

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
5 November 2009 (05.11.2009)

(10) International Publication Number
WO 2009/133464 A2

(51) International Patent Classification:
C12N 15/53 (2006.01) *C12P 19/04* (2006.01)
C12N 9/04 (2006.01)

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(21) International Application Number:
PCT/IB2009/005738

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(22) International Filing Date:
30 April 2009 (30.04.2009)

(81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
0807882.6 30 April 2008 (30.04.2008) GB
0807881.8 30 April 2008 (30.04.2008) GB
0811662.6 25 June 2008 (25.06.2008) GB
0817077.1 17 September 2008 (17.09.2008) GB
61/099,667 24 September 2008 (24.09.2008) US
61/099,698 24 September 2008 (24.09.2008) US
61/099,715 24 September 2008 (24.09.2008) US

(84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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Published:

- without international search report and to be republished upon receipt of that report (Rule 48.2(g))
- with sequence listing part of description (Rule 5.2(a))

(54) Title: OXIDATION PROCESS

(57) Abstract: A method of oxidising a saccharide, by contacting the saccharide with an alcohol dehydrogenase (ADH) enzyme selected from a quinone redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide (NAD⁺) redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide phosphate (NADP⁺) redox cofactor-dependent ADH, and any combination thereof is described. An oxidised saccharide obtainable by the method and products, in particular food products and paper products, containing the oxidised saccharide, are also described.



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OXIDATION PROCESSRelated applications

5 The present application relates to the subject-matter disclosed in UK patent application number 0807882.6 filed 30 April 2008 (attorney docket reference P033144GB (AFC)), UK patent application number 0811662.6 filed 25 June 2008 (attorney docket reference P033144GBR) and US patent application number USSN 61/099667 filed 24 September 2008 (attorney docket reference P033144USO), the
10 contents of each of which are incorporated herein by reference.

The present application also relates to the subject-matter disclosed in UK patent application number 0807881.8 filed 30 April 2008 (attorney docket reference P033172GB (SC)) and US patent application number USSN 61/099698 filed 24
15 September 2008 (attorney docket reference P033172USO), the contents of each of which are incorporated herein by reference.

The present application also relates to the subject-matter disclosed in UK patent application number 0817077.1 filed 17 September 2008 (attorney docket reference P033900GB (SPC)) and US patent application number USSN 61/099715 filed 24
20 September 2008 (attorney docket reference P033900USO), the contents of each of which are incorporated herein by reference.

Field of the Invention

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This invention relates to an oxidation process.

In particular, the present invention relates to a method for modifying polysaccharides.

30 More particularly, the present invention relates to a method of oxidising polysaccharides, as well as oxidised polysaccharides obtainable by the method and their use in a number of applications, particularly food products and paper products.

Description of the Prior Art

5 A number of hydrocolloids, pectin, alginate, carrageenans, potato starch and carboxymethyl cellulose are negatively charged due to galacturonate (Pectin), α -D-mannuronate and α -L-guluronate (Alginate), sulphate groups (carrageenans), phosphate groups (potato starch) and carboxymethyl groups (carboxymethyl-cellulose). These substitutions have a profound influence on the functionality of the hydrocolloids in complex food matrices. Whereas pectin, alginate, potato starch and
10 carrageenan are naturally occurring and are synthesized by plants and algae, carboxymethylcellulose is produced from cellulose by chemical treatment. Due to regulatory restriction and costs for approvals, only a few chemically modified hydrocolloids have been approved for use in foods.

15 A large number of food and feed products contain starch and therefore may be suitable for further processes like enzymatic modification. In particular, in the bakery process, control of starch retrogradation and recrystallization is of importance in slowing staling of bread.

20 Polysaccharide derivatives containing aldehyde groups and their use as paper additives are known in the art. For example, US 4675394 describes polysaccharide aldehydes, such as starch, gum and cellulose aldehydes and their preparation by a non-oxidative method which involves reacting the polysaccharide base, in the presence of alkali, with a derivatising acetal reagent and then hydrolyzing the
25 resulting acetal.

Oxidized saccharides, in particular oxidized polysaccharides, are useful as coupling agents in various technical fields, in particular in the pharmaceutical industry, where such compounds act to enhance the solubility and delivery of various
30 pharmaceuticals. For example, US2006198819 describes a method for producing a conjugate of a glycoprotein having at least one terminal galactose or derivative thereof, and a protractor group covalently bonded thereto, the method including a step of contacting the galactose-containing glycoprotein with galactose oxidase to oxidise the galactosyl group. The conjugates are stated to have increased *in vivo*
35 plasma half-life compared to non-conjugated glycoprotein.

US 4663448 describes aldehyde-containing heteropolysaccharides, in particular starch ether derivatives, and their preparation using the enzyme galactose oxidase, in which the C-6 position of the glycoside unit is oxidised to the aldehyde functionality.

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US 6265570 describes stable, solid water soluble starch aldehyde compositions and methods for their preparation by preparing a converted starch acetal and hydrolysis of the acetal under acid conditions to form the starch aldehyde.

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Chemical oxidation of polysaccharides such as starch to prepare aldehyde derivatives thereof is known in the art. For example, US 7247722 describes preparation of polysaccharide aldehydes using selective oxidation using nitroxyl radical mediator, such as 2,2,6,6-tetramethyl-1-piperidinyloxy (TEMPO) radical.

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WO 99/23240 describes a method for producing oxidised starch by using a reagent, such as TEMPO, which produces an oxoammonium ion, in conjunction with an oxidising enzyme, in particular an oxidase (such as laccase) or a peroxidase. However, in the process described in this document, it is the TEMPO which is the oxidising agent: the enzyme is used to regenerate the TEMPO to enable it to be used in catalytic quantities. Chemical oxidations of this type, however, often require harsh reagents and the regiospecificity of such chemical oxidations including the TEMPO method, is limited.

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There is therefore a need for an oxidation method for sugars which oxidises alcohol functionalities in sugar molecules more selectively, in particular at the C-6 or C-5 positions of hexose and pentose rings respectively. Furthermore, there is a need for methods for performing such oxidation reactions using milder reagents.

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Summary of the Invention

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In a first aspect, the invention comprises a method of oxidising a saccharide, by contacting the saccharide with an alcohol dehydrogenase (ADH) enzyme selected from a quinone redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide (NAD⁺) redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide phosphate (NADP⁺) redox cofactor-dependent ADH, and any combination thereof.

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In a second aspect, the invention comprises an oxidised saccharide obtained or obtainable by the above method.

5 In a third aspect, the invention comprises a product containing an oxidised saccharide obtained or obtainable by the above method.

Additional Aspects of the Present Invention

10 The present invention also encompasses methods comprising the use of – as well as the uses of – ADH active polypeptides that are co- or post-translationally processed during expression, for example by signal peptide cleavage. Post-translational cleavage may also occur at the C-terminal. Preferred co- or post-translational processing occurs at the N-terminal end to yield N-terminal truncated sequences.

15 Therefore in some embodiments of the present invention the effective fragment thereof (also referred to as functional fragment thereof) is the mature polypeptide produced by the native host or a suitable appropriate expression host.

20 The present invention also encompasses the co- or post-translationally processed ADH active polypeptides.

The present invention also encompasses nucleotide sequences that encode such co- or post-translationally processed active polypeptides.

25 In addition, the present invention encompasses an amino acid sequence that is expressed from or is expressible from all or part of said nucleotide sequences.

An example of a co- or post-translationally processed active polypeptide is presented as SEQ ID No. 1a.

30

Without wishing to be bound by theory, SEQ ID No. 2 may be optionally cleaved to SEQ ID No. 2a.

35 Without wishing to be bound by theory, SEQ ID No. 5 may be optionally cleaved to SEQ ID No. 5a.

Thus, the present invention also encompasses:

5 An amino acid sequence comprising SEQ ID No. 1A or an amino acid sequence having at least 75% amino acid sequence identity therewith but not SEQ ID No. 1.

10 An amino acid sequence comprising SEQ ID No. 1A or an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

15 An amino acid sequence comprising SEQ ID No. 2A or an amino acid sequence having at least 75% amino acid sequence identity therewith but not SEQ ID No. 2.

20 An amino acid sequence comprising SEQ ID No. 2A or an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

25 An amino acid sequence comprising SEQ ID No. 5A or an amino acid sequence having at least 75% amino acid sequence identity therewith but not SEQ ID No. 5.

30 An amino acid sequence comprising SEQ ID No. 5A or an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

35 A nucleotide sequence encoding any of said amino acid sequences.

A vector comprising said nucleotide sequence.

A host transformed with said nucleotide sequence or said vector.

The host may be a bacterial host, a fungal host, a yeast host or a plant host.

A method comprising expressing said nucleotide sequence or said vector.

Some Preferred Aspects of the Present Invention

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Preferred aspects of the present invention are apparent in the description and in the examples and in the claims.

Some preferred aspects include:

10

A method or a saccharide or a product or a use or an amino acid sequence or a nucleotide sequence according to the present invention wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme class EC 1.1.5.

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A method or a saccharide or a product or a use or an amino acid sequence or a nucleotide sequence according to the present invention wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme class EC 1.1.5.2.

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A method or a saccharide or a product or a use or an amino acid sequence or a nucleotide sequence according to the present invention wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme class EC 1.1.1.

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A method or a saccharide or a product or a use or an amino acid sequence or a nucleotide sequence according to the present invention wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme classes EC 1.1.1.1 and EC 1.1.1.2.

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A method or a saccharide or a product or a use or an amino acid sequence or a nucleotide sequence according to the present invention wherein the NAD⁺ or NADP⁺ cofactor is present in a concentration of 0.01-5000 ppm by weight.

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A method or a saccharide or a product or a use or an amino acid sequence or a nucleotide sequence according to the present invention wherein the NAD⁺ or NADP⁺ is present in a concentration of 0.10-1000 ppm by weight.

Brief Description of the Drawings

Fig. 1 illustrates an SDS-PAGE of extracellular broth from fermentation of a *Pichia*
5 *pastoris* recombinant strain harbouring the PQQ-ADH gene.

Fig. 2 illustrates the structure and fragment of glucose 1-ethyl oxime.

Fig. 3 illustrates the structure and fragment of glucose 1,6-bis(ethyl oxime).

10 Fig. 4 is a plasmid map of pENTRY-ADH containing the PQQ dependent ADH gene, Gateway compatible attLsites and the Zeocin selection marker.

Fig. 5 is a plasmid map of the *P. pastoris* destination vector pPIC2-DEST, which was
15 derived from pPIC3.5K (Invitrogen).

Fig. 6 is a plasmid map of the *P.pastoris* PQQ-ADH expression plasmid pPIC2-ADH.

Fig. 7 is a map of the plasmid pET3d-asd expressing the *E. coli* aldose sugar
20 dehydrogenase ylil.

Detailed Description of Preferred Embodiments

The present invention comprises in one aspect a method of oxidising a
25 polysaccharide by contacting the polysaccharide with an alcohol dehydrogenase (ADH) enzyme selected from a quinone redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide (NAD⁺) redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide phosphate (NADP⁺) redox cofactor-dependent ADH, and any combination thereof.

Saccharides

In this specification the term 'saccharide' is intended to cover all saccharides (sugars), including naturally occurring and synthetic and semi-synthetic saccharides.

35 The term encompasses monosaccharides (i.e. saccharides that cannot be hydrolyzed into simpler sugars), disaccharides (i.e. compounds having two

monosaccharide units (moieties) joined together by a glycoside bond), oligosaccharides (i.e. compounds having 3 to 10 monosaccharide units joined together by glycoside bonds in a branched or unbranched chain or a ring (optionally having a saccharide side chain). and polysaccharides. i.e. compounds having over 10 monosaccharide units joined together by a glycoside bond in a branched or unbranched chain or a ring (optionally having a saccharide side chain).

The saccharide may be bonded to other molecules, such as biomolecules, for example peptides, polypeptides/proteins (inc. enzymes), lipids and nucleic acids. However, it is preferred for the purposes of the present invention that the saccharide is formed from monosaccharide units only.

In one embodiment, the saccharide is a monosaccharide, i.e. a saccharide that cannot be hydrolyzed into a simpler sugar. The monosaccharide may have the D- or L-configuration, and may be an aldose or ketose.

In one embodiment, the monosaccharide is a hexose, examples of which include aldohexoses such as glucose, galactose, allose, altrose, mannose, gulose, idose and talose and ketohexoses such as fructose, tagatose, psicose and sorbose. Preferably, the hexose is glucose or galactose.

In another embodiment, the monosaccharide is a pentose, examples of which include aldopentoses such as ribose, arabinose, xylose and lyxose and ketopentoses such as ribulose and xylulose. Preferably, the pentose is arabinose or xylose.

In an alternative embodiment, the saccharide is a higher saccharide, i.e. a saccharide comprising more than one monosaccharide moiety joined together by glycoside bonds and which are generally hydrolysable into their constituent monosaccharides. Examples of such higher saccharides include disaccharides (2 monosaccharide moieties), oligosaccharides (3 to 10 monosaccharide moieties) and polysaccharides (more than 10 monosaccharide moieties). In this regard, the monosaccharide moieties which form the higher saccharide may be the same or different, and may each independently have the D- or L-configuration, and may each independently be aldose or ketose moieties.

The monosaccharide units which form the higher saccharide may have the same or different numbers of carbon atoms. In one embodiment, the monosaccharide moieties of the higher saccharide are hexose moieties, examples of which include aldohexoses such as glucose, galactose, allose, altrose, mannose, gulose, idose and talose and ketohexoses such as fructose, tagatose, psicose and sorbose. Preferably, the hexose moieties of such a higher saccharide are glucose moieties.

In another embodiment, the monosaccharide moieties of the higher saccharide are aldopentose moieties such as ribose, arabinose, xylose and lyxose and ketopentoses such as ribulose and xylulose. Preferably, the pentose moieties of such a higher saccharide are arabinose or xylose moieties.

The monosaccharide moieties which form the higher saccharide are joined together by glycoside bonds. When the monosaccharide moieties are hexose moieties, the glycoside bonds may be 1,4'- glycoside bonds (which may be 1,4'- α - or 1,4'- β - glycoside bonds), 1,6'-glycoside bonds (which may be 1,6'- α - or 1,6'- β -glycoside bonds), 1,2'- glycoside bonds (which may be 1,2'- α - or 1,2'- β -glycoside bonds), or 1,3'- glycoside bonds (which may be 1,3'- α - or 1,3'- β -glycoside bonds), or any combination thereof.

In one embodiment, the higher saccharide comprises 2 monosaccharide units (i.e. is a disaccharide). Examples of suitable disaccharides include lactose, maltose, cellobiose, sucrose, trehalose, isomaltulose and trehalulose.

In another embodiment, the higher saccharide comprises 3 to 10 monosaccharide units (i.e. is an oligosaccharide). The monosaccharide units may be in a chain, which may be branched or unbranched: such oligosaccharides are referred to in this specification as 'chain oligosaccharides'. Examples of such oligosaccharides include maltotriose, maltotetraose, maltopentaose, maltohexaose, maltoheptaose, cellobiose, cellotriose, cellotetraose, cellopentaose, cellohexaose and celloheptaose, as well as fructo-oligosaccharides (FOS) which consist of short chains of fructose molecules; mannanoligosaccharides, isomaltooligosaccharides, galactooligosaccharides and xylooligosaccharides.

Alternatively, the monosaccharide units which form the oligosaccharide may form a ring, which may optionally have a saccharide side chain: such oligosaccharides are referred to in this specification as 'cyclic oligosaccharides'. Typically, the ring consists of 5 to 8 monosaccharide units, preferably 6 to 8, and more preferably 6 monosaccharide units: the side chain, where present, typically consists of 1 to 4 monosaccharide units, preferably 1 or 2.

In particular, the cyclic oligosaccharide may be a cyclodextrin. Cyclodextrins (sometimes called cycloamyloses) make up a family of cyclic oligosaccharides, composed of 5 or more α -D-glucopyranoside units linked 1->4, as in amylose (a fragment of starch). The 5-membered macrocycle is not natural. Typical cyclodextrins contain a number of glucose monomers ranging from six to eight units in a ring, creating a cone shape. Particularly preferred cyclodextrins are α -cyclodextrin (6-membered sugar ring molecule), β -cyclodextrin: (7-membered sugar ring molecule) and γ -cyclodextrin (8-membered sugar ring molecule).

In another embodiment, the higher saccharide is a polysaccharide, comprising at least 10 monosaccharide units joined together by glycoside bonds. Typically such polysaccharides, comprise at least about 40, for example at least about 100, such as at least about 200, including at least about 500, for example at least about 1000, such as at least about 5000, for example about 10000, such as at least about 50000, for example about 100000, monosaccharide units.

The monosaccharide units in such a polysaccharide may be joined in a chain, which may be branched or unbranched: such polysaccharides are referred to in this specification as 'chain polysaccharides'. Alternatively, the monosaccharide units may be joined in a ring (which may have for example about 10 to about 200, preferably about 10 to about 100, more preferably about 10 to about 50, and most preferably about 10 to about 20, monosaccharide units), which may have one or more (preferably 1 or 2) side chains each comprising 1 to 6 (preferably 1 to 4, more preferably 1 or 2) monosaccharide units: such polysaccharides are referred to in this specification as 'cyclic polysaccharides'.

In some embodiments, the polysaccharide comprises from 10 to 500000 monosaccharide units. In other embodiments, the polysaccharide comprises from about 100 to about 1000 monosaccharide units. In other embodiments, the polysaccharide comprises from about 1000 to about 10000 monosaccharide units. In other embodiments, the polysaccharide comprises from about 10000 to about 100000 monosaccharide units. In some embodiments, the polysaccharide comprises from 40 to 3000, preferably about 200 to about 2500, monosaccharide units.

Examples of such polysaccharides include starch and derivatives thereof (such as cationic or anionic, oxidised or phosphated starch), amylose, amylopectin, glycogen, cellulose or a derivative thereof (such as carboxymethyl cellulose), alginic acid or a salt or derivative thereof, polydextrose, pectin, pullulan, carrageenan, locust bean gum and guar and derivatives thereof (such as cationic or anionic guar).

In one embodiment, the polysaccharide comprises starch or a derivative thereof. Starches are glucose polymers in which glucopyranose units are bonded by α -linkages. It is made up of a mixture of amylose and amylopectin. Amylose consists of a linear chain of several hundred glucose molecules linked together by 1,4'- α -glycoside linkages. In contrast amylopectin is a branched molecule made of several thousand glucose units, the main chain comprising 1,4'- α -glycoside linkages but having 1,6'- α -glycoside branches approximately every 25 glucose units.

Derivatives of starch are also oxidisable according to the present invention, provided that the derivative contains sufficient free primary hydroxyl groups for the enzyme to act upon (i.e. the starch has a degree of substitution of less than 1). Examples of suitable starches include substituted starches (eg carboxymethyl starch) and cationic, anionic, oxidised and phosphated starches.

In one embodiment, the polysaccharide comprises glycogen. Glycogen is a polysaccharide that is found in animals and is composed of a branched chain of glucose residues.

In one embodiment, the polysaccharide comprises cellulose or a derivative thereof. Cellulose is a polymer formed from several thousand glucose units bonded together by 1,4'- β -glycoside linkages. Derivatives of cellulose are known in the art, and

include hydroxyalkylcelluloses such as hydroxymethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose and hydroxypropylmethylcellulose and carboxyalkylcelluloses such as carboxymethylcellulose and carboxyethylcellulose. Derivatives of cellulose are also oxidisable according to the present invention, provided that the derivative contains sufficient free primary hydroxyl groups for the enzyme to act upon (i.e. the cellulose has a degree of substitution of less than 1).

Oxidation

The method of the invention comprises oxidising a saccharide, as defined and exemplified above, with an alcohol dehydrogenase (ADH) enzyme, as defined and exemplified herein.

The method of the invention results in oxidation of a proportion of the primary alcohol groups of the monosaccharide, or of the monosaccharide moieties of the higher saccharide, to aldehyde groups. The extent of oxidation, and the consequent degree of substitution (D.S.) of the resulting polymer (where the substrate is a higher saccharide), depends on factors such as the substrate, type and concentration of ADH enzyme employed, the type and concentration of cofactor (where used), and the reaction conditions such as temperature and pressure.

Typically, the method of the invention results in oxidation of at least 2%, such as at least 3%, for example at least 4%, such as at least 5%, for example at least 6%, of the primary alcohol groups of the monosaccharide, or of the monosaccharide moieties of the higher saccharide, to aldehyde groups. In particular, where the substrate is a higher saccharide (in particular, a polysaccharide) composed of glucose moieties, at least 2%, such as at least 3%, for example at least 4%, such as at least 5%, for example at least 6%, of the primary alcohol groups at the C-6 position of the glucose units of the higher saccharide, may be oxidised to aldehyde groups.

Therefore, the invention preferably comprises a method of oxidising a higher saccharide (in particular, a polysaccharide) formed from glucose moieties, wherein at least 2%, such as at least 3%, for example at least 4%, such as at least 5%, for example at least 6%, of the primary alcohol groups at the C-6 position of the glucose units of the polysaccharide, are oxidised to aldehyde groups, by contacting the

polysaccharide with an alcohol dehydrogenase (ADH) enzyme, as defined and exemplified herein.

The oxidation method of the present invention may result in some of the primary alcohol groups of the monosaccharide, or of the monosaccharide moieties of the higher saccharide, being oxidised to a carboxylic acid. The extent of oxidation of $-\text{CH}_2\text{OH}$ to $-\text{CO}_2\text{H}$ groups, and the consequent degree of substitution (D.S.) of the resulting polymer (where the substrate is a higher saccharide), depends on factors such as the substrate, the type and concentration of ADH enzyme employed, the type and concentration of cofactor (where used), and the reaction conditions such as temperature and pressure. Typically, the method of the invention results in oxidation of at least 0.05%, such as 0.05-0.5%, of the primary alcohol groups of the monosaccharide, or of the monosaccharide moieties of the higher saccharide, to carboxylic acid groups.

Alcohol Dehydrogenase

The method of the present invention employs, as an active ingredient, an alcohol dehydrogenase (ADH) enzyme. Alcohol dehydrogenase (ADH) is an oxidoreductase enzyme first discovered in the mid-1960s in *Drosophila melanogaster*. Alcohol dehydrogenases are a group of seven dehydrogenase enzymes that occur in many organisms and facilitate the interconversion between alcohols and aldehydes or ketones. In humans and many other animals, they serve to break down alcohols which could otherwise be toxic; in yeast and many bacteria, some alcohol dehydrogenases catalyze the opposite reaction as part of fermentation.

In this specification the term 'alcohol dehydrogenase', when used in isolation, covers all enzymes capable of acting on a $>\text{CH-OH}$ group to oxidise it to a $>\text{C=O}$ group (or the reverse reaction), in the presence or absence of a cofactor. Such enzymes are also known as 'aldehyde reductase' when the reverse reaction (i.e. reduction of a $>\text{C=O}$ group to a $>\text{CH-OH}$ group) occurs.

The activity of some ADH enzymes is dependent on the presence of a redox cofactor. Such ADH enzymes are referred to in this specification as 'redox cofactor-dependent alcohol dehydrogenases' and are used in this invention.

In particular, the ADH used in the present invention is selected from a quinone redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide (NAD^+) redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide phosphate (NADP^+) redox cofactor-dependent ADH, and any combination thereof. The function of the redox cofactors is described in more detail below.

The present invention is based on the surprising finding that quinone-dependent ADH and NAD^+ / NADP^+ dependent alcohol dehydrogenases are capable of selectively oxidising the primary alcohol groups of a monosaccharide, or of the monosaccharide moieties of a higher saccharide (in particular, of a polysaccharide) to aldehyde groups. This is contrary to what would have been expected as it would not previously have been thought that this type of alcohol dehydrogenase would be effective on this type of substrate. This has the potential to enable modification of the physico-chemical properties of saccharides, especially polysaccharides, by enzymatic techniques and avoid the use of harsh reagents.

In particular, the present invention is based on the surprising finding that quinone-dependent ADH and NAD^+ / NADP^+ dependent alcohol dehydrogenases are capable of selectively oxidising the C-6 or C-5 position of hexose or pentose rings, respectively.

Some alcohol dehydrogenases, especially ADHs falling within enzyme class (E.C.) 1.1.1, particularly E.C. 1.1.1.1 or E.C. 1.1.1.2, as well as those falling within enzyme class (E.C.) 1.2.1, generally function in conjunction with the redox cofactor nicotinamide adenine dinucleotide (NAD^+) or nicotinamide adenine dinucleotide phosphate (NADP^+), the reaction proceeding with the reduction of NAD^+ or NADP^+ to NADH or NADPH respectively.

Other alcohol dehydrogenases, especially those falling within enzyme class EC 1.1.5, particularly EC 1.1.5.2, generally function in conjunction with a quinone redox cofactor, particularly a quinone cofactor selected from pyrroloquinoline quinone (PQQ), tryptophyl tryptophanquinone (TTQ), topaquinone (TPQ), and lysine tyrosylquinone (LTQ), the quinone group being reduced to a di- or tetrahydroquinone group during the reaction.

In one embodiment, the ADH is selected from enzyme class (E.C.) 1.1.1 or 1.1.5. Of the ADH enzymes in E.C. 1.1.1, preferred are those in classification 1.1.1.1 or 1.1.1.2. Of the ADH enzymes in E.C. 1.1.5, preferred are those in classification 1.1.5.2.

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In another embodiment, the ADH is selected from the aldehyde reductases of enzyme class (E.C.) 1.2.1. These enzymes catalyse the opposite reaction of the ADHs and it is known that many enzymes can work as catalyst for both the forward and the reverse reaction depending on conditions.

10

In one embodiment, the ADH is obtainable or is obtained from a living organism. Suitable ADH's are of bacterial or fungal origin. Preferred are ADH enzymes of bacterial origin, especially *Pseudogluconobacter saccharoetogenes* ADH, *Lactobacillus kefir* ADH, *Thermoanaerobium brockii* ADH and *Escherichia coli* ASD, or an alcohol dehydrogenase enzyme having at least 70%, for example at least 75%, such as at least 80%, preferably at least 85%, more preferably at least 90%, even more preferably at least 95%, still more preferably at least 96%, such as at least 97%, yet more preferably at least 98%, and most preferably at least 99%, sequence identity to any thereof. Particularly preferred is *Pseudogluconobacter saccharoetogenes* ADH or an alcohol dehydrogenase enzyme having at least 70%, for example at least 75%, such as at least 80%, preferably at least 85%, more preferably at least 90%, even more preferably at least 95%, still more preferably at least 96%, such as at least 97%, yet more preferably at least 98%, and most preferably at least 99%, sequence identity thereto. Among ADH enzymes of fungal origin, *Saccharomyces cerevisiae* ADH, or an alcohol dehydrogenase enzyme having at least 70%, for example at least 75%, such as at least 80%, preferably at least 85%, more preferably at least 90%, even more preferably at least 95%, still more preferably at least 96%, such as at least 97%, yet more preferably at least 98%, and most preferably at least 99%, sequence identity thereto, is preferred.

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30

Amino acid sequences

Amino acid sequences of ADH enzymes having the specific properties as defined herein, particularly those of SEQ ID Nos. 1, 1A, 2, 2a, 3, 4, 5 or 5a, defined below, may be used in the present invention.

35

As used herein, the term "amino acid sequence" is synonymous with the term "polypeptide" and/or the term "protein". In some instances, the term "amino acid sequence" is synonymous with the term "peptide". In some instances, the term "amino acid sequence" is synonymous with the term "enzyme".

5

The amino acid sequence may be prepared/isolated from a suitable source, or it may be made synthetically or it may be prepared by use of recombinant DNA techniques.

10

The protein used in the present invention may be used in conjunction with other proteins, particularly other enzymes, for example amylases, proteases or lipases. Thus the present invention also covers a composition comprising a combination of enzymes wherein the combination comprises the ADH enzyme used in the present invention and another enzyme, which may be, for example, another ADH enzyme as described herein, or a protease. This aspect is discussed in a later section.

15

Sequence identity / sequence homology / variants / homologues / derivatives

20

The present invention also encompasses the use of polypeptides having a degree of sequence identity (sometimes referred to as sequence homology) with amino acid sequence(s) defined herein or with a polypeptide having the specific properties defined herein. The present invention encompasses, in particular, polypeptides having a degree of sequence identity with any of SEQ ID Nos. 1, 1A, 2, 2a, 3, 4, 5 or 5a, defined herein, or homologues thereof. Here, the term "homologue" means an entity having sequence identity with the subject amino acid sequences or the subject

25

nucleotide sequences. Here, the term "homology" can be equated with "sequence identity".

30

In a preferred embodiment, the enzyme has the amino acid sequence shown in SEQ ID No 1 or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

35

In a preferred embodiment, the enzyme has the amino acid sequence shown in SEQ ID No 1A or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least

80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

In a preferred embodiment, the enzyme has the amino acid sequence shown in SEQ ID No 2 or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

The enzyme may have the amino acid sequence shown in SEQ ID No. 2A or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

In a preferred embodiment, the enzyme has the amino acid sequence shown in SEQ ID No 3 or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

In a preferred embodiment, the enzyme has the amino acid sequence shown in SEQ ID No 4 or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

In a preferred embodiment, the enzyme has the amino acid sequence shown in SEQ ID No 5 or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

The enzyme may have the amino acid sequence shown in SEQ ID No. 5A or an amino acid sequence having at least 50%, preferably at least 55%, such as at least 60%, for example at least 65%, at least 70%, at least 75%, at least 80%, at least

85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

The homologous amino acid sequence and/or nucleotide sequence should provide
5 and/or encode a polypeptide which retains the functional activity and/or enhances the activity of the enzyme.

In the present context, a homologous sequence is taken to include an amino acid sequence which may be at least 50%, preferably at least 55%, such as at least 60%,
10 for example at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, identical to the subject sequence. Typically, the homologues will comprise the same active sites etc. as the subject amino acid sequence. Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical
15 properties/functions), in the context of the present invention it is preferred to express homology in terms of sequence identity.

Sequence identity comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These commercially
20 available computer programs use complex comparison algorithms to align two or more sequences that best reflect the evolutionary events that might have led to the difference(s) between the two or more sequences. Therefore, these algorithms operate with a scoring system rewarding alignment of identical or similar amino acids and penalising the insertion of gaps, gap extensions and alignment of non-similar
25 amino acids. The scoring system of the comparison algorithms include:

- i) assignment of a penalty score each time a gap is inserted (gap penalty score),
- ii) assignment of a penalty score each time an existing gap is extended with
30 an extra position (extension penalty score),
- iii) assignment of high scores upon alignment of identical amino acids, and
- iv) assignment of variable scores upon alignment of non-identical amino acids.

Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons.

5 The scores given for alignment of non-identical amino acids are assigned according to a scoring matrix also called a substitution matrix. The scores provided in such substitution matrices are reflecting the fact that the likelihood of one amino acid being substituted with another during evolution varies and depends on the physical/chemical nature of the amino acid to be substituted. For example, the
10 likelihood of a polar amino acid being substituted with another polar amino acid is higher compared to being substituted with a hydrophobic amino acid. Therefore, the scoring matrix will assign the highest score for identical amino acids, lower score for non-identical but similar amino acids and even lower score for non-identical non-similar amino acids. The most frequently used scoring matrices are the PAM
15 matrices (Dayhoff et al. (1978), Jones et al. (1992)), the BLOSUM matrices (Henikoff and Henikoff (1992)) and the Gonnet matrix (Gonnet et al. (1992)).

Suitable computer programs for carrying out such an alignment include, but are not limited to, Vector NTI (Invitrogen Corp.) and the ClustalV, ClustalW and ClustalW2
20 programs (Higgins DG & Sharp PM (1988), Higgins et al. (1992), Thompson et al. (1994), Larkin et al. (2007)). A selection of different alignment tools are available from the ExPASy Proteomics server at www.expasy.org. Another example of software that can perform sequence alignment is BLAST (Basic Local Alignment Search Tool), which is available from the webpage of National Center for
25 Biotechnology Information which can currently be found at <http://www.ncbi.nlm.nih.gov/> and which was firstly described in Altschul et al. (1990) J. Mol. Biol. **215**; 403-410.

30 Once the software has produced an alignment, it is possible to calculate % similarity and % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

In one embodiment, it is preferred to use the ClustalW software for performing sequence alignments. Preferably, alignment with ClustalW is performed with the
35 following parameters for pairwise alignment:

Substitution matrix:	Gonnet 250
Gap open penalty:	20
Gap extension penalty:	0.2
Gap end penalty:	None

ClustalW2 is for example made available on the internet by the European Bioinformatics Institute at the EMBL-EBI webpage www.ebi.ac.uk under tools – sequence analysis – ClustalW2. Currently, the exact address of the ClustalW2 tool is www.ebi.ac.uk/Tools/clustalw2.

Thus, the present invention also encompasses the use of variants, homologues and derivatives of any amino acid sequence of a protein as defined herein, particularly those of SEQ ID Nos. 1, 1A, 2, 2a, 3, 4, 5 or 5a, defined herein.

The sequences, particularly those of SEQ ID Nos. 1, 1A, 2, 2a, 3, 4, 5 or 5a, may also have deletions, insertions or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent substance. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the secondary binding activity of the substance is retained. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine, valine, glycine, alanine, asparagine, glutamine, serine, threonine, phenylalanine, and tyrosine.

The present invention also encompasses conservative substitution (substitution and replacement are both used herein to mean the interchange of an existing amino acid residue, with an alternative residue) that may occur i.e. like-for-like substitution such as basic for basic, acidic for acidic, polar for polar etc. Non-conservative substitution may also occur i.e. from one class of residue to another or alternatively involving the inclusion of unnatural amino acids such as ornithine (hereinafter referred to as Z), diaminobutyric acid ornithine (hereinafter referred to as B), norleucine ornithine (hereinafter referred to as O), pyriylalanine, thienylalanine, naphthylalanine and phenylglycine.

Conservative substitutions that may be made are, for example within the groups of basic amino acids (Arginine, Lysine and Histidine), acidic amino acids (glutamic acid and aspartic acid), aliphatic amino acids (Alanine, Valine, Leucine, Isoleucine), polar amino acids (Glutamine, Asparagine, Serine, Threonine), aromatic amino acids (Phenylalanine, Tryptophan and Tyrosine), hydroxyl amino acids (Serine, Threonine), large amino acids (Phenylalanine and Tryptophan) and small amino acids (Glycine, Alanine).

Replacements may also be made by unnatural amino acids include; α^* and α -disubstituted* amino acids, N-alkyl amino acids*, lactic acid*, halide derivatives of natural amino acids such as trifluorotyrosine*, p-Cl-phenylalanine*, p-Br-phenylalanine*, p-I-phenylalanine*, L-allyl-glycine*, β -alanine*, L- α -amino butyric acid*, L- γ -amino butyric acid*, L- α -amino isobutyric acid*, L- ϵ -amino caproic acid[#], 7-amino heptanoic acid*, L-methionine sulfone[#], L-norleucine*, L-norvaline*, p-nitro-L-phenylalanine*, L-hydroxyproline[#], L-thioprolin*, methyl derivatives of phenylalanine (Phe) such as 4-methyl-Phe*, pentamethyl-Phe*, L-Phe (4-amino)[#], L-Tyr (methyl)*, L-Phe (4-isopropyl)*, L-Tic (1,2,3,4-tetrahydroisoquinoline-3-carboxyl acid)*, L-diaminopropionic acid[#] and L-Phe (4-benzyl)*. The notation * has been utilised for the purpose of the discussion above (relating to homologous or non-conservative substitution), to indicate the hydrophobic nature of the derivative whereas # has been utilised to indicate the hydrophilic nature of the derivative, #* indicates amphipathic characteristics.

Variant amino acid sequences may include suitable spacer groups that may be inserted between any two amino acid residues of the sequence including alkyl groups such as methyl, ethyl or propyl groups in addition to amino acid spacers such as glycine or β -alanine residues. A further form of variation, involves the presence of one or more amino acid residues in peptoid form, will be well understood by those skilled in the art. For the avoidance of doubt, "the peptoid form" is used to refer to variant amino acid residues wherein the α -carbon substituent group is on the residue's nitrogen atom rather than the α -carbon. Processes for preparing peptides in the peptoid form are known in the art, for example Simon RJ *et al.* (1992), Horwell DC. (1995).

The ADH may be selected from *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1), *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1A), *Lactobacillus kefir* ADH (SEQ ID No 2), *Lactobacillus kefir* ADH (SEQ ID No 2a), *Saccharomyces cerevisiae* ADH (SEQ ID No 3) or *Thermoanaerobium brockii* ADH (SEQ ID No 4), *Escherichia coli* ASD (SEQ ID No 5) or *Escherichia coli* ASD (SEQ ID No 5a).

In preferred embodiments, the ADH is selected from *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1), *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1A), *Lactobacillus kefir* ADH (SEQ ID No 2), *Saccharomyces cerevisiae* ADH (SEQ ID No 3) or *Thermoanaerobium brockii* ADH (SEQ ID No 4), or *Escherichia coli* ASD (SEQ ID No 5).

In one preferred embodiment the ADH is selected from *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1) and *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1A).

In one aspect, preferably the ADH enzyme used in the present invention is in a purified form. The term "purified" means that a given component is present at a high level. The component is desirably the predominant active component present in a composition.

Isolated and/or purified

In one aspect, preferably the ADH enzyme used in the present invention is in an isolated form. The term "isolated" means that the product is at least substantially free from at least one other component with which the product is associated in the reaction mixture.

In one aspect, preferably the product according to the present invention is in a purified form. The term "purified" means that a given component is present at a high level. The component is desirably the predominant component present in a composition. Preferably, it is present at a level of at least about 90%, or at least about 95% or at least about 98%, said level being determined on a dry weight/dry weight basis with respect to the total composition under consideration.

Concentration

The ADH enzyme may be present in any concentration to enable it to perform the required function of oxidising the polysaccharide. The concentration of ADH required depends on factors such as the method of purification and the concentration of any cofactor (where present). Suitably, the ADH is present in a concentration of at least about 0.05 ppm (by weight), such as, e.g. at least about 1 ppm, at least about 10 ppm, at least about 100 ppm, at least about 150 ppm or at least about 200 ppm. Preferably, the ADH is present in a concentration of about 0.05-500 ppm, preferably about 0.1-200 ppm, more preferably about 0.2-100 ppm, even more preferably about 0.5-50 ppm, yet more preferably about 1-50 ppm, and most preferably about 1-10 ppm (by weight).

Redox cofactors

As noted above, ADH is preferably used in the present invention with a redox cofactor. In this specification the term 'redox cofactor' is defined as any non-protein chemical compound that assists the enzymatic redox reaction. The cofactor may be tightly bound or loosely bound to the enzyme, or unbound.

Cofactors can be divided into two broad groups: coenzymes and prosthetic groups. Coenzymes are small organic non-protein molecules that carry chemical groups between enzymes. These molecules are not bound tightly by enzymes and are released as a normal part of the catalytic cycle. In contrast, prosthetic groups form a permanent part of the protein structure.

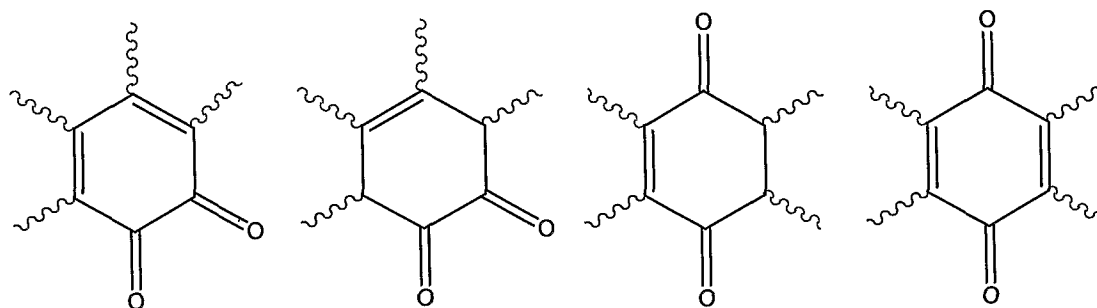
In one embodiment, the cofactor is nicotinamide adenine dinucleotide (NAD^+) or nicotinamide adenine dinucleotide phosphate (NADP^+). When these compounds are used as the cofactor, the reaction typically proceeds with the reduction of NAD^+ or NADP^+ to NADH or NADPH respectively. In this specification the terms NAD^+ and NADP^+ encompasses the redox cofactors nicotinamide adenine dinucleotide (NAD^+) or nicotinamide adenine dinucleotide phosphate whether in their oxidised (positively charged) form or their reduced form (usually described as NADH and NADPH).

NAD^+ or NADP^+ cofactors are particularly preferred when the ADH is an ADH enzyme in subclass 1.1.1, particularly ADH enzymes in E.C. 1.1.1.1 or 1.1.1.2, or is

an ADH enzyme in subclass 1.2.1. NAD^+ or NADP^+ cofactors are especially preferred when the ADH is *Lactobacillus kefir* ADH (SEQ ID No 2), *Saccharomyces cerevisiae* ADH (SEQ ID No 3) or *Thermoanaerobium brockii* ADH (SEQ ID No 4).

5 The enzyme cofactors may be present in any concentration to enable the enzyme to perform the required function of oxidising a saccharide. Suitably, the NAD^+ or NADP^+ cofactor is present in a concentration of about 0.01 to about 5000 ppm by weight. More preferably, the NAD^+ or NADP^+ is present in a concentration of about 0.10 to about 1000 ppm by weight.

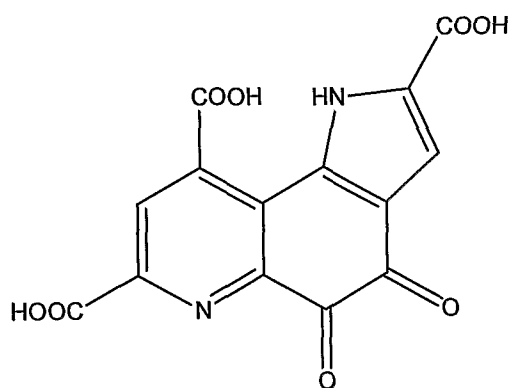
10 In another embodiment, the cofactor is a quinone cofactor. In this specification the term 'quinone cofactor' covers any compound including a 6-membered (saturated or partially unsaturated) ring having two carbonyl ($>\text{C}=\text{O}$) groups as ring substituents, and which is capable of acting as a cofactor for ADH. 1,4-quinones and 1,2-quinones,
15 for example those of the general formulae below (wherein the wavy bonds represent attachments to the remainder of the molecule, including molecules wherein two bonds together with the carbon atoms to which they are attached form a ring) are preferred. Quinone cofactors are particularly preferred when the ADH is an ADH enzyme in subclass 1.1.5, particularly ADH enzymes in E.C. 1.1.5.2, and especially
20 when the ADH enzyme is *Pseudogluconobacter saccharoketogenes* ADH (SEQ ID No 1) or *Escherichia coli* ADH (SEQ ID No 5).



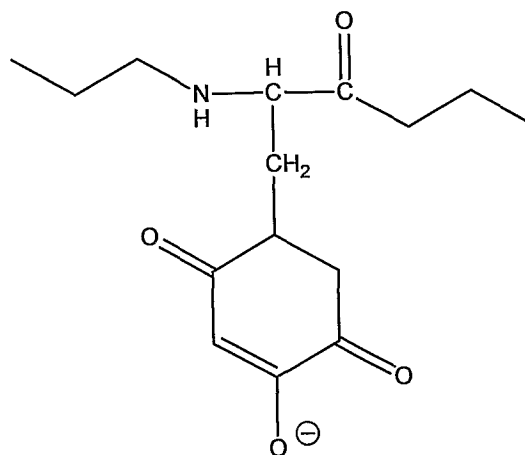
25 Preferably, the quinone cofactor is selected from from pyrroloquinoline quinone (PQQ), tryptophyl tryptophanquinone (TTQ), topaquinone (TPQ), and lysine tyrosylquinone (LTQ), the structures of which are set out below, or acceptable salts, esters or other derivatives thereof.

Acceptable salts of the quinone cofactors used in the present invention include the acid addition and base salts thereof. Suitable acid addition salts are formed from acids which form non-toxic salts. Examples include the acetate, adipate, aspartate, benzoate, besylate, bicarbonate/carbonate, bisulphate/sulphate, borate, camsylate, citrate, cyclamate, edisylate, esylate, formate, fumarate, gluceptate, gluconate, glucuronate, hexafluorophosphate, hibenzone, hydrochloride/chloride, hydrobromide/bromide, hydroiodide/iodide, isethionate, lactate, malate, maleate, malonate, mesylate, methylsulphate, naphthylate, 2-napsylate, nicotinate, nitrate, orotate, oxalate, palmitate, pamoate, phosphate/hydrogen phosphate/dihydrogen phosphate, pyroglutamate, saccharate, stearate, succinate, tannate, tartrate, tosylate, trifluoroacetate and xinofoate salts. Suitable base salts are formed from bases which form non-toxic salts. Examples include the aluminium, arginine, benzathine, calcium, choline, diethylamine, diolamine, glycine, lysine, magnesium, meglumine, olamine, potassium, sodium, tromethamine and zinc salts.

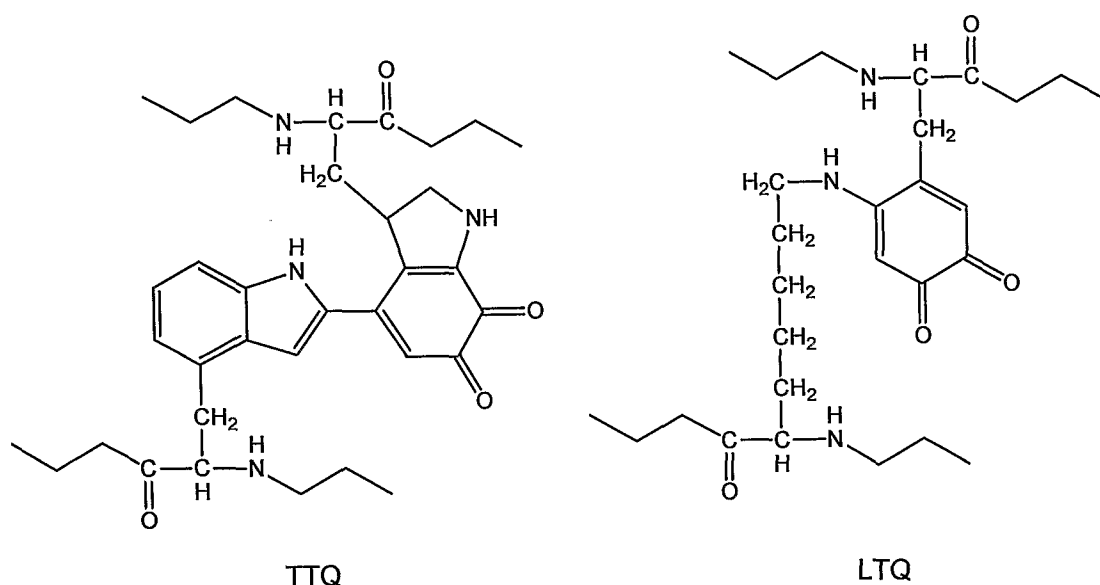
Acceptable esters of the quinone cofactors used in the present invention, in particular PQQ, include (C₁₋₆)alkyl esters, halo(C₁₋₆)alkyl esters, hydroxy(C₁₋₆)alkyl esters and (C₁₋₆)alkoxy(C₁₋₆)alkyl esters, and benzyl esters. Other acceptable derivatives include N-oxide derivatives.



PQQ



TPQ



5

More preferably, the quinone cofactor is pyrroloquinoline quinone (PQQ) or an acceptable salt, ester or other derivative thereof. Alcohol dehydrogenase enzymes used with PQQ as cofactor are referred to in this specification as "PQQ-ADH enzymes".

10

When the quinone cofactor is pyrroloquinoline quinone (PQQ), the PQQ may be made synthetically, for example as described in Buchi, G., J. H. Botkin, G. C. M. Lee, and K. Yakushijin, *J. Am. Chem. Soc.* (1985) **107**, 5555-5556. Alternatively, the PQQ may be obtained from natural sources, particularly foods, as described for example in Kumazawa et al., *Biochem. J.* (1995) **307**, 331-333. Examples of foodstuffs containing PQQ include broad bean, green soybeans, potato, sweet potato, parsley, cabbage, carrot, celery, green pepper, spinach, tomato, apple, banana, kiwi fruit, orange, papaya, green tea, oolong (tea), cola, whiskey, wine, sake, bread, fermented soybeans (natto), miso (bean paste) and tofu (bean curd).

Preferred sources of PQQ are plant extracts. A particularly preferred source of PQQ is green tea extract, as this is cheap and widely available.

20

When the quinone cofactor is PQQ, the PQQ is preferably present in a concentration of about 0.01 to about 1000 ppm, such as e.g., about 0.1 to about 500 ppm, about 0.15 to about 250 ppm or about 0.2 to about 100 ppm. More preferably, the PQQ is present in a concentration of about 0.25 to about 10 ppm.

25

When a quinone is used as cofactor with the ADH enzyme, a metal ion is preferably also used in conjunction with the ADH and quinone. Without wishing to be bound by theory, it is believed that the metal ion coordinates to the quinone and the substrate, thereby assisting transfer of hydrogen from the substrate to the quinone. Examples of suitable metal ions include alkali metal ions such as lithium, sodium and potassium ions, alkaline earth metal ions such as magnesium and calcium ions, and transition metal ions such as iron, manganese, cobalt, copper, molybdenum and zinc ions, or any combination thereof. Divalent or trivalent metal ions are preferred and calcium ions or iron (Fe^{2+} / Fe^{3+}) ions, or any combination thereof are particularly preferred.

According to Toyama *et al*, *Arch. Biochem. Biophys.* (2004) 428, 10-21, quino(hemo)protein alcohol dehydrogenases (ADH) that have pyrroloquinoline quinone (PQQ) as the cofactor group are classified into 3 groups, types I, II, and III. Type I ADH is a simple quinoprotein having PQQ as the only cofactor group, while type II and type III ADHs are quinohemoprotein having heme c as well as PQQ in the catalytic polypeptide. Type II ADH is a soluble periplasmic enzyme and is widely distributed in *Proteobacteria* such as *Pseudomonas*, *Ralstonia*, *Comamonas*, etc. In contrast, type III ADH is a membrane-bound enzyme working on the periplasmic surface solely in acetic acid bacteria. It consists of three subunits that comprise a quinohemoprotein catalytic subunit, a triheme cytochrome c subunit, and a third subunit of unknown function. The present invention embraces compositions and methods using all three types of ADH as defined in the above article; Type I ADH is preferred.

Combinations

The ADH enzyme may be used according to the present invention in combination with one or more further active agents. Such combinations may offer advantages, including synergy, when used together in the oxidation method of the invention.

In particular, the ADH enzyme may be used according to the present invention in combination with one or more further enzymes as active agents. Such combinations may offer advantages, including synergy, when used together in the oxidation method of the invention.

In one embodiment, the further enzyme is another ADH enzyme, so that two (or more) different ADH enzymes are used in combination.

- 5 In another embodiment, the ADH may be used in combination with a further active agent, capable of converting the aldehyde groups of the monosaccharide, or of the monosaccharide moieties of the higher saccharide, to carboxylic acid groups. Such a combination offers advantages in that the oxidized saccharide/polysaccharide would be rendered more suitable for ingestion for food applications. Examples of
10 such a further active agent capable of the above conversion to carboxylic acid include aldehyde dehydrogenase or oxidase (can be found in EC 1.2.).

Thus, in a preferred aspect, the method of the present invention comprises contacting the saccharide with an alcohol dehydrogenase (ADH) enzyme selected
15 from a quinone redox cofactor-dependent ADH and a nicotinamide adenine dinucleotide (NAD^+) or nicotinamide adenine dinucleotide phosphate (NADP^+) redox cofactor-dependent ADH, and an aldehyde dehydrogenase or oxidase.

Applications

20

The method of the present invention has a wide range of applications. In particular, the method of the present invention is useful in the food and paper industries.

In one aspect, the method of the present invention can be used to prepare modified
25 polysaccharides useful in the paper industry. Examples of polysaccharides that are typically relevant for the paper industry include cationic, anionic, oxidized and phosphated starches; carboxymethyl cellulose (CMC), guar, alginate, guar, cationic guar and anionic guar. Further details of suitable polysaccharides may be found in US2003/150573.

30

Thus, in one aspect, the invention comprises a paper product including an oxidised saccharide (in particular, an oxidised polysaccharide, as defined and exemplified above) prepared by the method of the invention, as defined above, either in its broadest aspect or a preferred aspect, as well as a method of producing a paper
35 product including such an oxidised saccharide (in particular, an oxidised polysaccharide).

A typical paper production method may include the following steps:

- 5 (a) Chemical or mechanical pulping to produce wood pulp which helps to release cellulose
- (b) Refining to process and soften the fibres
- (c) Dewatering on a mesh and forming of sheets
- (d) Pressing
- (e) Drying
- 10 (f) Calendaring to smooth the surface
- (g) Coating

The above steps may be varied within the ambit of knowledge of a person skilled in the art.

15

For application in the food industry, at least a portion of the saccharide may be comprised in a flour. The flour may be mixed with conventional ingredients to prepare a dough. Examples of such ingredients include yeast, water, egg, milk, salt, sugar, fat and oil. The dough may then be baked to prepare a baked product.

20

As an alternative application in the food industry, at least a portion of the saccharide is comprised in a sugar product, for example sucrose, invert sugar, glucose, fructose or maltose.

25 EXAMPLES

The PQQ-ADH enzyme used in the examples is SEQ ID NO. 1a, which is the enzyme prepared in "preparation 1".

30 Preparation 1: *Pseudogluconobacter saccharoetogenes* ADH

The gene encoding the *Pseudogluconobacter saccharoetogenes* PQQ-dependent alcohol dehydrogenase gene (PQQ-ADH) was synthesized as a codon optimized fragment, including its own signal sequence, and cloned into the pDONR/Zeo via the Gateway® BP recombination reaction (Invitrogen, Carlsbad, CA, USA) resulting in
35 the entry vector pENTRY-ADH (Fig. 4). SEQ ID No. 6 shows the DNA sequence of

the codon optimized PQQ-ADH gene (from Geneart AG (Regensburg, Germany)). Shown in italics are the sequences flanking the PQQ-ADH ORF. These flanking sequences contain the attB sites that facilitate the Gateway® BP dependent cloning of the gene into pDONR/Zeo.

5

To enable the expression of the PQQ-ADH in *Pichia pastoris*, the gene was cloned from pENTRY-ADH into pPIC2-DEST (Fig. 5) via the Gateway® LR recombination reaction. The resulting plasmid, pPIC2-ADH (Fig. 6) was linearized by *Sall* digestion, enabling integration of the construct into the HIS4 locus of *P. pastoris* GS115 upon
10 transformation. This vector contains the *P. pastoris* strong AOX1 promoter, allowing for strong methanol-inducible gene expression. For production of PQQ-ADH, *P. pastoris*::pPIC2-ADH was grown in a 2 liter B. Braun Biostat B fermentor according to standard *P. pastoris* fermentation protocols (Invitrogen, Carlsbad, CA USA). During fermentation the major fraction of the expressed PQQ-ADH was found in the
15 culture supernatant, with levels reaching 100-400 mg/l 72 hours after the start of methanol induction. The N-terminus of the mature protein was found to start at position 37 of the coding part, thus starting with AEPSKAGQSA.

The N-terminus of the PsADH expressed by *Pichia pastoris* was determined by
20 Edman degradation and analysis on a Procise® cLC capillary 491 protein sequencing system (Applied Biosystems).

Figure 5 is a plasmid map of the *P. pastoris* destination vector pPIC2-DEST, which was derived from pPIC3.5K (Invitrogen). The vector contains the methanol inducible
25 AOX1 promoter (PAOX1) and the AOX transcription terminator (AOX-TT). The Gateway® cassette was inserted between promoter and terminator of pPIC3.5K, and consists of the recombination sites attR1 and 2, the chloramphenicol resistance marker (cmR) and ccdB gene for negative selection in the Gateway® cloning procedure. Furthermore, the vector contains the HIS4 gene for selection in *P.*
30 *pastoris*, the kanamycin (Kan) and ampicillin (Amp) resistance genes for selection in *E. coli* (Kan).

Example 1 – Expression of the PQQ-ADH gene

A synthetic PQQ-ADH gene with a broad host codon usage was ordered and cloned
5 into Gateway compatible expression vectors. Acceptable expression levels (0.4 g/l)
were obtained after fermentation of a *Pichia pastoris* recombinant strain. A SDS-gel
analysis of extracellular broth showed a dominant band of the right size (Fig. 1).

Figure 1 is a SDS-PAGE of extracellular broth from fermentation of a *Pichia pastoris*
10 recombinant strain harboring the PQQ-ADH gene. The molecular weight markers
are as follows:

Lane 1: Fermentation broth, approximately 3 µg protein)

Lane 2: Fermentation broth (approximately 2 µg protein)

15 Lane 3: Fermentation broth (approximately 6 µg protein)

Nu-PAGE, 4-12%, Mes, +DTT

Expression could be estimated at the levels of 0.4 g/l.

Example 2 – Oxidation of maltotetraose and maltoheptaose

Maltotetraose (G4) and maltoheptaose (G7) were tested as potential oxidative
substrates for the PQQ-ADH enzyme.

25 Each reaction was carried out in a total volume of 250µl and consisted of:

12 mM G4 or 7 mM G7 (Sigma)

80 mM Na-phosphate buffer pH 7.0

4 mM CaCl₂ (Sigma)

30 360 µM PQQ (Fluka)

3.9 mM Phenazine methosulfate (Sigma)

0.1 mM 2,6-Dichlorophenolindophenol (Sigma)

Reactions were initiated by addition of 20 µl PQQ-ADH enzyme mixture and
35 incubated for 12 hrs at 25 °C. As a negative control samples were incubated with 20
µl water. Reactions were terminated by boiling for 2 min.

The reaction products were analyzed by FTMS and the products listed in Table 1 below were identified in PQQ-ADH treated samples.

5 Table 1: G4 and G7 Reaction products identified by FTMS

Substrate	Reaction product	Formula	Exact mass
G4	Maltotetra-1-uronic acid	$C_{24}H_{42}O_{22}Na_1$	705.20442
	Sodium maltotetra-1-uronate	$C_{24}H_{41}O_{22}Na_2$	727.18643
	Maltotetra-6-uronic acid	$C_{24}H_{40}O_{22}Na_1$	703.19035
	Maltotetraose-6-aldehyde	$C_{24}H_{40}O_{21}Na_1$	687.19543
	Maltotetraose	$C_{24}H_{42}O_{21}Na_1$	689.21004
G7	Maltohepta-1-uronic acid	$C_{42}H_{72}O_{37}Na_1$	1191.36124
	Sodium maltohepta-1-uronate	$C_{42}H_{71}O_{37}Na_2$	1213.34291
	Maltohepta-6-aldehyde	$C_{42}H_{70}O_{36}Na_1$	1173.35176
	Maltoheptaose	$C_{42}H_{72}O_{36}Na_1$	1175.36657

The relative abundance of Maltotetraose-6-aldehyde indicates around 5% conversion when maltotetraose is applied as a substrate. A lower conversion (1-2 %) to maltohepta-6-aldehyde is observed when maltoheptaose is used as a substrate.

10

It can be concluded from this example that PQQ-ADH can oxidize oligosaccharides at the C-1 and C-6 positions. The C-1-OH of the reducing end is oxidized to the carboxylic acid while modification at the C-6-OH yields the aldehyde as the major product and minor oxidation to the carboxylic acid.

15

Example 3 - Oxidation of starch by PQQ-ADH

Gelatinized wheat starch was tested as a substrate for PQQ-ADH, and the effects of Fe^{2+}/Fe^{3+} addition were investigated.

20

In a total volume of 570 μ l each reaction contained:

8 mg gelatinized wheat starch (Sigma)

90 mM Na-phosphate buffer pH 7.0

320 μ M PQQ

25

Specified concentrations of Fe^{2+} or Fe^{3+}

20 μ g PQQ-ADH

Samples were incubated at 40°C for 24 hrs and the reaction terminated by boiling for 2 min. The pH of the samples were brought to 4.5 by addition of 125 μ l 1 M sodium acetate. The starch polymer was degraded to monomers by addition of a mixture of α -amylase/glucoamylase, incubated at 70°C for 3 hrs and terminated by boiling for 10 min. pH was adjusted to 7.0 with 5 M NaOH.

40 μ l 0.5 M Ethylhydroxylamine was added to derivatize molecules with aldehyde groups. Ethylhydroxylamine modification of C-1 and C-1/C-6 glucose derived aldehydes is shown in Figs. 2 and 3. Samples were analyzed by FTMS.

Glucose 1,6-bis(ethyl oxime) represents glucosyl units in the starch polymer which have been oxidized to 6-aldehydes by PQQ-ADH. The ratio of glucose 1,6-bis(ethyl oxime) and glucose 1-ethyl oxime is a good measure of the ratio of the PQQ-ADH catalyzed conversion to C-6 glucosyl aldehyde within the starch polymer (Table 2).

Table 2: Oxidation of starch

Sample	Fe ²⁺ (mM)	Fe ³⁺ (mM)	Conversion ratio, %
1	0	0	2.3
2	0	0	2.2
3	0.02	0	5.3
4	0.2	0	5.2
5	0	0.1	6.6
6	0	1.0	3.4

It can be concluded from this example that PQQ-ADH can oxidize starch at the C-6 position of glucosyl units. Based on detection of the formed C-6 aldehyde a conversion rate of ~ 2% was obtained but this can be increased to ~ 5-6 % with the addition of Fe²⁺ or Fe³⁺.

Example 4 – Oxidation of various carbohydrates and polysaccharides

A wide range of carbohydrates and polysaccharides were tested as potential oxidative substrates for the PQQ-ADH enzyme. Each reaction was carried out in a total volume of 250 μ l and consisted of:

2% substrate

80 mM Na-phosphate buffer pH 7.0

4 mM CaCl₂

360 μM PQQ

5 3.9 mM Phenazine methosulfate

0.1 mM 2,6-Dichlorophenolindophenol (DCIP)

Reactions were initiated by addition of 20 μl PQQ-ADH enzyme mixture and incubated at 25 °C. In the assay DCIP serves as the electron acceptor and oxidation
10 of substrate was monitored by the reduction of DCIP to DCIPH₂ at 600 nm.

Oxidizing activity was observed for these substrates:

	Glucose
15	Maltose
	Maltotriose
	Maltotetraose
	Maltopentaose
	Maltohexaose
20	Maltoheptaose
	Amylose
	Amylopectin
	Glycogen
	Butanol
25	Xylose
	Trehalose
	Anhydrofructose
	Panose
	Cellobiose
30	Cellopentaose
	Melibiose
	Arabinose
	L-sorbose
	Stachyose
35	Sucrose
	α-cyclodextrin

β -cyclodextrin
 γ -cyclodextrin
polydextrose
pectin
5 Pullulan
carrageenan
locust bean gum
guar gum
alginate
10 carboxymethyl cellulose
 α -methyl glucose

It can be concluded from this example that PQQ-ADH shows oxidizing activity on a broad range of substrates.

Example 5 - Oxidation of guar gums

Four different guar gums with different viscosity profiles were treated with PQQ-ADH. The guar gums tested were Danisco products and these were Meyprodor 5, 50, 400 and Grindsted Guar 5000.

In a total volume of 700 ml each reaction contained:

5% Meyprodor 5, 1% Meyprodor 50, 0.5% Meyprodor 400 or 0.5% Grindsted Guar 5000 (all from Danisco A/S)

25 200 μ M PQQ (Sigma)

0.1 μ M FeCl₃ (Sigma)

pH was adjusted to 7.0 with 1M HCl.

Reactions were initiated by addition of 4 mg PQQ-ADH enzyme mixture and incubated at 25°C for 18 hrs.

30 The amount of negative charge in the guar products was investigated by Müttek particle charge detector where the guar gums are titrated with a cationic reagent (Table 3).

Table 3: Müték analysis of PQQ-ADH treated guar gums

Substrate	Control (ml)	PQQ-ADH treated (ml)
Grindsted Guar 5000	0.24	0.50
Meyprodor 400	0.35	0.71
Meyprodor 50	0.80	0.96
Meyprodor 5	3.28	3.52

5 It can be concluded from this example that PQQ-ADH can oxidize guar gum and introduce negative charges into the polysaccharide.

Example 6 - Oxidation of α - and β -cyclodextrin

10 α -cyclodextrin (α -CD) and β -cyclodextrin (β -CD) were tested as substrates for the PQQ-ADH enzyme. Each reaction was carried out in a total volume of 250 μ l and consisted of:

15 15 mM α -CD or β -CD (Sigma)
50 mM Na-phosphate buffer pH 7.0
320 μ M PQQ

Reactions were initiated by addition of 20 μ l PQQ-ADH enzyme mixture and incubated for 18 hrs at 40 °C. As a negative control samples were incubated with 20 μ l water. Reactions were terminated by boiling for 2 min.

20

The reaction products were analyzed by FTMS and the products listed in Table 4 were identified in PQQ-ADH treated samples.

Table 4: α -CD and β -CD reaction products identified by FTMS

Substrate	Reaction product	Formula	Exact mass	Relative abundance
α -CD	α -cyclodextrin	$C_{36}H_{60}O_{30}Na_1$	995.30617	100
	α -cyclodextrin-6-aldehyde	$C_{36}H_{58}O_{30}Na_1$	993.28936	0.1
	α -cyclodextrin-6-acid	$C_{36}H_{58}O_{31}Na_1$	1009.28029	0.002
β -CD	β -cyclodextrin	$C_{42}H_{70}O_{35}Na_1$	1157.35401	100
	β -cyclodextrin-6-aldehyde	$C_{42}H_{68}O_{35}Na_1$	1155.33957	0.2
	β -cyclodextrin-6-acid	$C_{42}H_{68}O_{36}Na_1$	1171.33214	0.003

It can be concluded from this example that PQQ-ADH can oxidize α -cyclodextrin and β -cyclodextrin at the C-6 position. Modification at the C-6-OH yields the aldehyde as the major product and a minor oxidation to the carboxylic acid is observed.

All publications mentioned in the above specification, and references cited in said publications, are herein incorporated by reference. Various modifications and variations of the described methods and system of the present invention will be apparent to those skilled in the art without departing from the scope and spirit of the present invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Claims

1. A method of oxidising a saccharide, by contacting the saccharide with an alcohol dehydrogenase (ADH) enzyme selected from a quinone redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide (NAD⁺) redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide phosphate (NADP⁺) redox cofactor-dependent ADH, and any combination thereof.
2. A method according to claim 1, wherein the alcohol dehydrogenase enzyme is in a purified form.
3. A method according to claim 1 or claim 2, wherein a redox cofactor is used with the alcohol dehydrogenase.
4. A method according to any one of claims 1 to 3, wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme class EC 1.1.5.
5. A method according to claim 4, wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme class EC 1.1.5.2.
6. A method according to claim 5, wherein the alcohol dehydrogenase enzyme is selected from *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1), *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1A), *Escherichia coli* ADH (SEQ ID No. 5) and *Escherichia coli* ASD (SEQ ID No. 5a) or an alcohol dehydrogenase enzyme having at least 70% sequence identity to any thereof.
7. A method according to claim 6, wherein the alcohol dehydrogenase enzyme is selected from *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1), *Pseudogluconobacter saccharoetogenes* ADH (SEQ ID No 1A), *Escherichia coli* ADH (SEQ ID No. 5) and *Escherichia coli* ADH (SEQ ID No. 5a) or an alcohol dehydrogenase enzyme having at least 75% (such as at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 96%, or at least 97%, or at least 98% or or at least 99%) sequence identity to any thereof.

8. A method according to any one of claims 1 to 3, wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme class EC 1.1.1.

5 9. A method according to claim 8, wherein the alcohol dehydrogenase is selected from alcohol dehydrogenases in enzyme classes EC 1.1.1.1 and EC 1.1.1.2.

10 10. A method according to claim 8 or claim 9, wherein the alcohol dehydrogenase enzyme is selected from *Lactobacillus kefir* ADH (SEQ ID No 2), *Lactobacillus kefir* ADH (SEQ ID No 2a), *Saccharomyces cerevisiae* ADH (SEQ ID No 3) or *Thermoanaerobium brockii* ADH (SEQ ID No 4) or an alcohol dehydrogenase enzyme having at least 70% sequence identity to any thereof; preferably wherein the alcohol dehydrogenase enzyme is selected from *Lactobacillus kefir* ADH (SEQ ID No 2), *Lactobacillus kefir* ADH (SEQ ID No 2a), *Saccharomyces*
15 *cerevisiae* ADH (SEQ ID No 3) or *Thermoanaerobium brockii* ADH (SEQ ID No 4) or an alcohol dehydrogenase enzyme having at least 75% (such as at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 96%, or at least 97%, or at least 98% or or at least 99%) sequence identity to any thereof..

20 11. A method according to any of claims 3 to 7, wherein the redox cofactor is a quinone cofactor.

12. A method according to claim 11, wherein the quinone cofactor is selected from pyrroloquinoline quinone (PQQ), tryptophyl tryptophanquinone (TTQ),
25 topaquinone (TPQ), and lysine tyrosylquinone (LTQ).

13. A method according to claim 12, wherein the redox cofactor is pyrroloquinoline quinone (PQQ).

30 14. A method according to claim 13, wherein the PQQ is derived from green tea extract.

15. A method according to claim 13 or claim 14, wherein the PQQ is present in a concentration of about 0.01 to about 1000 ppm by weight.

16. A method according to claim 15, wherein the PQQ is present in a concentration of about 0.2 to about 100 ppm by weight.

17. A method according to any one of claims 11 to 16, wherein a metal ion is used with the quinone cofactor.

18. A method according to claim 17, wherein the metal ion is a Fe^{2+} or Fe^{3+} ion, or a combination thereof.

19. A method according to any of claims 3, 8, 9 or 10, wherein the redox cofactor is selected from NAD^+ and NADP^+ .

20. A method according to claim 19, wherein the NAD^+ or NADP^+ is present in a concentration of about 0.01 to about 5000 ppm by weight.

21. A method according to claim 20, wherein the NAD^+ or NADP^+ is present in a concentration of about 0.10 to about 1000 ppm by weight.

22. A method according to any one of claims 1 to 21, wherein the concentration of alcohol dehydrogenase used is at least about 0.05 ppm by weight.

23. A method according to any one of claims 1 to 22, comprising oxidation of at least 2% of the primary alcohol groups of the saccharide to aldehyde groups.

24. A method according to claim 23, comprising oxidation of at least 6% of the primary alcohol groups of the saccharide to aldehyde groups.

25. A method according to any one of claims 1 to 24, wherein the saccharide is a polysaccharide comprising hexose moieties.

26. A method according to claim 25, wherein the hexose moieties of the polysaccharide are glucose moieties.

27. A method according to claim 25 or claim 26, comprising selective oxidation of alcohol groups at the C-6 position of the hexose moieties of the polysaccharide.

28. A method according to any one of claims 1 to 24, wherein the saccharide is a polysaccharide comprising pentose moieties.

29. A method according to claim 28, wherein the pentose moieties of the polysaccharide are arabinose or xylose moieties.

30. A method according to claim 28 or claim 29, comprising selective oxidation of alcohol groups at the C-5 position of the pentose moieties of the polysaccharide.

31. A method according to any one of claims 1 to 24, wherein the saccharide is a disaccharide.

32. A method according to claim 31, wherein the disaccharide is selected from lactose, maltose, cellobiose, sucrose, trehalose isomaltulose and trehalulose.

33. A method according to any one of claims 1 to 24, wherein the saccharide is an oligosaccharide

34. A method according to claim 33, wherein the oligosaccharide is a chain oligosaccharide.

35. A method according to claim 34, wherein the polysaccharide is selected from maltotriose, maltotetraose, maltopentaose, maltohexaose, maltoheptaose, cellobiose, cellotriose, cellotetraose, cellopentaose, cellohexaose, celloheptaose, a fructo-oligosaccharide, a mannanoligosaccharide; and an isomaltooligosaccharide, a galactooligosaccharide and a xylooligosaccharide.

36. A method according to claim 33, wherein the oligosaccharide is a cyclic oligosaccharide.

37. A method according to claim 36, wherein the cyclic oligosaccharide is a cyclodextrin selected from α -cyclodextrin, β -cyclodextrin and γ -cyclodextrin.

38. A method according to any one of claims 1 to 24, wherein the saccharide is a polysaccharide comprising at least 40 monosaccharide units.

39. A method according to claim 38, wherein the polysaccharide comprises at least 1000 monosaccharide units.

40. A method according to claim 38 or claim 39, wherein the polysaccharide is selected from starch, amylose, amylopectin, glycogen, arabinoxylan, a β -glucan, cellulose or a derivative thereof, alginic acid or a salt or derivative thereof, polydextrose, pectin, pullulan, carrageenan, locust bean gum and guar gum.

41. A method according to claim 40, wherein the polysaccharide is starch.

42. An oxidised saccharide obtainable by the method of any one of claims 1 to 41.

43. A product containing an oxidised saccharide obtainable by the method of any one of claims 1 to 41.

44. A product according to claim 43, selected from a food product and a paper product.

45. A product according to claim 44, which is a food product selected from dough and a baked product prepared from dough.

46. Use of an oxidised saccharide obtainable by the method of any one of claims 1 to 41 in the manufacture of food products or paper products.

47. Use of an alcohol dehydrogenase as defined in any one of claims 1 to 10 in the manufacture of paper products.

48. Use of an alcohol dehydrogenase selected from a quinone redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide (NAD^+) redox cofactor-dependent ADH, a nicotinamide adenine dinucleotide phosphate (NADP^+) redox cofactor-dependent ADH, and any combinations thereof for oxidising saccharides and/or for preparing food or paper products.

49. An amino acid sequence comprising SEQ ID No. 1A or an amino acid sequence having at least 75% amino acid sequence identity therewith but not SEQ ID No. 1.

50. An amino acid sequence according to claim 49 comprising SEQ ID No. 1A or an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

5

51. A nucleotide sequence encoding the amino acid sequence of claim 49 or claim 50.

52. A vector comprising the nucleotide sequence of claim 51.

10

53. A host transformed with the nucleotide sequence of claim 51 or the vector of claim 52.

54. A host according to claim 53 wherein the host is selected from a bacterial host, a fungal host or a yeast host.

15

55. A method comprising expressing the nucleotide sequence of claim 51 or the vector of claim 52.

20

56. An amino acid sequence comprising SEQ ID No. 2A or an amino acid sequence having at least 75% amino acid sequence identity therewith but not SEQ ID No. 2.

57. An amino acid sequence according to claim 56 comprising SEQ ID No. 2A or an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

25

58. A nucleotide sequence encoding the amino acid sequence of claim 56 or claim 57.

30

59. A vector comprising the nucleotide sequence of claim 58.

60. A host transformed with the nucleotide sequence of claim 58 or the vector of claim 59.

35

61. A host according to claim 60 wherein the host is selected from a bacterial host, a fungal host or a yeast host.

62. A method comprising expressing the nucleotide sequence of claim 58 or the vector of claim 59.

63. An amino acid sequence comprising SEQ ID No. 5A or an amino acid sequence having at least 75% amino acid sequence identity therewith but not SEQ ID No. 5.

64. An amino acid sequence according to claim 63 comprising SEQ ID No. 2A or an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, amino acid sequence identity therewith.

65. A nucleotide sequence encoding the amino acid sequence of claim 63 or claim 64.

66. A vector comprising the nucleotide sequence of claim 65.

67. A host transformed with the nucleotide sequence of claim 65 or the vector of claim 66.

68. A host according to claim 67 wherein the host is selected from a bacterial host, a fungal host or a yeast host.

69. A method comprising expressing the nucleotide sequence of claim 65 or the vector of claim 66.

70. A method according to claim 1 or any claim dependent thereon or a use according to claim 48 wherein said saccharide is selected from the group consisting of: Glucose, Maltose, Maltotriose, Maltotetraose, Maltopentaose, Maltohexaose, Maltoheptaose, Amylose, Amylopectin, Glycogen, Butanol, Xylose, Trehalose, Anhydrofructose, Panose, Cellobiose, Cellopentaose, Melibiose, Arabinose, L-sorbose, Stachyose, Sucrose, α -cyclodextrin, β -cyclodextrin, γ -cyclodextrin, polydextrose, pectin, Pullulan, carrageenan, locust

bean gum, guar gum, alginate, carboxymethyl cellulose, α -methyl glucose, and combinations thereof.

71. A method or a saccharide or a product or a use substantially as described herein
5 and with reference to the accompanying figures.

72. An amino acid sequence or a nucleotide sequence or a vector or a host or a
method substantially as described herein and with reference to the
accompanying figures.

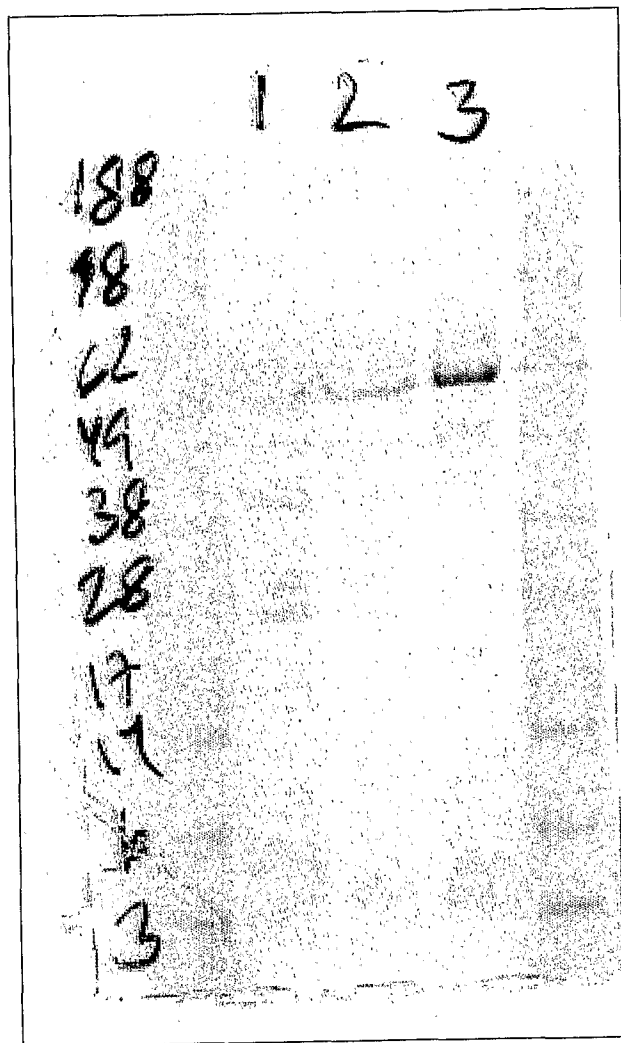
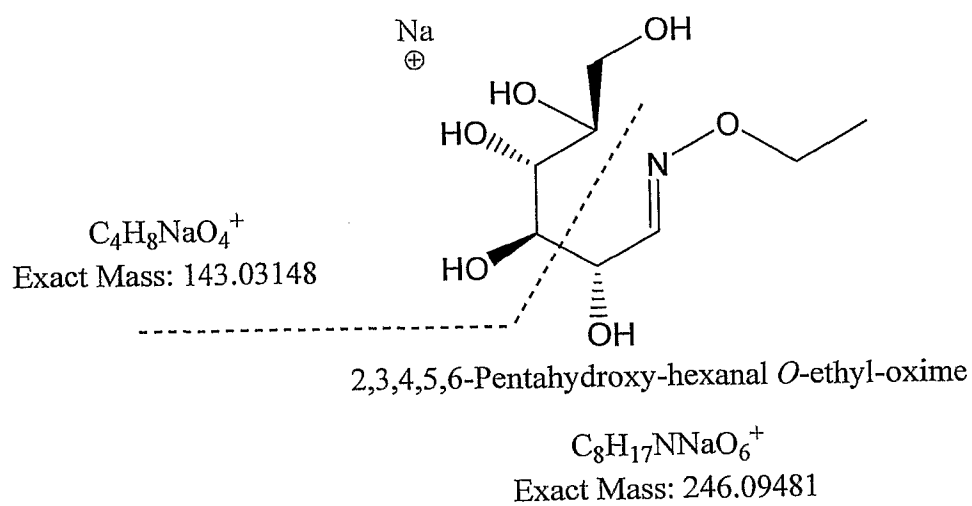
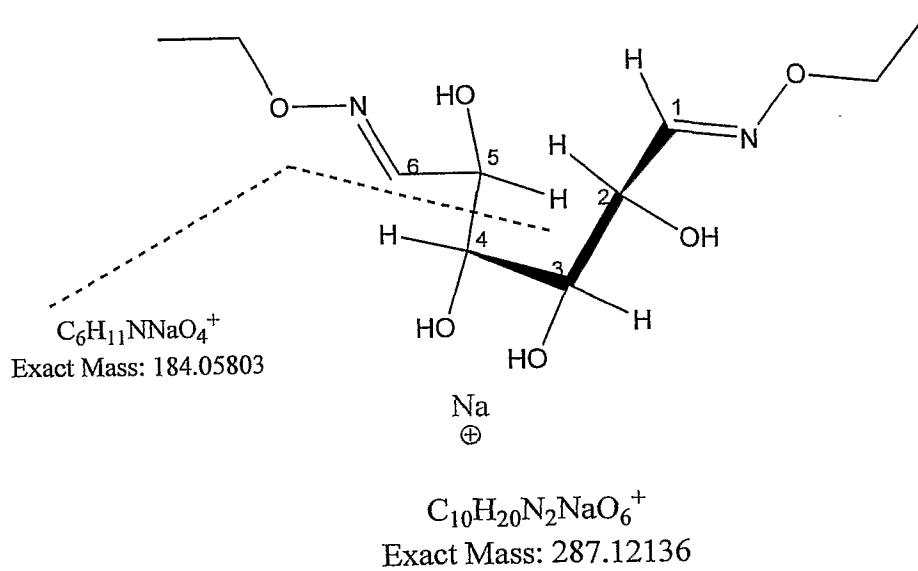


Fig. 1

2/4

**Fig. 2****Fig. 3**

3/4

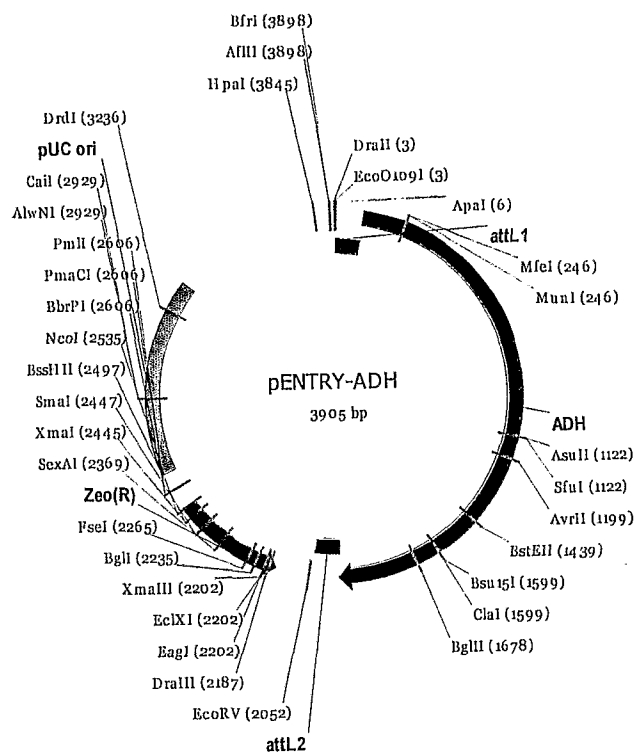


Fig. 4

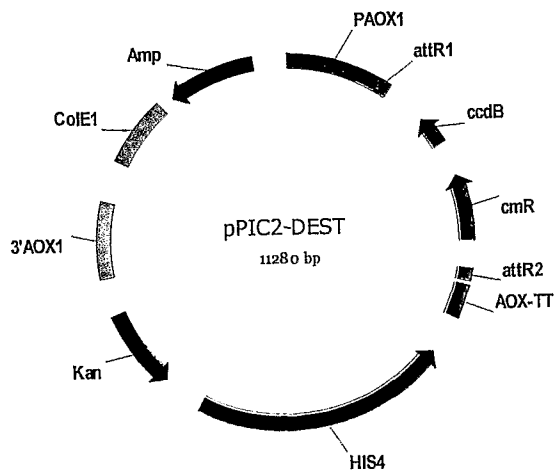
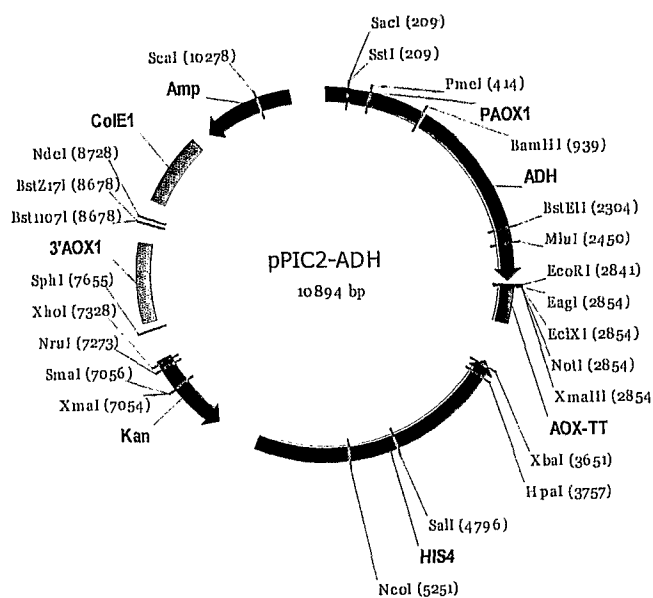
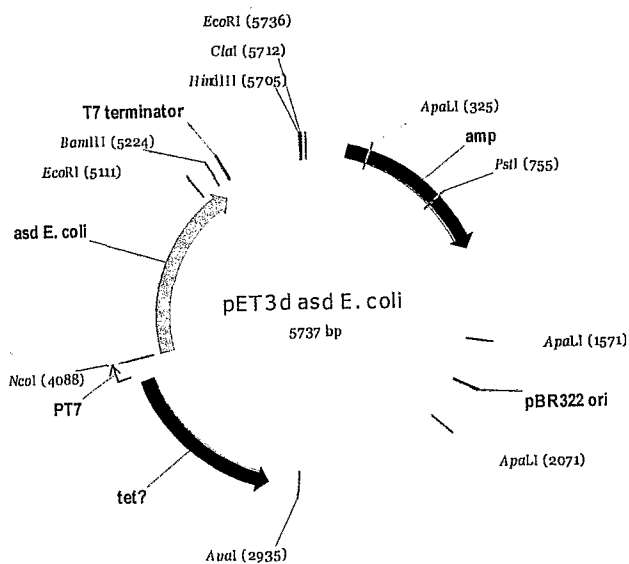


Fig. 5

**Fig. 6****Fig. 7**