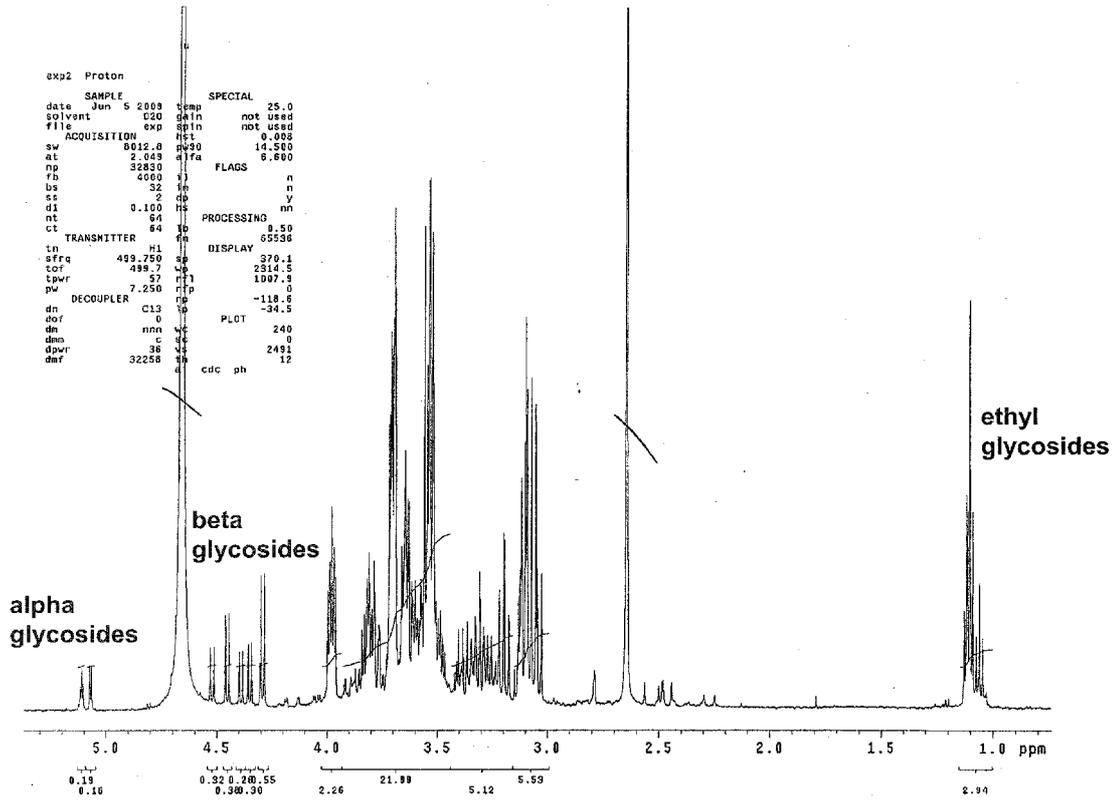


FIGURE 3

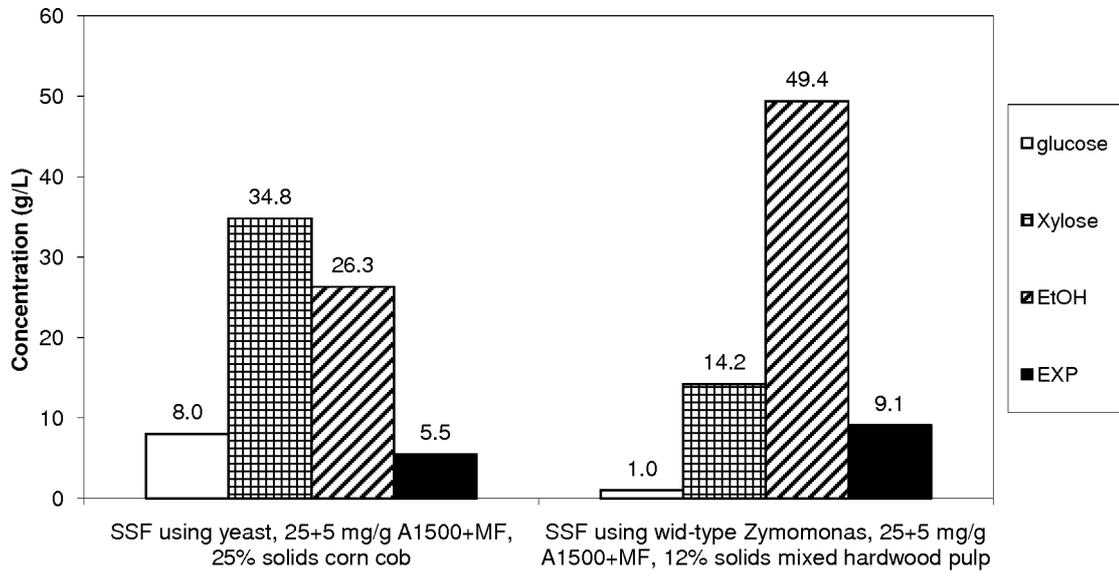


FIGURE 4

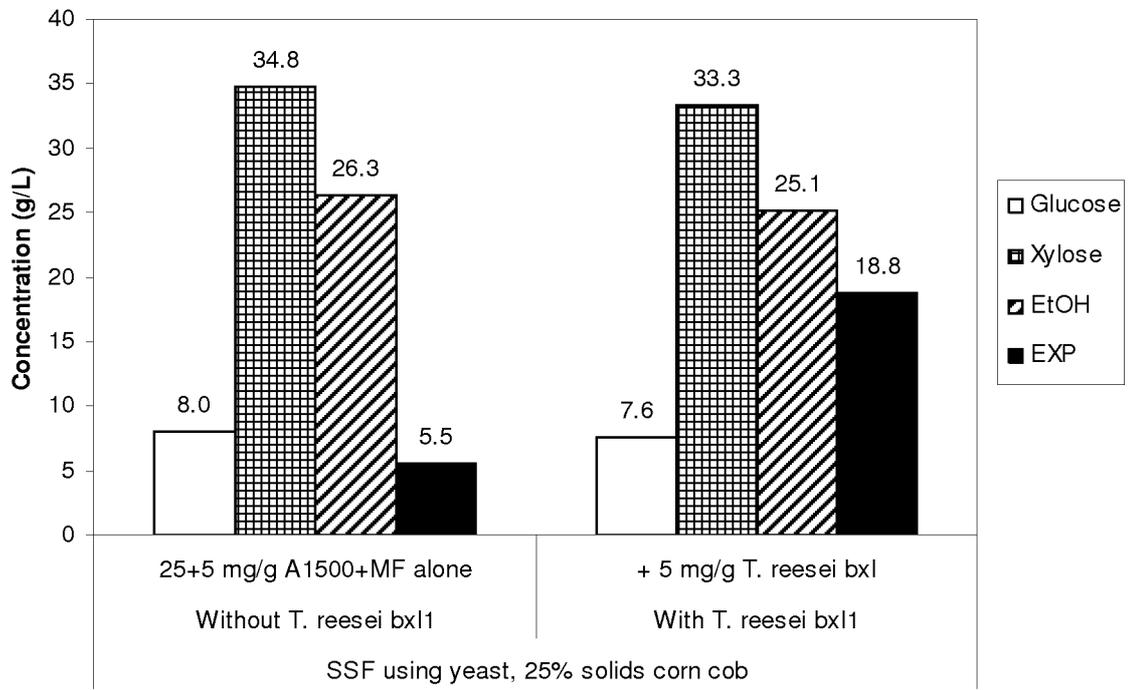


FIGURE 5

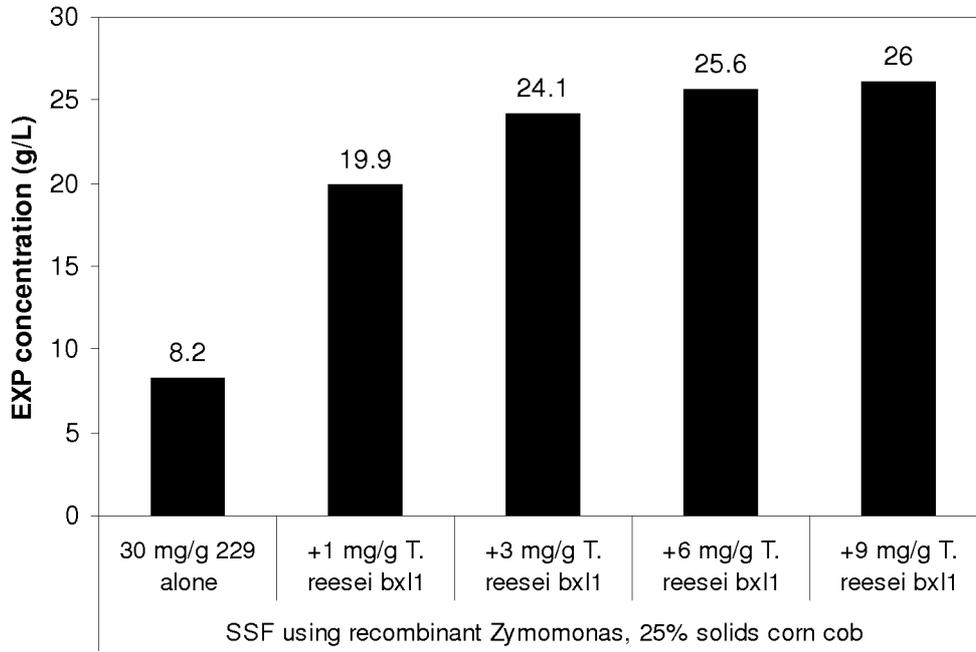


FIGURE 6

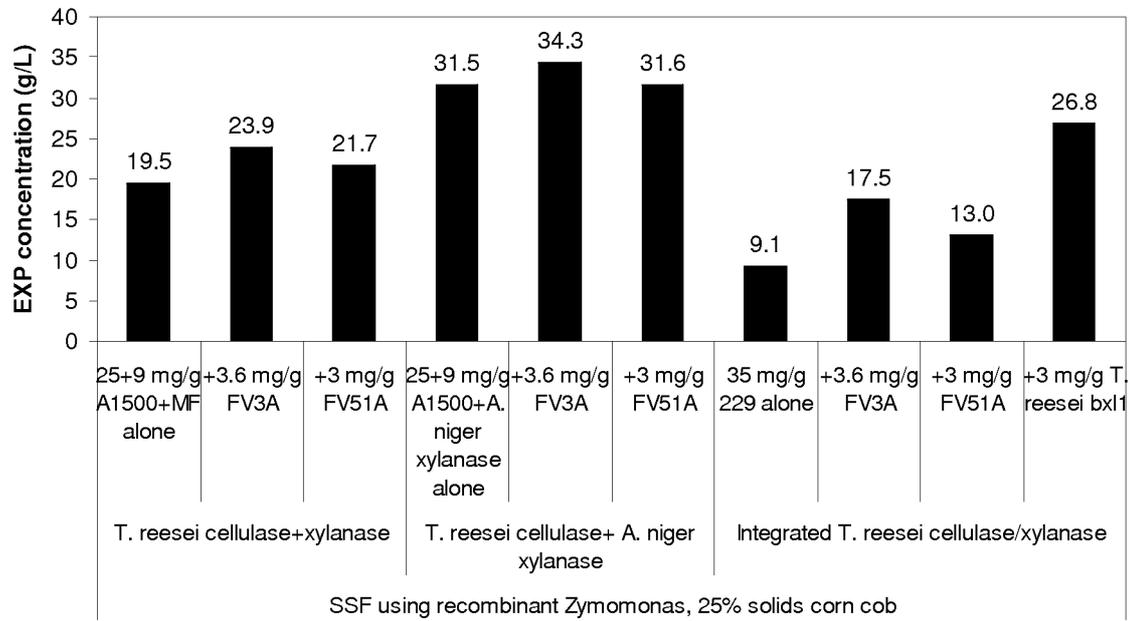


FIGURE 7

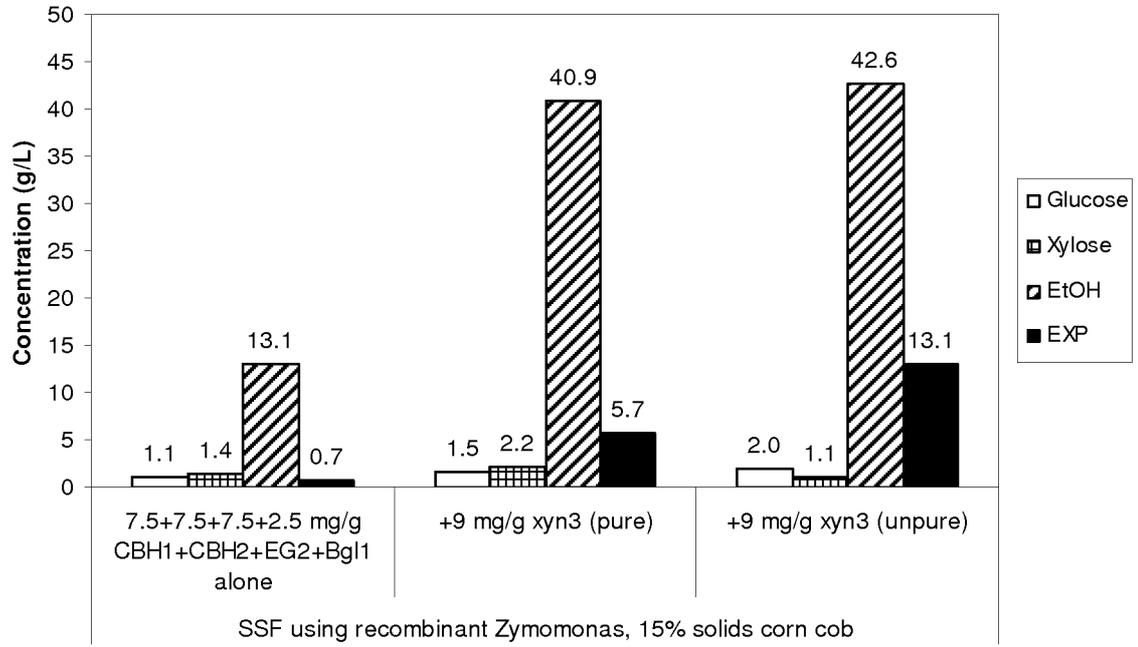


FIGURE 8

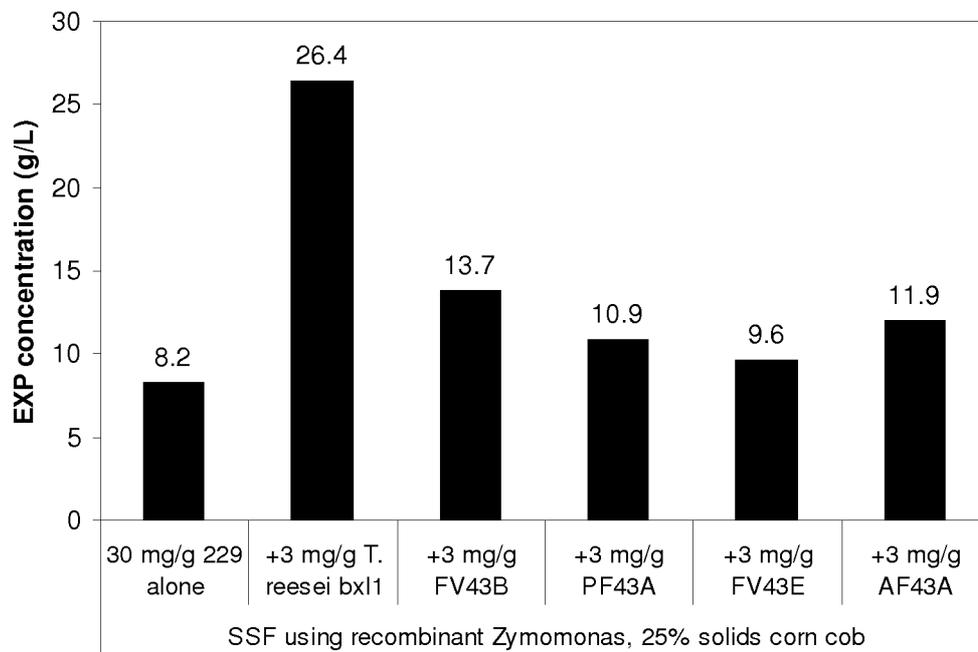


FIGURE 9

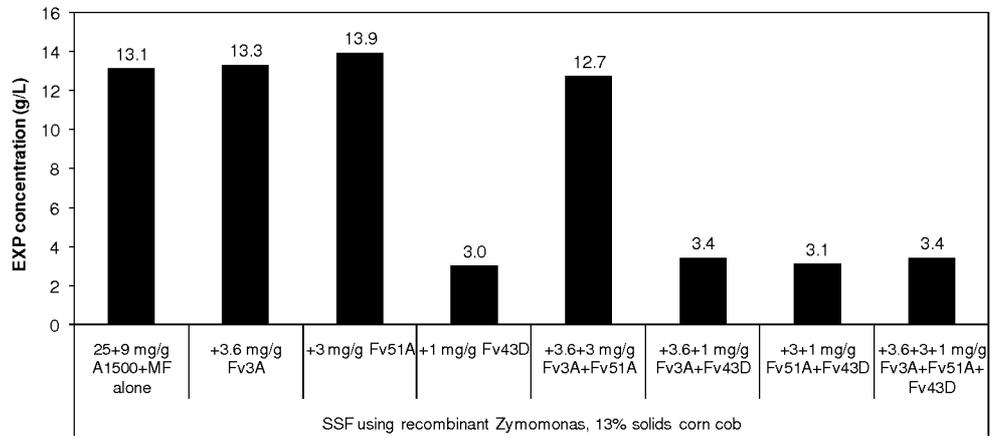


FIGURE 10

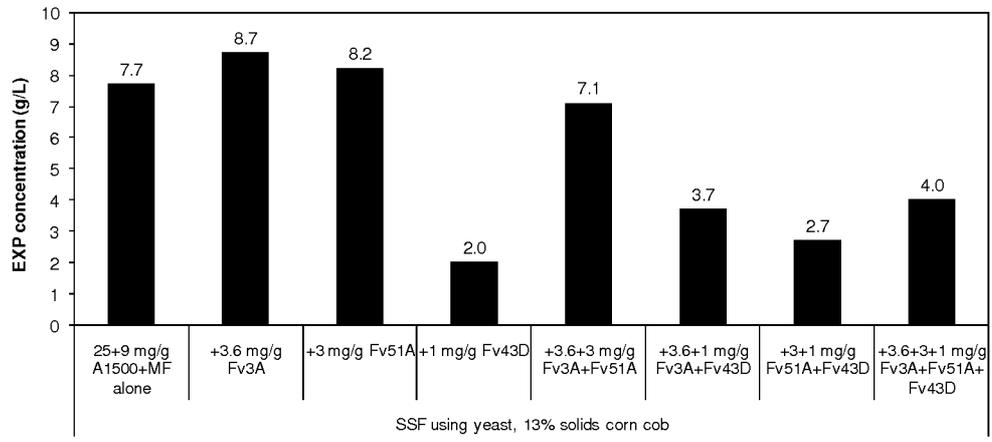


FIGURE 11

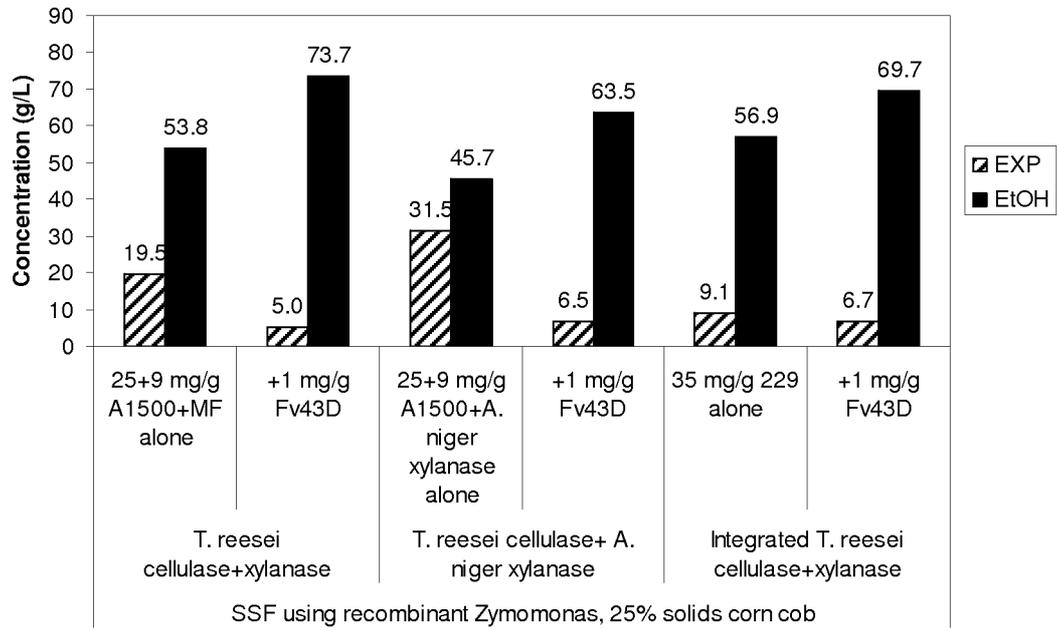


FIGURE 12

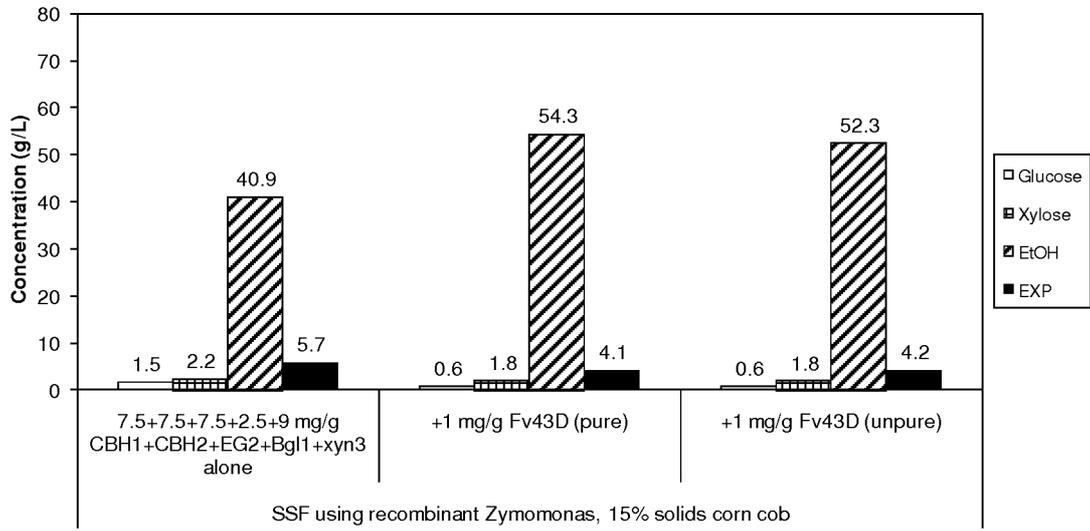


FIGURE 13

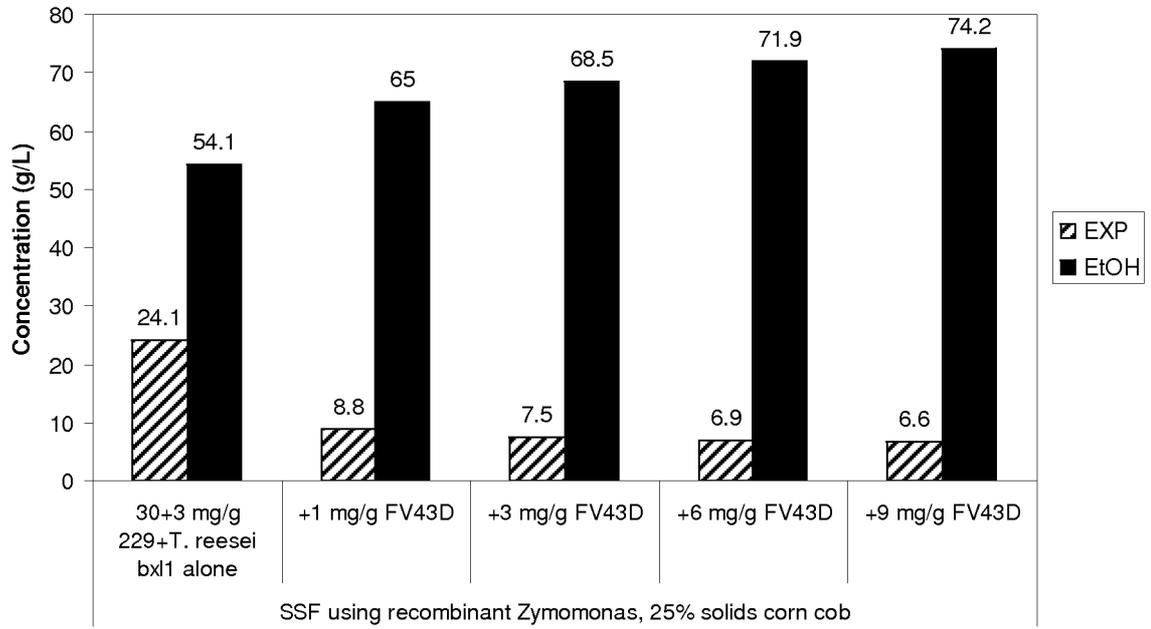


FIGURE 14A

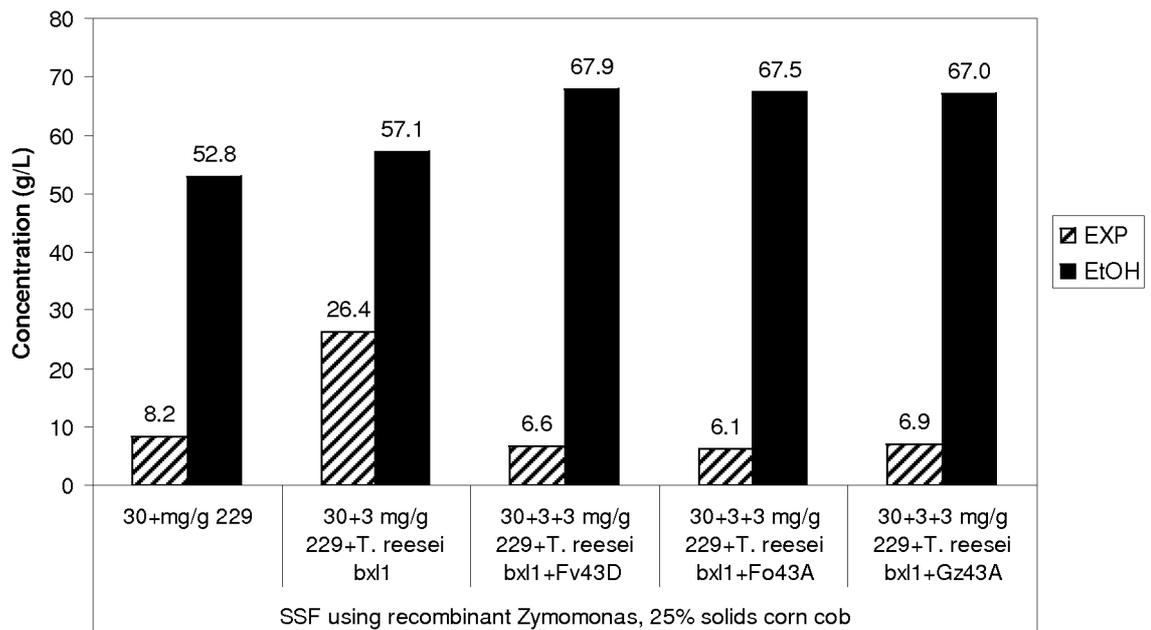


FIGURE 14B

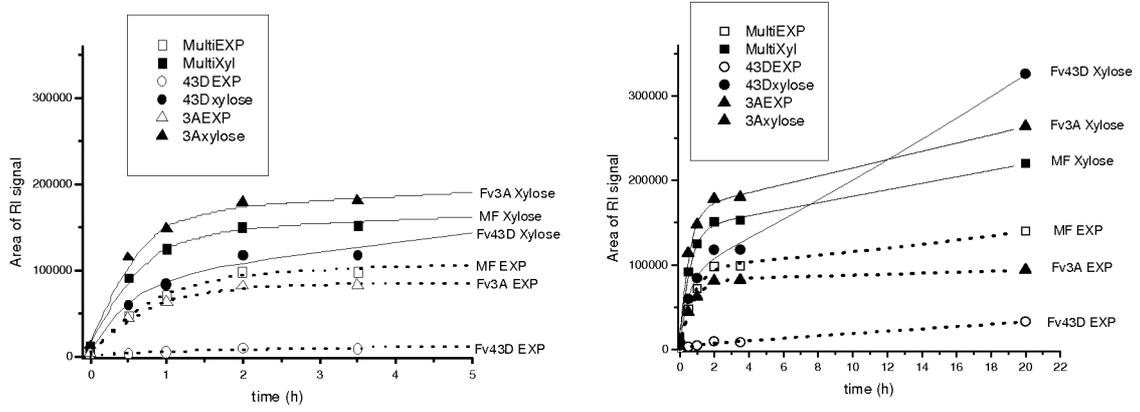


FIGURE 15

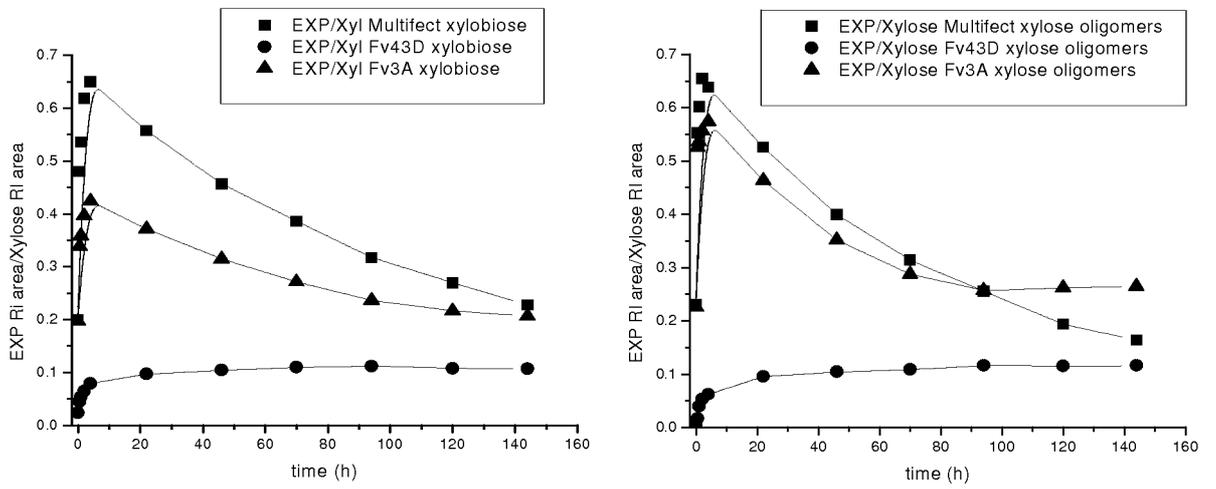


FIGURE 16

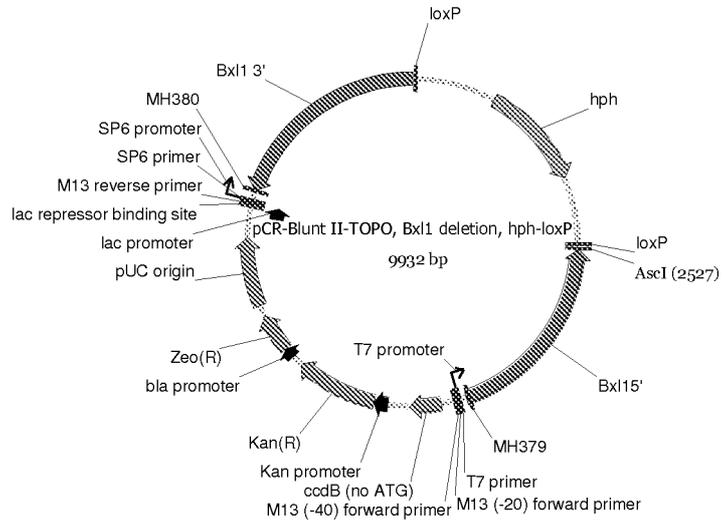


FIGURE 17

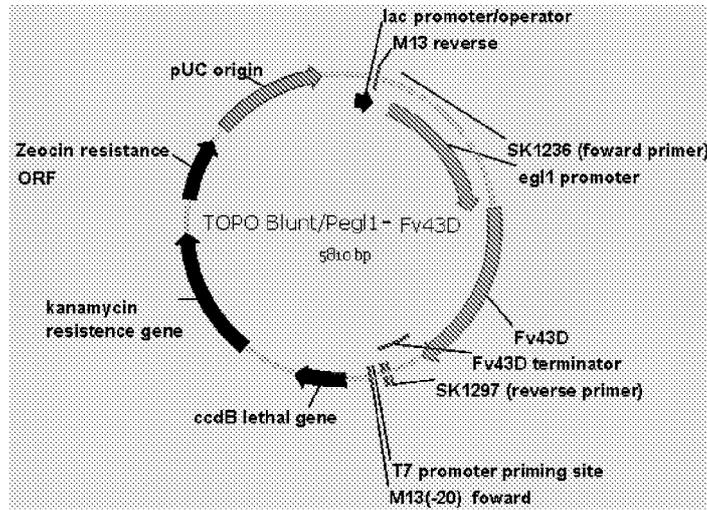


FIGURE 18

SEQ ID NO:1**Nucleotide sequence for Fv43D, GH43D family enzyme from *Fusarium verticillioides***

atgcagctcaagtttctgtcttcagcattggttgcctgtctttgaccggcaattgcgctgcgcaagacac
taatgatccctcctctgatcaccgacctctggtctgcggatccctcggctcatgtttcgagggca
aactctgggtttaccatctcagcagatcgaagccaatgtcgtcaacggcaccggaggcgctcagtac
gccatgagagattatcacacctattccatgaagaccatctatggaaaagatcccgttatcgaccatgg
cgtcgtctgtcagtcgatgatgtcccatgggccaagcagcaaatgtgggctcctgacgcagcttaca
agaacggcaaatattatctctacttccccgccaaggataaagatgagatcttcagaattggagttgct
gtctccaacaagcccagcggctctttcaaggccgacaagagctggatccccggtaacttacagatcga
tcctgctagctatgtcgacactaatggcgaggcacaacctcatctggggcggtatctggggcgccagc
tcaggcctggcaggatcacaagaccttaatgagtcgtggctcggcgacaaagctgctcccaacggc
accaacgcccctatctcctcagatcgccaagctaagcaaggacatgcacaagatcaccgagacccccg
cgatctcgtcatcctggccccgagacaggcaagccccctcaagcagaggacaataagcgacgatttt
tcgaggggcccctgggttcacaagcgcggcaagctgtactacctcatgtactctaccggcgacacgcac
ttcctcgtctacgcgacttccaagaacatctacggctccttatacctatcagggcaagattctcgacc
tggtgatgggtggactacgcgatggaagtattggtgagtacaagggacagtggtggttgttctttgcgg
atgcgcatacttctgaaaggattatctgagacaggtaaggcgaggaagatctggtatgacaaggat
ggcaagattttgcttactcgtcctaagatttag

FIGURE 19A**SEQ ID NO:2****Protein sequence of Fv43D**

mqlkflssallsltgncaaqdtndipplitdlwsadpsahvfegklwvypshdieanvvngtggaqy
amrdyhtysmkti ygkdpvidhgvalsvddvpwakqqmwapdaaykngkyylyfpakdkdeifrigva
vsnkpsgpfkadkswipgtysidpasyvdtngayliwgggiwggqlqawqdhktfneswlgdkaapng
tnalspqiaklskdmhkitetprdlvilapetgkplqaednkrrffegpwhkrklylylmystgdth
flvyatskniygpytyqgkildpvdgwtthgsiveykgqwwlffadahtsgkdylrqvkarkiydkd
gkilltrpki

FIGURE 19B

SEQ ID NO:3

Nucleotide sequence of Bxl1, a GH3 family β -xylosidase from *Trichoderma reesei*

atggtgaata	acgcagctct	tctcgccgcc	ctgtcggtc	tcctgccac	ggcctggcg	60
cagaacaatc	aaacatacgc	caactactct	gctcagggcc	agcctgatct	ctaccccgag	120
acacttgcca	cgctcacact	ctcgttcccc	gactgcgaac	atggccccct	caagaacaat	180
ctcgtctgtg	actcatcggc	eggctatgta	gagcgagccc	aggccctcat	ctcgtctctc	240
accctcgagg	agctcattct	caacacgcaa	aactcgggcc	ccggcgtgcc	tcgcctgggt	300
cttccgaact	accaagtctg	gaatgaggct	ctgcacggct	tggaccgcgc	caacttcgcc	360
accaagggcg	gccagttcga	atgggcgacc	tcggtcccca	tgcccatcct	caactacggcg	420
gccctcaacc	gcacattgat	ccaccagatt	gccgacatca	tctcgaccca	agctcgagca	480
ttcagcaaca	gcgccggtta	cggtctcgac	gtctatgcdc	caaacgtcaa	tggcttccga	540
agccccctct	ggggccgtgg	ccaggagacg	cccggcgaag	acgccttttt	cctcagctcc	600
gcttaccact	acaggtacat	cacgggcac	caggggtggc	tcgaccctga	gcacctcaag	660
ggtgcccga	cggtgaagca	ctttgcccga	tacgacctcg	agaactggaa	caaccagtcc	720
cgtctcggtt	tcgacgccat	cataactcag	caggacctct	ccgaatacta	caactccccag	780
ttcctcgctg	cggcccgtta	tgcaaagtca	cgcagcttga	tgtgcgcata	caactccgtc	840
aacggcgtgc	ccagctgtgc	caacagcttc	ttcctgcaga	cgcttttgcg	cgagagctgg	900
ggcttccccg	aatggggata	cgtctcgtcc	gattgcatg	ccgtctacaa	cgttttcaac	960
cctcatgact	acgccagcaa	ccagtctgca	gccgcccga	gctcaactgcy	agccggcacc	1020
gatatcgact	gcggtcagac	ttaccctggg	cacctcaacg	agtcttttgt	ggccggcgaa	1080
gtctcccgcg	gagagatcga	gcggtccgtc	acccgtctgt	acgccaacct	cgctccgtctc	1140
ggatacttcg	acaagaagaa	ccagtaccgc	tcgctcggtt	ggaaggatgt	cgtaagact	1200
gatgcctgga	acatctcgt	cgaggctgct	gttgaggcca	tcgtcctgct	caagaacgat	1260
ggcactctcc	ctctgtccaa	gaaggtgcdc	agcattgctc	tgatcggacc	atgggccaat	1320
gccacaacc	aatgcaagg	caactactat	ggcctgccc	catacctcat	cagccctctg	1380
gaagctgcta	agaaggccgg	ctatcacgtc	aactttgaac	tcggcacaga	gatcgccggc	1440
aacagcacca	ctggctttgc	caaggccatt	gctgccgcca	agaagtcgga	tgccatcatc	1500
tacctcggtg	gaattgacaa	caccattgaa	caggagggcg	ctgaccgcac	ggacattgct	1560
tggcccggta	atcagctgga	tctcatcaag	cagctcagcg	aggtcggcaa	acccttctgc	1620
gtcctgcaaa	tggcgggtgg	tcaggtagac	tcctcctcgc	tcaagagcaa	caagaaggtc	1680
aactccctcg	tctggggcgg	atatcccggc	cagtcgggag	gcgttgccct	cttcgacatt	1740
ctctctggca	agcgtgctcc	tgccggccga	ctggtcacca	ctcagtacct	ggctgagtat	1800
gttcaccaat	tccccagaa	tgacatgaac	ctccgaccgg	atggaaagtc	aaacctgga	1860
cagacttaca	tctggtacac	cggcaaacc	gtctacgagt	ttggcagtg	tctcttctac	1920
accaccttca	aggagactct	cgccagccac	ccaagagcc	tcaagttcaa	caactcatcg	1980
atcctctctg	ctcctcacc	cggatacact	tacagcgagc	agattcccgt	cttcaccttc	2040
gaggccaaca	tcaagaactc	gggcaagacg	gagtccccat	atcggccat	gctgtttggt	2100
cgcacaaagca	acgctggccc	agccccgtac	ccgaacaagt	ggctcgtcgg	attcgaccga	2160
cttgccgaca	tcaagcctgg	tcaactcttc	aagctcagca	tccccatccc	tgtcagtgct	2220
ctgcccgtg	ttgattctca	cggaaaccgg	attgtatacc	ccggcaagta	tgagctagcc	2280
ttgaacaccg	acgagtctgt	gaagcttgag	tttgagttgg	tgggagaaga	ggtaacgatt	2340
gagaactggc	cgttggagga	gcaacagatc	aaggatgcta	cacctgacgc	ataa	2394

FIGURE 20A

SEQ ID NO: 4

Protein sequence of Bxl1, a GH3 family β -xylosidase from *Trichoderma reesei*

mvnnaallaalsallptalagnnqtyanysagggpdlypetlatltlsfpdcehgplknnlvcdssag
yveraqualislftleelilntqnsppgvprlglpnyqvnealhgldranfatkggqfewatsfpmp
ltaalnrtlihqadiistqarafsnsgrylgdyapnvngfrsplwgrgqetpgedafflssayty
eyitgiqggvdpehlkvaatvkhfagydenwnnqsrllgfdaiitqqdlseyytpqflaaryaksrs
lmcaynsvngvpkansfflqtllreswgfpewgyvssdcdavynvfnphdyasnqssaasslragt
didcgqtypwhlnesfvagevsrgeiersvtrlyanlvrlgyfdkknqyrslgwkdvktdawnisye
aavegivllkndgtlplskkvrsialigpwanattmqgnyygpapylispleaakkagyhvnfelgt
eiagnsttgfakiaaakksdaiiylggidntieqegadrtiawpqnqldlikqlsevgkplvvlqm
gggqvdsslsknkvnslvwggypgqsggvalfdilsgkrapagrlvttqypaeyvhqfpqndmnlr
pdgksnpgqtyiwytgkpvye fgsglyfttfketlashpkslkfntssilsaphpgytyseqipvftf
eaniknsgktespytamlfvrtsnagpypnkwlvgfdrldikpghssklsipipvsalarvdshg
nrivypgkyelalntdesvklefelvgeevtienwpleeqqikdatpda

FIGURE 20B

SEQ ID NO:5**Nucleotide sequence for Fv3A, a GH3 family enzyme from *Fusarium verticillioides***

atgctgctcaatcttcaggtcgctgccagcgctttgtcgctttctcttttaggtggattggctgaggc
tgctacgccatataacccttccggactgtaccaaaggacctttgagcaagaatggaatctgcgatactt
cgttatctccagctaaaagagcggtgctctagttgctgctctgacgcccgaagagaaggtgggcaat
ctggtcaggtaaaatataccccccccataatcactattcggagattggagctgacttaacgcagcaa
tgcaactggtgcaccaagaatcggacttccaaggtacaactggtggaacgaagcccttcatggcctcg
ctggatctccaggtggtcgctttgccgacactcctccctacgacgcgccacatcatttccatgcct
cttctcatggccgctgctttcgacgatgatctgatccacgatatcggaacgctcgtcggcaccgaagc
gctgctgctcactaacggcggttggcggagtcgacttctggacaccaacgctcaacccttttaag
atcctcgctggggtcgctggctccgaaactccaggtgaagatgccttcatgtcagccggtatgctcgc
tataatcgtcaggggtctcgaaggcgataaggagcaacgacgtattggtgctacctgcaagcactatgc
tggaaacgactttgaggactggggaggcttcacgcgtcacgactttgatgccaagattactcctcagg
acttggctgagtactacgtcaggccttccaggagtgcaccctgatgcaaaggttggttccatcatg
tgcgctacaatgccgtgaacggcattcccgcatgcgcaaactcgtatctgcaggagacgatcctcag
agggcactggaactggacgcgcgataaacaactggatcactagtattgtggcgccatgcaggatatct
ggcagaatcacaagtatgtcaagaccaacgctgaaggtgccaggtagcttttgagaacggcatggat
tctagctgagagtataactactaccagcgatgtctccgattcgtacaagcaaggcctcttgactgagaa
gctcatggatcgttcttgaagcgccttttcgaagggtctggtcatactggtttctttgacggtgcc
aagcgcaatggaactcgctcagttttgcggtatgtcaacaccaaggaagctcaggatcttgcactcaga
tctgctgtggaggggtgctgttcttctaagaatgacggcactttgcctctgaagctcaagaagaagga
tagtggtgcaatgatcggattctggccaacgatacttccaagctgcagggtggttacagtggacgtg
ctccgttctccacagcccgtttatgcagctgagaagcttggctctgacaccaacgtggcttgggggt
ccgacactgcagaacagctcatctcatgataactggaccaccaatgctgttgcgagcgaagaagtc
tgattacattctacttttgggtggtcttgacgcctctgctgctggcgaggacagagatcgtgagaacc
ttgactggcctgagagccagctgacccttcttcagaagctctctagtctcggcaagccactggttggt
atccagcttgggtgatcaagtcgatgacaccgctcttttgaagaacaagaagattaacagtattctttg
ggccaattaccctggtcaggatggcggcactgcagctcatggacctgctcactggacgaaagagtcctg
ctggccgactaccctgcagcaatatcccagtaatacactgagcagattggcatgactgacatggac
ctcagacctaccaagtcggtgccagggagaacttatcgctggtactcaactccagttcttccctacgg
ctttggcctccactacaccaagttccaagccaagttcaagtccaacaagttgacggttgacatccaga
agcttctcaagggctgcagtgctcaatactccgatacttgcgcgctgcccccatccaagtttagtgct
aagaacaccggccgcattacctccgactttgtctctctggtctttatcaagagtgaagttggacctaa
gccttaccctctcaagacccttgcggttatggctcgcttgcatgatgtcgcgcttcatcgacgaagg
atatctcactggagtggacgttggataacattgcgcgacggggagagaatggtgatttgggttgtttat
cctgggacttacactctgttgcgtggatgagcctacgcaagccaagatccaggttacgctgactggaaa
gaaggctattttgataagtggcctcaagacccaagctctgcgtaa

FIGURE 21A

SEQ ID NO:6**Protein sequence of Fv3A**

mllnlqvaasalslsllgglaeaatpytlpdctkgpls kngicdtslspakraaalvaaltpeekvgn
lvsn**ATGAPRIGLPRYNWWNEALHGLAGSPGGRFADTPPYDAATSFPMPILLMAAAFDDDLIHDIGNVV**
GTEARAFTNGGWRGVDFWTPNVNPFKDPRWGRGSETPGEDALHVSRYARYIVRGLEGDKQRRIVATC
KHYAGNDFEDWGGFTRHDFDAKITPQDLAEYYVRPFQECTRDAKVGSIMCAYNAVNGIPACANSYLQE
TILRGHWNWTRDNNWITSDCGAMQDIWQNHKYVK**TNAEGAQVAFENGMD**ssceytttsdvsdsykqgl
lteklmdrslkrlfeglvhtgffdgakawnslsfadvntkeaqdlalrsaveg**AVLLKNDGTLPLKL**
KKKDSVAMIGFWANDTSKLQGGYSGRAPFLHSPLYAAEKLGLDTNVAWGPTLQNSSSHDNWTTNAVAA
AKKSDYILYFGGLDASAAGEDRDRENLDWPESQLTLLQKLSSLGKPLVVIQLGDQVDDTALLKNKKIN
SILWVNYPGQGGTAVMDLLTGRKSPAGRLPVTQYPSKYTEQIGMTDMDLRPTKSLPGRTYRWYSTPV
LPYGFGLHYTkfqakfksnkltfdiqkllkgcsaqysdtcalppiqvsvkntgritsdfvslvfikse
vgpkpyplktlaaygrlhdvapsstkdislewtldniarrgengdlvvyppgtytllldeptqakiqvt
ltgkkaildkwpqdpksa

FIGURE 21B

SEQ ID NO:7

Nucleotide sequence for Pf43A, a GH43 family enzyme from *Penicillium funiculosum*

atgcttcagcgaatttgcttatatatttaccactggctctattgagtggtggagtgaaagccgacaacc
 ctttgtgcagagcatctacaccgctgatccggcaccgatggatatacaatgaccgcgtttatgtcttca
 tggacatgacaacaccggagctacctactacaacatgacagactggcatctgttctcgtcagcagat
 atggcgaattggcaagatcatggcattccaatgagcctggccaatttcacctgggccaacgcgaatgc
 gtgggccccgcaagtcatccctcgcaacggccaattctacttttatgctcctgtccgacacaacgatg
 gttctatggctatcgggtgtgggagtgagcagcaccatcacagggtccataccatgatgctatcggcaaa
 ccgctagtagagaacaacgagattgatcccaccgtgttcacgacgatgacggtcaggcataacctgta
 ctgggaaatccagacctgtggtacgtcaaattgaaccaagatatgatatcgtacagcgggagcccta
 ctctactccactcaccacggctggatttggtactcgaacgggcaatgctcaacggccgaccactttt
 gaagaagctccatgggtatacaaacgcaacggcatctactatatcgctatgcagccgattggtgttc
 tgaggatattcgctactccacgggaaccagtgccactggccgtggacttatcgaggcgtcatcatgc
 cgaccaaggtagcagcttcaccaatcacgagggtattatcgacttccagaacaactcctactttttc
 taccacaacggcgctcttcccggcgaggcggctaccaacgatctgtatgtgtggagcaattcaaata
 caatgcagatggaaccattccgacgatcgaatgaccaccgcccgggtccagctcaaattgggactctca
 acccttacgtgcgacaggaagccgaaaacggcggcatggtcttcaggcatcactacggaggtttgtagc
 gaaggcgggaattgacgtcgggtttatcaacaatggcgattacatcaaagttaaggcgtagctttcgg
 ttcaggagcccattctttctcagcgcgggttgcttctgcaaatagcggcggcactattgcaatacacc
 tcggaagcacaactggtaacgtcgtgggcacttgtactgtcccagcactggcgggttggcagacttgg
 actaccgttacctgttctgtcagtggcgcactctgggaccaggatgtgtattttgttttcgggtgtag
 cggaacaggatacctgttcaactttgattattggcagttcgcataa

FIGURE 22A

SEQ ID NO:8

Protein sequence of Pf43A

mlqrfayilplallsvgvka**dnpfvqs**iytadpapmvyndrvyvfmdhdntgatyynmtdwhlfsad
 manwqdhgipmslanftwananawapqviprngqfyfyapvrhndgsmagvgsstitgpyhdaigk
 plvenneidptvfiddgqaylywgnpdlwyvklndmisysgsptqiplltagfgtrtgnarpttf
 eeapwvykrngiyyiayaadccsedirystgtsatgpwtyrgvimptqgssftnhegiidfqnnsyff
 yhngalpggggyqrsvcveqfkynadgti**ptiem**ttagpaqigtlnpyvrqEAETAAWSSGITTEVCS
 EGGIDVGF INNGDYIKVKGVAFGSGAHSFSARVASANSGGTIAIHLGSTTGLVGTCTVPSTGGWQTW
 TTVTCSVSGASGTQDVYFVFGSGGTGYLFNFDYWQFa

FIGURE 22B

SEQ ID NO:9**Nucleotide sequence for Fv43E, a GH43 family enzyme from *Fusarium verticillioides***

atgaaggataactggctcgtggcgtgggccacttctttgacgcggcactggctggcttgattggaca
ccgtcgcgccaccaccttcaacaatcctatcatctactcagactttccagataacgatgtattcctcg
gtccagataactactactacttctctgcttccaacttccacttcagcccaggagcaccggttttgaag
tctaaagatctgctaaactgggatctcatcggccattcaattccccgcctgaactttggcgacggcta
tgatcttcctcctggctcacgttattaccgtggaggacttgggcatcatccctcagatacagaaaga
gcaatggacagtggactggatcggctgcatcaacttctggcagacctgggtatacactgcctcatcg
cgggaagggtccatggtacaacaagggaaacttcgggtgataacaattgctactacgacaatggcatact
gatcgatgacgatgataccatgtatgtcgtatacgggtccgggtgagggtcaaagtatctcaactatctc
aggacggattcagccagggtcaaatctcaggtagttttcaagaacactgatattgggggtccaagacttg
gagggtaaccgcatgtacaagatcaacgggctctactatcctaaacgatagccaagtggcagtca
gacctggatttggaagtcgaaatcaccctggggcccttatgagtctaaggctctcgccgacaaagtca
ccccgcctatctctgggtggtaactcgccgcatcagggtagtctcataaagactccaatgggtggctgg
tacttcatgtcattcacttgggcctatcctgcccggccgtcttccgggtcttgaccgattacgtgggg
tagcgatgggtttcccattcttgtcaagggtgctaattggcgggatggggatcatcttaccacaacttc
ctggcacggatgggtgtgacaaagaattggacaaggactgataccttccgcggaacctcacttgctccg
tcctgggagtggaaaccataatccggacgtcaactccttcaactgtcaacaacggcctgactctccgcac
tgctagcattacgaaggatatttaccaggcggaggaacacgctatctcaccgaactcatgggtgatcatc
caacaggaatagtgaagattgatttctctccgatgaaggacggcgaccgggcccgggctttcagcgttt
cgagaccaaagtgcatacatcggattcatcgagataacggaaagttcacaatcgctacgaagcatgg
gatgaatatggatgagtggaaacggaacaacaacagacctgggacaaataaaagccacagctaattgtgc
cttctggaaggaccaagatctggctgagacttcaacttgataccaaccagcaggaactggcaact
atcttttcttacagttgggatggagtcaagtatgaaacactgggtcccaacttcaactgtacaatgg
ttgggcattctttattgcttaccgattcggcatcttcaacttcgccgagacggctttaggaggctcga
tcaaggttgagtctttcacagctgcatag

FIGURE 23A

SEQ ID NO:10**Protein sequence of Fv43E**

mkvywlvawatsltpalaglighrratt **fnnpiiysdfpdndvflgpdnyyfsasnfhfsgapvlk**
skdllnwdlighsiprlnfgdgydlppgsryyrggtwasslryrksngqwywigcinfwqtwvytass
pegpwynkgnfgdnncyydngiliddddtmyvvygsgevksqlsqdgfsqvsqvfkntdigvqdl
egnrmkinglyyilndspsgsqtwiwsksppwgyeskladkvtpisggnsphqgsliktpnggw
yfmsftwaypagrlpvlapitwgsdgfpilvkganggwgsyptlpgtdgvtknwtrtdtfrgtslap
swewnhnpdvnsftvnngltlrltasitkdiyqarntlshrthgdhptgivkidfspmkdgdraqlsaf
rdqsayigihrdngkftiatkhgmnmdewngtttdlgqikatanvpsgrtkiwlrlqldtnpagtgnt
ifsyswdgvkyetlgpnfklyngwaffiayrfgifnfaetalggsikvesftaa

FIGURE 23B

SEQ ID NO:11

Nucleotide sequence for Fv43B, a GH43 family enzyme from *Fusarium verticillioides*

atgCGcttctcttggctattgtgcccccttctagcgatgggaagtgctcttctgaaacgaagacgga
 tgtttcgacatacaccaaccctgtccttccaggatggcactcggatccatcgtgtatccagaaagatg
 gcctcttctctgCGtcacttcaacattcatctccttcccaggctctcccgtctatgcctcaaggat
 ctagtcaactggcgtctcatcagccatgtctggaaccgcgagaaacagttgcctggcattagctggaa
 gacggcaggacagcaacagggaatgtatgaccaaccattcgateaccacaagggaacatactacgtca
 tctgCGaataacctgggCGttggagatattattgggtgcatcttcaagaccaccaatccgtgggacgag
 agtagctggagtgacctgttaccttcaagccaaatcacatcgaccccgatctgttctgggatgatga
 cggaaagggttattgtgctacccatggcatcactctgcaggagattgatttggaaactggagagctta
 gccgagcttaataatctggaaccgacagggagtgtatggcctgaggggtcccatactacaagcgc
 gacggttactactatctcatgattgCCgaggggtggaactgCCgaagaccacgctatcacaatcgtcG
 ggCGcaagatcaccggccccatgaagcctacaataacaaccaatcttgaccaaccgCGgacat
 ctgagtacttccagactgtcgggtcacggtgatctgttccaagataccaagggaactgggtgggctt
 tgtcttgctactcgcacacagcagggagtttaccatgggCGgtgaagctgttttgttcaatgg
 cacatggaacaagggCGaatggccccagttgcaaccagtagcaggtcgcacgctggaaacctcctcc
 caaagcCGacgCGaaagcttcccggagatgggcccccaacgctgaccagacaactacaactgaag
 aagactaagaagatccctcctcacttctgtgacccatagagtccecaagagacggtgccttctcttctgC
 ttccaagggtctgcacatcgtgcctagtcgaaacaacggtaccggtagtggttGCCaggagatgaga
 ttgagctatcaggacagcagggcttagcttcatcggacgCGccaaactcactctgttcaaatat
 agtggtgatcgcacttcaagccaaagtcgcatgatcaggaagctggaatcacCGtttccgacgca
 gttcGaccatcgcacttggcattgttCGtcttctacaaccaaggcagcaacaagaaatctaagc
 ttgccttccgattccggGCCacaggagctcagaatgttctgcaaccgaaggtagtaccggtccccgat
 ggctgggagaagggCGtaatacagctacatcgcagggcagccaacgCGacgactacaaccttgagc
 ttCGagccacagaggcaagactctcgacatcgcgacagcatcagcaagtcttgtgagtggaggcagcG
 gttcatttgttggtagtttGcttggacctatgctacctgcaacggcaaggtctggagtggaatgt
 cccaagggaggtgatgtctatgtgaccaatggacttataagccCGtggcacaagagattgatcagG
 tgttttGtgaaatcagaattgtag

FIGURE 24A

SEQ ID NO:12

Protein sequence of Fv43B

mrfswllcpllamgsalpetktdvstytnpvlpgwhsdpsciqkdglflcvtstfisfpglpvyasrd
 lvnwrlishvwnrekqlpgiswktagqqqgmyaptiryhkgtyyviceylgvvgdiigvikttnpwde
 sswsdpvtfkpnhidpdlfwdddgvycathgitlqeidletgelspelniwngtggvwpegphiykr
 dgyyylmiaeggtaedhaitiararkitgpyeaynnnpiltnrgtseyfqtvghgdlfqdtkgnwwgl
 clatritaggvspmgreavlfngtwnkgewpklqpvrgrmpgnllpkptrnvpdgpfnadpdnynlk
 ktkkipphfvhhrvprdgafslsskglhivpsrnnvtgsvlpgdeielsgqrglafigrqrthtlfkyl
 svdidfkpsddqeagitvfrtqfdhidlgivr lptnqgsnkksklafrfratgaqnvppkvvppvd
 gwekgvislhieaanathynlgasshrgktdldiatasaslvsGGtgsfvgsllgpyatcngkgsGvec
 pkggdvyvtqwtYkpvaqeidhgvfvkseI

FIGURE 24B

SEQ ID NO:13

Nucleotide sequence for Af43A, a GH43 family enzyme from *Aspergillus fumigatus*

atggcagctccaagtttatcctaccccacaggtatccaatcgtataccaatcctctcttccctgggtg
gcactccgatcccagctgtgcctacgtagcggagcaagacaccttttctgcgtgacgtccactttca
ttgccttccccgggtcttctctttatgcaagccgagatctgcagaactggaaactggcaagcaatatt
ttcaatcggcccagccagatccctgatcttcgcgtcacggatggacagcagtcgggtatctatgcgcc
cactctgcgctatcatgagggccagttctacttgatcgtttcgtacctgggcccgcagactaagggct
tgctgtcacctcgtctgatccgtacgacgatgccgcgtggagcgatccgctcgaattcgcggta
ggcatcgaccggatattctctgggatcacgacgggacgggtctatgtcacgtccgcccagaccgat
gattaagcagtagacactcgatctgaagacggggcgattggcccgggtgactactacctcatgatcgca
ccggaggagtctggcccagggccgcacattacaagagagacggataactactacctcatgatcgca
gagggaggtagcagctcggccactcggagaccatggcgcgatctagaaccggacaggtccctggga
gccatacccgcaccaatccgctcttgtcgaacaagggcacctcggagtacttccagactgtgggcatg
cggacttgttccaggatgggaacggcaactggtgggcccgtggcgttgagcaccgatcagggcctgca
tggagaactatcccattgggtcgggagacgggtgctcgcggcccgcttgggagaagggtagtgggc
tgtcattcagcctgtgagaggccaaatgcagggccggtttccaccaccaaataagcaggttccctcgcg
gaggggaggatggatcaagcaaccgacaaagtggatttcaggcccggatcgaagataccggcgcac
ttccagtagtgggatatacccaagacagaggattttaccgtctcccctcggggccaccgaatactct
tcggctcacaccctcctttacaacctcaccggaactgcggacttcaagccggatgatggcctgtcgc
ttgttatgcgcaaacagaccgacacctgttcacgtacactgtggacgtgtctttgacccaaggtt
gccgatgaagaggcgggtgtgactgttttcttaccagcagcagcacatcgatcttggattgtcct
tctccagacaaccgaggggctgtcgttgtccttccgggttccgcgtggaaggccgcggtaactacgaag
gtcctcttccagaagccaccgtgcctgttcccaaggaatggtgtggacagaccatccggcttgagatt
caggccgtgagtgacaccgagtatgtcttgcggctgccccggctcggcacctgcacagaggcaaat
catcagccgcgcaactcgttgattgtcagtggtgatcgggacgggttactggctcgttgttggcg
tgtatgccacgtcgaacgggggtgccggatccacggccgcatatcagcagatggagatacgaagga
cggggccagatgattgattttggtcagtggtcccagactactga

FIGURE 25A

SEQ ID NO:14

Protein sequence of Af43A

maapslsyptgiqsytnplfpgwhsdpscayvaeqdtffcvststfiafpplplyasrdlqnwklasni
fnrpsqipdlrvtdgqqsgiyaptlryheggfyliivsylvpqtkgllftssdpyddaawsdplefavh
gidpdi fwdhdgtvyvtsaedqmikqytldlktgaigpvdylwngtggvwpegphiykrdgyylmia
eggtelghsetmarsrt rtgpwepyphnpllsnkgstseyfqtvghadlfqdngnwwavalstrsgpa
wknypmgretvlapaawekgewpviqqvrgmqgppppnkrvprgeggwikqpdkvdfprgskipah
fyywrypktedftvsprghpntlrlltspfnltgtadfkpddglslvmrkqtdtlftytvdvsfdpkv
adeeagvtvfltqqhidlgivllqtteglslsfrfrvegrgnyegplpeatvpvpkewcgqtirlei
qavsdt eyvfaaparhpaqrqiisranslivsgdtgrftgslvgvyatsnngagstpayisrwrvey
rgqmifgrvpsy

FIGURE 25B

SEQ ID NO:15

Nucleotide sequence of Fv51A, a GH51 family enzyme from *Fusarium verticillioides*

atggttcgcttcagttcaatcctagcggctgcggcttgcttcgtggctgttgagtcagtcacaatcaaggtcgac
 agcaagggcgaaacgctactagcggtcaccaatgatgcttccttcacgaggttggtattgacacaccactggcg
 atgattgggatgctaaacttggagctaggatatcaacaattccgggtgatgggtggcatctacgctgagctcatccgc
 aatcgtgctttccagtacagcaagaaataccctgtttctctatctggctggagaccatcaacgatgctaagctc
 tccctcaaccgtctcgacactcctctctccgacgctctccccgtttccatgaacgtgaagcctggaaagggcaag
 gccaaggagattgggttctcaacgaggggttactggggaatggatgtcaagaagcaaaagtacactggctctttc
 tgggttaagggcgcttacaagggccactttacagcttctttgcgatctaaccttaccgacgatgtctttggcagc
 gtcaaggtcaagccaagggccaacaagaagcagtggttgagcatgagtttgtgcttactcctaacaagaatgcc
 cctaacagcaacaacttttgcctacacctacgatccaaggtgagtaacaatcaaaactgggacgtgatgtat
 actgacaatttgtagggcgtgatggagctcttgacttcaacctcattagcttgttccctcccactacaagggc
 cgcaagaacgggtcttcgagttgatcttggccgaggtctcgaaggtctccaccccgtaaggtttaccgtctcagct
 gtatcgtgaacagtcgctgacttgtagaaaagagcctgctgcgcttccccgggtggtaacatgctcgagggcaaca
 ccaacaagacctggtgggactggaaggataacctcggaacctctccgcaaccgtcctggtttcgaggggtgtctgga
 actaccagcagaccatggtcttggaaatcttggagtaacctccagtgggctgaggacatgaaccttgaaatcagta
 ggttctataaaaatcagtgacgggtatgtgcatgctaacagatctcagttgtcggtgtctacgctggcctctccc
 tcgacggctccgtcaccccccaaggaccaactccagccctcatcgacgacgcgctcgacgagatcgaattcatcc
 gaggtcccgtcacttcaaagtggggaaagaagcgcgctgagctcggccaccccaagcctttcagactctcctacg
 ttgaagtcggaaacgaggaactggctcgctggttatcccactggctggaactctacaaggagtagcgttccccca
 tggttcctcgaggtatcaagaaagctcaccocgatctcaccgtcatctcctctggtgcttctattgaccccgttg
 gtaagaaggatgctggtttcgatattcctgctcctggaatcgggtgactaccaccttaccgagcctgatgttc
 ttggtgaggagttcaacctggttgataacaataagtatggtcacatcattggtgaggttgettctaccacccca
 acggtggaactggctggagtggttaaccttatgcttaccctgggtggtctctggtgtggcgaggccgtcgctc
 tctgcggttatgagcgaacgcgcgatcgtattcccggaacattctacgctcctatcctcaagaacgagaaccgtt
 ggcagtggtctatcaccatgatccaattcgccgcgactccgccatgaccacccgctccaccagctggtatgtct
 ggtcactcttcgagggccaccatgaccatactctccccaccaccgcccacttcgacccccctctactacgtcg
 ctggttaagaacgaggacaagggaaactcttatctggaaggggtgctgctataaacaccaccaaggggtgctgacgttc
 ccgtgtctctgctcctcaaggggtgtcaagcccgggtgctcaagctgagcttactctctgaccaacaaggagaagg
 atccttttgcgttcaatgatcctcacaagggcaacaatgttgttgataactaagaagactggttctcaagggcagatg
 gaaaggggtgcttcaacttcaagcttccctaacctgagcgtogctgttcttgagaccctcaagaagggaaagcctt
 actctagctag

FIGURE 26A

SEQ ID NO:16**Protein sequence of Fv51A**

mvrfssilaaaacfvavesvnikvdskggnatsghqygflhedinnsgdggiyaelirrafqyskky
pvslsgwrpindaklslnrldtplsdalpvsnmvkgpgkakeigflnegywgmdvkkqkytgsfwvk
gaykghftaslrslntddvfgsvkvkskankkqwvehefvltpnknapnsntfaitydpkgadgald
fnlislfpptykgrknglrvdlaealeglhpsllrfpggnmlegntnktwwdwdtlgplrnprgfeq
vwnyqqtghlgileylqwaedmnleiivgvyaglsldgsvtpkdqlqpliddaldeiefirgpvtskw
gkkraelghpkpfrlsyvevgnedwlagpytgwnsykeyrfpmfleaikkahpdltvissgasidpvg
kkdagfdipapggidyhpyrepdvlveefnlfdnnkyghii**gevasthpnggtgwsnglmpypwwisg**
vgeavalcgyernadripgtfyapilknenrwqwaitmiqfaadsamttrstswyvwslfaghpmtht
lpttadfdplyyvagknedkgtliwkgaaynttkgadvpvslsfkgvkpqaqaeltlltnkekdpfaf
ndphkgnnvvdtkktvlkadgkgafnfklnlsavavletlkkgkpyss

FIGURE 26B

SEQ ID NO:17**Nucleotide sequence for Xyn3, a GH10 xylanase from *Trichoderma reesei***

atgaaagcaaacgtcatcttgtgcctcctggccccctggcgccgctctccccaccgaaaccatcca
 cctcgacccccgagctcgccgctctccgcgccaacctcaccgagcgaacagccgacctctgggaccgcc
 aagcctctcaaagcatcgaccagctcatcaagagaaaaggcaagctctactttggcaccgccaccgac
 cgcgccctctccaacgggaaaagaacgcggccatcatccaggcagacctcggccaggtgacgcccga
 gaacagcatgaagtggcagtcgctcgagaacaaccaaggccagctgaactggggagacgcccgactatc
 tcgtcaactttgcccagcaaaacggcaagtcgatacgcggccacactctgatctggcactcgcagctg
 cctgctgggtgaacaatatcaacaacgcggatactctgcggcaagtcacccacccatgtctctac
 tgggttggcggtacaagggcaagattcgtgcttgggtgagttttgaacaccacatgcccttttct
 tagtccgctcctcctcctccttggaaacttctcacagttatagccgtatacaacattcgacaggaattt
 aggatgacaactactgacttgtgtgtgtgtgagggcagataggacgtggtcaatgaaatcttcaacg
 aggatggaacgctgcgctcttcagctctttccaggctcctcggcgaggagttagtctcgattgcctt
 cgtgctgctcgagatgctgaccttctgcccgtctttacatcaacgactacaatctcgaccgcgcaa
 ctatggcaaggtcaacggggtgaagacttacgtctccaagtggtatctcaaggagttcccattgacg
 gtattggtgagccacgacccctaaatgtccccattagagctctctttctagagccaaggcttgaagcc
 attcagggaactgacacgagagccttctctacaggaagccagtcacctctcagcggcgggaggctct
 ggtacgctgggtgcgctccagcagctggcaacggtaaccgtcaccgagctggccattaccgagctgga
 cattcagggggcaccgacgacggattacaccaagttgttcaagcatgcctgagcgtctccaagtgcg
 tcggcatcaccgctgtggggcatcagtgacaaggttaagttgcttcccctgtctgtgcttatcaactgta
 agcagcaacaactgatgctgtctgtctttacctaggactcgtggcgtgccagcaccacccctcttctg
 tttgacgcaacttcaaccccaagccggcatataacagcattgttggcatcttacaatag

FIGURE 27A**SEQ ID NO:18****Protein sequence for Xyn3**

mkanvilc1laplvaalptetihldpelaalranltertadlwdrqasqsidqlikrkgklyfgtatd
 rgllqreknaaiiqadlgqvtpensmkwqslennqqqlnwgdadylvnfaqngksirghtliwhsql
 pawvnninnadtlrqvirthvstvvgrykgkirawdvneifnedgtrssvfsrllgeefvsiafra
 ardadpsarlyindyndranygkvnglkyvskwisqgvpidgigsqshlsgggsgtlgalqqlat
 vpvteaiteldiqgapttdyqtqvvaclsvskcvgitvwgisdkdswrastnpllfdanfnpkpayn
 sivgilq

FIGURE 27B

SEQ ID NO:19

Nucleotide sequence xlnA, a xylanase from *Aspergillus tubingensis*

```

aagctctgca gtcccgtact gtttaccaaa atgcccaggcc actggtggat atacaacttt      60
gtaatacgtt gcccgagtca gcccctactc cctgatgggt tcccactccc tagttacttc      120
ctactgggta gtaggctcct agagtggggt aaagtttgcc aagggttag ccccgactctt      180
gtttatgctt ggctagggcag gacctgggta agttgatggc tcctgcattc ctacctgagt      240
atttccagct ataagcgaga ttggccatac tottcagcga gtccggatgg tccgcgccga      300
ggttgacctt gecttcatca cctacacaaa gaaactcctcg gccaaactccc ggtggccttc      360
gagctccaaa gtaccttcgc gacctttggc cagtgtttct cgcagcgttt actgagccta      420
aggcttgcta caataaataa agagacataa ccttgccagta catacgtctt gtatgagcga      480
ggaactgtgt tcagtagtag atcagtgggt acataatcat gaacatgact tctgagccag      540
aaaaccttct gcagggaacc ggtgaagaaa ccccacttcc ccgcctccac taactgcagc      600
ccctttatcc gectgcccgc catttagcca aatgtagtcc atttagccaa gtgcggtcca      660
tttagccaag tccagtgcct aggttgggtc ctacacagga aacggccatg aatgtagaca      720
caactataga actgtcccta gaaataggct cgaggttggt agagcgttta aggtgatgcg      780
gcaaaatgca tatgactgag ttgcttcaac gtgcagggga aagggataaa tagtcttttt      840
cgcagaatat aaatagaggt agagcgggct cgcagcaata ttgaccagga caggccttct      900
tttccagttg catacatcca ttcacagcat tcagctttct tcaatcatca tgagagtcac      960
tgcggctttt gcaggctctt tggctcagcc attcgcgcct cctgccccag aacctgatct      1020
ggtgtcgcga agtgcgggta tcaactacgt gcaaaactac aacggcaacc ttggtgattt      1080
caectacgac gagagtgcg gaacattttc catgtaactgg gaagatggag tgagctccga      1140
ctttgtcggt ggtctgggct ggaccaactgg ttcttctaag tgagtgactg tattctttaa      1200
ccaaggctca ggatctaacc tctttcagcg ctatcaccta ctctgccgaa tacagcgtct      1260
ctggctccgc ttccctacctc gctgtgtaag gctgggtcaa ctatcctcaa gctgagtaact      1320
acatcgtoga ggattacggt gattataacc cttgcagttc ggccacaagc cttggtaccg      1380
tgtactctga tggaaagcacc taccaagtct gcaccgacac tcgaacaaac gaaccgtcca      1440
tcacgggaac aagcaacttc acgcagtaact tctccgttcg agagagcacg cgcacatctg      1500
gaacgggtgac tgttgccaac catttcaact tetgggcgca ccatgggttc ggcaatagcg      1560
acttcaatta tcaggctcgt gcggtggaag catggagcgg tgctggcagc gctagtgtca      1620
caatctcttc ttgagagatt agtgccttag tagtcggaag atatcaacgc ggcagtttgc      1680
tctcaggtag tgtgatgate ggatccggtc tetgggggta cattgaggct gtataagttg      1740
ttgtggggcc gagctgtcag cggtcgggtt ttcagcttgc acagataatc aactctogtt      1800
ttctatctct tgcgtttcct cgctgcttat cctatccata gataattatt ttgccacta      1860
ccacaacttg ttcggtcgca gtatcactc cgagcaaggc attgggaaat gggggatgcg      1920
gggtgctgag tacctctaaa cctagggcat tttaaaggat atttaccctc cagatattct      1980
atagatacag acttcttagg actgcgggta atatagagag cgaaatttct acagttcgat      2040
gcagttcaat gcga
    
```

FIGURE 28A

SEQ ID NO:20

Protein sequence for xlnA

MKVTAAFAGLLVTAFAAPAFEPDLVSRSAGIN YVQNYNGNLGDF TYDESAGTFSMYWEDGVSSDFVVLG
WTTGSSNAITYSAEYSASGSASYLAVYGWVNPQAEYY IVEDYGDYNPCSSATSLGTVYSDGSTYQVCTD
TRTNEPSITGTSTFTQYF SVRESTRTS GTVTVANHFNFWAHHGFGNSDFNYQVVAVEAWSGAGSASVT IS
S

FIGURE 28B

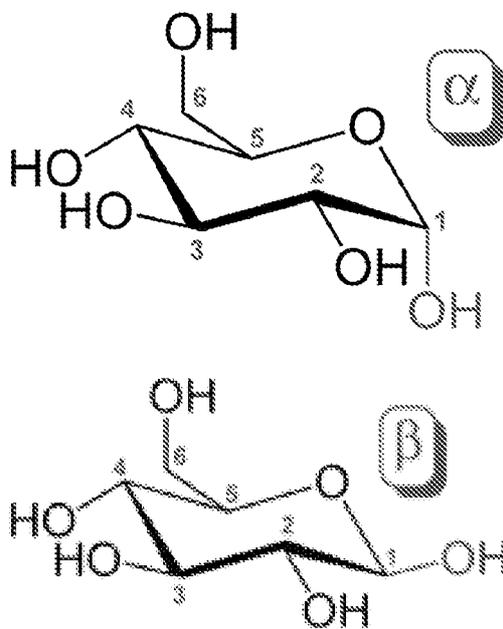


FIGURE 29

SEQ ID NO:21

Nucleotide sequence for Gz43A, a GH43 family enzyme from *Gibberella zeae*

atgaagtccaagttgttattcccactcctctcttttcggttggtcaaagtccttgccaccaacgacgactgtcctctcatcactag
tagatggactgcggtatccttcggctcatgtctttaacgacaccttggtctaccctctcatgacatcgatgctggattg
agaatgatcctgatggaggccagtaagccatgagagattaccoatgtctactctatcgacaagatctacggttccctgccggtc
gatcacggtagcggccctgtcagtgaggatgtcccctgggctctcgacagatgtgggctcctgacgctgcccacaagaacgg
caaatactacctatacttccctgcccagaagacaaggatgatattcttcagaatcggcgttgctgtctaccaacccccggcggac
cattcgtcccgacaagagttggatcctcacactttcagcatcgaccccgcagtttctcgtcgtatgatgatgacagagcctac
ttggcatggggtggtatcatgggtggccagcttcaacgatggcaggataaagaacaagtacaacgaatctggcactgagccagg
aaacggcaccgctgccttgagccctcagattgccaagctgagcaaggacatgcacactctggcagagaagcctcgcgacatgc
tcattcttgacccaagactggcaagccgctcctttctgaggatgaagaccgacgcttctcgaaggaccctggattcacaag
cgcaacaagatttactacctcacctactctactggcacaaccactatcttctctatgcgacttcaaagaccctatgggtcc
ttacacctaccagggcagaattctggagccagttgatggctggactactcactctagtatcgtcaagtaccagggtcagtggt
ggctatcttctacgtagccaagacatctggcaaggactatcttcgccaggtaaaggctaagaagatttggtagcatagcaaa
ggaaagatcttgacaaaagaagccttga

FIGURE 30A

SEQ ID NO:22

Protein sequence of Gz43A

mkskllfpllsfvqgslatnddcplitsrwtadpsahvfndtlwlypshdidagfendpdggqyamrdyh
vysidkiyglpvdhgtalsvedvpwasrqmwapdaahkngkyylyfpakdkddifrigvavsptpgg
pfvpdkswiphtfsidpasfvdddraylawggimggqlqrwqdknkynesgtepngtaalspqiak
lskdmhtlaekprdmliildpktgkpllsededrrffegpwihkrnkyylytystgtthylvyatsktp
yppytyqgrilepvdgwtthssivkyqgqwwlfyhdaktsgkdylrqvkakkiwydskgkiltkkp

FIGURE 30B

SEQ ID NO:23

Nucleotide sequence for Fo43A, a GH43 family enzyme from *Fusarium oxysporum*

atgcagctcaagtttctgtcttcagcattgctggttctctctgaccagcaaatgctgctgcaagacac
taatgacattcctcccctgatcaccgacctctggtccgcagatccctcggctcatgttttcgaaggca
agctctgggtttaccatctcacgacatcgaagccaatggtgtcaacggcacaggaggcgtcaatac
gccatgagggattaccatacctactccatgaagagcatctatggtaaagatcccggttgcgaccacgg
cgtcgtctctcagtcgatgacggtccctggggaagcagcaaatgtgggctcctgacgcagctcata
agaacggcaaatattatctgtacttccccgccaaggacaaggatgagatcttcagaattggagttgct
gtctccaacaagcccagcgggtcctttcaaggccgacaagagctggatccctggcagctacagtatcga
tcctgctagctacgtcgacactgataacgaggcctacctcatctggggcggtatctggggcggccagc
tccaagcctggcaggataaaaaagaactttaacgagtcggtggattggagacaaggctgctcctaacggc
accaatgccctatctcctcagatcgccaagctaagcaaggacatgcacaagatcaccgaaacaccccg
cgatctcgtcattctcgccccgagacaggcaagcctcttcaggctgaggacaacaagcgacgattct
tcgagggcccttggatccacaagcgcggcaagctttactacctcatgtactccaccggtgataccca
ttccttgtctacgctacttccaagaacatctacggctccttataacctaccggggcaagattcttgatcc
tgttgatgggtggactactcatggaagtattggtgagtataagggacagtggtggcttttcttgctg
atgcgcatagctctggtaaggattaccttcgacaggtgaaggcgaggaagatctgggatgacaagaac
ggcaagatcttgcttcaccgtccttag

FIGURE 31A

SEQ ID NO:24

Protein sequence of Fo43A

Mqlkflssallfsltskcaaqdtndipplitdlwsadpsahvfegklwvypshdieanvvnegtggagy
amrdyhtysmksiygkdpvvdhgvalsvddvpwakqqmwapdaahkngkylyfpakdkdeifrigva
vsnkpsgpfkadmkipgtysidpasyvdtneayliwgggiwggqlqawqdkknfneswigkaapng
tnalspqiaklskdmhkitetprdlvilapetgkplqaednkrrffegpwihkrklylmystgdth
flvyatskniygyptyrgkildpvdgwtthgsiveykgqwwlffadahtsgkdylrqvkarkiydkn
gkillhrp

FIGURE 31B

Fv43D ---MQLKFLSSALLLSLTGNCAAQDNDIPPLITDLWSADDPSAHVFEGKLVVYPSHDIEA
Fo43A ---MQLKFLSSALLLSLTGNCAAQDNDIPPLITDLWSADDPSAHVFEGKLVVYPSHDIEA
Gz43A ---MKSLLFP--LLSFVG--QSLATNDDCPLITSRWTADPSAHVFENDTLWLPSHDIDA
Pf43A --MLQRFAIILPLALLSVG--VKADN----PFVQSIYTADPAPMVYNDRVYVFMHDHNTG
Fv43A --MWLTSPLLFASLLGLTGVALADN-----PIVQDIYTADPAPMVYNGRVYLFTHGHDNDG
Fv43B --MRFSWLLCPLLAMGSALPETKTDVSTYTNVPLPGWHSDPSC-IQKDGFLCVTSTFIS
Af43A -----MAAPSLSYPTGIQSYTNPLFPGWHSDPSCAYVAEQDTFFCVTSTFI
Pf43B ----MSRSILPYASVFALLGGAIAP----FLVLNSDFDPSLIETSSGYAFGTGTNGV
Fv43E MKVYVWLVAWATSLTPALAGLIGHRRATTFNNPIIYSDFDNVFLGPDNYYSASNFHF

Fv43D NVVNGTGGAQYAMRDYHTYSMKTIYCKDPVIDHGVALSVDDVPWAKQOMWAPDAAYK--N
Fo43A NVVNGTGGAQYAMRDYHTYSMKSIYCKDPVVDHGVALSVDDVPWAKQOMWAPDAAHK--N
Gz43A GFENDPDGGQYAMRDYHVYSIDKIYGSLP--VDHGVALSVEDVPWASRQMWAPDAAHK--N
Pf43A -----ATYNNMTDWHLFSADMANWQD---HGIPMSLANFTWANANAWAPQVIPR--N
Fv43A -----STDFNMTDWRLFSADMVNWQH---HGVPMSLKTFSWANSRAWAGQVVAR--N
Fv43B FP----GLPVYASRDLVNWRLISHVWNRE---KQLPGISWKTAGQQQGMYPATIRYH--K
Af43A AFP----GLPLYASRDLQNWKLASNIFNRP---SQIPDLR-VTDGQQSGIYAPTLRYH--E
Pf43B N-----AQVASSFDFNTWTLLSGT-----DALPGFPFSPWASSPQIWAAPDLVKA-D
Fv43E SP----GAPVLKSKDLLNWDLIGHSIPRLNFGDGYDLPPGSRYYRG--GTWASSLRYSKN

Fv43D GKYYLYFFPAK-DK-DEIFRIGVAVSNKPSGPFK---ADK-SWIPGTYSIDPASYVDTNGE
Fo43A GKYYLYFFPAK-DK-DEIFRIGVAVSNKPSGPFK---ADK-SWIPGTYSIDPASYVDTDNE
Gz43A GKYYLYFFPAK-DK-DDIFRIGVAVSPTPGPFV---PDK-SWIPHTFSIDPASFVDDDDR
Pf43A GQFYFYAPVR-HN-DGSMAIGVGVSTITGYPH---DAIGKPLVENNEIDPTVFIDDDGQ
Fv43A GKFYFYVPVRNAK-TGMAIGVGVSTNIGPYT---DALGKPLVENNEIDPTVYIDTDGQ
Fv43B GTYYVICEYLVG--DIIGVIFKTTNPWDESSWS---DPV---TFKPNHIDPDFWDDDGK
Af43A GQFYLVIVSYLGP--QTKGLLFTSSDPYDDAAWS---DPL---EFVAVHIDPDFIFWDHGT
Pf43B GTYVMYFASASAASDSGKHCVGAATATSPEGPYTPVDSAVACPLDQGAIDANGFIDTDGT
Fv43E GQWYWIGCIN-----FWQTWVYTASSPEGPWY---NKGNFGDNNCYYDNGILIDDDT

Fv43D AYLWGGI-WGGQLQAWQDHKTFNESWLGDKAAPNGTNALSPQIAKLSKDMHKITETPRD
Fo43A AYLWGGI-WGGQLQAWQDKKNFNESWIGDKAAPNGTNALSPQIAKLSKDMHKITETPRD
Gz43A AYLWGGI-MGGQLQAWQDKKNYNES--GTEPG-NGTAALSPQIAKLSKDMHTLAEKPRD
Pf43A AYLWGGI-----NPDLWYVKNLQDMIYSYSGSPTQ
Fv43A AYLWGGI-----NPGLYYVKNLQDMLSYSGSINK
Fv43B VYCATHG----ITLQEI DLETGELSPELNIWNGTGGVWPEGPHIYKRDGYLLMIAEGGT
Af43A VYVTSABED-QMIKQYTLDLKGTGAIGPVDYLWNGTGGVWPEGPHIYKRDGYLLMIAEGGT
Pf43B IYVVYKID-----GNSLDGDGTHPTPIMLQQMEADGT
Fv43E MYVVYSGSEVKSQLSQDGFSSQVKSQVVFKNTDIGVQDLEGNRMKYKING-----LYYI

Fv43D LVILAPETGKPLQAEDNKRRFFEGP-----WVHKRGKLYLLMYSTG-----
Fo43A LVILAPETGKPLQAEDNKRRFFEGP-----WIHKRGKLYLLMYSTG-----
Gz43A MLILDPKTGKPLSEDEDRRFFEGP-----WIHKRNKIYYLTYSTG-----
Pf43A IPLTTAGFGTRTGNARPTTFEAP-----WVYKRNKIYYIAYAAD-----
Fv43A VSLTTAGFGSRPNNAQRPTTFEGP-----WLYKRNLIYYMIYAAN-----
Fv43B ----AEDHAI TIARARKITGPYEAYNNNPILTNRGTSEYFQTVGHGDLFQDTKGNWWGLC
Af43A ----ELGHSETMARSRTTGPWEPYPHNPLLSNKGTSYFQTVGHADLFQDGNGNWWAVA
Pf43B --TPTGSPQLIDRSDLDGPLIEAP-----SLLLSNGIYYLSFSN-----
Fv43E LNDSPSGSQTWIWKSKSPWGPYESKVLADKVTPIISGNSPHQGSLLIKTPNGGWY-----

Fv43D -DTHFLVYATSKN---IYGPYT-----YQKILDPVDG-----WTTHG
Fo43A -DTHFLVYATSKN---IYGPYT-----YRGIKILDPVDG-----WTTHG
Gz43A -TTHYLVIYATSKT---PYGPYT-----YQGRILEPVDG-----WTTHS
Pf43A CCSEDIRYSTGTS---ATGPWT-----YRGVIMPTQGS-----FTNHE
Fv43A CCSEDIRYSTGTS---ATGPWT-----YRGVVMNKAGRS-----FTNHP
Fv43B LATRITAQGVSPMGREAVLFGTWNKGEWPKLQPVVRGMPGNLLPKPTRN-----VPGD
Af43A LSTRSGPAWKNYPMGRETVLAPAAWEKGEWVPIQPVRGQMGG--PFPNKR----VPRGE
Pf43B YYNTNYDTSYAYASSITGPWT-----KQSAPYAPLLVGT-----ETSND
Fv43E FMSFTWAYPAGRLPVLAPITWG-----SDGFPILVKGGANGGSSYPTLPGT

FIGURE 32-1

Fv43D SIVEYKQWVWLFAD-AHTSGKDYLRQVKARKIWDKDG-----KILLTRPKI-----
Fo43A SIVEYKQWVWLFAD-AHTSGKDYLRQVKARKIWDKNG-----KILLHRP-----
Gz43A SIVKYQGQWVWLFYHD-AKTSKDYLRQVKAKKIWDYDSKG-----KILTCKP-----
Pf43A GIIDFQNNSYFFYHNGALPGGGGYQRSVCVEQFKYNADG-----TIPTIEMTTAG-----
Fv43A GIIDFENNSYFFYHNGALDGGSGYTRSVAVESFKYSGD-----LIPEIKMTTQ-----
Fv43B GPFNADPDNYNLKTKKIPPHFVHHRVPRDGAFLSSKG-----LHIVPSRNNVTGSLVLP
Af43A GGWIKQPDKVDLFRPGSKIPAHFQYWRYPKTEDFTVSPRGHPNTRLRLTSPFYNLTG-----
Pf43B GALSAPGGADFSVDGKMLFHANLNGQDISGGRALFAAS-----ITEASDVVTLQ-----
Fv43E DGVTKNWTRTDTFRGTSLAPSWEWNHNPVNSFTVNNGLTLRTASITKDIYQARN-----

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A -----PAQIGTLNPNYVRQEAETAAWSSGITTEVCSEGGIDVGFINNG
Fv43A -----PAQLKSLNPNYVQEAETIAWSEGIETEVCSEGGLNVAFIGDNG
Fv43B DEIELSGQRGLAFIGRRQTHLTKYSVDIDFKPKSDDQEAETVFRVTFQFDHIDLGIIVRLP
Af43A -TADFKPDDGLSLVMRQTDLFTYTVDVSPDKVADEEAGVTVFLTQQQHIDLGIIVLLQ
Pf43B -----
Fv43E -----TLSHRTHGDHPTGIVKIDFSPMKDGDRAGLSAFRDQSAYIGIHRDNCK

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A DYIK-----VKGVAFGS-GAHSFSARVASANSGGTIAIHLGSTTGLVGTCTV
Fv43A DYIK-----VKGVDGFGSTGAKTF SARVASNSSGGKIELRLGSKTGKLVGTCTV
Fv43B TNQGSNKKSKLAFRFRATGAQNVPAK---VVPVDPGWEKGVISLHIEAANATHYNLQAS
Af43A TTEG----LSSLFRFRVEGRGNYEGPLPEATVVPVKEWCGQTIRLEIQAVSDTEYVFAAA
Pf43B -----
Fv43E FTIAT---KHGMNMDWNGTTTDLGQIKATANVPSGRTKIWLRLQLDTPAGTGNTIFIS

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A PSTGGWQWTWTVTCSVSGASGTQ-----DVYFVFGSGTGYLEFN-----FDYWQFA
Fv43A TTTGNWQTYKTVDPCVSGATGTS-----DLFFVFTGSGSGSLEFN-----FNWWQFS
Fv43B --SHRGKTLDIATASASLVSGGTGSFVGSLLGPYATCNGKSGVCEPKGGDVVYVQWYTK
Af43A PARHPAQRQIISRANSLIVSGDTGRFTGSLVGVYATSNG-GAGSTP-----AYLSRWRYE
Pf43B -----
Fv43E YSWDGVKYEITLGNPKLYNG-----WAFIAYRFGIFNFAETALGGSIKVESFT

Fv43D -----
Fo43A -----
Gz43A -----
Pf43A -----
Fv43A -----
Fv43B PVAQEIDHGTVFKSEL
Af43A GRGQMIDFGRVVPSY-
Pf43B -----
Fv43E AA-----

FIGURE 32-2

SEQ ID NO: 25**Protein sequence of XynB3, a GH43 family enzyme from *Geobacillus stearothermophilus***

MSKIKNPILTGFHPDPSICRVGDDYYIAVSTFEWFPGVRIYHSDLKNWRLVARPLNRLSQLNMIGNPDS
GGVWAPHLSDGKFWLIYTDVKVVEGQWKDGHNYLVTCDTIDGAWSDPIYLNSSGFDPSLFHDEDGRKY
LVNMYWDHRVDHHPFYGIVLQEYSVEQKKLVGEPKIFKGTDLRITEGPHLYKINGYYYYLLTAEGGTRYN
HAATIARSTSLYGPYEVHPDNPLLTSPYPRNPLQKAGHASIVHTHTDEWFLVHLTGRPLPREGQPPLLEH
RGYCPLGRETAIQRLEWKDGWPYVVGNGGPSLEIDGPSVEEVSWEKDYDEKDDFDGDTLNHHFQTLRIPL
GEDIATLKARPGHLRLYGRESLTSRFTQAFVARRWQHFFVAETKVSFRPTTFQQSAGLVNYYNTQNWTT
LQITWHEEKGRILELMTCDHLVVDQPLRGREIVVPDDIEYVYLRVTVQATTYKYSYSFDGMNWIDLPVTF
ESYKLSDDYIKSRAAF TGAFVGMHCRDGSQNNYADFDFLYKEL

FIGURE 33

SEQ ID NO:26

Protein sequence of Bgl1, a GH3 family β -glucosidase from *Trichoderma reesei*

mryrtaaalalatgpfaradshstsgasaeavvppagtpwgtaydkakaalaklnlqdkvgivsgv
nggpcvgnvspaskisypslclqdgplgvrystgstaftpgvqaastwdvnlirergqfigeevkasg
ihvilgpvagplgktpqgggrnwefgvdpyltgiamgqtingiqsvgvqatakhyilneqelnretis
snpddrtlhelytwpfadavqanvasvmcsynkvnttwacedqytlqtvldqldqfpgyvmtdwnaqh
ttvqsansgldmsmpgtdfngnrlwgpaltnavnsnqvptsrvdmdvtrilaawyltgqdgagyps
fnisrnlvqgnhktnvraiardgivllkndanilplkkpasiavvgsaaaignharnspscndkgcddga
lmgwgsavnyfyvapydaintrassqgtqvtlsntdntssgasaargkdvaivfitadsgegyit
vegnagdrnldpwhngnalvqavagansnivvvhsvgaiileqilalpqvkvavwaglpseqsgna
lvdvlwgdvpsgklvytiakspndytrivsggsdsfseglfidykhfddanitpryefgyglstyk
fnysrlsvlstaksgpatgavvpqggsdlfnvatvtvdiansgqvtgaevaqllyitypssaprtppk
qlrgfaklnltpgqsgtatfnirrrdlsywdtasqkwvpsgsfgisvgassrdirltstlsva

FIGURE 34

SEQ ID NO:39

Nucleotide sequence of XlnD, a GH3 enzyme from *Aspergillus japonicus*

ATGGCTGTGGCGGCTCTTGCTCTGCTGGCTCTACTGCC TCAAGCTCTGGGGCAACATAACAGCAGCTACG
 TGGATTACAACGTCGAAGCCAATCCGGACTTGTTCACAAATGTCTAGACACAATCTCCCTGTCCTTCCC
 CGACTGCCAGAGCGGTCCCTCTGAGCAAGAACCCTGCTCTGCGACTCGACTGCCCTGCCCTATGACCGCGCC
 GCGGCTCTGGTCTCCCTCTTACCCTCGAGGAAC TTATCGCCAACACTGGTAACACCAGCCCGGTGTCC
 CTCGTCTGGGTCTGCCCTCATAACCAGGTCTGGAGTGAGGCCCTGCATGGCCTGGCTCGCGCCAACCTTAC
 CGACAACGGGGCTTACAGCTGGGCGACGTCTTCCCTCACCCATTCTCTCCGCAGCGGCCCTTCAATCGC
 ACCCTGATCAACCAGATCGCCTCCATTATTTGACTCAGGGCCGTGCCTTCAACAACGCCGGCCGCTTTG
 GCCTCGACGTCTACTCGCCAAACATCAATACCTTCCGCCATCCAGTCTGGGGTCTGGGACAGGAACTCC
 TGGCGAGGATGCGTACACTCTTACGGCCGCTACGCCTACGAATACATCACGGGTATCCAGGGTGGTGTG
 AACCCAGAGCATCTGAAGCTCGCCGCGACAGCCAAGCACTTTGCCGGCTACGACATCGAGAATGGGACA
 ACCACTCCCGGCTGGGGAACGATGTCAACATTACGCAGCAAGACCTGGCCGAGTACTACAGCCCGCAGTT
 CCTCGTCGCCGCGCGACGCCACGTCCACAGCTTCATGTGCTCCTACAACGCGTTAACGGAGTGCC
 AGCTGCTCCAACACCTTCTTTCTGCAGACCCTCTGCGCGACACCTTCTCCTTCGTGCGACCAGGCTACG
 TCTCCGGCGACTGCGGCGCGTCTACGGCGTCTTCAACCCCCACGGCTACGCGGCAACGAGCCCAGCGC
 CGCCGCGGATGCCATCTCGCCGGCACTGACATTGACTGCGGCACCTCCTATCAATATCACTTCAACGAG
 TCCATCACCACCGGGCTGTGCGCCGCGACGACATCGAGCGTGGTTTCATCCGGCTGTACGCCAACCTCG
 TCGAGCTGGGCTACTTCGACGGCAACAGCAGCAGCAACCCGTACCGCAGCCTGGGCTGGCCCGACGT
 CCAGAAGACAGACGCATGGAACATTTCTTACGAGGCGGCGAGTCAAGGCATCGTCTCTGAAGAACGAC
 GGCACCCCTCCCTCTTGCTCCCTTCCGAGGGCAAGAACAATCCATCGCCCTCATCGGCCCTGGGCCA
 ACGCCACCACCCAGCTCCAGGGTAACTACTACGGCGACGCGCCATACCTCATCAGCCCGGTCGACGCCTT
 CACGGCCGCGGGTACACAGTACACTACGCCCGGCGACGGAGATCTCGACGAACTCGACGGCGAACTTC
 AGCGCCGCGCTCTCCGCGGCGCGCGCCGACACCATCGTATTCTTGGGGGGCATCGATAACACCATCG
 AAGCCGAAGCCCAAGACCGCAGCTCGATCGCTGGCCCGGCAACCAACTCGAGCTGATCTCGCAACTCGC
 GCGCAGAAATCCGACGACCAGCCCTTGGTGGTGTACCAGATGGGCGGCGGCCAGGTCGACTCCTCCGCC
 CTCAAATCCAACGCGAAGGTCAACGCCCTCCTCTGGGGCGGCTACCCGGGCCAATCCGGCGGCCTCGCC
 TGCGCGACATCTCACGGGCGCGCGCCCCCGCGGCCCTCACCACGACCCAGTACCCGGCCGCTTA
 CGCCGAGAGCTTCTCGGCCCTCGACATGAACCTGCGGCCGAATGAGACTACACAGAACCCGGGCCAGACC
 TACATGTGGTACACCGCGAGCCCTTACGCCCTCGGCCACGGCCTGTTCTACACCACCTTCAACGCTT
 CCTCAGCCCAAGCAGCGAAGACGAAGTATACCTTCAACATCACCGACCTCACCTCCGCGCACACCCAGA
 CACCACGACCGTCGGCCAACGCACCCTTCTCAACTTACAGCCTCCATCACGAACTCCGGACAGAGGGAT
 TCCGATTACACCGCCCTGGTGTACGCCAACACCTCGACTGCGGGCCCCCTCCCGTACCCGAATAAATGGC
 TCGTCGGGTTGACCGGCTCGCCGCGGTGGCGAAGGAGGGCGGCACGGCCGAGTTGAATGTGCCGGTGGC
 GGTGGATCGGTTGGCGAGGGTGGATGAAGCGGGTAAACCCGTGCTGTTTCCGGGGCGGTATGAGGTGGCC
 CTGAATAATGAGCGGAGGTGCTGGTTCGAGGTGGAGTTGGTGGGTGAGCAGGTTGTGCTGTTGAAGTGGC
 CGGAGGAGGTGCAGGGGGTGGCGGGGATGAGTAG

FIGURE 35A

SEQ ID NO:40**Protein sequence of XlnD**

mavaalalla llpgalgqhn ssyvdyneva npdlfpqcld tislspdcq sgplsknlvc
dstaspydra aalvslftle eliantgnts pgvprlglpp yqvwsealhg laranftdng
ayswatsfps pilsaaafnr tlinqiasii stqgrafnna grfgldvysp nintfrhpvw
grgqetpged aytltayay eyitgiqggv npehlklaat akhfagydie nwdnhsrlgn
dvnitqqdla eyytpqflva ardahvhsfm csynavngvp scsntfflqt llrdtfsfvd
hgyvsgdcga vygvfnphgy aanepsaaad ailagtdidc gtsyqyhfe sittgavard
diergfirly anlvelgyfd gnssssnpyr slgwpdvqkt dawnisyaa vegivllknd
gtlplaspse gknksialig pwanattqlq gnnygdapyl ispvdaftaa gytvhyapgt
eistnstanf saalsaaraa dtivflggid ntieaeaqr ssiawpqnql elisqlaaqk
sddqplvvyq mgggqvdsaa lksnakvna lwggyppqsg glalrdiltg arapagrltt
tqypaayaes fsaladmnlrp nettqnpqgt ymwytgepvy afghglfytt fnassaqaak
tkytnitdl tsaahpdttt vgqrtlfnft asitnsgqrd sdytalvyan tstagpspyp
nkwlvqfdrl aavakeggta elnvpvavdr larvdeagnt vlfpgryeva lnnerevvve
velvgeqvvl lkwpveevqgv agde

FIGURE 35B

SEQ ID NO:41**Nucleotide sequence of Fv30A, a GH30 enzyme from *Fusarium verticillioides***

atgctcttctcgctcgttcttccctacccttgcccttcaagccagcctggcgctcggcgatacatccgt
tactgtcgacaccagccagaaactccaggtcatcgatggctttgggtgtctcagaagcctacggccaag
ccaaacaattccaaaacctcggctcctggaccacagaaagagggcctcgatcttctcttcaactaca
accggcgcaggcttatccatcatccgaaacaagatcggctgcgacgcctccaactccatcaccagcac
caacaccgacaaccagataagcaggctgtttaccatthttgacggcgatgatgatgggtcaggatgggt
ttagcaaacaggccatgagctatgggtgtagatactatctacgctaatactggtctgcgcctgtatac
atgaagtcagcccagagtatgggcccgtctctgcggtacacctgggtgtgtcgtgctcctctggagattg
gagacatcgttacgttgagatgatagctgagtacctctcctactacaagcaggctggcatcccagtg
cgcacgttgattcctcaatgaggggtgacggctcggactttatgctctcaactgccgaacaggctgca
gatgtcattcctcttctacacagcgtttgagtcgaagggccttggcgatatcaagatgacgtgctg
tgataacatcggttggaagtcacagatggactataccgccaaagctggctgagcttgaggtggagaag
atctatctgtcatcacatcccacgagtactccagcagcccccaaccagcctatgaactactacattgcc
acctggatgtccgagggagctgccaatgaccaggcattttgccacagcgtggtacgtcaacggcggttc
caacgaaggtttcacatgggcagtcaagatcgcaaacggcatcgtcaatgccgacctctcagcgtata
tctactgggagggcggttgagaccaacaacaaggggtctctatctcacgtcatcgacacggacggtaac
aagtttaccatatacctcgattctctgggccattgctcactggtcgcgccatattcgcctgggtgcgca
tagactttcgacttcagggtggtgtgcaagatacgattggtgggtgcgtttgagaacggtgatggcagtg
tcgtcatgggtgctcaccactctggcactgctgctcagactgtggacctgggtgtttcggaagtagc
ttctcaacagctcaggctttcacttcggatgctgaggcgcagatggctcgataccaaggtgactctgtc
cgacggctcgtgtcaaggttacggctcccgggtgcacgggtgctcgtcactgtgaagctcacaacagcaaaa
gctccaaaccgggtctcaactgctgtttctgcgcaatctgccccactccaactagtgttaagcacacc
ttgactcaccagaagacttcttcaacaacactctcgaccgccaaggcccaacctccactcagactac
ctctgtagttgagtcagccaaggcgggtgaaataccctgtccccctgtagcatccaagggatcctcga
agagtgctcccaagaaggggtaccaagaagaccactacgaagaagggctcccaccaatcgcaaacggcg
catagtgctactcatcgtcgatgccgccatggaagttaccgtcgtggccactgcaccaactaa

FIGURE 36A

SEQ ID NO:42**Protein sequence of Fv30A**

mlfslvlptlafgaslalgdtsvtvdtsqklqvidgfgvseayghakqfqnlgppgqkeglldllfntt
tgaglsiirnkiqcdasnsitstntdnpdkqavyhfdgdddgggsaqsmgrlcgtpgvscssgdwrhry
vemiaeylsyykqagipvshvgflnegdgsdfmlstaeqaadvipllhsalqskglgdikmtccdng
wksqmdytaklaelevekylsvitsheyssspnqpmnttlptwmsegaandqafatawyvnggsnegf
twavkiaqgivnadlsaiyywegvetnknkslshvidtdgkftissilwaihwsrhirpgahrilst
sgvvqdtivgafenvdgsvmmvltnsqtaaqtdlvgvsgssfstafaftsdaeaqmvdkvtlsdgrv
kvtvpvhgvvtvklttaksskpvstavsqaqsaptptsvkhtlthqktssttlstakaptstqttsvve
sakavkypvppvaskgssksapkkgtkktttkgshqshkhsathrrcrhgryrrghctn

FIGURE 36B

SEQ ID NO:43

Nucleotide sequence of Fv30B, a GH30 enzyme from *Fusarium verticillioides*

atgaatcctttatctctcggccttgccgccttgagccttctgggctacgtgggtgtcaactttgttgc
 agccttccccacggattcaaaactcaggctccgaagtcttgatttctgtcaatggccacgttaaacc
 aagagcttgacggatttgggtgcttcacaagcattccaacggggccgaagacattcttgaaaagacggg
 ctgtccaaagaagggactcagcatgtactggacttgctgttcagcaaggatatcgggtgccccgttctc
 tatcctgcgtaatggcattggctcaagcaacagttctgacaagaacttcatgaattcaatcgagccat
 tctcgccaggctcaccggagcaaaagccacactacgtctgggatggctatgatagcggacaactcacc
 gtcgctcaagaagcattcaagagaggattgaagttcctctatggcgatgcttgggtccgctcctgggta
 catgaagacaaccacgatgagaataacggggggtatttgtgtgggtgttacaggtgctcctgcgctt
 ctggcgactgaagcaggcttacgcagactactgctgcagtggggtgagttctaccgcaagtgcaggc
 gtcaaggtcaccaacctaggattccttaacgagcctcagttcgccgctccctacgcccgcagtgctgc
 taacggcacacaggctgcccacttcatacgtgactgggcaagacaatcagaaaacgaggtatccacg
 accttacaatcgccctgctgtgatggcgagggtgggatctccaagaagatatgatggctgggttgact
 gctggacctgatccggcaatcaactacctcagtgctgactgggcaacggctacgtttcaccaccgaa
 ccatccgctttcaacaacaaagaagacgtggctcaccgagtgggctgatctcacaggccagttcacgc
 cctacacgttctacaacaatagcggtcagggggaaggtatgacctgggctggccgatccagacggcg
 cttgtagatgccaatgtcagcggcttctctattggatcggagccgagaaactcgaccaccaacagtg
 tctgatcaacatgatcggcgacaaggtcatccctccaagaggttctgggcctttgcatccttcagtc
 gggttgctagacctgggtgctcgtcgcatgaagccacgagctccgcttctctgggtcacagtcagttca
 tttctgaataccgacggtaactgtcgcgacgcaggtgctgaacaacgacacgggtgctcacagtggtga
 actcgttgtctctggcacaggtcgaaatcctcatagcttgaagccggtttttgaccgataattctaag
 atttgactgccttgaagcatttgaaggctactggaaaggggtcatttcagactacgattcctcctcga
 tctcttgtagctttgttacagatttctaacaagacaatattacttgaagaagacgactatgagggc
 tgctttgatcaagttgactatgtctagatggttgggtgtaaattctcctaacaatcttggtgggctgctt
 atttcggcttagttacgcaacgtcatgttcagtggtgccgaaagccgaaccacgaaaatagctcacaag
 accattctggattttgacacgataagatcctgcctttttttcatacttggtcctctctttcacttgg
 cgaaatatgctggttttacgtatccatgctctccc

FIGURE 37A

SEQ ID NO:44

Protein sequence of Fv30B

mnplslglaalsllgyvgvnfvaafptdsngsevllsvnghvkhqeldgfgasqafqraedilgkdg
 lskegtqhvdllfksdigagfsilrngigssnsdknfmnsiepfspgspgakphyvwdgydsgqlt
 vaeafkrglkflygdawsapgyktnhdennggylcgvgtgaacasgdwkqayadyllqwvefyrksg
 vkvtnlgflnepqfaapyagmlsngtqaadfirvlgktirkrgihdltiaccdgegwdlqedmmaglt
 agpdpainylsvvtghgyvsppnhplsttkktwltewadltgqftpytfynnsgqgegmtwagriqta
 lvdanvsgflywigaensttnsalinmigdkvipskrfwafasfsrfarpgarrieatssvplvtvss
 flntdgtvatqvlndtvahsvqlvvsgrnphslkpfldnsndltalkhkatgkgsfqtppr
 slvsfvtdf*

FIGURE 37B

SEQ ID NO:45

Nucleotide sequence of Fv39A, a GH39 enzyme from *Fusarium verticillioides*

atgcactacgctaccctcaccactttggtgctggctctgaccaccaacgtcgctgcacagcaaggcac
 agcaactgtcgcacctctccaaaaatcatggaccggcgaaggcccttggttcaggcttcatatacggct
 ggctgacaacggaacaagcgtcgacacctccataccagatttcttggtaactgacatcaaattcaac
 tcaaaccgcgcggtggcgcccaaatcccatcactgggttgggcccagaggtggctatgaaggatacct
 cggccgcttcaactcaaccttaccactatcgaccacgcgcaagataaacgctgactttatcttgt
 tgctcatgacctctggggtgcggtggcgggcagggttcaaactcccgttctctggcgacaatggc
 aattggactgagatggagttattctggaatcagcttgtgtctgacttgaaggctcataatatgctgga
 aggtcttgtgattgatgttgggaatgagcctgatattgatattctttgggatcgcccggtggtcgagt
 ttcttgagtattacaatcgcgcgaccactacttccggtgagctactactgatccatacgtatttac
 agtgagctgactggcgaattagaaaaacacttcccaaaactcttctcagtgcccagccatggcaca
 ttctcccattctgtccgatgataaatggcatacctggcttcaatcagtagcggtaacaagacagtcc
 ctgatatttactcctggcatcagattggcgcttgggaacgtgagccggacagcactatccccgacttt
 accaccttgcggcgcaatatggcgcttcccgagaagccaattgacgtcaatgagtagcctgcacgcga
 tgagcaaaatccagccaactccgtctactacctctctcaactagagcgtcataaccttagaggcttcc
 gcgcaaaactgggtagcggatctgacctccacaactggatgggcaacttgatttacagcactaccggt
 acctcggaggggacttactacctaatggtgaatggcaggcttacaagtagctatgcggccatggcagg
 gcagagacttgtgaccaaagcatcgtcggacttgaagtttgatgtctttgccactaagcaaggcgtga
 agattaagattatagccggcagcagaccggttcaagcaaagtataacatcaaaatcagcgggttggaa
 gtagcaggacttcttaagatgggtacggtaaggtccggacttctcgggtcactggggtgggcccga
 tggaaaggttgacgggctgttgatttgggggagaagaagtatacttattcggccaatacgggtgagca
 gccctctacttga

FIGURE 38A

SEQ ID NO:46

Protein sequence of Fv39A

mhyatllttlvlallttnvaaqqgtatvdlsknhgpakalgsgfiygwpdngtsvdtsipdflvtdikfn
 snrgggaqipslgwarggyegylgrfnstlsnyrtrkynadfillphdlwgadggggsnspfpgdng
 nwtemlfwnqlvsdlkahnmleglvidvwnepdidifwdrpwsqfleynratkllrktlpktllsg
pamahspilsddkwtlqsvagnktpdiyswhqigawerepdstipdftlraqygvpekpidvne
yaardeqnpansvyylsqlerhnlrglranwgssdlhnwmgnliysttgtsegtyypngewqaykyy
 aamagqrlvtkassdlkfdvfatkqrkikiiagtrtvqakynikisglevaglpkmgtvkvrtyrfd
 wagpngkvdgpvdlgekytysantvsspst

FIGURE 38B

SEQ ID NO:47**Nucleotide sequence of Fv39B, a GH39 enzyme from *Fusarium verticillioides***

atgtggttaatcaaggcctgttccgtcctcgccgctctctccactgtagctgctgacagccccgggtcc
 caccatcgacttctcctccaacactggagagcctcagcatctcgctgctggtatcctgtacggatatac
 ccgacgatgggaaccagatcccagatgatcttctctctggctttggcttcaactactatcgcggtgca
 ggtgccaagtctctcatggatggagttatgacgaggctggcttccagcagcgttttgaaagcgcgca
 taacaactacatcgtcacgcgctcgtcacaacggcggctttgtcttgctgctgaatgacctctggggct
 ttgattgttcttctaacaacgatacctcactggccagcagataatggcgattggctcctatgac
 aagttcgttcaggcgattattgccaatgtcaagaagtaacaatgcaggaaggcttggctcattgatata
 ctggaacgagccagagggggctgttctggggcccgtagcattgaccaatggcttcagatgtggggctc
 gcgctggcatcaattcaagtaagtactagataacctctgaggacggatggacaagaactgactgtct
 attcagtgatgccttcggggacagcgtgtgacatccggaccaactcttgcaggcagccgggaacaa
 acgatgactggtggacccaatgggcccattcgtcaagaacaacgactccatccccgaccaatacgc
 tggcacgaggaaggaggctcaggttccaacttcgagaacagctacggcgtcctgcaacaaattctcac
 taaatcggctcttccccaacgccaatcaacatcaacgaatacgtacgttcaatgaacaagtccccg
 ccggttctgccttctggatctcccagttcgagcgcgtaatactatcggtcttcgcggaattggcta
 ggaggcactcaacttcacgatctggccgctagtcttctgtccaagcctgacctcggactacgcttc
 cacgggatactttgccaatggagactggtgggtgtataactactactctcacaacatgacgggacagc
 gcgttctgacttcgggtgtcttccgatggaaggctggatgcttatgcaacgggtggatactacggcgcg
 acggctagagtattgcttggctgccatccgctacgactggtaacttatgatgtgacattctctggct
 gacaaagtgggtctgccatcttctggaacacttcaggttaggacttggaaagttgctgtgggcagtg
 atgtgcattacagccaggtgggttctcctcaggatctgggtaactatggtcacactattagcaacgg
 caggttaccttgccgttctatcagactgatgatgtgactacatacgcgatgggagttcaaattctag

FIGURE 39A**SEQ ID NO:48****Protein sequence of Fv39B**

mwlikacsvlaalstvaadspgptidfsntgepqhlaagilygipddgnqipdllsgfgfnyyrga
 gaqvshgwsydeagfqqr fesahnniyvtrrhnggfvlldlwgfdcssnndtspggdngdwssyd
 kfvqaiianvkynmqeglvidiwnepggcfwgrsidqwlqmwgrgwhqfndafgdsvltsgptlag
 epgtnddwwtqwaqfvknndsipdqyawheeggsgsnfensygvllqqiltkyglpqrqinineyatfn
 eqvpagsafwisqferrnaiglrgnwlgtqlhdlaasllskpdpdyastgyfangdwwvynyshn
 mtgqrvstsvssdgrldayatvdtartarvllgchpvtgtydvtfsgltklglpssgtlqvrtwkf
 avgsdvhysqvgspqdlgnyghtisngqvtlpyqtddvttiyawefkf*

FIGURE 39B

SEQ ID NO:49

Nucleotide sequence of XynB, a GH39 enzyme from *Thermoanaerobacter saccharolyticum*

```

atggtaaaaa taaagatacc aaaaaattct gatggcaaaa aattcaccag tagatggaga
tattgtgtag gtacaggaag gttgggactt gcgctgcaaa aagagtacat ggatacttta
aaatthgtga aagaaaatat agacttcaag tatataagag gacatggcct tttgtgcgac
gatgtaggta tttaccgtga ggacgtagta ggcaacgatg taaggccatt ttacaatttc
acgtatatag atagaatctt tgattcattt ttggaattag ggataaggcc atttgttgaa
gtcggattta tgcctaaaag attagcatct ggtacacaga cagtatttta ttgggagggga
aatgtcacc ctcctaaaaga ttatgaaaaa tggagcaacc ttataaaagc tgttgtttca
cattttatat caaggtatgg catagatgaa gtcgtaaaaa ggccatttga aatatggaat
gagccaaacc taaaagagtt ttggaaagat gctgatgaga aagaatactt caagctgtac
aaggttactg caaaggcgat taaagaagta aatgagaatt tgcaggtagg aggacctgct
atatgtgggtg gtgctgacta ctggatagaa gattttttga atttctgcta tgaagaaaat
gttcctggtg attttgtatc gcgacacgca tatacgtcta agcaagggtga atatacgcca
catctcatat accaggagat tatgccatct gaatacatgc taaacgaatt caaaacagtg
agagagatca taaaaaactc acatthtccg aaccttccgt ttcataaac ggagtacaat
acatcttaca gtccattaaa tcctgtacat gatacgcctt ttaatgcggc gtatcttgcg
aggatthttaa gtgaaggcgg agattatggt gattcatttt cctattggac gtttagcgat
gtgthtgaag aaagagatgt gccaaagatcg cagthtcatg gaggatttgg actagttgca
ttgaataaga taccaaaagcc gactthtccac atgthttaat thtcaatgc tatgggagaa
gagggtgcttt acagagataa ccatatgctt ataactagaa gggatgatgg gtcgattgca
ttgattgctt ggaatgagat aatggagaaa acagaaaatc cagataagga atatgaactg
gaaatacctg taggattcaa agatgtcttt ataaagaaac agatgataga tgaggatcac
ggcaatcctt ggggtacgtg gatacacatg ggaaggccga gattcccaag taaagaacaa
attaagactt taagggatat tgcaaagcct aaaatcaaaa caggtagagc cacatcaaat
gatggctatg taaatthgaa atthtagatt gggaaaaatg ctgtggtatt gthtgaattg
actgaagtaa tggatgaaac aaacacttat ataggacttg atgatagcaa gataaacgga
tattga
    
```

FIGURE 40A

SEQ ID NO:50

Protein sequence of XynB

```

MIKVRVPDFS DKKFSDRWRY CVGTGRLGLA LQKEYIETLK YVKENIDFKY IRGHLLCDD
VGIYREDVVG DEVKPFYNFT YIDRIFDSFL EIGIRPFVEI GFMPKKLASG TQTVFYWEGN
VTPPKDYEKW SDLVKAVLHH FISRYGIEEV LKWPFEIWNE PNLKEFWKDA DEKEYFKLYK
VTAKAIKEVN ENLKVGGPAI CGGADYWIED FLNFCYEENV PVDFVSRHAT TSKQGEYTPH
LIYQEIMPSE YMLNEFKTVR EIIKNSHFPN LPFHTEYNT SYSPQNPVHD TPFNAAYIAR
ILSEGSDYVD SFSYWTFSDV FEERDVPRSQ FHGGFGLVAL NMIPKPTFYT FKFFNAMGEE
MLYRDEHMLV TRRDDGSVAL IAWNEVMDKT ENPDEDYEVE IPVRFRDVFI KRQLIDEEHG
NPWGTWIHMG RPRYPSKEQV NTLREVAKPE IMTSQPVAND GYLNLFKFLG KNAVVLYELT
ERIDESSTYI GLDDSKINGY
    
```

FIGURE 40B

SEQ ID NO:51

Nucleotide sequence of XylA, A GH52 enzyme from *Geobacillus stearothermophilus*

```

atgccaacca atgtatTTTT caacgccccat cactcgccgg ttggggcgct tggcagcttt
acgctagggt ttccgggaaa aagcggagga ctggacttgg aactcgcccg accgccacgg
caaaatgtct ttattggcgt tgagtcgccg catgagccgg ggctgtatca tatectcca
ttcgcggaaa cagcaggcga ggatgaaagc aaacgatatg acattgaaaa tcctgatccg
aatccgcaaa aaccaaaacat tctcatcccc tttgcgaaag aggagatcaa gcgcgaattc
tgtgtggcaa cggatacatg gaaagctggg gatttaacgt ttacgattta ttccgccgta
aaggcgggtc ctgatcccga aacagcggcc gaggaagaac tcaagttggc gttggtccca
gctgtcattg tcgagatgac gatcgataac acgaacggaa caagaacacg acggggcgttt
ttcggattcg aaggcaccga cccgtatacc tcgatgcggc ggatcgatga tacatgcccg
cagctgcgcg ggtcgggtca agggcggatt ttgggcattg tatccaagga tgaggggtgtt
cgctcagcgc tgcattttag catggaggat atcttaacgg cgactctcga agaaaactcg
acgtttgggc ttgggaaagt cgggtgcgta atcgttgatg tgccggcggg agaaaagaaa
acgtatcaat ttgctgtttg tttttaccgc ggtggttatg ttaccgcagg aatggatgcc
tcttattttt acaccggtt cttccataat atcgaagaag tcggtcttta tgcgttagag
caggccgagg tgttaaagga gcaggcgttc cgttcgaatg aactcattga aaaagaatgg
ctctccgatg atcaaaagt tatgatggcg cacgcgatcc gcagctacta tggcaataca
caactgcttg agcatgaagg aaagccgatt tgggtcgtta atgaaggcga gtaccggatg
atgaatacgt ttgatctcac cgtcgaccag ctcttttttg agttgaaaat gaatccgtgg
acggtgaaaa atgtgcttga cttctatgtc gagcgctaca gctatgagga tcgtgtccgt
ttcccaggag atgagacgga atatcccggc ggcatacagc tcaactcatga tatgggagtc
gctaacacgt tctcgcgtcc gcattactcg tcatatgagc tatacggaat cagcggctgc
ttttcgcata tgacgcacga acagctcgtc aactgggtgc tttgcgcggc ggtatacatc
gaacaaacga aagactgggc atggcgcgac cggcggctta cgatcttga acaatgtctc
gaaagcatgg tcgctcgtga tcatccggat ccagaaaagc ggaacggcgt gatggggctt
gacagcaccg gcaccatggg tggagcggaa atcacaacgt atgatagttt ggatgtttcc
ctcggccagg cgcgcaacaa tttatatttg gcaggaaaat gttgggctgc ctatgtggcg
ctcgaaaagt tgttccgcga tgtcggcaaa gaagaactgg ctgcattggc aagggagcag
gcggaaaaat gcgccgcgac gattgtcagt cacgtgacgg aggacgggta tatcccagcc
gtgatgggag aaggaaatga ctcgaaaatc atcccgcta ttgaggggct tgtgtttcct
tactttacga actgccatga ggcgttaaga gaagacggac gttttggaga ctatattcgt
gcaactgcgac aacatttgca atatgtgttg cgggaaggaa tttgcctatt cccggaacggg
ggatggaaaa tttcctcgac aagcaacaac tcgtggttga gcaaaattha cttatgccag
tttattgccc gccgattttt aggggtgggaa tgggatgaac aaggaaaacg agctgatgcg
getcatgttg cgtggctcac gcacccgacg ctctccattt ggagttggag cgaccaaatt
atcgctggcg aaatcagcgg cagcaaatat taccgcgcgg gcgtgacgag ctttttatgg
ttggaggagg gggaaatga

```

FIGURE 41A

SEQ ID NO:52**Protein sequence of XylA**

mptnlffnah hspvgafasf tlgfpgksgg ldlelarppr qnvligvesl hesglyhvlp
fletaeedes krydienpdp npqkpnlip fakeeiqref hvatdtwkag dltftiyspv
kavpnpetad eeelklalvp aviventidn tngtrarra fgefegtdpyt smriddtcp
qlrgvgggri lsivskdegv rsalhfsmed iltaqleenw tfglgkvgal ivdvpagekk
tyqfavcfyr ggyvtagmda syfytrffqn ieevglyale qaevlkeqsf rsnklikew
lsddqtfmma hairsyygnt qllehegkpi wvnegeyrm mntfdltdq lffelklnpw
tvknlldlyv erysyedrvr fpgeeteyps gisfthdmgv antfsrphys syelygisgc
fshmtheqlv nwlcaavyi eqtkdwawrd krlaileqcl esmvrrdhp peqrngvmgl
dstrtmggae ittydsldvs lgqarnnlyl agkcwaayva leklfrdvdk eelaalageq
aekcaativs hvtdagyipa imgegndski ipaieglvfp yftncheald engrfgayiq
alrnhlqyvl regiclfpdg gwkisstsnn swlskiylcq fiarhilgwe wdeggkrada
ahvawlhpt lsiwswsdqi iageitgsky yprgvtsilw leege

FIGURE 41B

SEQ ID NO:53

Nucleotide sequence of Xyl1, a GH54 enzyme from *Trichoderma koningii* (*Hypocrea koningii*)

ATGCTCTCCAACGCTCGTATCATCGCAGCGGGCTGTATTGCTGCAGGCTCTCTCGTTGCT
 GCTGGGCCTTGTGACATCTACTCCTCGGGCGGAACGCCTTGGGTTGCCGCCACAGCACC
 ACTCGAGCTCTGTTCAGCGCTTATACCGGCCCGTTATACCAGGTAAGCGCGGCTCCGAT
 GGTGCCACAACCGCCATATCGCCCCCTCAAGTGGTGTGGCCAACGCTGCCGCTCAAGAT
 GCTTTCTGTGCGGGAACACTACATGCCCTCATTACCATCATATACGACCAGTCGGGTCGCGGC
 AACCATCTCAGGGAGGCCCGCCGGCGGCTTCAGCGGCCGGAATCCAACGGCTATGAC
 AACCTGGCTAGTGCAATTGGGGCGCCGGTAACACTCAACGGCCAGAAGGCGTATGGAGTT
 TTCGTGTCTCCAGGAACGGGGTATCGGAATAACGCTGCCAGCGGCACAGCCAAAGGAGAT
 GCCCGGAGGGCATGTATGCGGTTCTCGATGGTACACACTACAACGGCGCCTGCTGCTTT
 GACTATGGCAACGCCGAGACCAACAGCCCGGATACAGGCAACGGTCATATGGAGGCCATC
 TATTTTGGCGACAGCACGTCTGGGGTACTGGCTCAGGCAAGGGTCCGTGGATCATGGCT
 GATCTCGAGAACGGCTTGTCTCAGGCTCCAGTCCCGGCAACAATGCCGGTATCCGCTCC
 ATCTCGTACCGGTTTCGTCACTGCAGCGATCAAGGGGCAGCCAAACCAATGGGCAATCCGT
 GGCGGCAATGCTGCGTCTGGCTCGCTGTCAACTTCTACAGCGCGGCTCGCCACAAGTC
 TCCGGATAACAATCCGATGAGCAAAGAGGGCGCCATCATTCTCGGCATTGGCGGCGACAAC
 AGCAACGGCGGCCAGGGCACATTCTATGAGGGCGTCATGACCTCTGGATATCCTTCCGAT
 GCAACAGAGAATTCAGTGCAAGCCAACATCGTAGCTGCCA

FIGURE 42A

SEQ ID NO:54

Protein sequence of Xyl1

MLSNARIIAA GCIAAGSLVA AGPCDIYSSG GTPCVAAHST TRALFSAYTG PLYQVCRGSD
 GATTAISPLS SGVANAAAQD AFCAGTTCLI TIIYDQSGRG NHLREAPPGG FSGPESNGYD
 NLASAIGAPV TLNGQKAYGV FVSPGTGYRN NAASGTAKGD AAEGMYAVLD GTHYNGACCF
 DYGNAETNSR DTGNHMEAI YFGDSTVWGT GSGKGPWIMA DLENGLFSGS SPGNAGDPS
 ISYRFVTAAI KGQPNQWAIK GGNAASGSLT TFYSGARPQV SGYNPMSKEG AIILGIGGDN
 SNGGQGTIFYE GVMTSGYPSD ATENSVQANI VAARYAVAPL TSGPALTVGS SISLRATTAC
 CTRYIAHSG STVNTQVVSS SSATALKQQA SWTVRAGLAN NACFSFESQD TSGSYIRHSN
 FGLVLNANDG SKLFAEDATF CTQAGINGQG SSIRSWSYPT RYFRHYNNTL YIASNGGVHV
 FDATAAFNDD VSFVVS GGFA

FIGURE 42B

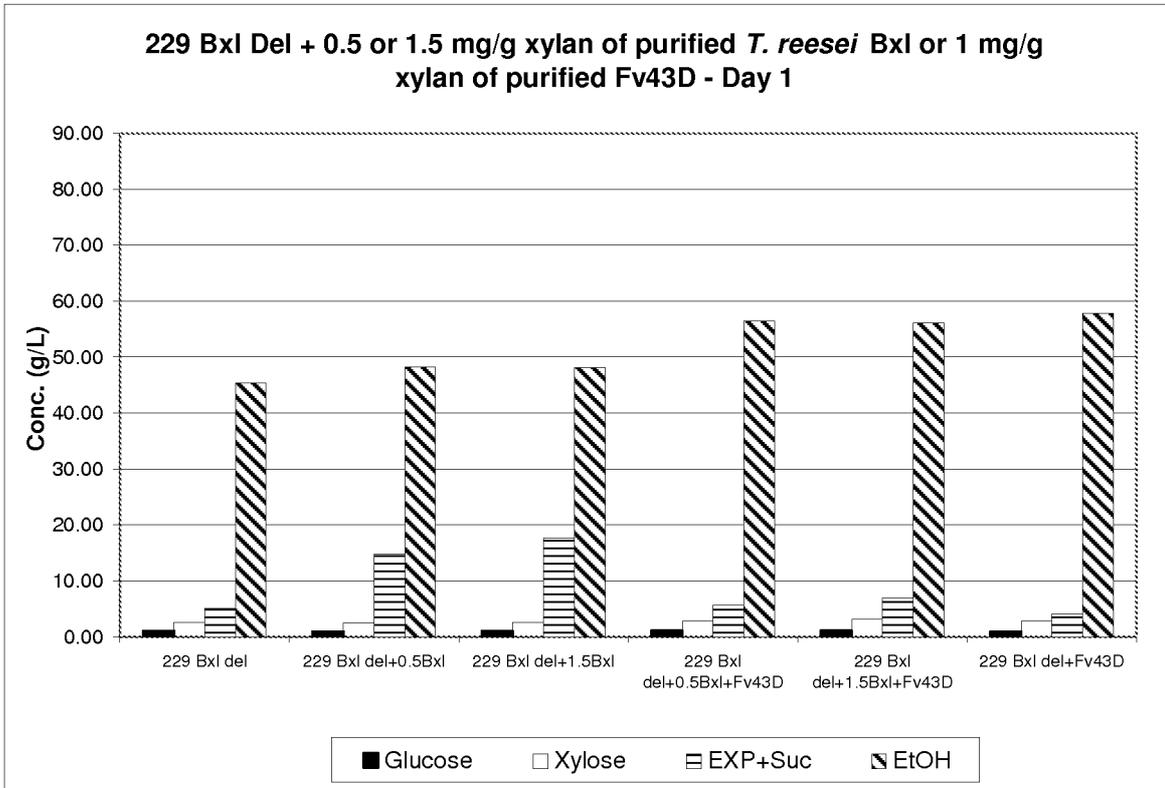


FIGURE 43A

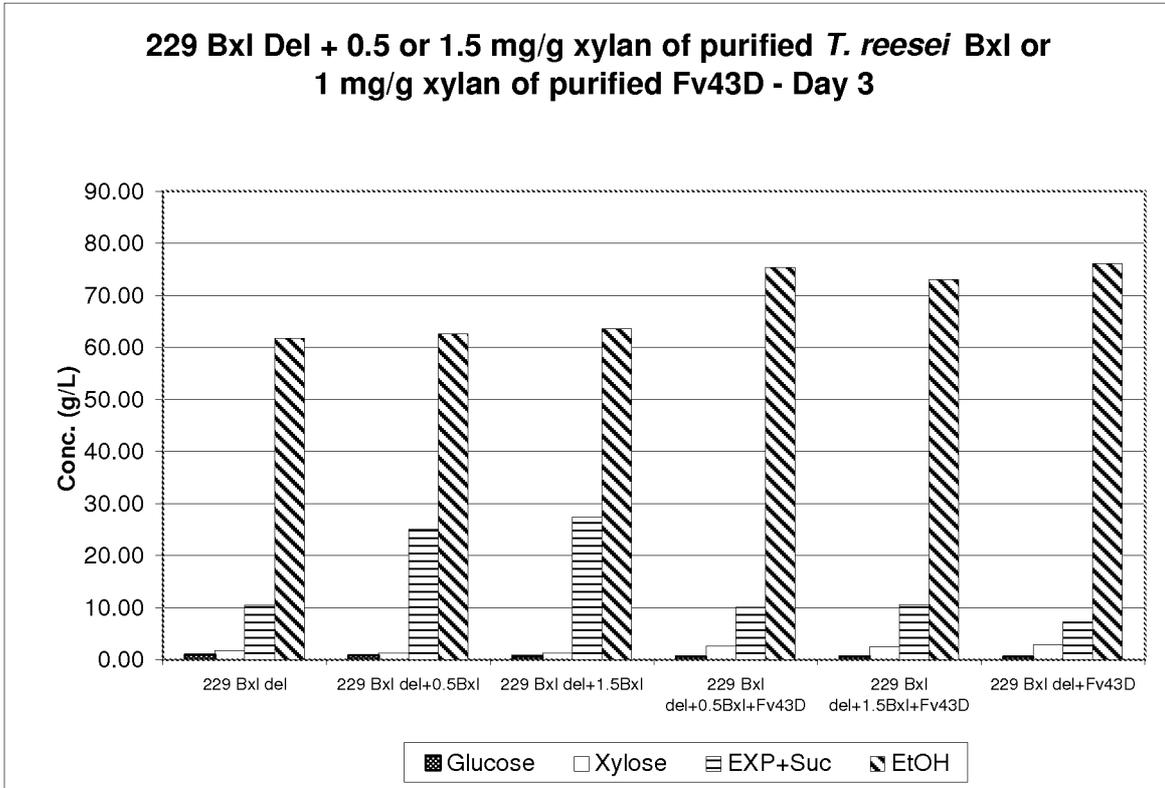


FIGURE 43B