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(54) Title: GLYCOSYL HYDROLASES

(57) Abstract: The invention relates to polypeptides having hydrolytic activity and polynucleotides encoding the polypeptides. The invention also relates to nucleic acid constructs, vectors, and host cells comprising the polynucleotides as well as methods of producing and using the polypeptides.

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GLYCOSYL HYDROLASES

Reference to a Sequence Listing

This application contains a Sequence Listing in computer readable form, which is incorporated herein by reference.

Background of the Invention

Field of the Invention

The present invention relates to polypeptides comprising a Glyco_hydro_114 pFam domain (PF03537) having hydrolytic activity and polynucleotides encoding the polypeptides. The invention also relates to nucleic acid constructs, vectors, and host cells comprising the polynucleotides as well as methods of producing and using the polypeptides.

Description of the Related Art

Enzymes have been used in detergents for decades. Usually a cocktail of various enzymes is added to detergent compositions. The enzyme cocktail often comprises various enzymes, wherein each enzyme targets it specific substrate e.g. amylases are active towards starch stains, proteases on protein stains and so forth. Textiles and surfaces such as laundry and dishes become soiled with many different types of soiling. The soiling may compose of proteins, grease, starch etc. Biofilm is an example of soiling and the presence of biofilm provides several disadvantages. Biofilm comprises an extracellular polymeric matrix, composed of e.g. polysaccharides, extracellular DNA (eDNA), and proteins. The extracellular polymeric matrix may be sticky or glueing, which when present on textile, give rise to redeposition or backstaining of soil resulting in a greying of the textile. Another drawback is that malodor may be trapped within the organic structure. Biofilm is therefore not desirable in textiles and surfaces associated with cleaning such as washing machines etc. As biofilm is a complex mixture of polysaccharides, proteins, DNA etc. there is a need for enzymes which effectively prevent, remove or reduce components of such soiling e.g. polysaccharides of components hereof on items such of fabrics. There is a need for enzymes which effectively remove or reduce components of organic soiling such as polysaccharides in e.g. the EPS in cleaning processes such as laundry and hard surface cleaning. The object of the present invention is to provide enzymes, which are compatible with cleaning compositions e.g. detergents and which effectively reduce polysaccharides associated e.g. with EPS.

Summary of the Invention

The present invention provides polypeptides with hydrolase activity, wherein the polypeptides comprise the Pfam database domain Glyco_hydro_114 (Pfam domain id PF03537,

Pfam version 31.0 Finn (2016). Nucleic Acids Research, Database Issue 44:D279-D285). The domain is a functional domain providing hydrolytic activity to the polypeptide. The invention further provides detergent compositions comprising polypeptides comprising the Glyco_hydro_114 domain and the use of such polypeptides for cleaning e.g. deep cleaning in cleaning processes. The polypeptides of the present invention comprising the Glyco_hydro_114 domain have beneficial properties such as cleaning e.g. deep cleaning in cleaning processes. Cleaning processes include laundry and dish wash.

In a first aspect, the present invention relates to a Glyco_hydro_114 glycosyl hydrolase comprising one, two or all three of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) and GXXGX[FY][LYFI]D (SEQ ID NO 97), wherein the Glyco_hydro_114 glycosyl hydrolase has hydrolytic activity, and wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(w) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(y) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(z) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(aa) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least

97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(bb) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(cc) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(dd) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(ee) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

The present invention also relates to glycosyl hydrolases e.g. polypeptide comprising at least one Glyco_hydro_114 glycosyl hydrolase domain. In particular, the invention relates to polypeptides selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(w) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(y) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(z) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(aa) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(bb) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(cc) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(dd) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(ee) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95;

(ff) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96;

(gg) a variant of the polypeptide selected from the group consisting of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30 and SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 and SEQ ID NO 96, wherein the variant has hydrolytic and/or deacetylase activity and comprises one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 positions;

(hh) a polypeptide comprising the polypeptide of (a) to (l) and a N-terminal and/or C-terminal His-tag and/or HQ-tag;

(ii) a polypeptide comprising the polypeptide of (a) to (l) and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; and

(jj) a fragment of the polypeptide of (a) to (l) having hydrolytic and/or deacetylase activity and having at least 90% of the length of the mature polypeptide.

The invention further relates to a cleaning composition e.g. a detergent composition, a ADW composition, a laundry composition, comprising a polypeptide according to the invention.

One aspect relates to a cleaning composition comprising:

a) at least 0.001 ppm of at least one Glyco_hydro_114 glycosyl hydrolase according to the invention; and

b) one or more cleaning composition components, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

The invention also relates to a method for laundering an item comprising the steps of:

a. Exposing an item to a wash liquor comprising a polypeptide according to the invention or a cleaning composition comprising a polypeptide according to the invention;

b. Completing at least one wash cycle; and

c. Optionally rinsing the item, wherein the item is a textile.

The invention further relates to a method for laundering an item comprising the steps of:

a. exposing an item to a wash liquor comprising a Glyco_hydro_114 glycosyl hydrolase according to the invention or a composition according to the invention;

b. completing at least one wash cycle; and

c. optionally rinsing the item,

wherein the item is a textile.

The invention further relates to use of a polypeptide according to the invention for cleaning e.g. deep cleaning of an item, such as textile e.g. fabric. The invention further relates to the use of a polypeptide according to the invention,

(i) for preventing, reducing or removing stickiness of the item;

(ii) for pretreating stains on the item;

(iii) for preventing, reducing or removing redeposition of soil during a wash cycle;

(iv) for preventing, reducing or removing adherence of soil to the item;

(v) for maintaining or improving whiteness of the item;

(vi) for preventing, reducing or removing malodor from the item,

wherein the item is a textile.

The invention further relates to the use of a Glyco_hydro_114 glycosyl hydrolase in a cleaning process, such as laundry and/or dish wash. The invention also relates to the use of a Glyco_hydro_114 glycosyl hydrolase,

i. for preventing, reducing or removing stickiness of the item;

ii. for preventing, reducing or removing biofilm or biofilm components

iii. for reducing or removing pel stains on the item;

iv. for preventing, reducing or removing redeposition of soil during a wash cycle;

v. for preventing, reducing or removing adherence of soil to the item;

vi. for maintaining or improving whiteness of the item;

vii. for preventing, reducing or removing malodor from the item,

wherein the item is a textile.

In one aspect, the invention relates to a granule comprising;

(a) a core comprising a Glyco_hydro_114 glycosyl hydrolase according to the invention, and

(b) optionally a coating consisting of one or more layer(s) surrounding the core.

The invention further relates to a polynucleotide encoding the polypeptide of the invention. A nucleic acid construct or expression vector comprising a polynucleotide encoding a polypeptide of the invention, which is operably linked to one or more control sequences that direct the production of the polypeptide in an expression host. The invention further relates to a recombinant host cell comprising a polynucleotide encoding a polypeptide of the invention, which is operably linked to one or more control sequences that direct the production of the polypeptide, wherein the method may further comprise cultivating a cell, which in its wild-type form produces the polypeptide, under conditions conducive for production of the polypeptide and optionally recovering the polypeptide.

Overview of sequences

SEQ ID NO 1 DNA encoding full length polypeptide from *Pseudomonas sp-62208*

SEQ ID NO 2 polypeptide derived from SEQ ID NO 1

SEQ ID NO 3 mature polypeptide obtained from *Pseudomonas sp-62208*

SEQ ID NO 4 DNA encoding full length polypeptide from *Environmental bacterial community A*

SEQ ID NO 5 polypeptide derived from SEQ ID NO 4

SEQ ID NO 6 mature polypeptide obtained from *Environmental bacterial community A*

SEQ ID NO 7 DNA encoding full length polypeptide from *Thermus rehai*

SEQ ID NO 8 polypeptide derived from SEQ ID NO 7

SEQ ID NO 9 mature polypeptide obtained from *Thermus rehai*

SEQ ID NO 10 DNA encoding full length polypeptide from *Environmental bacterial community LE*

SEQ ID NO 11 polypeptide derived from SEQ ID NO 10

SEQ ID NO 12 mature polypeptide obtained from *Environmental bacterial community LE*

SEQ ID NO 13 DNA encoding full length polypeptide from *Burkholderia sp-63093*

SEQ ID NO 14 polypeptide derived from SEQ ID NO 13

SEQ ID NO 15 mature polypeptide obtained from *Burkholderia sp-63093*

SEQ ID NO 16 DNA encoding full length polypeptide from *Myxococcus macrosporus*

SEQ ID NO 17 polypeptide derived from SEQ ID NO 16

SEQ ID NO 18 mature polypeptide obtained from *Myxococcus macrosporus*

SEQ ID NO 19 DNA encoding full length polypeptide from *Gallaecimonas pentaromativorans*

SEQ ID NO 20 polypeptide derived from SEQ ID NO 19

SEQ ID NO 21 mature polypeptide obtained from *Gallaecimonas pentaromativorans*

SEQ ID NO 22 DNA encoding full length polypeptide from *Nonomuraea coxensis*

SEQ ID NO 23 polypeptide derived from SEQ ID NO 22

SEQ ID NO 24 mature polypeptide obtained from *Nonomuraea coxensis*

SEQ ID NO 25 DNA encoding full length polypeptide from *Glycomyces rutgersensis*

SEQ ID NO 26 polypeptide derived from SEQ ID NO 25

SEQ ID NO 27 mature polypeptide obtained from *Glycomyces rutgersensis*

SEQ ID NO 28 DNA encoding full length polypeptide from *Environmental bact. community XE*

SEQ ID NO 29 polypeptide derived from SEQ ID NO 28

SEQ ID NO 30 mature polypeptide obtained from *Environmental bact. community XE*

SEQ ID NO 31 DNA encoding full length polypeptide from *Paraburkholderia phenazinium*

SEQ ID NO 32 polypeptide derived from SEQ ID NO 31

SEQ ID NO 33 mature polypeptide obtained from *Paraburkholderia phenazinium*

SEQ ID NO 34 motif [G]X[FY][LYF]D

SEQ ID NO 35 motif AYX[SET]XX[EAS]

SEQ ID NO 36 signal peptide MKKPLGKIVASTALLISVAFSSSIASA

SEQ ID NO 37 HHHHHHPR His -tag

SEQ ID NO 38 DNA encoding full length polypeptide from *Microbial community*

SEQ ID NO 39 polypeptide derived from SEQ ID NO 38

SEQ ID NO 40 mature polypeptide obtained from *Microbial community*

SEQ ID NO 41 DNA encoding full length polypeptide from *Myxococcus virescens*

SEQ ID NO 42 polypeptide derived from SEQ ID NO 40

SEQ ID NO 43 mature polypeptide obtained from *Myxococcus virescens*

SEQ ID NO 44 DNA encoding full length polypeptide from *Myxococcus fulvus*

SEQ ID NO 45 polypeptide derived from SEQ ID NO 43

SEQ ID NO 46 mature polypeptide obtained from *Myxococcus fulvus*

SEQ ID NO 47 DNA encoding full length polypeptide from *Myxococcus macrosporus*

SEQ ID NO 48 polypeptide derived from SEQ ID NO 47

SEQ ID NO 49 mature polypeptide obtained from *Myxococcus macrosporus*

SEQ ID NO 50 DNA encoding full length polypeptide from *Myxococcus stipitatus*

SEQ ID NO 51 polypeptide derived from SEQ ID NO 50

SEQ ID NO 52 mature polypeptide obtained from *Myxococcus stipitatus*

SEQ ID NO 53 DNA encoding full length polypeptide from *Myxococcus macrosporus*

SEQ ID NO 54 polypeptide derived from SEQ ID NO 53

SEQ ID NO 55 mature polypeptide obtained from *Myxococcus macrosporus*

SEQ ID NO 56 DNA encoding full length polypeptide from *Pseudomonas seleniipraecipitans*

SEQ ID NO 57 polypeptide derived from SEQ ID NO 56

SEQ ID NO 58 mature polypeptide obtained from *Pseudomonas seleniipraecipitans*

SEQ ID NO 59 DNA encoding full length polypeptide from *Pseudomonas migulae*

SEQ ID NO 60 polypeptide derived from SEQ ID NO 59

SEQ ID NO 61 mature polypeptide obtained from *Pseudomonas migulae*

SEQ ID NO 62 DNA encoding full length polypeptide from *Pseudomonas corrugata*

SEQ ID NO 63 polypeptide derived from SEQ ID NO 62

SEQ ID NO 64 mature polypeptide obtained from *Pseudomonas corrugata*

SEQ ID NO 65 DNA encoding full length polypeptide from *Pseudomonas pelagia*

SEQ ID NO 66 polypeptide derived from SEQ ID NO 65

SEQ ID NO 67 mature polypeptide obtained from *Pseudomonas pelagia*

SEQ ID NO 68 DNA encoding full length polypeptide from *Pseudomonas aeruginosa PAO1*

SEQ ID NO 69 polypeptide derived from SEQ ID NO 68

SEQ ID NO 70 mature polypeptide obtained from *Pseudomonas aeruginosa PAO1*

SEQ ID NO 71 DNA encoding full length polypeptide from *Streptomyces griseofuscus*

SEQ ID NO 72 polypeptide derived from SEQ ID NO 71

SEQ ID NO 73 mature polypeptide obtained from *Streptomyces griseofuscus*

SEQ ID NO 74 DNA encoding full length polypeptide from *Lysinibacillus xylanilyticus*

SEQ ID NO 75 polypeptide derived from SEQ ID NO 74

SEQ ID NO 76 mature polypeptide obtained from *Lysinibacillus xylanilyticus*

SEQ ID NO 77 DNA encoding full length polypeptide from *Tumebacillus ginsengisoli*

SEQ ID NO 78 polypeptide derived from SEQ ID NO 77

SEQ ID NO 79 mature polypeptide obtained from *Tumebacillus ginsengisoli*

SEQ ID NO 80 DNA encoding full length polypeptide from *Lysinibacillus boronitolerans*

SEQ ID NO 81 polypeptide derived from SEQ ID NO 80

SEQ ID NO 82 mature polypeptide obtained from *Lysinibacillus boronitolerans*

SEQ ID NO 83 DNA encoding full length polypeptide from *Microbulbifer hydrolyticus*

SEQ ID NO 84 polypeptide derived from SEQ ID NO 83

SEQ ID NO 85 mature polypeptide obtained from *Microbulbifer hydrolyticus*

SEQ ID NO 86 DNA encoding full length polypeptide from *Carnobacterium inhibens subsp. gilichinskyi*

SEQ ID NO 87 polypeptide derived from SEQ ID NO 86

SEQ ID NO 88 mature polypeptide obtained from *Carnobacterium inhibens subsp. gilichinskyi*

SEQ ID NO 89 DNA encoding full length polypeptide from environmental bacterial community

SEQ ID NO 90 polypeptide derived from SEQ ID NO 89

SEQ ID NO 91 mature polypeptide obtained from environmental bacterial community

SEQ ID NO 92 DNA encoding full length polypeptide from *Pseudomonas composti*

SEQ ID NO 93 polypeptide derived from SEQ ID NO 92

SEQ ID NO 94 mature polypeptide obtained from *Pseudomonas composti*

SEQ ID NO 95 mature polypeptide obtained from *Paraburkholderia phenazinium*

SEQ ID NO 96 mature polypeptide obtained from *Burkholderia sp-63093*

SEQ ID NO 97: motif GXXGX[FY][LYFI]D

SEQ ID NO 98: motif [ILFQV]N[RW]G[FL]

SEQ ID NO 99: motif DTLDS[YF]

SEQ ID NO 100: motif G[VL]FLDTLDSF[QTH]L[LMQ]

SEQ ID NO 101: motif DT[VIMA][GD][DNW][VIL][DEN]

SEQ ID NO 102: motif [SETC]IG[EQA][ALI]EXY

SEQ ID NO 103: motif [QL]N[AS]PEL

SEQ ID NO 104: motif [KLYMQ]XX[PV]QN[SA]PE

Definitions

Activity: The present inventions relates to glycosyl hydrolases (EC 3.2.1.-), which are a widespread group of enzymes that hydrolyse the glyosidic bond between two or more carbohydrates or between a carbohydrate and a non-carbohydrate moiety. A classification of glycoside hydrolases in families based on amino acid sequence similarities has been proposed. The polypeptides of the invention comprise at least one glycosyl hydrolase domain and are in the present context defined as glycosyl hydrolases. Thus, polypeptides of the invention hydrolyse

glyosidic bonds and the polypeptide of the invention have hydrolytic activity. The glycosyl hydrolase domain comprised in the polypeptide of the invention may be classified as a Glyco_hydro_114 (Pfam domain id PF03537, Pfam version 31.0 Finn (2016). Nucleic Acids Research, Database Issue 44:D279-D285). The polypeptides of the invention may further comprise a polysaccharide deacetylase domain (CE4) and in a preferred embodiment the polypeptides of the invention have hydrolytic and/or deacetylase activity. Polypeptides according to the invention having hydrolytic and/or deacetylase activity includes Glyco_hydro_114 glycosyl hydrolases. A Glyco_hydro_114 glycosyl hydrolase is in the context of the present invention a glycosyl hydrolase comprising glycosyl hydrolase domain (DUF297), which here is termed Glyco_hydro_114 (Pfam domain id PF03537, Pfam version 31.0 Finn (2016). The Glyco_hydro_114 glycosyl hydrolase domain is located at position 9 to 218 in SEQ ID NO 3, at position 14 to 247 in SEQ ID NO 6, at position 222 to 420 in SEQ ID NO 9, at position 18 to 229 in SEQ ID NO 76, at position 31 to 241 in SEQ ID NO 79, at position 14 to 226 in SEQ ID NO 82, at position 56 to 199 in SEQ ID NO 73, at position 12 to 221 in SEQ ID NO 15, at position 205 to 427 in SEQ ID NO 18, at position 206 to 428 in SEQ ID NO 12, at position 6 to 204 in SEQ ID NO 21, at position 11 to 237 in SEQ ID NO 24, at position 16 to 240 in SEQ ID NO 27, at position 10 to 243 in SEQ ID NO 30, at position 22 to 231 in SEQ ID NO 33, at position 9 to 218 in SEQ ID NO 40, at position 205 to 427 in SEQ ID NO 43, at position 202 to 424 in SEQ ID NO 46, at position 213 to 435 in SEQ ID NO 49, at position 207 to 429 in SEQ ID NO 52, at position 213 to 435 in SEQ ID NO 55, at position 60 to 269 in SEQ ID NO 58, at position 9 to 218 in SEQ ID NO 61, at position 9 to 218 in SEQ ID NO 64, at position 10 to 219 in SEQ ID NO 67, at position 6 to 215 in SEQ ID NO 70, at position 181 to 310 in SEQ ID NO 85, at position 27 to 226 in SEQ ID NO 88, at position 173 to 292 in SEQ ID NO 91, at position 5 to 210 in SEQ ID NO 94, at position 22 to 231 in SEQ ID NO 95, at position 12 to 221 in SEQ ID NO 96. The polypeptides of the invention are glycosyl hydrolases preferably Glyco_hydro_114 glycosyl hydrolases. In one preferred embodiment, the polypeptides of the invention are endo-alpha-1,4-polygalactosaminidases. The polypeptides of the invention have at least hydrolytic activity to glyosidic bond and may also have deacetylase activity. In the context of the present invention the Glyco_hydro_114 glycosyl hydrolase is a PelA enzyme, which is active towards the polysaccharide pel, present in many biofilms. The pellicle (PEL) polysaccharide is synthesized e.g. by *Pseudomonas aeruginosa* and is an important biofilm constituent critical for bacterial virulence and persistence. Pel is a cationic polymer composed of partially acetylated 1→4 glycosidic linkages of N-acetylgalactosamine and N-acetylglucosamine that promotes cell-cell interactions within the biofilm matrix through electrostatic interactions with extracellular DNA (Jennings et al. PNAS Sept 2015, vol.112, no36, 11353-11358; Marmont et.al. J Biol Chem. 2017 Nov 24;292(47):19411-19422. 2017).

Allelic variant: The term “allelic variant” means any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and

may result in polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

Biofilm: A biofilm is organic matter produced by any group of microorganisms in which cells stick to each other or stick to a surface, such as a textile, dishware or hard surface or another kind of surface. These adherent cells are frequently embedded within a self-produced matrix of extracellular polymeric substance (EPS). Biofilm EPS is a polymeric conglomeration generally composed of extracellular DNA, proteins, and polysaccharides. Biofilms may form on living or non-living surfaces. The microbial cells growing in a biofilm are physiologically distinct from planktonic cells of the same organism, which, by contrast, are single-cells that may float or swim in a liquid medium. Bacteria living in a biofilm usually have significantly different properties from planktonic bacteria of the same species, as the dense and protected environment of the film allows them to cooperate and interact in various ways. One benefit of this environment for the microorganisms is increased resistance to detergents and antibiotics, as the dense extracellular matrix and the outer layer of cells protect the interior of the community. On laundry biofilm or EPS producing bacteria can be found among the following species: *Acinetobacter sp., Aeromicrobium sp., Brevundimonas sp., Microbacterium sp., Micrococcus luteus, Pseudomonas sp., Staphylococcus epidermidis, and Stenotrophomonas sp*. In one aspect, the biofilm producing strain is *Pseudomonas*. In one aspect, the EPS producing strain is *Pseudomonas aeruginosa*, *Pseudomonas alcaliphila* or *Pseudomonas fluorescens*. In one embodiment, the biofilm is caused by microorganisms or group of microorganisms which produce Pel. In another embodiment, the biofilm produce a polysaccharide that is degradable by the Glyco_hydro_114 glycosyl hydrolases of the invention. The biofilm that may be formed on the surface e.g. such as textiles may be caused by any microorganism or group of microorganisms that forms PelA-dependent biofilm including but not limited to; *Acinetobacter sp., Aeromicrobium sp., Brevundimonas sp., Microbacterium sp., Micrococcus luteus, Staphylococcus epidermidis, Staphylococcus aureus*, *Pseudomonas sp., Pseudomonas aeruginosa*, *Pseudomonas alcaliphila*, *Pseudomonas fluorescens*, *Stenotrophomonas sp*., *Paraburkholderia*, *Burkolderia* sp., *Candida* sp., *Bordetella pertussis Yersinia pestis, Escherichia coli* and *Aspergillus* sp.

Catalytic domain: The term “catalytic domain” means the region of an enzyme containing the catalytic machinery of the enzyme.

Clade: A clade is a group of polypeptides clustered together on the basis of homologous features traced to a common ancestor. Polypeptide clades can be visualized as phylogenetic trees and a clade is a group of polypeptides that consists of a common ancestor and all its lineal descendants. Example 5 describes generation of phylogenetic trees.

cDNA: The term "cDNA" means a DNA molecule that can be prepared by reverse transcription from a mature, spliced, mRNA molecule obtained from a eukaryotic or prokaryotic cell. cDNA lacks intron sequences that may be present in the corresponding genomic DNA. The

initial, primary RNA transcript is a precursor to mRNA that is processed through a series of steps, including splicing, before appearing as mature spliced mRNA.

Coding sequence: The term "coding sequence" means a polynucleotide, which directly specifies the amino acid sequence of a polypeptide. The boundaries of the coding sequence are generally determined by an open reading frame, which begins with a start codon such as ATG, GTG, or TTG and ends with a stop codon such as TAA, TAG, or TGA. The coding sequence may be a genomic DNA, cDNA, synthetic DNA, or a combination thereof.

Control sequences: The term "control sequences" means nucleic acid sequences necessary for expression of a polynucleotide encoding a mature polypeptide of the present invention. Each control sequence may be native (*i.e.*, from the same gene) or foreign (*i.e.*, from a different gene) to the polynucleotide encoding the polypeptide or native or foreign to each other. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the polynucleotide encoding a polypeptide.

Deep cleaning: The term "deep cleaning" means disruption, reduction or removal of organic components such as polysaccharides e.g. Pel, proteins, DNA, soil or other components present in organic matter such as biofilm.

Cleaning component: The cleaning component e.g. a detergent adjunct ingredient is different to the polypeptides of this invention. The precise nature of these additional cleaning or adjunct components, and levels of incorporation thereof, will depend on the physical form of the composition and the nature of the operation for which it is to be used. Suitable cleaning components include, but are not limited to the components described below such as surfactants, builders, flocculating aid, chelating agents, dye transfer inhibitors, enzymes, enzyme stabilizers, enzyme inhibitors, catalytic materials, bleach activators, hydrogen peroxide, sources of hydrogen peroxide, preformed peracids, polymeric agents, clay soil removal/anti-redeposition agents, brighteners, suds suppressors, dyes, perfumes, structure elasticizing agents, fabric softeners, carriers, hydrotropes, builders and co-builders, fabric huing agents, anti-foaming agents, dispersants, processing aids, and/or pigments.

Cleaning Composition: The term cleaning composition includes "detergent composition" and refers to compositions that find use in the removal of undesired compounds from items to be cleaned, such as textiles. The detergent composition may be used to e.g. clean textiles for both household cleaning and industrial cleaning. The terms encompass any materials/compounds selected for the particular type of cleaning composition desired and the form of the product (e.g., liquid, gel, powder, granulate, paste, or spray compositions) and includes, but is not limited to, detergent compositions (e.g., liquid and/or solid laundry detergents

and fine fabric detergents; fabric fresheners; fabric softeners; and textile and laundry pre-spotters/pretreatment). In addition to containing the enzyme of the invention, the detergent formulation may contain one or more additional enzymes (such as proteases, amylases, lipases, cutinases, cellulases, endoglucanases, xyloglucanases, pectinases, pectin lyases, xanthanases, peroxidases, haloperoxygenases, catalases and mannanases, or any mixture thereof), and/or detergent adjunct ingredients such as surfactants, builders, chelators or chelating agents, bleach system or bleach components, polymers, fabric conditioners, foam boosters, suds suppressors, dyes, perfume, tannish inhibitors, optical brighteners, bactericides, fungicides, soil suspending agents, anti-corrosion agents, enzyme inhibitors or stabilizers, enzyme activators, transferase(s), hydrolytic enzymes, oxido reductases, bluing agents and fluorescent dyes, antioxidants, and solubilizers.

Enzyme Detergency benefit: The term "enzyme detergency benefit" is defined herein as the advantageous effect an enzyme may add to a detergent compared to the same detergent without the enzyme. Important detergency benefits which can be provided by enzymes are stain removal with no or very little visible soils after washing and/or cleaning, prevention or reduction of redeposition of soils released in the washing process (an effect that also is termed anti-redeposition), restoring fully or partly the whiteness of textiles which originally were white but after repeated use and wash have obtained a greyish or yellowish appearance (an effect that also is termed whitening). Textile care benefits, which are not directly related to catalytic stain removal or prevention of redeposition of soils, are also important for enzyme detergency benefits. Examples of such textile care benefits are prevention or reduction of dye transfer from one fabric to another fabric or another part of the same fabric (an effect that is also termed dye transfer inhibition or anti-backstaining), removal of protruding or broken fibers from a fabric surface to decrease pilling tendencies or remove already existing pills or fuzz (an effect that also is termed anti-pilling), improvement of the fabric-softness, colour clarification of the fabric and removal of particulate soils which are trapped in the fibers of the fabric or garment. Enzymatic bleaching is a further enzyme detergency benefit where the catalytic activity generally is used to catalyze the formation of bleaching components such as hydrogen peroxide or other peroxides.

Expression: The term "expression" includes any step involved in the production of a polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

Expression vector: The term "expression vector" means a linear or circular DNA molecule that comprises a polynucleotide encoding a polypeptide and is operably linked to control sequences that provide for its expression.

Fragment: The term "fragment" means a polypeptide or a catalytic domain having one or more (*e.g.*, several) amino acids absent from the amino and/or carboxyl terminus of a mature polypeptide or domain; wherein the fragment has activity.

Host cell: The term "host cell" means any cell type that is susceptible to transformation, transfection, transduction, or the like with a nucleic acid construct or expression vector comprising a polynucleotide of the present invention. The term “host cell” encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication.

Isolated: The term “isolated” means a substance in a form or environment that does not occur in nature. Non-limiting examples of isolated substances include (1) any non-naturally occurring substance, (2) any substance including, but not limited to, any enzyme, variant, nucleic acid, protein, peptide or cofactor, that is at least partially removed from one or more or all of the naturally occurring constituents with which it is associated in nature; (3) any substance modified by the hand of man relative to that substance found in nature; or (4) any substance modified by increasing the amount of the substance relative to other components with which it is naturally associated (*e.g.*, recombinant production in a host cell; multiple copies of a gene encoding the substance; and use of a stronger promoter than the promoter naturally associated with the gene encoding the substance). An isolated substance may be present in a fermentation broth sample; e.g. a host cell may be genetically modified to express the polypeptide of the invention. The fermentation broth from that host cell will comprise the isolated polypeptide.

Improved wash performance: The term “improved wash performance” is defined herein as an enzyme displaying an increased wash performance in a detergent composition relative to the wash performance of same detergent composition without the enzyme e.g. by increased stain removal or less re-deposition. The term “improved wash performance” includes wash performance in laundry.

Laundering: The term “laundering” relates to both household laundering and industrial laundering and means the process of treating textiles with a solution containing a cleaning or detergent composition of the present invention. The laundering process can for example be carried out using e.g. a household or an industrial washing machine or can be carried out by hand.

Malodor: By the term ”malodor” is meant an odor which is not desired on clean items. The cleaned item should smell fresh and clean without malodors adhered to the item. One example of malodor is compounds with an unpleasant smell, which may be produced by microorganisms. Another example is unpleasant smells can be sweat or body odor adhered to an item which has been in contact with human or animal. Another example of malodor can be the odor from spices, which sticks to items for example curry or other exotic spices which smells strongly.

Mature polypeptide: The term “mature polypeptide” means a polypeptide in its final form following translation and any post-translational modifications, such as N-terminal processing, C-terminal truncation, glycosylation, phosphorylation, etc. In some aspects, the mature polypeptide is amino acids 1 to 904 of SEQ ID NO 2 and amino acids -32 to -1 of SEQ ID NO 2 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence shown

in SEQ ID NO 3. In some aspects, the mature polypeptide is amino acids 1 to 281 of SEQ ID NO 5 and amino acids -21 to -1 of SEQ ID NO 5 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence shown in SEQ ID NO 6. In some aspects, the mature polypeptide is amino acids 1 to 458 of SEQ ID NO 8 and amino acids -18 to -1 of SEQ ID NO 8 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 9. In some aspects, the mature polypeptide is amino acids 1 to 468 of SEQ ID NO 11 and amino acids -26 to -1 of SEQ ID NO 11 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 12. In some aspects, the mature polypeptide is amino acids 1 to 266 of SEQ ID NO 14 and amino acids -45 to -1 of SEQ ID NO 14 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 15. In some aspects, the mature polypeptide is amino acids 1 to 467 of SEQ ID NO 17 and amino acids -28 to -1 of SEQ ID NO 17 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 18. In some aspects, the mature polypeptide is amino acids 1 to 882 of SEQ ID NO 20 and amino acids -16 to -1 of SEQ ID NO 20 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 21. In some aspects, the mature polypeptide is amino acids 1 to 279 of SEQ ID NO 23 and amino acids -21 to -1 of SEQ ID NO 23 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 24. In some aspects, the mature polypeptide is amino acids 1 to 276 of SEQ ID NO 26 and amino acids -22 to -1 of SEQ ID NO 26 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 27. In some aspects, the mature polypeptide is amino acids 1 to 277 of SEQ ID NO 29 and amino acids -26 to -1 of SEQ ID NO 29 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 30. In some aspects, the mature polypeptide is amino acids 1 to 271 of SEQ ID NO 32 and amino acids -29 to -1 of SEQ ID NO 32 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 33. In some aspects, the mature polypeptide is amino acids 1 to 905 of SEQ ID NO 39 and amino acids -32 to -1 of SEQ ID NO 39 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 40. In some aspects, the mature polypeptide is amino acids 1 to 467 of SEQ ID NO 42 and amino acids -28 to -1 of SEQ ID NO 42 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 43. In some aspects, the mature polypeptide is amino acids 1 to 464 of SEQ ID NO 45 and amino acids -18 to -1 of SEQ ID NO 45 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 46. In some aspects, the mature polypeptide is amino acids 1 to 475 of SEQ ID NO 48 and amino acids -24 to -1 of SEQ ID NO 48 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 49. In some aspects, the mature polypeptide is amino acids 1 to 469 of SEQ ID NO 51 and amino acids -24 to -1 of SEQ ID NO 51 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 52. In some aspects, the

mature polypeptide is amino acids 1 to 475 of SEQ ID NO 54 and amino acids -24 to -1 of SEQ ID NO 54 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 55. In some aspects, the mature polypeptide is amino acids 1 to 906 of SEQ ID NO 57 and amino acids -49 to -1 of SEQ ID NO 57 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 58. In some aspects, the mature polypeptide is amino acids 1 to 905 of SEQ ID NO 60 and amino acids -32 to -1 of SEQ ID NO 60 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 61. In some aspects, the mature polypeptide is amino acids 1 to 905 of SEQ ID NO 63 and amino acids -32 to -1 of SEQ ID NO 63 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 64. In some aspects, the mature polypeptide is amino acids 1 to 906 of SEQ ID NO 66 and amino acids -31 to -1 of SEQ ID NO 66 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 67. In some aspects, the mature polypeptide is amino acids 1 to 257 of SEQ ID NO 69 and in some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 70. In some aspects, the mature polypeptide is amino acids 1 to 269 of SEQ ID NO 72 and amino acids -43 to -1 of SEQ ID NO 72 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 73. In some aspects, the mature polypeptide is amino acids 1 to 260 of SEQ ID NO 75 and amino acids -26 to -1 of SEQ ID NO 75 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 76. In some aspects, the mature polypeptide is amino acids 1 to 275 of SEQ ID NO 78 and amino acids -30 to -1 of SEQ ID NO 78 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 79. In some aspects, the mature polypeptide is amino acids 1 to 268 of SEQ ID NO 81 and amino acids -28 to -1 of SEQ ID NO 81 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 82. In some aspects, the mature polypeptide is amino acids 1 to 313 of SEQ ID NO 84 and amino acids -16 to -1 of SEQ ID NO 84 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 85. In some aspects, the mature polypeptide is amino acids 1 to 257 of SEQ ID NO 87 and amino acids -24 to -1 of SEQ ID NO 87 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 88. In some aspects, the mature polypeptide is amino acids 1 to 296 of SEQ ID NO 90 and amino acids -24 to -1 of SEQ ID NO 90 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 91. In some aspects, the mature polypeptide is amino acids 1 to 897 of SEQ ID NO 93 and amino acids -26 to -1 of SEQ ID NO 93 is a signal peptide. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 94. In some aspects, the mature polypeptide is amino acids 1 to 271 of SEQ ID NO 95. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 95. In some aspects, the mature polypeptide is amino acids 1 to 271 of SEQ ID NO 96. In some aspects, the mature polypeptide is the amino acid sequence having SEQ ID NO 96.

It is known in the art that a host cell may produce a mixture of two of more different mature polypeptides (*i.e.*, with a different C-terminal and/or N-terminal amino acid) expressed by the same polynucleotide. It is also known in the art that different host cells process polypeptides differently, and thus, one host cell expressing a polynucleotide may produce a different mature polypeptide (*e.g.*, having a different C-terminal and/or N-terminal amino acid) as compared to another host cell expressing the same polynucleotide.

Mature polypeptide coding sequence: The term "mature polypeptide coding sequence" means a polynucleotide that encodes a mature polypeptide having activity. In one aspect, the mature polypeptide coding sequence is nucleotides 97 to 2808 of SEQ ID NO 1 and nucleotides 1 to 96 of SEQ ID NO 1 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 64 to 906 of SEQ ID NO 4 and nucleotides 1 to 63 of SEQ ID NO 4 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 55 to 1428 of SEQ ID NO 7 and nucleotides 1 to 54 of SEQ ID NO 7 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 79 to 1482 of SEQ ID NO 10 and nucleotides 1 to 78 of SEQ ID NO 10 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 136 to 933 of SEQ ID NO 13 and nucleotides 1 to 135 of SEQ ID NO 13 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 85 to 1485 of SEQ ID NO 16 and nucleotides 1 to 84 of SEQ ID NO 16 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 49 to 2694 of SEQ ID NO 19 and nucleotides 1 to 48 of SEQ ID NO 19 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 64 to 900 of SEQ ID NO 22 and nucleotides 1 to 63 of SEQ ID NO 22 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 67 to 894 of SEQ ID NO 25 and nucleotides 1 to 66 of SEQ ID NO 25 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 79 to 909 of SEQ ID NO 28 and nucleotides 1 to 78 of SEQ ID NO 28 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 88 to 900 of SEQ ID NO 31 and nucleotides 1 to 87 of SEQ ID NO 31 encodes a signal peptide.

In one aspect, the mature polypeptide coding sequence is nucleotides 97 to 2811 of SEQ ID NO 38 and nucleotides 1 to 96 of SEQ ID NO 38 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 85 to 1485 of SEQ ID NO 41 and nucleotides 1 to 84 of SEQ ID NO 41 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 55 to 1446 of SEQ ID NO 44 and nucleotides 1 to 54 of SEQ ID NO 44 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 1497 of SEQ ID NO 47 and nucleotides 1 to 72 of SEQ ID NO 47 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 1479 of SEQ ID NO 50 and nucleotides 1 to 72 of SEQ ID NO 50 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 1497 of SEQ ID NO 53 and nucleotides 1 to 72

of SEQ ID NO 53 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 148 to 2865 of SEQ ID NO 56 and nucleotides 1 to 147 of SEQ ID NO 56 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 97 to 2811 of SEQ ID NO 59 and nucleotides 1 to 96 of SEQ ID NO 59 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 97 to 2811 of SEQ ID NO 62 and nucleotides 1 to 96 of SEQ ID NO 62 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 94 to 2811 of SEQ ID NO 65 and nucleotides 1 to 93 of SEQ ID NO 65 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 1 to 771 of SEQ ID NO 68. In one aspect, the mature polypeptide coding sequence is nucleotides 130 to 936 of SEQ ID NO 71 and nucleotides 1 to 129 of SEQ ID NO 71 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 79 to 858 of SEQ ID NO 74 and nucleotides 1 to 78 of SEQ ID NO 74 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 91 to 915 of SEQ ID NO 77 and nucleotides 1 to 90 of SEQ ID NO 77 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 85 to 888 of SEQ ID NO 80 and nucleotides 1 to 84 of SEQ ID NO 80 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 49 to 987 of SEQ ID NO 83 and nucleotides 1 to 48 of SEQ ID NO 83 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 843 of SEQ ID NO 86 and nucleotides 1 to 72 of SEQ ID NO 86 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 960 of SEQ ID NO 89 and nucleotides 1 to 72 of SEQ ID NO 89 encodes a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 79 to 2769 of SEQ ID NO 92 and nucleotides 1 to 78 of SEQ ID NO 92 encodes a signal peptide.

Nucleic acid construct: The term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or is modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature or which is synthetic, which comprises one or more control sequences.

Nomenclature: For purposes of the present invention, the nomenclature [E/Q] means that the amino acid at this position may be a glutamic acid (Glu, E) or a glutamine (Gln, Q). Likewise, the nomenclature [V/G/A/I] means that the amino acid at this position may be a valine (Val, V), glycine (Gly, G), alanine (Ala, A) or isoleucine (Ile, I), and so forth for other combinations as described herein. Unless otherwise limited further, the amino acid X is defined such that it may be any of the 20 natural amino acids.

Operably linked: The term “operably linked” means a configuration in which a control sequence is placed at an appropriate position relative to the coding sequence of a polynucleotide such that the control sequence directs expression of the coding sequence.

Sequence identity: The relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter “sequence identity”.

For purposes of the present invention, the sequence identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *J. Mol. Biol.* 48: 443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice *et al.*, 2000, *Trends Genet.* 16: 276-277), preferably version 5.0.0 or later. The parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix. The output of Needle labeled "longest identity" (obtained using the –nobrief option) is used as the percent identity and is calculated as follows:

(Identical Residues x 100)/(Length of Alignment – Total Number of Gaps in Alignment)

Variant: The term "variant" means a polypeptide having hydrolase activity comprising an alteration, *i.e.*, a substitution, insertion, and/or deletion, at one or more (*e.g.*, several) positions. A substitution means replacement of the amino acid occupying a position with a different amino acid; a deletion means removal of the amino acid occupying a position; and an insertion means adding an amino acid adjacent to and immediately following the amino acid occupying a position.

Detailed Description of the Invention

Various enzymes are applied in cleaning processes each targeting specific types of soiling such as protein, starch and grease soiling. Enzymes are now standard ingredients in detergents for laundry and dish wash. The effectiveness of these commercial enzymes provides detergents which removes much of the soiling. However, organic matters such as EPS (extracellular polymeric substance) comprised in much biofilm constitute a challenging type of soiling due to the complex nature of such organic matters. None of the commercially available detergents effectively remove or reduce EPS related soiling. Biofilm is produced by a group of microorganisms in which cells stick to each other or stick to a surface, such as a textile, dishware or hard surface or another kind of surface. These adherent cells are frequently embedded within a self-produced matrix of extracellular polymeric substance (EPS), which constitute 50% to 90% of the biofilm's total organic matter. EPS is mostly composed of polysaccharides (exopolysaccharides) and proteins, but include other macro-molecules such as DNA, lipids and human substances. EPS is the construction material of bacterial settlements and either remain attached to the cell's outer surface, or is secreted into its growth medium. EPS is required for the development and integrity of biofilms produced by a wide variety of bacteria. The inventors have shown that the Glyco_hydro_114 polypeptides comprising the Glyco_hydro_114 glycosyl hydrolase domain and/or the deacetylase CE4 domain have hydrolytic activity to the exopolysaccharide Pel and thus having the potential to reduce or remove components of EPS and thus reduce or remove EPS related soiling of e.g. textiles. It is well known that polypeptides deriving from organisms may share common structural elements, which can be identified by comparing the primary structures e.g. amino acid sequences and grouping the polypeptides according to sequence homology. However, common structural elements may also be identified

by comparing the three-dimensional (3D) structure of various polypeptides. Both approaches have been applied in the present invention.

These approaches identified polypeptides, which derive from organisms from divergent taxonomic groups but share structural elements common for the identified group.

The polypeptides of the invention comprise a domain termed here as CE4_PelA_like domain, which are represented by a protein PelA that is encoded by a gene in the pelA-G gene cluster for pellicle production and biofilm formation in *Pseudomonas aeruginosa*. PelA and most of the family members contain a domain of unknown function, DUF297 (PF03537), in the N-terminus and a C-terminal domain that shows high sequence similarity to the catalytic domain of the six-stranded barrel rhizobial NodB-like proteins, which remove N-linked or O-linked acetyl groups from cell wall polysaccharides and belong to the larger carbohydrate esterase 4 (CE4) superfamily. The polypeptides of the present invention comprise the Glyco_hydro_114 domain and several motifs. One example is GX[FY][LYF]D (SEQ ID NO 34) situated in positions corresponding to positions 113 to 117 in *Pseudomonas sp-62208* (SEQ ID NO 3). Another motif which may be comprised by the polypeptides of the invention is AYX[SET]XX[EAS] (SEQ ID NO 35) situated in positions corresponding to positions 53 to 58 in *Pseudomonas sp-62208* (SEQ ID NO 3). The polypeptides in Glyco_hydro_114 can be separated into distinct sub-clusters, where we denoted one sub-cluster comprising the motif GX[FY][LYF]D (SEQ ID NO 34) or the motif GXXGX[FY][LYFI]D (SEQ ID NO 97) as family FLD. Another motif characteristic of this domain is AYX[SET]XX[EAS] (SEQ ID NO 35).

One embodiment of the invention relates a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase polypeptide comprising the DUF297 domain and preferably comprising one, two or all three of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97), wherein the polypeptide has hydrolytic activity, and wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(w) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(y) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(z) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(aa) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(bb) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(cc) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(dd) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(ee) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(ff) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

The polypeptides of the invention preferably belong to the cluster FLD, which comprises the a glycosyl hydrolytic domain Glyco_hydro_114 and have hydrolytic activity. In some embodiment, the polypeptides additionally comprise a CE4 domain and have deacetylase activity.

The polypeptides of the FLD clade, which includes all PelA Glyco_hydro_114 glycosyl hydrolases comprising the amino acids sequence shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 and SEQ ID NO 96. The FLD-clade (or polypeptides of the FLD-domain) may be divided in two further clades or sub-clades (see figure 3), which again may be divided into further sub-clades, see below. These sub-clades are termed NRG and IGEAE clades and comprises polypeptides of bacterial origin having hydrolase activity, wherein the polypeptides comprise a Glyco_hydro_114 domain and belong to the FLD clade.

The polypeptides of the NRG clade comprise the motif example [ILFQV]N[RW]G[FL] (SEQ ID NO 98), corresponding to amino acids FNRGF at positions 155 to 159 of SEQ ID NO 3 where N and G (corresponding to position 156 and 158 of SEQ ID NO 3) is fully conserved in NRG clade. Examples of polypeptides of the NRG clade includes SEQ ID NO 3, SEQ ID NO 9, SEQ ID NO 15, SEQ ID NO 21, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 94, SEQ ID NO 95, and SEQ ID NO 96.

One embodiment of the invention relates a glycosyl hydrolase preferably a Glyco_hydro_114 glycosyl hydrolase comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98), wherein the glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(e) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(f) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(g) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(h) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(i) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(k) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(n) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(o) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

The NRG sub-clade may be further be divided into yet another subgroup, which here is termed DTLDS clade (se figure 3). The DTLDS clade comprises polypeptides of bacterial origin having hydrolase activity, wherein the polypeptides comprise a Glyco_hydro_114 domain and belong to the NRG clade (and the FLD-clade). The polypeptides of the clade comprise the motif example DTLDS[YF] (SEQ ID NO 99), corresponding to amino acids DTLDSF positions 117 to 122 of SEQ ID NO 3 where DTLDS (corresponding to positions 117 and 121 of SEQ ID NO 3) is fully conserved in DTLDS clade, and D at position 117 is part of the substrate binding pocket and one of the two putative catalytic site residues. Examples of polypeptides of the DTLDS clade includes SEQ ID NO 3, SEQ ID NO 15, SEQ ID NO 21, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 94, SEQ ID NO 95, and SEQ ID NO 96.

One embodiment of the invention relates a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98) and/or the motif DTLDS[YF] (SEQ ID NO 99), wherein the glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98) and/or the motif DTLDS[YF] (SEQ ID NO 99), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(d) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(e) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(f) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(g) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(h) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(j) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(l) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

The DTLDS sub-clade may be further be divided into yet another subgroup, which here is termed GVFLD clade (se figure 3). The GVFLD clade comprises polypeptides of bacterial origin having

hydrolase activity, wherein the polypeptides comprise a Glyco_hydro_114 domain and belong to the DTLDS clade (and the NRG and FLD-clade). The GVFLD clade comprises polypeptides of bacterial origin having hydrolase activity, wherein the polypeptides comprise a Glyco_hydro_114 domain and belonging to the DTLDS clade (and the NRG and FLD-clade). The polypeptides of the GVFLD clade comprise the motif G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), corresponding to amino acids GLFLDTLDSFQLL positions 113 to 125 of SEQ ID NO 3 where D (corresponding to position 117 of SEQ ID NO 3) is fully conserved in GVFLD clade, part of the substrate binding pocket, and one of the two putative catalytic site residues. Examples of polypeptides of the GVFLD clade includes SEQ ID NO 3, SEQ ID NO 40, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, and SEQ ID NO 94.

One embodiment of the invention relates a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase comprising the motifs [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and/or G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), wherein the glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70; and

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase comprising the motifs [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and/or G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(c) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(e) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(f) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67; and

(g) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94.

The NRG sub-clade may be further be divided into another subgroup, which here is termed DTVG clade (se figure 3). The DTVG clade comprises polypeptides of bacterial origin having hydrolase activity, wherein the polypeptides comprise a Glyco_hydro_114 domain and belong to the NRG clade (and the FLD clade). The polypeptides of the clade comprise the motif example DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), corresponding to amino acids DTVGNIN in SEQ ID NO 76 at positions 134 to 140 of SEQ ID NO 76, where D and T (corresponding to position 134 and 135 of SEQ ID NO 76) is fully conserved in the DTVG clade. Examples of polypeptides of the DTVG clade is SEQ ID NO 76 and SEQ ID NO 82.

One embodiment of the invention relates a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98) and/or the motif DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), wherein the glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 76; and

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase, comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98) and/or the motif DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82.

The glycosyl hydrolases of the FLD clade, may as mentioned above be divided into two clades the clades termed NRG and the IGEAE (see figure 3). The IGEAE comprises polypeptides of bacterial origin having hydrolase activity, wherein the polypeptides comprise a Glyco_hydro_114 domain and belong to the FLD clade. The polypeptides of the clade comprise the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), corresponding to amino acids EIGAIEEY at positions 262 to 269 of SEQ ID NO 12 where G and E (corresponding to position 264 and 267 of SEQ ID NO 12) are fully conserved in IGEAE clade. Residue A at position 265 is part of the substrate binding pocket. Examples of polypeptides of the IGEAE clade is SEQ ID NO 6, SEQ ID NO 12, SEQ ID NO 18, SEQ ID NO 30, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52 and SEQ ID NO 55.

One embodiment of the invention relates a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase comprising the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), wherein the glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 6;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase, comprising the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(b) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(d) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(f) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(g) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(h) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(i) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

The IGEAE sub-clade may be further be divided into another subgroup, which here is termed QNSPEL clade (se figure 3). The QNSPEL clade comprises polypeptides of bacterial origin having hydrolase activity, comprising a Glyco_hydro_114 domain and belonging to the IGEAE clade. The polypeptides of the clade comprise the motif example [QL]N[AS]PEL (SEQ ID NO 103), corresponding to amino acids QNSPEL at positions 370 to 375 of SEQ ID NO 12 where P, E and L (corresponding to position 373 to 375 of SEQ ID NO 12) are fully conserved in QNSPEL clade. Another conserved motif of this clade is [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104), located at positions 366 to 374 in SEQ ID NO 12, and corresponding to peptide KVVPQNSPE in SEQ ID NO 12. Examples of polypeptides of the QNSPEL clade is SEQ ID NO 12, SEQ ID NO 18, SEQ ID NO 30, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52 and SEQ ID NO 55.

One embodiment of the invention relates a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase comprising the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) and/or one or both motifs [QL]N[AS]PEL (SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104), wherein the glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase comprising the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) and/or one or both motifs [QL]N[AS]PEL (SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(c) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(e) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(g) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(h) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

Thus, in one embodiment the Glyco_hydro_114 glycosyl hydrolase comprises one, two or all three of the motifs; GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the motif ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

In another embodiment the Glyco_hydro_114 glycosyl hydrolase comprises one, two or all three of the motifs; GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 6;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

The polypeptides of the invention have activity to the exopolysaccharide Pel, which is a component of some biofilm matrix. One embodiment of the invention relates to the use of a polypeptide according to the invention for reduction or removal of Pel, wherein in the Pel is comprised in a biofilm. In particular, the polypeptides of the invention have activity in detergents and is useful in cleaning processes such as laundry and/or dish wash e.g. for deep cleaning of surfaces such as textiles and hard surfaces. The present disclosure also provides a method for preventing, reduction or removal of Pel containing organic soiling on an item comprising applying at least one polypeptide of the invention to an item and optionally rinse the item. The item is preferably a textile or a hard surface, such as dish ware.

Organic matters such as EPS or components hereof may have glue-like properties and the presence of biofilm on e.g. textiles may result in items or areas on items which are “sticky”. Soil will in general adhere to the sticky areas and such soil has shown difficult to remove by commercially available detergent compositions. Further, when dirty laundry items are washed together with less dirty laundry items the dirt present in the wash liquor tend to stick to the organic matter and e.g. EPS. As a result, the laundry item is more “soiled” after wash than before wash. This effect may also be termed re-deposition. The Glyco_hydro_114 glycosyl hydrolase polypeptides comprising one or more of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), [QL]N[AS]PEL (SEQ ID NO 103) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) as defined above are useful in reducing or removing re-deposition.

The Glyco_hydro_114 glycosyl hydrolase polypeptides comprising one or more of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), [QL]N[AS]PEL (SEQ ID NO 103) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) as defined above are useful in reducing or removing malodor of items being washed. The inventors have surprisingly found that the polypeptides comprising one or more of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID

NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), [QL]N[AS]PEL (SEQ ID NO 103) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) as defined above are useful in reducing or removing laundry associated Pel.

The polypeptides of the present invention are useful in cleaning compositions and are effective in deep cleaning of surfaces such as fabrics. The polypeptides of the present invention are effective in reducing or removing polysaccharide soiling from e.g. organic matter. One example of organic matter is biofilm, which is produced by various microorganisms. The extracellular polymeric matrix of biofilm, EPS is composed of polysaccharides, extracellular DNA and proteins. Biofilm EPS may be sticky or glueing, which when present on textile, may give rise to re-deposition or backstaining of soil resulting in a greying of the textile. Another drawback of organic matter e.g. biofilm is the malodor as various malodor related molecules are often associated with organic matter e.g. biofilm. One aspect of the invention relates to a laundering method for laundering an item comprising the steps of:

a. exposing an item to a wash liquor comprising a polypeptide or a cleaning composition comprising a polypeptide selected from the group consisting of SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 and SEQ ID NO 96 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto, wherein the polypeptide has hydrolytic and/or deacetylase activity;

b. completing at least one wash cycle; and

c. optionally rinsing the item,

wherein the item is a textile.

The polypeptides of the invention are therefore useful for prevention, reduction or removal of malodor and for prevention, reduction of re-deposition and improving whiteness.

One embodiment of the invention relates to the use of polypeptide selected from the group consisting of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto for deep cleaning of an item, wherein the item is a textile. One embodiment of the invention relates to the use of polypeptide selected from the group consisting of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9,

SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 and SEQ ID NO 96 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto;

(i) for preventing, reducing or removing stickiness of the item;

(ii) for pretreating stains on the item;

(iii) for preventing, reducing or removing redeposition of soil during a wash cycle;

(iv) for preventing, reducing or removing adherence of soil to the item;

(v) for maintaining or improving whiteness of the item;

(vi) for preventing, reducing or removal malodor from the item,

wherein the item is a textile. The textile may e.g. be cotton or polyester or a mixture hereof.

Further methods and uses are described in the “use” section below.

One embodiment of the invention relates to a polypeptide having at least 60%, 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 polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30,SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 or SEQ ID NO 96.

One embodiment of the invention relates a Glyco_hydro_114 glycosyl hydrolase polypeptide, wherein the polypeptide has hydrolytic activity, and wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(w) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(y) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(z) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(aa) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(bb) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(cc) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(dd) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(ee) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95;

(ff) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase polypeptide, wherein the polypeptide has hydrolytic activity, and wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(w) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(y) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(z) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(aa) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(bb) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(cc) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(dd) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(ee) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

Another preferred embodiment of the invention relates a Glyco_hydro_114 glycosyl hydrolase polypeptide comprising one, two or all three of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97), wherein the polypeptide has hydrolytic activity, and wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(w) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(y) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(z) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(aa) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(bb) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(cc) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(dd) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(ee) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

In one embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 2 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 2.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 5 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 5.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 8 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 8.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 11 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 11.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 14 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 14.

In some embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 17 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 7.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 20 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 20.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 23 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 23.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 26 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 26.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 29 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 29.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 32 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 32.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 39 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 39.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 42 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 42.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 45 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 45.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 48 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 48.

v In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 51 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 51.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 54 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 54.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 57 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 57.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 60 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 60.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 63 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 63.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 66 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 66.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 69 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 69.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 72 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 72.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 75 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 75.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 78 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 78.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 81 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 81.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 84 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 84.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 87 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 87.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 90 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 90.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 93 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 93.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 95 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 95.

In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO 96 of 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%, and wherein the polypeptide has at least at least 70% of the hydrolytic and/or deacetylase activity of the mature polypeptide of SEQ ID NO 96.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 3 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In

another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 2. In another aspect, the polypeptide comprises or consists of amino acids 1 to 904 of SEQ ID NO 2.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 3; comprises the amino acid sequence shown in SEQ ID NO 3 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 3 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 3.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 6 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 5. In another aspect, the polypeptide comprises or consists of amino acids 1 to 281 of SEQ ID NO 5.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 6; comprises the amino acid sequence shown in SEQ ID NO 6 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 6 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 6.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 9 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 8. In another aspect, the polypeptide comprises or consists of amino acids 1 to 458 of SEQ ID NO 8.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 9; comprises the amino acid sequence shown in SEQ ID NO 9 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 9 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 9.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 12 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 11. In another aspect, the polypeptide comprises or consists of amino acids 1 to 468 of SEQ ID NO 11.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 12; comprises the amino acid sequence shown in SEQ ID NO 12 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 12 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 12.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 15 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 14. In another aspect, the polypeptide comprises or consists of amino acids 1 to 266 of SEQ ID NO 14.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 15; comprises the amino acid sequence shown in SEQ ID NO 15 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 15 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 15.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 18 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 17. In another aspect, the polypeptide comprises or consists of amino acids 1 to 467 of SEQ ID NO 17.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 18; comprises the amino acid sequence shown in SEQ ID NO

18 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 18 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 18.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 21 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 20. In another aspect, the polypeptide comprises or consists of amino acids 1 to 882 of SEQ ID NO 20.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 21; comprises the amino acid sequence shown in SEQ ID NO 21 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 21 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 21.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 24 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 23. In another aspect, the polypeptide comprises or consists of amino acids 1 to 279 of SEQ ID NO 23.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 24; comprises the amino acid sequence shown in SEQ ID NO 24 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 24 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 24.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 27 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity.

In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 26. In another aspect, the polypeptide comprises or consists of amino acids 1 to 276 of SEQ ID NO 26.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 27; comprises the amino acid sequence shown in SEQ ID NO 27 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 27 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 27.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 30 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 29. In another aspect, the polypeptide comprises or consists of amino acids 1 to 277 of SEQ ID NO 29.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 30; comprises the amino acid sequence shown in SEQ ID NO 30 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 30 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 30.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 33 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 32. In another aspect, the polypeptide comprises or consists of amino acids 1 to 271 of SEQ ID NO 32.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 33; comprises the amino acid sequence shown in SEQ ID NO 33 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 33 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 33.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 40 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 39. In another aspect, the polypeptide comprises or consists of amino acids 1 to 905 of SEQ ID NO 39.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 40; comprises the amino acid sequence shown in SEQ ID NO 40 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 40 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 40.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 43 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 42. In another aspect, the polypeptide comprises or consists of amino acids 1 to 467 of SEQ ID NO 42.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 43; comprises the amino acid sequence shown in SEQ ID NO 43 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 43 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 43.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 46 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 45. In another aspect, the polypeptide comprises or consists of amino acids 1 to 464 of SEQ ID NO 45.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 46; comprises the amino acid sequence shown in SEQ ID NO

46 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 46 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 46.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 49 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 48. In another aspect, the polypeptide comprises or consists of amino acids 1 to 475 of SEQ ID NO 48.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 49; comprises the amino acid sequence shown in SEQ ID NO 49 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 49 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 49.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 52 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 51. In another aspect, the polypeptide comprises or consists of amino acids 1 to 469 of SEQ ID NO 51.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 52; comprises the amino acid sequence shown in SEQ ID NO 52 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 52 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 52.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 55 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID

NO 54. In another aspect, the polypeptide comprises or consists of amino acids 1 to 475 of SEQ ID NO 54.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 55; comprises the amino acid sequence shown in SEQ ID NO 55 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 55 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 55.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 58 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 57. In another aspect, the polypeptide comprises or consists of amino acids 1 to 906 of SEQ ID NO 57.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 58; comprises the amino acid sequence shown in SEQ ID NO 58 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 58 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 58.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 61 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 60. In another aspect, the polypeptide comprises or consists of amino acids 1 to 905 of SEQ ID NO 60.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 61; comprises the amino acid sequence shown in SEQ ID NO 61 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 61 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 61.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 64 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 63. In another aspect, the polypeptide comprises or consists of amino acids 1 to 905 of SEQ ID NO 63.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 64; comprises the amino acid sequence shown in SEQ ID NO 64 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 64 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 64.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 67 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 66. In another aspect, the polypeptide comprises or consists of amino acids 1 to 906 of SEQ ID NO 66.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 67; comprises the amino acid sequence shown in SEQ ID NO 67 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 67 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 67.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 70 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 69. In another aspect, the polypeptide comprises or consists of amino acids 1 to 257 of SEQ ID NO 69.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 70; comprises the amino acid sequence shown in SEQ ID NO 70 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 70 and a N-terminal and/or C-terminal extension of between 1 and 10

amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 70.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 73 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 72. In another aspect, the polypeptide comprises or consists of amino acids 1 to 269 of SEQ ID NO 72.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 73; comprises the amino acid sequence shown in SEQ ID NO 73 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 73 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 73.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 76 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 75. In another aspect, the polypeptide comprises or consists of amino acids 1 to 260 of SEQ ID NO 75.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 76; comprises the amino acid sequence shown in SEQ ID NO 76 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 76 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 76.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 79 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 78. In another aspect, the polypeptide comprises or consists of amino acids 1 to 275 of SEQ ID NO 78.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 79; comprises the amino acid sequence shown in SEQ ID NO 79 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 79 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 79.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 82 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 81. In another aspect, the polypeptide comprises or consists of amino acids 1 to 268 of SEQ ID NO 81.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 82; comprises the amino acid sequence shown in SEQ ID NO 82 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 82 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 82.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 85 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 84. In another aspect, the polypeptide comprises or consists of amino acids 1 to 313 of SEQ ID NO 84.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 85; comprises the amino acid sequence shown in SEQ ID NO 85 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 85 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 85.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 88

or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 87. In another aspect, the polypeptide comprises or consists of amino acids 1 to 257 of SEQ ID NO 87.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 88; comprises the amino acid sequence shown in SEQ ID NO 88 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 88 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 88.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 91 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 90. In another aspect, the polypeptide comprises or consists of amino acids 1 to 296 of SEQ ID NO 90.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 91; comprises the amino acid sequence shown in SEQ ID NO 91 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 91 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 91.

In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 94 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO 93. In another aspect, the polypeptide comprises or consists of amino acids 1 to 897 of SEQ ID NO 93.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 94; comprises the amino acid sequence shown in SEQ ID NO 94 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 94 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 94.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 95; comprises the amino acid sequence shown in SEQ ID NO 95 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 95 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 95. In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 95 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity.

In one embodiment, the polypeptide preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 96; comprises the amino acid sequence shown in SEQ ID NO 96 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; comprises the amino acid sequence of SEQ ID NO 96 and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; or is a fragment thereof having hydrolytic and/or deacetylase activity and having at least 50% such as at least 60%, 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% of the length of SEQ ID NO 96. In some embodiment, the polypeptide has been isolated. A polypeptide of the present invention preferably comprises or consists of the amino acid sequence shown in SEQ ID NO 96 or an allelic variant thereof; or is a fragment thereof having hydrolytic and/or deacetylase activity.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 3.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 6.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 9.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 12.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 15.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 18.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 21.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 24.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 27.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 30.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 33.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 40.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 43.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 46.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 49.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 52.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 55.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 58.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 61.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 64.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 67.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 70.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 73.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 76.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 79.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 82.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 85.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 88.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 91.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 94.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 95.

In some aspect, the invention relates to a polypeptide which comprises or consists of the amino acid sequence shown in SEQ ID NO 96.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 3 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 3 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 6 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 6 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 9 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 9 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 12 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 12 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 15 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 15 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 18 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or

insertions introduced into the mature polypeptide shown in SEQ ID NO 18 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 21 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 21 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 24 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 24 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 27 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 27 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 30 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 30 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 33 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 33 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 40 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 40 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 43 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 43 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 46 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 46 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 49 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 49 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 52 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 52 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 55 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 55 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 58 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 58 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 61 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 61 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 64 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 64 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 67 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or

insertions introduced into the mature polypeptide shown in SEQ ID NO 67 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 70 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 70 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 73 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 73 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 76 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 76 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 79 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 79 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 82 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 82 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 85 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 85 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 88 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 88 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 91 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 91 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 94 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 94 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 95 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 95 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In some embodiment, the present invention relates to variants of the mature polypeptide shown in SEQ ID NO 96 comprising a substitution, deletion, and/or insertion at one or more (*e.g.*, several) positions. In some embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the mature polypeptide shown in SEQ ID NO 96 is up to 10, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

The amino acid changes may be of a minor nature, that is conservative amino acid substitutions or insertions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of 1-30 amino acids; small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an antigenic epitope or a binding domain.

Examples of conservative substitutions are within the groups of basic amino acids (arginine, lysine and histidine), acidic amino acids (glutamic acid and aspartic acid), polar amino acids (glutamine and asparagine), hydrophobic amino acids (leucine, isoleucine and valine), aromatic amino acids (phenylalanine, tryptophan and tyrosine), and small amino acids (glycine, alanine, serine, threonine and methionine). Amino acid substitutions that do not generally alter specific activity are known in the art and are described, for example, by H. Neurath and R.L. Hill, 1979, *In*, *The Proteins*, Academic Press, New York. Common substitutions are Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly.

Essential amino acids in a polypeptide can be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, 1989, *Science* 244: 1081-1085). In the latter technique, single alanine mutations are

introduced at every residue in the molecule, and the resultant molecules are tested for hydrolytic and/or deacetylase activity to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton *et al.*, 1996, *J. Biol. Chem.* 271: 4699-4708. The active site of the enzyme or other biological interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction, or photoaffinity labeling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos *et al.*, 1992, *Science* 255: 306-312; Smith *et al.*, 1992, *J. Mol. Biol.* 224: 899-904; Wlodaver *et al.*, 1992, *FEBS Lett.* 309: 59-64. The identity of essential amino acids can also be inferred from an alignment with a related polypeptide.

Single or multiple amino acid substitutions, deletions, and/or insertions can be made and tested using known methods of mutagenesis, recombination, and/or shuffling, followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer, 1988, *Science* 241: 53-57; Bowie and Sauer, 1989, *Proc. Natl. Acad. Sci. USA* 86: 2152-2156; WO 95/17413; or WO 95/22625. Other methods that can be used include error-prone PCR, phage display (*e.g.*, Lowman *et al.*, 1991, *Biochemistry* 30: 10832-10837; U.S. Patent No. 5,223,409; WO 92/06204), and region-directed mutagenesis (Derbyshire *et al.*, 1986, *Gene* 46: 145; Ner *et al.*, 1988, *DNA* 7: 127).

Mutagenesis/shuffling methods can be combined with high-throughput, automated screening methods to detect activity of cloned, mutagenized polypeptides expressed by host cells (Ness *et al.*, 1999, *Nature Biotechnology* 17: 893-896). Mutagenized DNA molecules that encode active polypeptides can be recovered from the host cells and rapidly sequenced using standard methods in the art. These methods allow the rapid determination of the importance of individual amino acid residues in a polypeptide.

The polypeptide may be a hybrid polypeptide in which a region of one polypeptide is fused at the N-terminus or the C-terminus of a region of another polypeptide.

The polypeptide may be a fusion polypeptide or cleavable fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide of the present invention. A fusion polypeptide is produced by fusing a polynucleotide encoding another polypeptide to a polynucleotide of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fusion polypeptide is under control of the same promoter(s) and terminator. Fusion polypeptides may also be constructed using intein technology in which fusion polypeptides are created post-translationally (Cooper *et al.*, 1993, *EMBO J.* 12: 2575-2583; Dawson *et al.*, 1994, *Science* 266: 776-779).

A fusion polypeptide can further comprise a cleavage site between the two polypeptides. Upon secretion of the fusion protein, the site is cleaved releasing the two polypeptides. Examples of cleavage sites include, but are not limited to, the sites disclosed in Martin *et al.*, 2003, *J. Ind. Microbiol. Biotechnol.* 3: 568-576; Svetina *et al.*, 2000, *J. Biotechnol.* 76: 245-251; Rasmussen-

Wilson *et al.*, 1997, *Appl. Environ. Microbiol.* 63: 3488-3493; Ward *et al.*, 1995, *Biotechnology* 13: 498-503; and Contreras *et al.*, 1991, *Biotechnology* 9: 378-381; Eaton *et al.*, 1986, *Biochemistry* 25: 505-512; Collins-Racie *et al.*, 1995, *Biotechnology* 13: 982-987; Carter *et al.*, 1989, *Proteins: Structure, Function, and Genetics* 6: 240-248; and Stevens, 2003, *Drug Discovery World* 4: 35-48.

Sources of Polypeptides Having Polypeptide Activity

A polypeptide having hydrolytic and/or deacetylase activity of the present invention may be obtained from microorganisms of any genus. For purposes of the present invention, the term "obtained from" as used herein in connection with a given source shall mean that the polypeptide encoded by a polynucleotide is produced by the source or by a strain in which the polynucleotide from the source has been inserted. In one aspect, the polypeptide obtained from a given source is secreted extracellularly. In one aspect, the polypeptide is a *Pseudomonas* polypeptide, *e.g.*, a polypeptide obtained from *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*. In one aspect, the polypeptide is a *Bacterial* polypeptide, *e.g.*, a polypeptide obtained from *Environmental bacterial community A*, *Environmental bacterial community LE* or *Environmental bacterial community XE.* In one aspect, the polypeptide is a *Thermus* polypeptide, *e.g.*, a polypeptide obtained from *Thermus rehai.* In one aspect, the polypeptide is a *Burkholderia* polypeptide, *e.g.*, a polypeptide obtained from *Burkholderia sp-63093.* In one aspect, the polypeptide is a *Myxococcus* polypeptide, *e.g.*, a polypeptide obtained from *Myxococcus macrosporus, Myxococcus virescens*, *Myxococcus fulvus* or *Myxococcus stipitatus*. In one aspect, the polypeptide is a *Gallaecimonas* polypeptide, *e.g.*, a polypeptide obtained from *Gallaecimonas pentaromativorans.* In one aspect, the polypeptide is a *Nonomuraea* polypeptide, *e.g.*, a polypeptide obtained from *Nonomuraea coxensis.* In one aspect, the polypeptide is a *Paraburkholderia* polypeptide, *e.g.*, a polypeptide obtained from *Paraburkholderia phenazinium.* In one aspect, the polypeptide is a *Microbulbifer* polypeptide, *e.g.*, a polypeptide obtained from *Microbulbifer hydrolyticus*. In one aspect, the polypeptide is a *Carnobacterium* polypeptide, *e.g.*, a polypeptide obtained from *Carnobacterium inhibens subsp. gilichinskyi*.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase i.e. a polypeptide comprising the Glyco_hydro_114 domain is bacterial. In one embodiment, the Glyco_hydro_114 glycosyl hydrolase i.e. a polypeptide comprising the Glyco_hydro_114 domain is derived from *Pseudomonas* e.g. *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*. In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Pseudomonas*, preferably *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*, wherein the Glyco_hydro_114 glycosyl

hydrolase comprising one or more, or even all of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100).

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Pseudomonas*, preferably *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*, wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 58;

(c) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 61;

(d) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 64;

(e) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 67; and

(f) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 94.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase, wherein the Glyco_hydro_114 glycosyl hydrolase is obtained from *Pseudomonas*, preferably *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*, and wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(d) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(e) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67; and

(f) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94.

One preferred embodiment relates to a Glyco_hydro_114 glycosyl hydrolase, wherein the Glyco_hydro_114 glycosyl hydrolase is obtained from *Pseudomonas*, preferably *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*, wherein the Glyco_hydro_114 glycosyl comprises four, five or six of the motifs selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) and wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(d) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(e) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67; and

(f) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase i.e. a polypeptide comprising the Glyco_hydro_114 domain is bacterial. In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Myxococcus*, preferably *Myxococcus macrosporus, Myxococcus virescens*, *Myxococcus fulvus* or *Myxococcus stipitatus*, wherein the Glyco_hydro_114 glycosyl hydrolase comprising one or more, or even all of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Myxococcus*, preferably *Myxococcus macrosporus, Myxococcus virescens*, *Myxococcus fulvus* or *Myxococcus stipitatus*, wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 18;

(b) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 43;

(c) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 46;

(d) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 49;

(e) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 52; and

(f) a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 55.

One preferred embodiment relates to A Glyco_hydro_114 glycosyl hydrolase, wherein the Glyco_hydro_114 glycosyl hydrolase is obtained from *Myxococcus*, preferably *Myxococcus macrosporus, Myxococcus virescens*, *Myxococcus fulvus* or *Myxococcus stipitatus*, wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;
(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;
(c) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;
(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;
(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and
(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

One preferred embodiment relates to A Glyco_hydro_114 glycosyl hydrolase, wherein the Glyco_hydro_114 glycosyl hydrolase is obtained from *Myxococcus*, preferably *Myxococcus macrosporus, Myxococcus virescens*, *Myxococcus fulvus* or *Myxococcus stipitatus*, wherein the Glyco_hydro_114 glycosyl comprises four, five or six of the motifs selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) and wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of:

(a) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;
(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;
(c) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;
(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;
(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and
(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Thermus*, preferably *Thermus rehai*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Thermus*, preferably *Thermus rehai*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 9.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Burkholderia*, preferably *Burkholderia sp-63093*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Burkholderia*, preferably *Burkholderia sp-63093* wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 15 or a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 96.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Gallaecimonas*, preferably *Gallaecimonas pentaromativorans*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Gallaecimonas*, preferably *Gallaecimonas pentaromativorans*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 21.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Nonomuraea*, preferably *Nonomuraea coxensis*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Nonomuraea*, preferably *Nonomuraea coxensis*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%,

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 polypeptide of SEQ ID NO 24.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Glycomyces*, preferably *Glycomyces rutgersensis*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Glycomyces*, preferably *Glycomyces rutgersensis*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 27.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Paraburkholderia*, preferably *Paraburkholderia phenazinium*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Paraburkholderia*, preferably *Paraburkholderia phenazinium*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 33 or a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 95.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Streptomyces*, preferably *Streptomyces griseofuscus*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Streptomyces*, preferably *Streptomyces griseofuscus*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 73.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Lysinibacillus*, preferably *Lysinibacillus xylanilyticus*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34),

AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DT[VIMA][GD][DNW][VIL][DEN](SEQ ID NO 101). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Lysinibacillus*, preferably *Lysinibacillus xylanilyticus*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 76 or a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 82.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Tumebacillus*, preferably *Tumebacillus ginsengisoli*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Tumebacillus*, preferably *Tumebacillus ginsengisoli*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 79.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Microbulbifer*, preferably *Microbulbifer hydrolyticus*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Microbulbifer*, preferably *Microbulbifer hydrolyticus*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 85.

In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Carnobacterium*, preferably *Carnobacterium inhibens subsp. gilichinskyi*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises one or more, or even all of the motif(s)GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97). In one embodiment, the Glyco_hydro_114 glycosyl hydrolase is obtained from *Carnobacterium*, preferably *Carnobacterium inhibens subsp. gilichinskyi*, wherein the Glyco_hydro_114 glycosyl hydrolase is a polypeptide having at least 60%, 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 polypeptide of SEQ ID NO 88.

It will be understood that for the aforementioned species, the invention encompasses both the perfect and imperfect states, and other taxonomic equivalents, *e.g.*, anamorphs, regardless of the species name by which they are known. Those skilled in the art will readily recognize the identity of appropriate equivalents.

Strains of these species are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Centraalbureau Voor Schimmelcultures (CBS), and Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL).

The polypeptide may be identified and obtained from other sources including microorganisms isolated from nature (*e.g.*, soil, composts, water, etc.) or DNA samples obtained directly from natural materials (*e.g.*, soil, composts, water, etc.) using the above-mentioned probes. Techniques for isolating microorganisms and DNA directly from natural habitats are well known in the art. A polynucleotide encoding the polypeptide may then be obtained by similarly screening a genomic DNA or cDNA library of another microorganism or mixed DNA sample. Once a polynucleotide encoding a polypeptide has been detected with the probe(s), the polynucleotide can be isolated or cloned by utilizing techniques that are known to those of ordinary skill in the art (see, *e.g.*, Sambrook *et al.*, 1989, *supra*).

Polynucleotides

The present invention also relates to polynucleotides encoding a polypeptide of the present invention, as described herein. In some embodiment, the polynucleotide encoding the polypeptide of the present invention has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 1 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 4 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a

sequence identity to the mature polypeptide coding sequence of SEQ ID NO 7 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 10 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 13 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 16 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 19 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 22 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 25 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 28 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 31 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 38 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 41 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 44 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 47 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 50 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 53 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 56 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 59 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 62 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 65 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a

sequence identity to the mature polypeptide coding sequence of SEQ ID NO 68 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 71 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 74 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 77 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 80 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 83 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 86 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 89 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 92 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 95 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

In some embodiment, the present invention relates to a polynucleotide encoding a polypeptide having hydrolytic and/or deacetylase activity, wherein the polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO 98 of at least 60%, *e.g.*, 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%. In a further embodiment, the polynucleotide has been isolated.

The techniques used to isolate or clone a polynucleotide are known in the art and include isolation from genomic DNA or cDNA, or a combination thereof. The cloning of the polynucleotides from genomic DNA can be effected, *e.g.*, by using the well-known polymerase chain reaction (PCR) or antibody screening of expression libraries to detect cloned DNA fragments with shared structural features. See, *e.g.*, Innis *et al.*, 1990, *PCR: A Guide to Methods and Application*, Academic Press, New York. Other nucleic acid amplification procedures such as ligase chain reaction (LCR), ligation activated transcription (LAT) and polynucleotide-based amplification (NASBA) may be used. Modification of a polynucleotide encoding a polypeptide of the present invention may be necessary for synthesizing polypeptides substantially similar to the polypeptide. The term “substantially similar” to the polypeptide refers to non-naturally occurring forms of the polypeptide.

Nucleic Acid Constructs

The present invention also relates to nucleic acid constructs comprising a polynucleotide of the present invention operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

The polynucleotide may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides utilizing recombinant DNA methods are well known in the art.

The control sequence may be a promoter, a polynucleotide that is recognized by a host cell for expression of a polynucleotide encoding a polypeptide of the present invention. The promoter contains transcriptional control sequences that mediate the expression of the polypeptide. The promoter may be any polynucleotide that shows transcriptional activity in the host cell including variant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a bacterial host cell are the promoters obtained from the *Bacillus amyloliquefaciens* alpha-amylase gene (*amyQ*), *Bacillus licheniformis* alpha-amylase gene (*amyL*), *Bacillus licheniformis* penicillinase gene (*penP*), *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), *Bacillus subtilis* levansucrase gene (*sacB*), *Bacillus subtilis xylA* and *xylB* genes, *Bacillus thuringiensis cryIIIA* gene (Agaisse and Lereclus, 1994, *Molecular Microbiology* 13: 97-107), *E. coli lac* operon, *E. coli trc* promoter (Egon *et al.*, 1988, *Gene* 69: 301-315), *Streptomyces coelicolor* agarase gene (*dagA*), and prokaryotic beta-lactamase gene (Villa-Kamaroff *et al.*, 1978, *Proc. Natl. Acad. Sci. USA* 75: 3727-3731), as well as the *tac* promoter (DeBoer *et al.*, 1983, *Proc. Natl. Acad. Sci. USA* 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Gilbert *et al.*, 1980, *Scientific American* 242: 74-94; and in Sambrook *et al.*, 1989, *supra*. Examples of tandem promoters are disclosed in WO 99/43835.

Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a filamentous fungal host cell are promoters obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (*glaA*), *Aspergillus oryzae* TAKA amylase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Fusarium oxysporum* trypsin-like protease (WO 96/00787), *Fusarium venenatum* amyloglucosidase (WO 00/56900), *Fusarium venenatum* Daria (WO 00/56900), *Fusarium venenatum* Quinn (WO 00/56900), *Rhizomucor miehei* lipase, *Rhizomucor miehei* aspartic proteinase, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I,

Trichoderma reesei cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* xylanase III, *Trichoderma reesei* beta-xylosidase, and *Trichoderma reesei* translation elongation factor, as well as the NA2-tpi promoter (a modified promoter from an *Aspergillus* neutral alpha-amylase gene in which the untranslated leader has been replaced by an untranslated leader from an *Aspergillus* triose phosphate isomerase gene; non-limiting examples include modified promoters from an *Aspergillus niger* neutral alpha-amylase gene in which the untranslated leader has been replaced by an untranslated leader from an *Aspergillus nidulans* or *Aspergillus oryzae* triose phosphate isomerase gene); and variant, truncated, and hybrid promoters thereof. Other promoters are described in U.S. Patent No. 6,011,147.

In a yeast host, useful promoters are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH1, ADH2/GAP), *Saccharomyces cerevisiae* triose phosphate isomerase (TPI), *Saccharomyces cerevisiae* metallothionein (CUP1), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos *et al.*, 1992, *Yeast* 8: 423-488.

The control sequence may also be a transcription terminator, which is recognized by a host cell to terminate transcription. The terminator is operably linked to the 3'-terminus of the polynucleotide encoding the polypeptide. Any terminator that is functional in the host cell may be used in the present invention.

Preferred terminators for bacterial host cells are obtained from the genes for *Bacillus clausii* alkaline protease (*aprH*), *Bacillus licheniformis* alpha-amylase (*amyL*), and *Escherichia coli* ribosomal RNA (*rrnB*).

Preferred terminators for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase, *Aspergillus oryzae* TAKA amylase, *Fusarium oxysporum* trypsin-like protease, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* xylanase III, *Trichoderma reesei* beta-xylosidase, and *Trichoderma reesei* translation elongation factor.

Preferred terminators for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos *et al.*, 1992, *supra*.

The control sequence may also be an mRNA stabilizer region downstream of a promoter and upstream of the coding sequence of a gene which increases expression of the gene.

Examples of suitable mRNA stabilizer regions are obtained from a *Bacillus thuringiensis cryIIIA* gene (WO 94/25612) and a *Bacillus subtilis* SP82 gene (Hue *et al.*, 1995, *Journal of Bacteriology* 177: 3465-3471).

The control sequence may also be a leader, a nontranslated region of an mRNA that is important for translation by the host cell. The leader is operably linked to the 5'-terminus of the polynucleotide encoding the polypeptide. Any leader that is functional in the host cell may be used.

Preferred leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase.

Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3'-terminus of the polynucleotide and, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence that is functional in the host cell may be used.

Preferred polyadenylation sequences for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase *Aspergillus oryzae* TAKA amylase, and *Fusarium oxysporum* trypsin-like protease.

Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Mol. Cellular Biol.* 15: 5983-5990.

The control sequence may also be a signal peptide coding region that encodes a signal peptide linked to the N-terminus of a polypeptide and directs the polypeptide into the cell's secretory pathway. The 5'-end of the coding sequence of the polynucleotide may inherently contain a signal peptide coding sequence naturally linked in translation reading frame with the segment of the coding sequence that encodes the polypeptide. Alternatively, the 5'-end of the coding sequence may contain a signal peptide coding sequence that is foreign to the coding sequence. A foreign signal peptide coding sequence may be required where the coding sequence does not naturally contain a signal peptide coding sequence. Alternatively, a foreign signal peptide coding sequence may simply replace the natural signal peptide coding sequence in order to enhance secretion of the polypeptide. However, any signal peptide coding sequence that directs the expressed polypeptide into the secretory pathway of a host cell may be used.

Effective signal peptide coding sequences for bacterial host cells are the signal peptide coding sequences obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus*

licheniformis subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus stearothermophilus* neutral proteases (*nprT*, *nprS*, *nprM*), and *Bacillus subtilis prsA*. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

Effective signal peptide coding sequences for filamentous fungal host cells are the signal peptide coding sequences obtained from the genes for *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Aspergillus oryzae* TAKA amylase, *Humicola insolens* cellulase, *Humicola insolens* endoglucanase V, *Humicola lanuginosa* lipase, and *Rhizomucor miehei* aspartic proteinase.

Useful signal peptides for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding sequences are described by Romanos *et al.*, 1992, *supra*.

The control sequence may also be a propeptide coding sequence that encodes a propeptide positioned at the N-terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to an active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding sequence may be obtained from the genes for *Bacillus subtilis* alkaline protease (*aprE*), *Bacillus subtilis* neutral protease (*nprT*), *Myceliophthora thermophila* laccase (WO 95/33836), *Rhizomucor miehei* aspartic proteinase, and *Saccharomyces cerevisiae* alpha-factor.

Where both signal peptide and propeptide sequences are present, the propeptide sequence is positioned next to the N-terminus of a polypeptide and the signal peptide sequence is positioned next to the N-terminus of the propeptide sequence.

It may also be desirable to add regulatory sequences that regulate expression of the polypeptide relative to the growth of the host cell. Examples of regulatory sequences are those that cause expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory sequences in prokaryotic systems include the *lac*, *tac*, and *trp* operator systems. In yeast, the ADH2 system or GAL1 system may be used. In filamentous fungi, the *Aspergillus niger* glucoamylase promoter, *Aspergillus oryzae* TAKA alpha-amylase promoter, and *Aspergillus oryzae* glucoamylase promoter, *Trichoderma reesei* cellobiohydrolase I promoter, and *Trichoderma reesei* cellobiohydrolase II promoter may be used. Other examples of regulatory sequences are those that allow for gene amplification. In eukaryotic systems, these regulatory sequences include the dihydrofolate reductase gene that is amplified in the presence of methotrexate, and the metallothionein genes that are amplified with heavy metals. In these cases, the polynucleotide encoding the polypeptide would be operably linked to the regulatory sequence.

Expression Vectors

The present invention also relates to recombinant expression vectors comprising a polynucleotide of the present invention, a promoter, and transcriptional and translational stop signals. The various nucleotide and control sequences may be joined together to produce a recombinant expression vector that may include one or more convenient restriction sites to allow for insertion or substitution of the polynucleotide encoding the polypeptide at such sites. Alternatively, the polynucleotide may be expressed by inserting the polynucleotide or a nucleic acid construct comprising the polynucleotide into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (*e.g.*, a plasmid or virus) that can be conveniently subjected to recombinant DNA procedures and can bring about expression of the polynucleotide. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector may be a linear or closed circular plasmid.

The vector may be an autonomously replicating vector, *i.e.*, a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.*, a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one that, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids that together contain the total DNA to be introduced into the genome of the host cell, or a transposon, may be used.

The vector preferably contains one or more selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

Examples of bacterial selectable markers are *Bacillus licheniformis* or *Bacillus subtilis dal* genes, or markers that confer antibiotic resistance such as ampicillin, chloramphenicol, kanamycin, neomycin, spectinomycin, or tetracycline resistance. Suitable markers for yeast host cells include, but are not limited to, ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, *adeA* (phosphoribosylaminoimidazole-succinocarboxamide synthase), *adeB* (phosphoribosyl-aminoimidazole synthase), *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hph* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenyltransferase), and *trpC* (anthranilate synthase), as well as equivalents thereof. Preferred for use in an *Aspergillus* cell are *Aspergillus nidulans* or *Aspergillus oryzae amdS* and *pyrG* genes and a *Streptomyces*

hygroscopicus bar gene. Preferred for use in a *Trichoderma* cell are *adeA*, *adeB*, *amdS*, *hph*, and *pyrG* genes.

The selectable marker may be a dual selectable marker system as described in WO 2010/039889. In one aspect, the dual selectable marker is an *hph-tk* dual selectable marker system.

The vector preferably contains an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the polynucleotide's sequence encoding the polypeptide or any other element of the vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, 400 to 10,000 base pairs, and 800 to 10,000 base pairs, which have a high degree of sequence identity to the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding polynucleotides. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term "origin of replication" or "plasmid replicator" means a polynucleotide that enables a plasmid or vector to replicate *in vivo*.

Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAMß1 permitting replication in *Bacillus*.

Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6.

Examples of origins of replication useful in a filamentous fungal cell are AMA1 and ANS1 (Gems *et al.*, 1991, *Gene* 98: 61-67; Cullen *et al.*, 1987, *Nucleic Acids Res.* 15: 9163-9175; WO 00/24883). Isolation of the AMA1 gene and construction of plasmids or vectors comprising the gene can be accomplished according to the methods disclosed in WO 00/24883.

More than one copy of a polynucleotide of the present invention may be inserted into a host cell to increase production of a polypeptide. An increase in the copy number of the polynucleotide can be obtained by integrating at least one additional copy of the sequence into

the host cell genome or by including an amplifiable selectable marker gene with the polynucleotide where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the polynucleotide, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, *e.g.*, Sambrook *et al.*, 1989, *supra*).

Host Cells

The present invention also relates to recombinant host cells, comprising a polynucleotide of the present invention operably linked to one or more control sequences that direct the production of a polypeptide of the present invention. A construct or vector comprising a polynucleotide is introduced into a host cell so that the construct or vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier. The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The choice of a host cell will to a large extent depend upon the gene encoding the polypeptide and its source.

The host cell may be any cell useful in the recombinant production of a polypeptide of the present invention, *e.g.*, a prokaryote or a eukaryote.

The prokaryotic host cell may be any Gram-positive or Gram-negative bacterium. Gram-positive bacteria include, but are not limited to, *Bacillus*, *Clostridium*, *Enterococcus*, *Geobacillus*, *Lactobacillus*, *Lactococcus*, *Oceanobacillus*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*. Gram-negative bacteria include, but are not limited to, *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neisseria*, *Pseudomonas*, *Salmonella*, and *Ureaplasma*.

The bacterial host cell may be any *Bacillus* cell including, but not limited to, *Bacillus alkalophilus*, *Bacillus altitudinis*, *Bacillus amyloliquefaciens*, *B. amyloliquefaciens* subsp. *plantarum*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus methylotrophicus*, *Bacillus pumilus*, *Bacillus safensis, Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* cells.

The bacterial host cell may also be any Streptococcus cell including, but not limited to, Streptococcus equisimilis, Streptococcus pyogenes, Streptococcus uberis, and Streptococcus equi subsp. Zooepidemicus cells.

The bacterial host cell may also be any Streptomyces cell including, but not limited to, Streptomyces achromogenes, Streptomyces avermitilis, Streptomyces coelicolor, Streptomyces griseus, and Streptomyces lividans cells.

The introduction of DNA into a *Bacillus* cell may be effected by protoplast transformation (see, *e.g.*, Chang and Cohen, 1979, *Mol. Gen. Genet.* 168: 111-115), competent cell

transformation (see, *e.g.*, Young and Spizizen, 1961, *J. Bacteriol.* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *J. Mol. Biol.* 56: 209-221), electroporation (see, *e.g.*, Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or conjugation (see, *e.g.*, Koehler and Thorne, 1987, *J. Bacteriol.* 169: 5271-5278). The introduction of DNA into an *E. coli* cell may be effected by protoplast transformation (see, *e.g.*, Hanahan, 1983, *J. Mol. Biol.* 166: 557-580) or electroporation (see, *e.g.*, Dower *et al.*, 1988, *Nucleic Acids Res.* 16: 6127-6145). The introduction of DNA into a *Streptomyces* cell may be effected by protoplast transformation, electroporation (see, *e.g.*, Gong *et al.*, 2004, *Folia Microbiol.* (*Praha*) 49: 399-405), conjugation (see, *e.g.*, Mazodier *et al.*, 1989, *J. Bacteriol.* 171: 3583-3585), or transduction (see, *e.g.*, Burke *et al.*, 2001, *Proc. Natl. Acad. Sci. USA* 98: 6289-6294). The introduction of DNA into a *Pseudomonas* cell may be effected by electroporation (see, *e.g.*, Choi *et al.*, 2006, *J. Microbiol. Methods* 64: 391-397) or conjugation (see, *e.g.*, Pinedo and Smets, 2005, *Appl. Environ. Microbiol.* 71: 51-57). The introduction of DNA into a *Streptococcus* cell may be effected by natural competence (see, *e.g.*, Perry and Kuramitsu, 1981, *Infect. Immun.* 32: 1295-1297), protoplast transformation (see, *e.g.*, Catt and Jollick, 1991, *Microbios* 68: 189-207), electroporation (see, *e.g.*, Buckley *et al.*, 1999, *Appl. Environ. Microbiol.* 65: 3800-3804), or conjugation (see, *e.g.*, Clewell, 1981, *Microbiol. Rev.* 45: 409-436). However, any method known in the art for introducing DNA into a host cell can be used.

The host cell may also be a eukaryote, such as a mammalian, insect, plant, or fungal cell.

The host cell may be a fungal cell. “Fungi” as used herein includes the phyla Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota as well as the Oomycota and all mitosporic fungi (as defined by Hawksworth *et al.*, *In*, *Ainsworth and Bisby’s Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK).

The fungal host cell may be a yeast cell. “Yeast” as used herein includes ascosporogenous yeast (*Endomycetales*), basidiosporogenous yeast, and yeast belonging to the *Fungi Imperfecti* (*Blastomycetes*). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in *Biology and Activities of Yeast* (Skinner, Passmore, and Davenport, editors, *Soc. App. Bacteriol. Symposium Series* No. 9, 1980).

The yeast host cell may be a *Candida, Hansenula, Kluyveromyces, Pichia, Saccharomyces, Schizosaccharomyces,* or *Yarrowia* cell, such as a *Kluyveromyces lactis, Saccharomyces carlsbergensis, Saccharomyces cerevisiae, Saccharomyces diastaticus, Saccharomyces douglasii, Saccharomyces kluyveri, Saccharomyces norbensis, Saccharomyces oviformis, or Yarrowia lipolytica* cell.

The fungal host cell may be a filamentous fungal cell. “Filamentous fungi” include all filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth *et al.*, 1995, *supra*). The filamentous fungi are generally characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex polysaccharides. Vegetative

growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

The filamentous fungal host cell may be an *Acremonium, Aspergillus, Aureobasidium, Bjerkandera, Ceriporiopsis, Chrysosporium, Coprinus, Coriolus, Cryptococcus, Filibasidium, Fusarium, Humicola, Magnaporthe, Mucor, Myceliophthora, Neocallimastix, Neurospora, Paecilomyces, Penicillium, Phanerochaete, Phlebia, Piromyces, Pleurotus, Schizophyllum, Talaromyces, Thermoascus, Thielavia, Tolypocladium, Trametes,* or *Trichoderma* cell.

For example, the filamentous fungal host cell may be an A*spergillus awamori, Aspergillus foetidus, Aspergillus fumigatus, Aspergillus japonicus, Aspergillus nidulans, Aspergillus niger, Aspergillus oryzae, Bjerkandera adusta, Ceriporiopsis aneirina, Ceriporiopsis caregiea, Ceriporiopsis gilvescens, Ceriporiopsis pannocinta, Ceriporiopsis rivulosa, Ceriporiopsis subrufa, Ceriporiopsis subvermispora, Chrysosporium inops, Chrysosporium keratinophilum, Chrysosporium lucknowense, Chrysosporium merdarium, Chrysosporium pannicola, Chrysosporium queenslandicum, Chrysosporium tropicum, Chrysosporium zonatum, Coprinus cinereus, Coriolus hirsutus, 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, Fusarium venenatum, Humicola insolens, Humicola lanuginosa, Mucor miehei, Myceliophthora thermophila, Neurospora crassa, Penicillium purpurogenum, Phanerochaete chrysosporium, Phlebia radiata, Pleurotus eryngii, Thielavia terrestris, Trametes villosa, Trametes versicolor, Trichoderma harzianum, Trichoderma koningii, Trichoderma longibrachiatum, Trichoderma reesei,* or *Trichoderma viride* cell.

Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known *per se*. Suitable procedures for transformation of *Aspergillus* and *Trichoderma* host cells are described in EP 238023, Yelton *et al.*, 1984, *Proc. Natl. Acad. Sci. USA* 81: 1470-1474, and Christensen *et al.*, 1988, *Bio/Technology* 6: 1419-1422. Suitable methods for transforming *Fusarium* species are described by Malardier *et al.*, 1989, *Gene* 78: 147-156, and WO 96/00787. Yeast may be transformed using the procedures described by Becker and Guarente, *In* Abelson, J.N. and Simon, M.I., editors, *Guide to Yeast Genetics and Molecular Biology*, *Methods in Enzymology*, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito *et al.*, 1983, *J. Bacteriol.* 153: 163; and Hinnen *et al.*, 1978, *Proc. Natl. Acad. Sci. USA* 75: 1920.

Methods of Production

The present invention also relates to methods of producing a polypeptide of the present invention, comprising (a) cultivating a cell, which in its wild-type form produces the polypeptide,

under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide.

The present invention also relates to methods of producing a polypeptide of the present invention, comprising (a) cultivating a recombinant host cell of the present invention under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide.

The host cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cells may be cultivated by shake flask cultivation, or small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

The polypeptide may be detected using methods known in the art that are specific for the polypeptides having hydrolytic and/or deacetylase activity. These detection methods include, but are not limited to, use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide.

The polypeptide may be recovered using methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures including, but not limited to, collection, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. In one aspect, a fermentation broth comprising the polypeptide is recovered.

The polypeptide may be purified by a variety of procedures known in the art 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, or extraction (see, *e.g.*, *Protein Purification*, Janson and Ryden, editors, VCH Publishers, New York, 1989) to obtain substantially pure polypeptides.

In an alternative aspect, the polypeptide is not recovered, but rather a host cell of the present invention expressing the polypeptide is used as a source of the polypeptide.

Fermentation Broth Formulations or Cell Compositions

The present invention also relates to a fermentation broth formulation or a cell composition comprising a polypeptide of the present invention. The fermentation broth product further comprises additional ingredients used in the fermentation process, such as, for example, cells

(including, the host cells containing the gene encoding the polypeptide of the present invention which are used to produce the polypeptide of interest), cell debris, biomass, fermentation media and/or fermentation products. In some embodiments, the composition is a cell-killed whole broth containing organic acid(s), killed cells and/or cell debris, and culture medium.

The term "fermentation broth" as used herein refers to a preparation produced by cellular fermentation that undergoes no or minimal recovery and/or purification. For example, fermentation broths are produced when microbial cultures are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis (*e.g.*, expression of enzymes by host cells) and secretion into cell culture medium. The fermentation broth can contain 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 some embodiments, the fermentation broth contains spent cell culture medium, extracellular enzymes, and viable and/or nonviable microbial cells.

In some embodiment, the fermentation broth formulation and cell compositions comprise a first organic acid component comprising at least one 1-5 carbon organic acid and/or a salt thereof and a second organic acid component comprising at least one 6 or more carbon organic acid and/or a salt thereof. In a specific embodiment, the first organic acid component is acetic acid, formic acid, propionic acid, a salt thereof, or a mixture of two or more of the foregoing and the second organic acid component is benzoic acid, cyclohexanecarboxylic acid, 4-methylvaleric acid, phenylacetic acid, a salt thereof, or a mixture of two or more of the foregoing.

In one aspect, the composition contains an organic acid(s), and optionally further contains killed cells and/or cell debris. In one embodiment, the killed cells and/or cell debris are removed from a cell-killed whole broth to provide a composition that is free of these components.

The fermentation broth formulations or cell compositions may further comprise a preservative and/or anti-microbial (*e.g.*, bacteriostatic) agent, including, but not limited to, sorbitol, sodium chloride, potassium sorbate, and others known in the art.

The cell-killed whole broth or composition may contain the unfractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the cell-killed whole broth or composition contains the spent culture medium and cell debris present after the microbial cells (*e.g.*, filamentous fungal cells) are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis. In some embodiments, the cell-killed whole broth or composition contains the spent cell culture medium, extracellular enzymes, and killed filamentous fungal cells. In some embodiments, the microbial cells present in the cell-killed whole broth or composition can be permeabilized and/or lysed using methods known in the art.

A whole broth or cell composition as described herein is typically a liquid, but may contain insoluble components, such as killed cells, cell debris, culture media components, and/or

insoluble enzyme(s). In some embodiments, insoluble components may be removed to provide a clarified liquid composition.

The whole broth formulations and cell compositions of the present invention may be produced by a method described in WO 90/15861 or WO 2010/096673.

Enzyme Compositions

The invention relates to compositions comprising a Polypeptide of the present invention in combination with one or more additional component(s). The choice of additional components is within the skill of the artisan and includes conventional ingredients, including the exemplary non-limiting components set forth below.

Some embodiments of the invention relate to a composition comprising:

a) at least 0.001 ppm of at least one polypeptide having hydrolytic and/or deacetylase activity, wherein the polypeptide is selected for the group consisting of: SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 and polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto;

b) one or more adjunct ingredient.

Some embodiments of the invention relate to a cleaning composition comprising:

a) at least 0.001 ppm of at least one polypeptide having hydrolytic and/or deacetylase activity, wherein the polypeptide is selected for the group consisting of: SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 and polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto;

b) one or more cleaning composition component, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

Some embodiments of the invention relate to a cleaning composition comprising:

a) at least 0.001 ppm of at least one polypeptide having hydrolytic and/or deacetylase activity, wherein the polypeptide comprises one or more motif selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103), and [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104); and

b) one or more cleaning composition component, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

One embodiment relates to a cleaning composition comprising:

a) at least 0.001 ppm of at least one polypeptide having hydrolytic and/or deacetylase activity e.g. a Glyco_hydro_114 glycosyl hydrolase, wherein the polypeptide is selected from the group consisting of:

i) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

ii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

iii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

iv) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

vi) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

vii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

viii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

ix) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

xi) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

xii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

xiii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

xiv) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

xv) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

xvi) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

xvii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

xviii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

xix) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

xx) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

xxi) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

xxii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

xxiii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

xxiv) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

xxv) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

xxvi) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

xxvii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

xxviii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

xxix) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

xxx) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

xxxi) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95;

xxxii) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96; and

b) one or more cleaning composition component, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

The choice of cleaning components may include, for textile care, the consideration of the type of textile to be cleaned, the type and/or degree of soiling, the temperature at which cleaning

is to take place, and the formulation of the detergent product. Although components mentioned below are categorized by general header according to a particular functionality, this is not to be construed as a limitation, as a component may comprise additional functionalities as will be appreciated by the skilled artisan.

Surfactants

The detergent composition may comprise one or more surfactants, which may be anionic and/or cationic and/or non-ionic and/or semi-polar and/or zwitterionic, or a mixture thereof. In a particular embodiment, the detergent composition includes a mixture of one or more nonionic surfactants and one or more anionic surfactants. The surfactant(s) is typically present at a level of from about 0.1% to 60% by weight, such as about 1% to about 40%, or about 3% to about 20%, or about 3% to about 10%. The surfactant(s) is chosen based on the desired cleaning application, and may include any conventional surfactant(s) known in the art.

When included therein the detergent will usually contain from about 1% to about 40% by weight of an anionic surfactant, such as from about 5% to about 30%, including from about 5% to about 15%, or from about 15% to about 20%, or from about 20% to about 25% of an anionic surfactant. Non-limiting examples of anionic surfactants include sulfates and sulfonates, in particular, linear alkylbenzenesulfonates (LAS), isomers of LAS, branched alkylbenzenesulfonates (BABS), phenylalkanesulfonates, alpha-olefinsulfonates (AOS), olefin sulfonates, alkene sulfonates, alkane-2,3-diylbis(sulfates), hydroxyalkanesulfonates and disulfonates, alkyl sulfates (AS) such as sodium dodecyl sulfate (SDS), fatty alcohol sulfates (FAS), primary alcohol sulfates (PAS), alcohol ethersulfates (AES or AEOS or FES, also known as alcohol ethoxysulfates or fatty alcohol ether sulfates), secondary alkanesulfonates (SAS), paraffin sulfonates (PS), ester sulfonates, sulfonated fatty acid glycerol esters, alpha-sulfo fatty acid methyl esters (alpha-SFMe or SES) including methyl ester sulfonate (MES), alkyl- or alkenylsuccinic acid, dodecenyl/tetradecenyl succinic acid (DTSA), fatty acid derivatives of amino acids, diesters and monoesters of sulfo-succinic acid or salt of fatty acids (soap), and combinations thereof.

When included therein the detergent will usually contain from about 1% to about 40% by weigh of a cationic surfactant, for example from about 0.5% to about 30%, in particular from about 1% to about 20%, from about 3% to about 10%, such as from about 3% to about 5%, from about 8% to about 12% or from about 10% to about 12%. Non-limiting examples of cationic surfactants include alkyldimethylethanolamine quat (ADMEAQ), cetyltrimethylammonium bromide (CTAB), dimethyldistearylammonium chloride (DSDMAC), and alkylbenzyldimethylammonium, alkyl quaternary ammonium compounds, alkoxylated quaternary ammonium (AQA) compounds, ester quats, and combinations thereof.

When included therein the detergent will usually contain from about 0.2% to about 40% by weight of a nonionic surfactant, for example from about 0.5% to about 30%, in particular from about 1% to about 20%, from about 3% to about 10%, such as from about 3% to about 5%, from about 8% to about 12%, or from about 10% to about 12%. Non-limiting examples of nonionic surfactants

include alcohol ethoxylates (AE or AEO), alcohol propoxylates, propoxylated fatty alcohols (PFA), alkoxylated fatty acid alkyl esters, such as ethoxylated and/or propoxylated fatty acid alkyl esters, alkylphenol ethoxylates (APE), nonylphenol ethoxylates (NPE), alkylpolyglycosides (APG), alkoxylated amines, fatty acid monoethanolamides (FAM), fatty acid diethanolamides (FADA), ethoxylated fatty acid monoethanolamides (EFAM), propoxylated fatty acid monoethanolamides (PFAM), polyhydroxyalkyl fatty acid amides, or N-acyl N-alkyl derivatives of glucosamine (glucamides, GA, or fatty acid glucamides, FAGA), as well as products available under the trade names SPAN and TWEEN, and combinations thereof.

When included therein the detergent will usually contain from about 0.1% to about 10% by weight of a semipolar surfactant. Non-limiting examples of semipolar surfactants include amine oxides (AO) such as alkyldimethylamineoxide, N-(coco alkyl)-N,N-dimethylamine oxide and N-(tallow-alkyl)-N,N-bis(2-hydroxyethyl)amine oxide, and combinations thereof.

When included therein the detergent will usually contain from about 0.1% to about 10% by weight of a zwitterionic surfactant. Non-limiting examples of zwitterionic surfactants include betaines such as alkyldimethylbetaines, sulfobetaines, and combinations thereof.

Builders and Co-Builders

The detergent composition may contain about 0-65% by weight, such as about 5% to about 50% of a detergent builder or co-builder, or a mixture thereof. In a dish wash detergent, the level of builder is typically 40-65%, particularly 50-65%. The builder and/or co-builder may particularly be a chelating agent that forms water-soluble complexes with Ca and Mg. Any builder and/or co-builder known in the art for use in cleaning detergents may be utilized. Non-limiting examples of builders include zeolites, diphosphates (pyrophosphates), triphosphates such as sodium triphosphate (STP or STPP), carbonates such as sodium carbonate, soluble silicates such as sodium metasilicate, layered silicates (e.g., SKS-6 from Hoechst), ethanolamines such as 2-aminoethan-1-ol (MEA), diethanolamine (DEA, also known as 2,2'-iminodiethan-1-ol), triethanolamine (TEA, also known as 2,2',2"-nitrilotriethan-1-ol), and (carboxymethyl)inulin (CMI), and combinations thereof.

The detergent composition may also contain 0-50% by weight, such as about 5% to about 30%, of a detergent co-builder. The detergent composition may include a co-builder alone, or in combination with a builder, for example a zeolite builder. Non-limiting examples of co-builders include homopolymers of polyacrylates or copolymers thereof, such as poly(acrylic acid) (PAA) or copoly(acrylic acid/maleic acid) (PAA/PMA). Further non-limiting examples include citrate, chelators such as aminocarboxylates, aminopolycarboxylates and phosphonates, and alkyl- or alkenylsuccinic acid. Additional specific examples include 2,2',2"-nitrilotriacetic acid (NTA), ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTPA), iminodisuccinic acid (IDS), ethylenediamine-N,N'-disuccinic acid (EDDS), methylglycinediacetic acid (MGDA), glutamic acid-N,N-diacetic acid (GLDA), 1-hydroxyethane-1,1-diphosphonic acid (HEDP), ethylenediaminetetra(methylenephosphonic acid) (EDTMPA), diethylenetriaminepentakis(methylenephosphonic acid) (DTMPA or DTPMPA), N-(2-

hydroxyethyl)iminodiacetic acid (EDG), aspartic acid-N-monoacetic acid (ASMA), aspartic acid-N,N-diacetic acid (ASDA), aspartic acid-N-monopropionic acid (ASMP), iminodisuccinic acid (IDA), N-(2-sulfomethyl)-aspartic acid (SMAS), N-(2-sulfoethyl)-aspartic acid (SEAS), N-(2-sulfomethyl)-glutamic acid (SMGL), N-(2-sulfoethyl)-glutamic acid (SEGL), N-methyliminodiacetic acid (MIDA), α-alanine-N,N-diacetic acid (α-ALDA), serine-N,N-diacetic acid (SEDA), isoserine-N,N-diacetic acid (ISDA), phenylalanine-N,N-diacetic acid (PHDA), anthranilic acid-N,N-diacetic acid (ANDA), sulfanilic acid-N,N-diacetic acid (SLDA) , taurine-N,N-diacetic acid (TUDA) and sulfomethyl-N,N-diacetic acid (SMDA), N-(2-hydroxyethyl)ethylenediamine-N,N',N''-triacetic acid (HEDTA), diethanolglycine (DEG), diethylenetriamine penta(methylenephosphonic acid) (DTPMP), aminotris(methylenephosphonic acid) (ATMP), and combinations and salts thereof. Further exemplary builders and/or co-builders are described in, e.g., WO 09/102854, US 5977053.

Bleaching Systems

The detergent may contain 0-30% by weight, such as about 1% to about 20%, of a bleaching system. Any bleaching system comprising components known in the art for use in cleaning detergents may be utilized. Suitable bleaching system components include sources of hydrogen peroxide; sources of peracids; and bleach catalysts or boosters.

Sources of hydrogen peroxide:

Suitable sources of hydrogen peroxide are inorganic persalts, including alkali metal salts such as sodium percarbonate and sodium perborates (usually mono- or tetrahydrate), and hydrogen peroxide—urea (1/1).

Sources of peracids:

Peracids may be (a) incorporated directly as preformed peracids or (b) formed in situ in the wash liquor from hydrogen peroxide and a bleach activator (perhydrolysis) or (c) formed in situ in the wash liquor from hydrogen peroxide and a perhydrolase and a suitable substrate for the latter, e.g., an ester.

a) Suitable preformed peracids include, but are not limited to, peroxycarboxylic acids such as peroxybenzoic acid and its ring-substituted derivatives, peroxy-α-naphthoic acid, peroxyphthalic acid, peroxylauric acid, peroxystearic acid, ε-phthalimidoperoxycaproic acid [phthalimidoperoxyhexanoic acid (PAP)], and o-carboxybenzamidoperoxycaproic acid; aliphatic and aromatic diperoxydicarboxylic acids such as diperoxydodecanedioic acid, diperoxyazelaic acid, diperoxysebacic acid, diperoxybrassylic acid, 2-decyldiperoxybutanedioic acid, and diperoxyphthalic, -isophthalic and -terephthalic acids; perimidic acids; peroxymonosulfuric acid; peroxydisulfuric acid; peroxyphosphoric acid; peroxysilicic acid; and mixtures of said compounds. It is understood that the peracids mentioned may in some cases be best added as suitable salts, such as alkali metal salts (e.g., Oxone®) or alkaline earth-metal salts.

b) Suitable bleach activators include those belonging to the class of esters, amides, imides, nitriles or anhydrides and, where applicable, salts thereof. Suitable examples are tetraacetylethylenediamine (TAED), sodium 4-[(3,5,5-trimethylhexanoyl)oxy]benzene-1-

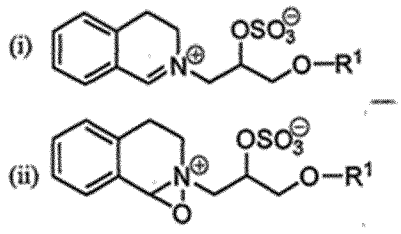
sulfonate (ISONOBS), sodium 4-(dodecanoyloxy)benzene-1-sulfonate (LOBS), sodium 4-(decanoyloxy)benzene-1-sulfonate, 4-(decanoyloxy)benzoic acid (DOBA), sodium 4-(nonanoyloxy)benzene-1-sulfonate (NOBS), and/or those disclosed in WO98/17767. A particular family of bleach activators of interest was disclosed in EP624154 and particularly preferred in that family is acetyl triethyl citrate (ATC). ATC or a short chain triglyceride like triacetin has the advantage that they are environmentally friendly. Furthermore, acetyl triethyl citrate and triacetin have good hydrolytical stability in the product upon storage and are efficient bleach activators. Finally, ATC is multifunctional, as the citrate released in the perhydrolysis reaction may function as a builder.

Bleach catalysts and boosters

The bleaching system may also include a bleach catalyst or booster.

Some non-limiting examples of bleach catalysts that may be used in the compositions of the present invention include manganese oxalate, manganese acetate, manganese-collagen, cobalt-amine catalysts and manganese triazacyclononane (MnTACN) catalysts; particularly preferred are complexes of manganese with 1,4,7-trimethyl-1,4,7-triazacyclononane (Me3-TACN) or 1,2,4,7-tetramethyl-1,4,7-triazacyclononane (Me4-TACN), in particular Me3-TACN, such as the dinuclear manganese complex [(Me3-TACN)Mn(O)3Mn(Me3-TACN)](PF6)2, and [2,2',2''-nitrilotris(ethane-1,2-diylazanylylidene-κN-methanylylidene)triphenolato-κ3O]manganese(III). The bleach catalysts may also be other metal compounds; such as iron or cobalt complexes.

In some embodiments, where a source of a peracid is included, an organic bleach catalyst or bleach booster may be used having one of the following formulae:



(iii) and mixtures thereof; wherein each R1 is independently a branched alkyl group containing from 9 to 24 carbons or linear alkyl group containing from 11 to 24 carbons, preferably each R1 is independently a branched alkyl group containing from 9 to 18 carbons or linear alkyl group containing from 11 to 18 carbons, more preferably each R1 is independently selected from the group consisting of 2-propylheptyl, 2-butyloctyl, 2-pentylnonyl, 2-hexyldecyl, dodecyl, tetradecyl, hexadecyl, octadecyl, isononyl, isodecyl, isotridecyl and isopentadecyl.

Other exemplary bleaching systems are described, e.g. in WO2007/087258, WO2007/087244, WO2007/087259, EP1867708 (Vitamin K) and WO2007/087242. Suitable photobleaches may for example be sulfonated zinc or aluminium phthalocyanines.

Metal care agents

Metal care agents may prevent or reduce the tarnishing, corrosion or oxidation of metals, including aluminium, stainless steel and non-ferrous metals, such as silver and copper. Suitable examples include one or more of the following:

(a) benzatriazoles, including benzotriazole or bis-benzotriazole and substituted derivatives thereof. Benzotriazole derivatives are those compounds in which the available substitution sites on the aromatic ring are partially or completely substituted. Suitable substituents include linear or branch-chain Ci-C20- alkyl groups (e.g., C1-C20- alkyl groups) and hydroxyl, thio, phenyl or halogen such as fluorine, chlorine, bromine and iodine.

(b) metal salts and complexes chosen from the group consisting of zinc, manganese, titanium, zirconium, hafnium, vanadium, cobalt, gallium and cerium salts and/or complexes, the metals being in one of the oxidation states II, III, IV, V or VI. In one aspect, suitable metal salts and/or metal complexes may be chosen from the group consisting of Mn(II) sulphate, Mn(II) citrate, Mn(II) stearate, Mn(II) acetylacetonate, K^TiF6 (e.g., K2TiF6), K^ZrF6 (e.g., K2ZrF6), CoSO4, Co(NOs)2 and Ce(NOs)3, zinc salts, for example zinc sulphate, hydrozincite or zinc acetate.;

(c) silicates, including sodium or potassium silicate, sodium disilicate, sodium metasilicate, crystalline phyllosilicate and mixtures thereof.

Further suitable organic and inorganic redox-active substances that act as silver/copper corrosion inhibitors are disclosed in WO 94/26860 and WO 94/26859. Preferably the composition of the invention comprises from 0.1 to 5% by weight of the composition of a metal care agent, preferably the metal care agent is a zinc salt.

Hydrotropes

The detergent may contain 0-10% by weight, for example 0-5% by weight, such as about 0.5 to about 5%, or about 3% to about 5%, of a hydrotrope. Any hydrotrope known in the art for use in detergents may be utilized. Non-limiting examples of hydrotropes include sodium benzenesulfonate, sodium p-toluene sulfonate (STS), sodium xylene sulfonate (SXS), sodium cumene sulfonate (SCS), sodium cymene sulfonate, amine oxides, alcohols and polyglycolethers, sodium hydroxynaphthoate, sodium hydroxynaphthalene sulfonate, sodium ethylhexyl sulfate, and combinations thereof.

Polymers

The detergent may contain 0-10% by weight, such as 0.5-5%, 2-5%, 0.5-2% or 0.2-1% of a polymer. Any polymer known in the art for use in detergents may be utilized. The polymer may function as a co-builder as mentioned above, or may provide antiredeposition, fiber protection, soil release, dye transfer inhibition, grease cleaning and/or anti-foaming properties. Some

polymers may have more than one of the above-mentioned properties and/or more than one of the below-mentioned motifs. Exemplary polymers include (carboxymethyl)cellulose (CMC), poly(vinyl alcohol) (PVA), poly(vinylpyrrolidone) (PVP), poly(ethyleneglycol) or poly(ethylene oxide) (PEG), ethoxylated poly(ethyleneimine), carboxymethyl inulin (CMI), and polycarboxylates such as PAA, PAA/PMA, poly-aspartic acid, and lauryl methacrylate/acrylic acid copolymers , hydrophobically modified CMC (HM-CMC) and silicones, copolymers of terephthalic acid and oligomeric glycols, copolymers of poly(ethylene terephthalate) and poly(oxyethene terephthalate) (PET-POET), PVP, poly(vinylimidazole) (PVI), poly(vinylpyridine-N-oxide) (PVPO or PVPNO) and polyvinylpyrrolidone-vinylimidazole (PVPVI). Suitable examples include PVP-K15, PVP-K30, ChromaBond S-400, ChromaBond S- 403E and Chromabond S-100 from Ashland Aqualon, and Sokalan® HP 165, Sokalan® HP 50 (Dispersing agent), Sokalan® HP 53 (Dispersing agent), Sokalan® HP 59 (Dispersing agent), Sokalan® HP 56 (dye transfer inhibitor), Sokalan® HP 66 K (dye transfer inhibitor) from BASF. Further exemplary polymers include sulfonated polycarboxylates, polyethylene oxide and polypropylene oxide (PEO-PPO) and diquaternium ethoxy sulfate. Other exemplary polymers are disclosed in, e.g., WO 2006/130575. Salts of the above-mentioned polymers are also contemplated. Particularly preferred polymer is ethoxylated homopolymer Sokalan® HP 20 from BASF, which helps to prevent redeposition of soil in the wash liquor.

Fabric hueing agents

The detergent compositions of the present invention may also include fabric hueing agents such as dyes or pigments, which when formulated in detergent compositions can deposit onto a fabric when said fabric is contacted with a wash liquor comprising said detergent compositions and thus altering the tint of said fabric through absorption/reflection of visible light. Fluorescent whitening agents emit at least some visible light. In contrast, fabric hueing agents alter the tint of a surface as they absorb at least a portion of the visible light spectrum. Suitable fabric hueing agents include dyes and dye-clay conjugates, and may also include pigments. Suitable dyes include small molecule dyes and polymeric dyes. Suitable small molecule dyes include small molecule dyes selected from the group consisting of dyes falling into the Colour Index (C.I.) classifications of Direct Blue, Direct Red, Direct Violet, Acid Blue, Acid Red, Acid Violet, Basic Blue, Basic Violet and Basic Red, or mixtures thereof, for example as described in WO2005/03274, WO2005/03275, WO2005/03276 and EP1876226 (hereby incorporated by reference). The detergent composition preferably comprises from about 0.00003 wt% to about 0.2 wt%, from about 0.00008 wt% to about 0.05 wt%, or even from about 0.0001 wt% to about 0.04 wt% fabric hueing agent. The composition may comprise from 0.0001 wt% to 0.2 wt% fabric hueing agent, this may be especially preferred when the composition is in the form of a unit dose pouch. Suitable hueing agents are also disclosed in, e.g. WO 2007/087257 and WO2007/087243.

Enzymes

The detergent additive as well as the detergent composition may comprise one or more additional enzymes such as one or more lipase, cutinase, an amylase, carbohydrase, cellulase,

pectinase, mannanase, arabinase, galactanase, xylanase, oxidase, e.g., a laccase, and/or peroxidase.

In general, the properties of the selected enzyme(s) should be compatible with the selected detergent, (i.e., pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.), and the enzyme(s) should be present in effective amounts.

Cellulases

Suitable cellulases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Suitable cellulases include cellulases from the genera Bacillus, Pseudomonas, Humicola, Fusarium, Thielavia, Acremonium, e.g., the fungal cellulases produced from Humicola insolens, Myceliophthora thermophila and Fusarium oxysporum disclosed in US 4,435,307, US 5,648,263, US 5,691,178, US 5,776,757 and WO 89/09259.

Especially suitable cellulases are the alkaline or neutral cellulases having colour care benefits. Examples of such cellulases are cellulases described in EP 0 495 257, EP 0 531 372, WO 96/11262, WO 96/29397, WO 98/08940. Other examples are cellulase variants such as those described in WO 94/07998, EP 0 531 315, US 5,457,046, US 5,686,593, US 5,763,254, WO 95/24471, WO 98/12307 and WO99/001544.

Other cellulases are endo-beta-1,4-glucanase enzyme having a sequence of at least 97% identity to the amino acid sequence of position 1 to position 773 of SEQ ID NO2 of WO 2002/099091 or a family 44 xyloglucanase, which a xyloglucanase enzyme having a sequence of at least 60% identity to positions 40-559 of SEQ ID NO 2 of WO 2001/062903.

Commercially available cellulases include Celluzyme™, and Carezyme™ (Novozymes A/S) Carezyme Premium™ (Novozymes A/S), Celluclean ™ (Novozymes A/S), Celluclean Classic™ (Novozymes A/S), Cellusoft™ (Novozymes A/S), Whitezyme™ (Novozymes A/S), Clazinase™, and Puradax HA™ (Genencor International Inc.), and KAC-500(B)™ (Kao Corporation).

Mannanases

Suitable mannanases include those of bacterial or fungal origin. Chemically or genetically modified mutants are included. The mannanase may be an alkaline mannanase of Family 5 or 26. It may be a wild-type from Bacillus or Humicola, particularly B. agaradhaerens, B. licheniformis, B. halodurans, B. clausii, or H. insolens. Suitable mannanases are described in WO 1999/064619. A commercially available mannanase is Mannaway (Novozymes A/S).

Peroxidases/Oxidases

Suitable peroxidases/oxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from Coprinus, e.g., from C. cinereus, and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257. Commercially available peroxidases include Guardzyme™ (Novozymes A/S).

Lipases and Cutinases:

Suitable lipases and cutinases include those of bacterial or fungal origin. Chemically modified or protein engineered mutant enzymes are included. Examples include lipase from Thermomyces, e.g. from T. lanuginosus (previously named Humicola lanuginosa) as described in EP258068 and EP305216, cutinase from Humicola, e.g. H. insolens (WO96/13580), lipase from strains of Pseudomonas (some of these now renamed to Burkholderia), e.g. P. alcaligenes or P. pseudoalcaligenes (EP218272), P. cepacia (EP331376), P. sp. strain SD705 (WO95/06720 & WO96/27002), P. wisconsinensis (WO96/12012), GDSL-type Streptomyces lipases (WO10/065455), cutinase from Magnaporthe grisea (WO10/107560), cutinase from Pseudomonas mendocina (US5,389,536), lipase from Thermobifida fusca (WO11/084412), Geobacillus stearothermophilus lipase (WO11/084417), lipase from Bacillus subtilis (WO11/084599), and lipase from Streptomyces griseus (WO11/150157) and S. pristinaespiralis (WO12/137147).

Other examples are lipase variants such as those described in EP407225, WO92/05249, WO94/01541, WO94/25578, WO95/14783, WO95/30744, WO95/35381, WO95/22615, WO96/00292, WO97/04079, WO97/07202, WO00/34450, WO00/60063, WO01/92502, WO07/87508 and WO09/109500.

Preferred commercial lipase products include Lipolase™, Lipex™; Lipolex™ and Lipoclean™ (Novozymes A/S), Lumafast (originally from Genencor) and Lipomax (originally from Gist-Brocades).

Still other examples are lipases sometimes referred to as acyltransferases or perhydrolases, e.g. acyltransferases with homology to Candida antarctica lipase A (WO10/111143), acyltransferase from Mycobacterium smegmatis (WO05/56782), perhydrolases from the CE 7 family (WO09/67279), and variants of the M. smegmatis perhydrolase in particular the S54V variant used in the commercial product Gentle Power Bleach from Huntsman Textile Effects Pte Ltd (WO10/100028).

Amylases:

Suitable amylases include alpha-amylases and/or a glucoamylases and may be of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Amylases include, for example, alpha-amylases obtained from Bacillus, e.g., a special strain of Bacillus licheniformis, described in more detail in GB 1,296,839.

Suitable amylases include amylases having SEQ ID NO 2 in WO 95/10603 or variants having 90% sequence identity to SEQ ID NO 3 thereof. Preferred variants are described in WO 94/02597, WO 94/18314, WO 97/43424 and SEQ ID NO 4 of WO 99/019467, such as variants with substitutions in one or more of the following positions: 15, 23, 105, 106, 124, 128, 133, 154, 156, 178, 179, 181, 188, 190, 197, 201, 202, 207, 208, 209, 211, 243, 264, 304, 305, 391, 408, and 444.

Different suitable amylases include amylases having SEQ ID NO 6 in WO 02/010355 or variants thereof having 90% sequence identity to SEQ ID NO 6. Preferred variants of SEQ ID NO 6 are those having a deletion in positions 181 and 182 and a substitution in position 193.

Other amylases which are suitable are hybrid alpha-amylase comprising residues 1-33 of the alpha-amylase derived from B. amyloliquefaciens shown in SEQ ID NO 6 of WO 2006/066594 and residues 36-483 of the B. licheniformis alpha-amylase shown in SEQ ID NO 4 of WO 2006/066594 or variants having 90% sequence identity thereof. Preferred variants of this hybrid alpha-amylase are those having a substitution, a deletion or an insertion in one of more of the following positions: G48, T49, G107, H156, A181, N190, M197, I201, A209 and Q264. Most preferred variants of the hybrid alpha-amylase comprising residues 1-33 of the alpha-amylase derived from B. amyloliquefaciens shown in SEQ ID NO 6 of WO 2006/066594 and residues 36-483 of SEQ ID NO 4 are those having the substitutions:

M197T;

H156Y+A181T+N190F+A209V+Q264S; or

G48A+T49I+G107A+H156Y+A181T+N190F+I201F+A209V+Q264S.

Further amylases which are suitable are amylases having SEQ ID NO 6 in WO 99/019467 or variants thereof having 90% sequence identity to SEQ ID NO 6. Preferred variants of SEQ ID NO 6 are those having a substitution, a deletion or an insertion in one or more of the following positions: R181, G182, H183, G184, N195, I206, E212, E216 and K269. Particularly preferred amylases are those having deletion in positions R181 and G182, or positions H183 and G184.

Additional amylases which can be used are those having SEQ ID NO 1, SEQ ID NO 3, SEQ ID NO 2 or SEQ ID NO 7 of WO 96/023873 or variants thereof having 90% sequence identity to SEQ ID NO 1, SEQ ID NO 2, SEQ ID NO 3 or SEQ ID NO 7. Preferred variants of SEQ ID NO 1, SEQ ID NO 2, SEQ ID NO 3 or SEQ ID NO 7 are those having a substitution, a deletion or an insertion in one or more of the following positions: 140, 181, 182, 183, 184, 195, 206, 212, 243, 260, 269, 304 and 476, using SEQ ID 2 of WO 96/023873 for numbering. More preferred variants are those having a deletion in two positions selected from 181, 182, 183 and 184, such as 181 and 182, 182 and 183, or positions 183 and 184. Most preferred amylase variants of SEQ ID NO 1, SEQ ID NO 2 or SEQ ID NO 7 are those having a deletion in positions 183 and 184 and a substitution in one or more of positions 140, 195, 206, 243, 260, 304 and 476.

Other amylases which can be used are amylases having SEQ ID NO 2 of WO 08/153815, SEQ ID NO 10 in WO 01/66712 or variants thereof having 90% sequence identity to SEQ ID NO 2 of WO 08/153815 or 90% sequence identity to SEQ ID NO 10 in WO 01/66712. Preferred variants of SEQ ID NO 10 in WO 01/66712 are those having a substitution, a deletion or an insertion in one of more of the following positions: 176, 177, 178, 179, 190, 201, 207, 211 and 264.

Further suitable amylases are amylases having SEQ ID NO 2 of WO 09/061380 or variants having 90% sequence identity to SEQ ID NO 2 thereof. Preferred variants of SEQ ID NO 2 are those having a truncation of the C-terminus and/or a substitution, a deletion or an insertion in one of more of the following positions: Q87, Q98, S125, N128, T131, T165, K178, R180, S181, T182, G183, M201, F202, N225, S243, N272, N282, Y305, R309, D319, Q320, Q359, K444 and G475. More preferred variants of SEQ ID NO 2 are those having the substitution in one of more of the following positions: Q87E,R, Q98R, S125A, N128C, T131I, T165I, K178L, T182G, M201L, F202Y, N225E,R, N272E,R, S243Q,A,E,D, Y305R, R309A, Q320R, Q359E, K444E and G475K and/or deletion in position R180 and/or S181 or of T182 and/or G183. Most preferred amylase variants of SEQ ID NO 2 are those having the substitutions:

N128C+K178L+T182G+Y305R+G475K;

N128C+K178L+T182G+F202Y+Y305R+D319T+G475K;

S125A+N128C+K178L+T182G+Y305R+G475K; or

S125A+N128C+T131I+T165I+K178L+T182G+Y305R+G475K wherein the variants are C-terminally truncated and optionally further comprises a substitution at position 243 and/or a deletion at position 180 and/or position 181.

Further suitable amylases are amylases having SEQ ID NO 1 of WO13184577 or variants having 90% sequence identity to SEQ ID NO 1 thereof. Preferred variants of SEQ ID NO 1 are those having a substitution, a deletion or an insertion in one of more of the following positions: K176, R178, G179, T180, G181, E187, N192, M199, I203, S241, R458, T459, D460, G476 and G477. More preferred variants of SEQ ID NO 1 are those having the substitution in one of more of the following positions: K176L, E187P, N192FYH, M199L, I203YF, S241QADN, R458N, T459S, D460T, G476K and G477K and/or deletion in position R178 and/or S179 or of T180 and/or G181. Most preferred amylase variants of SEQ ID NO 1 are those having the substitutions:

E187P+I203Y+G476K

E187P+I203Y+R458N+T459S+D460T+G476K

wherein the variants optionally further comprise a substitution at position 241 and/or a deletion at position 178 and/or position 179.

Further suitable amylases are amylases having SEQ ID NO 1 of WO10104675 or variants having 90% sequence identity to SEQ ID NO 1 thereof. Preferred variants of SEQ ID NO 1 are those having a substitution, a deletion or an insertion in one of more of the following positions: N21, D97, V128 K177, R179, S180, I181, G182, M200, L204, E242, G477 and G478. More preferred variants of SEQ ID NO 1 are those having the substitution in one of more of the following positions: N21D, D97N, V128I K177L, M200L, L204YF, E242QA, G477K and G478K and/or deletion in position R179 and/or S180 or of I181 and/or G182. Most preferred amylase variants of SEQ ID NO 1 are those having the substitutions:

N21D+D97N+V128I

wherein the variants optionally further comprise a substitution at position 200 and/or a deletion at position 180 and/or position 181.

Other suitable amylases are the alpha-amylase having SEQ ID NO 12 in WO01/66712 or a variant having at least 90% sequence identity to SEQ ID NO 12. Preferred amylase variants are those having a substitution, a deletion or an insertion in one of more of the following positions of SEQ ID NO 12 in WO01/66712: R28, R118, N174; R181, G182, D183, G184, G186, W189, N195, M202, Y298, N299, K302, S303, N306, R310, N314; R320, H324, E345, Y396, R400, W439, R444, N445, K446, Q449, R458, N471, N484. Particular preferred amylases include variants having a deletion of D183 and G184 and having the substitutions R118K, N195F, R320K and R458K, and a variant additionally having substitutions in one or more position selected from the group: M9, G149, G182, G186, M202, T257, Y295, N299, M323, E345 and A339, most preferred a variant that additionally has substitutions in all these positions.

Other examples are amylase variants such as those described in WO2011/098531, WO2013/001078 and WO2013/001087.

Commercially available amylases are Duramyl™, Termamyl™, Fungamyl™, Stainzyme ™, Stainzyme Plus™, Natalase™, Liquozyme X and BAN™ (from Novozymes A/S), and Rapidase™, Purastar™/Effectenz™, Powerase, Preferenz S1000, Preferenz S100 and Preferenz S110 (from Genencor International Inc./DuPont).

Proteases:

Suitable proteases include those of bacterial, fungal, plant, viral or animal origin e.g. vegetable or microbial origin. Microbial origin is preferred. Chemically modified or protein engineered mutants are included. It may be an alkaline protease, such as a serine protease or a metalloprotease. A serine protease may for example be of the S1 family, such as trypsin, or the S8 family such as subtilisin. A metalloproteases protease may for example be a thermolysin from e.g. family M4 or other metalloproteases such as those from M5, M7 or M8 families.

The term "subtilases" refers to a sub-group of serine protease according to Siezen et al., Protein Engng. 4 (1991) 719-737 and Siezen et al. Protein Science 6 (1997) 501-523. Serine proteases are a subgroup of proteases characterized by having a serine in the active site, which forms a covalent adduct with the substrate. The subtilases may be divided into 6 sub-divisions, i.e. the Subtilisin family, the Thermitase family, the Proteinase K family, the Lantibiotic peptidase family, the Kexin family and the Pyrolysin family.

Examples of subtilases are those derived from *Bacillus* such as *Bacillus lentus, Bacillus alkalophilus, Bacillus subtilis, Bacillus amyloliquefaciens, Bacillus pumilus* and *Bacillus gibsonii* described in; US7262042 and WO09/021867, and *Subtilisin lentus*, *Subtilisin* Novo, *subtilisin* Carlsberg, *Bacillus licheniformis*, *subtilisin* BPN', *subtilisin* 309, *subtilisin* 147 and *subtilisin* 168 and e.g. protease PD138 described in (WO93/18140). Other useful proteases may be those described in WO01/016285 and WO02/016547. Examples of trypsin-like proteases are trypsin (e.g. of porcine or bovine origin) and the *Fusarium* protease described in WO94/25583 and

WO05/040372, and the chymotrypsin proteases derived from *Cellumonas* described in WO05/052161 and WO05/052146. A further preferred protease is the alkaline protease from *Bacillus lentus* DSM 5483, as described for example in WO95/23221, and variants thereof which are described in WO92/21760, WO95/23221, EP1921147 and EP1921148.

Examples of metalloproteases are the neutral metalloprotease as described in WO07/044993 (Proctor & Gamble/Genencor Int.) such as those derived from *Bacillus amyloliquefaciens*.

Examples of useful proteases are the variants described in: WO89/06279 WO92/19729, WO96/034946, WO98/20115, WO98/20116, WO99/011768, WO01/44452, WO03/006602, WO04/03186, WO04/041979, WO07/006305, WO11/036263, WO11/036264, especially the variants with substitutions in one or more of the following positions: 3, 4, 9, 15, 24, 27, 42, 55, 59, 60, 66, 74, 85, 96, 97, 98, 99, 100, 101, 102, 104, 116, 118, 121, 126, 127, 128, 154, 156, 157, 158, 161, 164, 176, 179, 182, 185, 188, 189, 193, 198, 199, 200, 203, 206, 211, 212, 216, 218, 226, 229, 230, 239, 246, 255, 256, 268 and 269 wherein the positions correspond to the positions of the *Bacillus lentus* protease shown in SEQ ID NO 1 of WO 2016/001449. More preferred the protease variants may comprise one or more of the mutations selected from the group consisting of: S3T, V4I, S9R, S9E, A15T, S24G, S24R, K27R, N42R, S55P, G59E, G59D, N60D, N60E, V66A, N74D, S85R, A96S, S97G, S97D, S97A, S97SD, S99E, S99D, S99G, S99M, S99N, S99R, S99H, S101A, V102I, V102Y, V102N, S104A, G116V, G116R, H118D, H118N, A120S, S126L, P127Q, S128A, S154D, A156E, G157D, G157P, S158E, Y161A, R164S, Q176E, N179E, S182E, Q185N, A188P, G189E, V193M, N198D, V199I, Y203W, S206G, L211Q, L211D, N212D, N212S, M216S, A226V, K229L, Q230H, Q239R, N246K, N255W, N255D, N255E, L256E, L256D T268A and R269H. The protease variants are preferably variants of the *Bacillus lentus* protease (Savinase®) shown in SEQ ID NO 1 of WO2016/001449, the *Bacillus amylolichenifaciens* protease (BPN') shown in SEQ ID NO 2 of WO2016/001449. The protease variants preferably have at least 80% sequence identity to SEQ ID NO 1 or SEQ ID NO 2 of WO 2016/001449.

A protease variant comprising a substitution at one or more positions corresponding to positions 171, 173, 175, 179, or 180 of SEQ ID NO 1 of WO2004/067737, wherein said protease variant has a sequence identity of at least 75% but less than 100% to SEQ ID NO 1 of WO2004/067737.

Suitable commercially available protease enzymes include those sold under the trade names Alcalase®, Duralase™, Durazym™, Relase®, Relase® Ultra, Savinase®, Savinase® Ultra, Primase®, Polarzyme®, Kannase®, Liquanase®, Liquanase® Ultra, Ovozyme®, Coronase®, Coronase® Ultra, Blaze®, Blaze Evity® 100T, Blaze Evity® 125T, Blaze Evity® 150T, Neutrase®, Everlase® and Esperase® (Novozymes A/S), those sold under the tradename Maxatase®, Maxacal®, Maxapem®, Purafect Ox®, Purafect OxP®, Puramax®, FN2®, FN3®, FN4®, Excellase®, Excellenz P1000™, Excellenz P1250™, Eraser®, Preferenz P100™, Purafect Prime®, Preferenz P110™, Effectenz P1000™, Purafect®™, Effectenz P1050™, Purafect

Ox®™, Effectenz P2000™, Purafast®, Properase®, Opticlean® and Optimase® (Danisco/DuPont), Axapem™ (Gist-Brocases N.V.), BLAP (sequence shown in Figure 29 of US5352604) and variants hereof (Henkel AG) and KAP (*Bacillus alkalophilus* subtilisin) from Kao.

Peroxidases/Oxidases

A peroxidase according to the invention is a peroxidase enzyme comprised by the enzyme classification EC 1.11.1.7, as set out by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB), or any fragment derived therefrom, exhibiting peroxidase activity.

Suitable peroxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from Coprinopsis, e.g., from C. cinerea (EP 179,486), and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257.

A suitable peroxidase includes a haloperoxidase enzyme, such as chloroperoxidase, bromoperoxidase and compounds exhibiting chloroperoxidase or bromoperoxidase activity. Haloperoxidases are classified according to their specificity for halide ions. Chloroperoxidases (E.C. 1.11.1.10) catalyze formation of hypochlorite from chloride ions. Preferably, the haloperoxidase is a vanadium haloperoxidase, i.e., a vanadate-containing haloperoxidase. Haloperoxidases have been isolated from many different fungi, in particular from the fungus group dematiaceous hyphomycetes, such as Caldariomyces, e.g., C. fumago, Alternaria, Curvularia, e.g., C. verruculosa and C. inaequalis, Drechslera, Ulocladium and Botrytis.

Haloperoxidases have also been isolated from bacteria such as Pseudomonas, e.g., P. pyrrocinia and Streptomyces, e.g., S. aureofaciens.

A suitable oxidase includes in particular, any laccase enzyme comprised by the enzyme classification EC 1.10.3.2, or any fragment derived therefrom exhibiting laccase activity, or a compound exhibiting a similar activity, such as a catechol oxidase (EC 1.10.3.1), an o-aminophenol oxidase (EC 1.10.3.4), or a bilirubin oxidase (EC 1.3.3.5). Preferred laccase enzymes are enzymes of microbial origin. The enzymes may be derived from plants, bacteria or fungi (including filamentous fungi and yeasts). Suitable examples from fungi include a laccase derivable from a strain of Aspergillus, Neurospora, e.g., N. crassa, Podospora, Botrytis, Collybia, Fomes, Lentinus, Pleurotus, Trametes, e.g., T. villosa and T. versicolor, Rhizoctonia, e.g., R. solani, Coprinopsis, e.g., C. cinerea, C. comatus, C. friesii, and C. plicatilis, Psathyrella, e.g., P. condelleana, Panaeolus, e.g., P. papilionaceus, Myceliophthora, e.g., M. thermophila, Schytalidium, e.g., S. thermophilum, Polyporus, e.g., P. pinsitus, Phlebia, e.g., P. radiata (WO 92/01046), or Coriolus, e.g., C. hirsutus (JP 2238885). Suitable examples from bacteria include a laccase derivable from a strain of Bacillus. A laccase derived from Coprinopsis or Myceliophthora is preferred; in particular, a laccase derived from Coprinopsis cinerea, as disclosed in WO 97/08325; or from Myceliophthora thermophila, as disclosed in WO 95/33836.

Dispersants

The detergent compositions of the present invention can also contain dispersants. In particular, powdered detergents may comprise dispersants. Suitable water-soluble organic materials include the homo- or co-polymeric acids or their salts, in which the polycarboxylic acid comprises at least two carboxyl radicals separated from each other by not more than two carbon atoms. Suitable dispersants are for example described in Powdered Detergents, Surfactant science series volume 71, Marcel Dekker, Inc.

Dye Transfer Inhibiting Agents

The detergent compositions of the present invention may also include one or more dye transfer inhibiting agents. Suitable polymeric dye transfer inhibiting agents include, but are not limited to, polyvinylpyrrolidone polymers, polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinyloxazolidones and polyvinylimidazoles or mixtures thereof. When present in a subject composition, the dye transfer inhibiting agents may be present at levels from about 0.0001 % to about 10%, from about 0.01% to about 5% or even from about 0.1% to about 3% by weight of the composition.

Fluorescent whitening agent

The detergent compositions of the present invention will preferably also contain additional components that may tint articles being cleaned, such as fluorescent whitening agent or optical brighteners. Where present the brightener is preferably at a level of about 0.01% to about 0.5%. Any fluorescent whitening agent suitable for use in a laundry detergent composition may be used in the composition of the present invention. The most commonly used fluorescent whitening agents are those belonging to the classes of diaminostilbene-sulfonic acid derivatives, diarylpyrazoline derivatives and bisphenyl-distyryl derivatives. Examples of the diaminostilbene-sulfonic acid derivative type of fluorescent whitening agents include the sodium salts of: 4,4'-bis-(2-diethanolamino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulfonate, 4,4'-bis-(2,4-dianilino-s-triazin-6-ylamino) stilbene-2.2'-disulfonate, 4,4'-bis-(2-anilino-4-(N-methyl-N-2-hydroxy-ethylamino)-s-triazin-6-ylamino) stilbene-2,2'-disulfonate, 4,4'-bis-(4-phenyl-1,2,3-triazol-2-yl)stilbene-2,2'-disulfonate and sodium 5-(2H-naphtho[1,2-d][1,2,3]triazol-2-yl)-2-[(E)-2-phenylvinyl]benzenesulfonate. Preferred fluorescent whitening agents are Tinopal DMS and Tinopal CBS available from Ciba-Geigy AG, Basel, Switzerland. Tinopal DMS is the disodium salt of 4,4'-bis-(2-morpholino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulfonate. Tinopal CBS is the disodium salt of 2,2'-bis-(phenyl-styryl)-disulfonate. Also preferred are fluorescent whitening agents is the commercially available Parawhite KX, supplied by Paramount Minerals and Chemicals, Mumbai, India. Other fluorescers suitable for use in the invention include the 1-3-diaryl pyrazolines and the 7-alkylaminocoumarins. Suitable fluorescent brightener levels include lower levels of from about 0.01, from 0.05, from about 0.1 or even from about 0.2 wt % to upper levels of 0.5 or even 0.75 wt%.

Soil release polymers

The detergent compositions of the present invention may also include one or more soil release polymers which aid the removal of soils from fabrics such as cotton and polyester based fabrics, in particular the removal of hydrophobic soils from polyester based fabrics. The soil release polymers may for example be nonionic or anionic terephthalte based polymers, polyvinyl caprolactam and related copolymers, vinyl graft copolymers, polyester polyamides see for example Chapter 7 in Powdered Detergents, Surfactant science series volume 71, Marcel Dekker, Inc. Another type of soil release polymers is amphiphilic alkoxylated grease cleaning polymers comprising a core structure and a plurality of alkoxylate groups attached to that core structure. The core structure may comprise a polyalkylenimine structure or a polyalkanolamine structure as described in detail in WO2009/087523 (hereby incorporated by reference). Furthermore, random graft co-polymers are suitable soil release polymers. Suitable graft co-polymers are described in more detail in WO2007/138054, WO2006/108856 and WO2006/113314 (hereby incorporated by reference). Suitable polyethylene glycol polymers include random graft co-polymers comprising: (i) hydrophilic backbone comprising polyethylene glycol; and (ii) side chain(s) selected from the group consisting of: C4-C25 alkyl group, polypropylene, polybutylene, vinyl ester of a saturated C1-C6 mono-carboxylic acid, Cl-C 6 alkyl ester of acrylic or methacrylic acid, and mixtures thereof. Suitable polyethylene glycol polymers have a polyethylene glycol backbone with random grafted polyvinyl acetate side chains. The average molecular weight of the polyethylene glycol backbone can be in the range of from 2,000 Da to 20,000 Da, or from 4,000 Da to 8,000 Da. The molecular weight ratio of the polyethylene glycol backbone to the polyvinyl acetate side chains can be in the range of from 1: 1 to 1:5, or from 1: 1.2 to 1:2. The average number of graft sites per ethylene oxide units can be less than 1, or less than 0.8, the average number of graft sites per ethylene oxide units can be in the range of from 0.5 to 0.9, or the average number of graft sites per ethylene oxide units can be in the range of from 0.1 to 0.5, or from 0.2 to 0.4. A suitable polyethylene glycol polymer is Sokalan HP22. Other soil release polymers are substituted polysaccharide structures especially substituted cellulosic structures such as modified cellulose deriviatives such as those described in EP 1867808 or WO 2003/040279 (both are hereby incorporated by reference). Suitable cellulosic polymers include cellulose, cellulose ethers, cellulose esters, cellulose amides and mixtures thereof. Suitable cellulosic polymers include anionically modified cellulose, nonionically modified cellulose, cationically modified cellulose, zwitterionically modified cellulose, and mixtures thereof. Suitable cellulosic polymers include methyl cellulose, carboxy methyl cellulose, ethyl cellulose, hydroxyl ethyl cellulose, hydroxyl propyl methyl cellulose, ester carboxy methyl cellulose, and mixtures thereof.

Anti-redeposition agents

The detergent compositions of the present invention may also include one or more anti-redeposition agents such as carboxymethylcellulose (CMC), polyvinyl alcohol (PVA),

polyvinylpyrrolidone (PVP), polyoxyethylene and/or polyethyleneglycol (PEG), homopolymers of acrylic acid, copolymers of acrylic acid and maleic acid, and ethoxylated polyethyleneimines. The cellulose based polymers described under soil release polymers above may also function as anti-redeposition agents.

Rheology Modifiers

The detergent compositions of the present invention may also include one or more rheology modifiers, structurants or thickeners, as distinct from viscosity reducing agents. The rheology modifiers are selected from the group consisting of non-polymeric crystalline, hydroxy-functional materials, polymeric rheology modifiers which impart shear thinning characteristics to the aqueous liquid matrix of a liquid detergent composition. The rheology and viscosity of the detergent can be modified and adjusted by methods known in the art, for example as shown in EP 2169040. Other suitable cleaning composition components include, but are not limited to, anti-shrink agents, anti-wrinkling agents, bactericides, binders, carriers, dyes, enzyme stabilizers, fabric softeners, fillers, foam regulators, hydrotropes, perfumes, pigments, sod suppressors, solvents, and structurants for liquid detergents and/or structure elasticizing agents.

Formulation of detergent products

The detergent composition of the invention may be in any convenient form, e.g., a bar, a homogenous tablet, a tablet having two or more layers, a pouch having one or more compartments, a regular or compact powder, a granule, a paste, a gel, or a regular, compact or concentrated liquid.

Pouches can be configured as single or multicompartments. It can be of any form, shape and material which is suitable for hold the composition, e.g. without allowing the release of the composition to release of the composition from the pouch prior to water contact. The pouch is made from water soluble film which encloses an inner volume. Said inner volume can be divided into compartments of the pouch. Preferred films are polymeric materials preferably polymers which are formed into a film or sheet. Preferred polymers, copolymers or derivates thereof are selected polyacrylates, and water soluble acrylate copolymers, methyl cellulose, carboxy methyl cellulose, sodium dextrin, ethyl cellulose, hydroxyethyl cellulose, hydroxypropyl methyl cellulose, malto dextrin, poly methacrylates, most preferably polyvinyl alcohol copolymers and, hydroxypropyl methyl cellulose (HPMC). Preferably the level of polymer in the film for example PVA is at least about 60%. Preferred average molecular weight will typically be about 20,000 to about 150,000. Films can also be of blended compositions comprising hydrolytically degradable and water soluble polymer blends such as polylactide and polyvinyl alcohol (known under the Trade reference M8630 as sold by MonoSol LLC, Indiana, USA) plus plasticisers like glycerol, ethylene glycerol, propylene glycol, sorbitol and mixtures thereof. The pouches can comprise a solid laundry cleaning composition or part components and/or a liquid cleaning composition or part components separated by the water soluble film. The compartment for liquid components can be different in composition than compartments containing solids: US2009/0011970 A1.

Detergent ingredients can be separated physically from each other by compartments in water dissolvable pouches or in different layers of tablets. Thereby negative storage interaction between components can be avoided. Different dissolution profiles of each of the compartments can also give rise to delayed dissolution of selected components in the wash solution.

A liquid or gel detergent, which is not unit dosed, may be aqueous, typically containing at least 20% by weight and up to 95% water, such as up to about 70% water, up to about 65% water, up to about 55% water, up to about 45% water, up to about 35% water. Other types of liquids, including without limitation, alkanols, amines, diols, ethers and polyols may be included in an aqueous liquid or gel. An aqueous liquid or gel detergent may contain from 0-30% organic solvent. A liquid or gel detergent may be non-aqueous.

Granular detergent formulations

Non-dusting granulates may be produced, e.g. as disclosed in US 4,106,991 and 4,661,452 and may optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molar weights of 1000 to 20000; ethoxylated nonylphenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty acids; and mono- and di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in GB 1483591. Liquid enzyme preparations may, for instance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lactic acid or boric acid according to established methods. Protected enzymes may be prepared according to the method disclosed in EP 238,216.

The glycosyl hydrolase e.g. Glyco_hydro_114 glycosyl hydrolase may be formulated as a granule for example as a co-granule that combines one or more enzymes. Each enzyme will then be present in more granules securing a more uniform distribution of enzymes in the detergent. This also reduces the physical segregation of different enzymes due to different particle sizes. Methods for producing multi-enzyme co-granulate for the detergent industry is disclosed in the IP.com disclosure IPCOM000200739D.

Another example of formulation of enzymes by the use of co-granulates are disclosed in WO 2013/188331, which relates to a detergent composition comprising (a) a multi-enzyme co- granule; (b) less than 10 wt zeolite (anhydrous basis); and (c) less than 10 wt phosphate salt (anhydrous basis), wherein said enzyme co-granule comprises from 10 to 98 wt% moisture sink component and the composition additionally comprises from 20 to 80 wt% detergent moisture sink component. The multi-enzyme co-granule may comprise an enzyme of the invention and one or more enzymes selected from the group consisting of proteases, lipases, cellulases, xyloglucanases, perhydrolases, peroxidases, lipoxygenases, laccases, hemicellulases, proteases, cellulases, cellobiose dehydrogenases, xylanases, phospho lipases, esterases, cutinases, pectinases, mannanases, pectate lyases, keratinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, tannases, pentosanases, lichenases glucanases, arabinosidases, hyaluronidase, chondroitinase,

amylases, and mixtures thereof. WO 2013/188331 also relates to a method of treating and/or cleaning a surface, preferably a fabric surface comprising the steps of (i) contacting said surface with the detergent composition as claimed and described herein in aqueous wash liquor, (ii) rinsing and/or drying the surface.

An embodiment of the invention relates to an enzyme granule/particle comprising the glycosyl hydrolase e.g Glyco_hydro_114 glycosyl hydrolase. The granule is composed of a core, and optionally one or more coatings (outer layers) surrounding the core. Typically, the granule/particle size, measured as equivalent spherical diameter (volume based average particle size), of the granule is 20-2000 µm, particularly 50-1500 µm, 100-1500 µm or 250-1200 µm. The core may include additional materials such as fillers, fibre materials (cellulose or synthetic fibres), stabilizing agents, solubilising agents, suspension agents, viscosity regulating agents, light spheres, plasticizers, salts, lubricants and fragrances. The core may include binders, such as synthetic polymer, wax, fat, or carbohydrate. The core may comprise a salt of a multivalent cation, a reducing agent, an antioxidant, a peroxide decomposing catalyst and/or an acidic buffer component, typically as a homogenous blend. The core may consist of an inert particle with the enzyme absorbed into it, or applied onto the surface, *e.g.*, by fluid bed coating. The core may have a diameter of 20-2000 µm, particularly 50-1500 µm, 100-1500 µm or 250-1200 µm. The core can be prepared by granulating a blend of the ingredients, *e.g.*, by a method comprising granulation techniques such as crystallization, precipitation, pan-coating, fluid bed coating, fluid bed agglomeration, rotary atomization, extrusion, prilling, spheronization, size reduction methods, drum granulation, and/or high shear granulation.

Methods for preparing the core can be found in Handbook of Powder Technology; Particle size enlargement by C. E. Capes; Volume 1; 1980; Elsevier.

The core of the enzyme granule/particle may be surrounded by at least one coating, *e.g.*, to improve the storage stability, to reduce dust formation during handling, or for coloring the granule. The optional coating(s) may include a salt coating, or other suitable coating materials, such as polyethylene glycol (PEG), methyl hydroxy-propyl cellulose (MHPC) and polyvinyl alcohol (PVA). Examples of enzyme granules with multiple coatings are shown in WO 93/07263 and WO 97/23606. The coating may be applied in an amount of at least 0.1% by weight of the core, *e.g.*, at least 0.5%, 1% or 5%. The amount may be at most 100%, 70%, 50%, 40% or 30%. The coating is preferably at least 0.1 µm thick, particularly at least 0.5 µm, at least 1 µm or at least 5 µm. In a one embodiment, the thickness of the coating is below 100 µm. In another embodiment, the thickness of the coating is below 60 µm. In an even more particular embodiment the total thickness of the coating is below 40 µm. The coating should encapsulate the core unit by forming a substantially continuous layer. A substantially continuous layer is to be understood as a coating having few or no holes, so that the core unit it is encapsulating/enclosing has few or none uncoated areas. The layer or coating should be homogeneous in thickness. The coating can further contain other materials as known in the art, *e.g.*, fillers, antisticking agents, pigments, dyes, plasticizers and/or binders, such as titanium dioxide, kaolin, calcium carbonate or talc. A salt coating may comprise at least 60% by weight w/w of a salt,

e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 99% by weight w/w. The salt may be added from a salt solution where the salt is completely dissolved or from a salt suspension wherein the fine particles is less than 50 µm, such as less than 10 µm or less than 5 µm. The salt coating may comprise a single salt or a mixture of two or more salts. The salt may be water soluble, and may have a solubility at least 0.1 grams in 100 g of water at 20°C, preferably at least 0.5 g per 100 g water, *e.g.*, at least 1 g per 100 g water, *e.g.*, at least 5 g per 100 g water. The salt may be an inorganic salt, *e.g.*, salts of sulfate, sulfite, phosphate, phosphonate, nitrate, chloride or carbonate or salts of simple organic acids (less than 10 carbon atoms, *e.g.*, 6 or less carbon atoms) such as citrate, malonate or acetate. Examples of cations in these salts are alkali or earth alkali metal ions, the ammonium ion or metal ions of the first transition series, such as sodium, potassium, magnesium, calcium, zinc or aluminium. Examples of anions include chloride, bromide, iodide, sulfate, sulfite, bisulfite, thiosulfate, phosphate, monobasic phosphate, dibasic phosphate, hypophosphite, dihydrogen pyrophosphate, tetraborate, borate, carbonate, bicarbonate, metasilicate, citrate, malate, maleate, malonate, succinate, lactate, formate, acetate, butyrate, propionate, benzoate, tartrate, ascorbate or gluconate. In particular alkali- or earth alkali metal salts of sulfate, sulfite, phosphate, phosphonate, nitrate, chloride or carbonate or salts of simple organic acids such as citrate, malonate or acetate may be used. The salt in the coating may have a constant humidity at 20°C above 60%, particularly above 70%, above 80% or above 85%, or it may be another hydrate form of such a salt (*e.g.*, anhydrate). The salt coating may be as described in WO 00/01793 or WO 2006/034710. Specific examples of suitable salts are NaCl ($CH_{20°C}$=76%), Na_2CO_3 ($CH_{20°C}$=92%), $NaNO_3$ ($CH_{20°C}$=73%), Na_2HPO_4 ($CH_{20°C}$=95%), Na_3PO_4 ($CH_{25°C}$=92%), NH_4Cl ($CH_{20°C}$ = 79.5%), $(NH_4)_2HPO_4$ ($CH_{20°C}$ = 93,0%), $NH_4H_2PO_4$ ($CH_{20°C}$ = 93.1%), $(NH_4)_2SO_4$ ($CH_{20°C}$=81.1%), KCl ($CH_{20°C}$=85%), K_2HPO_4 ($CH_{20°C}$=92%), KH_2PO_4 ($CH_{20°C}$=96.5%), KNO_3 ($CH_{20°C}$=93.5%), Na_2SO_4 ($CH_{20°C}$=93%), K_2SO_4 ($CH_{20°C}$=98%), $KHSO_4$ ($CH_{20°C}$=86%), $MgSO_4$ ($CH_{20°C}$=90%), $ZnSO_4$ ($CH_{20°C}$=90%) and sodium citrate ($CH_{25°C}$=86%). Other examples include NaH_2PO_4, $(NH_4)H_2PO_4$, $CuSO_4$, $Mg(NO_3)_2$ and magnesium acetate. The salt may be in anhydrous form, or it may be a hydrated salt, i.e. a crystalline salt hydrate with bound water(s) of crystallization, such as described in WO 99/32595. Specific examples include anhydrous sodium sulfate (Na_2SO_4), anhydrous magnesium sulfate ($MgSO_4$), magnesium sulfate heptahydrate ($MgSO_4 \cdot 7H_2O$), zinc sulfate heptahydrate ($ZnSO_4 \cdot 7H_2O$), sodium phosphate dibasic heptahydrate ($Na_2HPO_4 \cdot 7H_2O$), magnesium nitrate hexahydrate ($Mg(NO_3)_2(6H_2O)$), sodium citrate dihydrate and magnesium acetate tetrahydrate. Preferably the salt is applied as a solution of the salt, *e.g.*, using a fluid bed.

One embodiment of the present invention provides a granule, which comprises:

(a) a core comprising a Glyco_hydro_114 glycosyl hydrolase according to the invention, and

(b) optionally a coating consisting of one or more layer(s) surrounding the core.

One embodiment of the invention relates to a granule, which comprises:

(a) a core comprising a Glyco_hydro_114 glycosyl hydrolase having at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or 100% sequence identity to the amino acid sequence shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 or SEQ ID NO 96, and

(b) optionally a coating consisting of one or more layer(s) surrounding the core.

Medical cleaning

The present invention further relates to methods of cleaning a medical device and to the use of a composition comprising a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase and at least one adjunct ingredient for cleaning of a medical device. The invention further relates to a method of preventing biofilm formation on a medical device e.g. an indwelling medical device or implant comprising coating the device with at least one Glyco_hydro_114 glycosyl hydrolase.

One embodiment of the invention relates to a method of preventing biofilm formation on a medical device e.g. an indwelling medical device or implant comprising coating the device with at least one Glyco_hydro_114 glycosyl hydrolase.

The polypeptides suitable for use in medical cleaning and in compositions for medical cleaning are described above and include polypeptides which comprises one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and/or polypeptide selected from the group consisting of polypeptides having the amino acid sequence of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 or SEQ ID NO 96 and polypeptides having at least 60%, 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 hereto.

One aspect of the invention relates to a method of cleaning a medical device, wherein the method comprises

a) contacting the medical device with the composition comprising a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase, for a period effective to clean the

medical device;

b) cleaning, the medical device; and

c) optionally disinfect the medical device.

One aspect of the invention relates to a method of cleaning a medical device, wherein the method comprises

a) contacting the medical device with the composition comprising a Glyco_hydro_114 glycosyl hydrolase, which comprises one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and/or is selected from the group consisting of Glyco_hydro_114 glycosyl hydrolases having the amino acid sequence of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 or SEQ ID NO 96 and polypeptides having at least 60%, 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 hereto, for a period effective to clean the medical device;

b) cleaning, the medical device; and

c) optionally disinfect the medical device.

One embodiment relates to a composition comprising a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase, which comprises one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and/or is selected from the group consisting of glycosyl hydrolases having the amino acid sequence of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 and polypeptides having at least 60%, 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 hereto and preferably an adjunct ingredient. The composition may be an anti-biofouling composition and the composition may be a cleaning or pharmaceutical composition. The adjunct ingredient may be any excipient suitable for e.g. cleaning or pharmaceutical compositions. The adjuncts/ excipients are within the choice of the skilled artisan. The adjunct ingredient may be

selected from the group consisting of surfactants, builders, chelators or chelating agents, bleach system or bleach components, polymers, fabric conditioners, foam boosters, suds suppressors, dyes, perfume, tannish inhibitors, optical brighteners, bactericides, fungicides, soil suspending agents, anti-corrosion agents, enzyme inhibitors or stabilizers, enzyme activators, transferase(s), hydrolytic enzymes, oxido reductases, bluing agents and fluorescent dyes, antioxidants, and solubilizers. The compositions may be used for detaching biofilm or preventing biofilm formation on surfaces such as medical devices.

One embodiment of the invention relates to the use of a composition comprising a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase, which comprises one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and/or is selected from the group consisting glycosyl hydrolases having the amino acid sequence of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 and polypeptides having at least 60%, 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 hereto and preferably an adjunct ingredient for cleaning a medical device or an implant.

The medical device may be characterized in that at least a portion of a patient-contactable surface of said device is coated with composition comprising a Glyco_hydro_114 glycosyl hydrolase of the invention. The medical device or implant may be any device or implant that is susceptible to biofilm formation. The medical device may be selected from the group consisting of a catheter such as a central venous catheter, intravascular catheter, urinary catheter, Hickman catheter, peritoneal dialysis catheter, endrotracheal catheter, or wherein the device is a mechanical heart valve, a cardiac pacemaker, an arteriovenous shunt, a scleral buckle, a prosthetic joint, a tympanostomy tube, a tracheostomy tube, a voice prosthetic, a penile prosthetic, an artificial urinary sphincter, a synthetic pubovaginal sling, a surgical suture, a bone anchor, a bone screw, an intraocular lens, a contact lens, an intrauterine device, an aortofemoral graft, a vascular graft, a needle, a Luer-Lok connector, a needleless connector and a surgical instrument.

Uses

The polypeptides of the invention having hydrolytic activity may be used for cleaning e.g. deep cleaning of an item, such as a textile. One embodiment of the invention relates to the use of a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase in a cleaning process, such as laundry and/or dish wash.

In a preferred embodiment, the Glyco_hydro_114 glycosyl hydrolase polypeptides of the invention comprise one or more of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97). In a preferred embodiment the Glyco_hydro_114 glycosyl hydrolase comprising one or more of the motif(s) selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103) and [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

In some embodiments of the invention relate to the use of glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase according to the invention for prevention reduction or removal of malodor. Some embodiment of the invention relates to the use of a polypeptide of the invention for prevention or reduction of anti-redeposition and improvement of whiteness of a textile subjected to multiple washes. One embodiment of the invention relates to the use of a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase according to the invention for deep cleaning of an item, wherein item is a textile. One embodiment of the invention relates to the use of a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase polypeptide according to the invention

(i) for preventing, reducing or removing stickiness of the item;
(ii) for pretreating stains on the item;
(iii) for preventing, reducing or removing redeposition of soil during a wash cycle;
(iv) for preventing, reducing or removing adherence of soil to the item;
(v) for maintaining or improving whiteness of the item;
(vi) for preventing, reducing or removal malodor from the item,

wherein the item is a textile.

One embodiment of the invention relates to the use of a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase polypeptide according to the invention for deep cleaning of an item, wherein item is a textile. One embodiment of the invention relates to the use of a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase polypeptide,

(i) for preventing, reducing or removing stickiness of the item;
(ii) for pretreating stains on the item;
(iii) for preventing, reducing or removing redeposition of soil during a wash cycle;
(iv) for preventing, reducing or removing adherence of soil to the item;
(v) for maintaining or improving whiteness of the item;
(vi) for preventing, reducing or removal malodor from the item, optionally wherein the item is a textile, wherein the glycosyl hydrolase polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(w) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(y) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(z) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(aa) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(bb) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(cc) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(dd) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(ee) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95;

(ff) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

One preferred embodiment relates to the use of a Glyco_hydro_114 glycosyl hydrolase,

i. for preventing, reducing or removing stickiness of the item;
ii. for preventing, reducing or removing biofilm or biofilm components
iii. for reducing or removing pel stains on the item;
iv. for preventing, reducing or removing redeposition of soil during a wash cycle;
v. for preventing, reducing or removing adherence of soil to the item;
vi. for maintaining or improving whiteness of the item;
vii. for preventing, reducing or removal malodor from the item,

wherein the item is a textile.

One preferred embodiment relates to the use of a Glyco_hydro_114 glycosyl hydrolase,

i. for preventing, reducing or removing stickiness of the item;
ii. for preventing, reducing or removing biofilm or biofilm components

iii. for reducing or removing pel stains on the item;

iv. for preventing, reducing or removing redeposition of soil during a wash cycle;

v. for preventing, reducing or removing adherence of soil to the item;

vi. for maintaining or improving whiteness of the item;

vii. for preventing, reducing or removal malodor from the item,

wherein the item is a textile and wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(w) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(y) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(z) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(aa) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(bb) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(cc) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(dd) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(ee) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95;

(ff) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

One preferred embodiment relates to the use of a Glyco_hydro_114 glycosyl hydrolase,

i. for preventing, reducing or removing stickiness of the item;
ii. for preventing, reducing or removing biofilm or biofilm components
iii. for reducing or removing pel stains on the item;
iv. for preventing, reducing or removing redeposition of soil during a wash cycle;
v. for preventing, reducing or removing adherence of soil to the item;

vi. for maintaining or improving whiteness of the item;

vii. for preventing, reducing or removal malodor from the item,

wherein the item is a textile and wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(w) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(y) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(z) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(aa) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(bb) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(cc) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(dd) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(ee) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

The polypeptides of the invention are particularly useful in cleaning processes such as laundry, where the polypeptide effectively reduces biofilm components such as Pel comprising biofilm as shown in the examples below. One embodiment of the invention relates to a method for laundering an item comprising the steps of:

a. exposing an item to a wash liquor comprising the Glyco_hydro_114 glycosyl hydrolase or a composition comprising a Glyco_hydro_114 glycosyl hydrolase;
b. completing at least one wash cycle; and
c. optionally rinsing the item,

wherein the item is a textile.

One preferred embodiment of the invention relates to a method for laundering an item comprising the steps of:

d. exposing an item to a wash liquor comprising a glycosyl hydrolase, preferably a Glyco_hydro_114 glycosyl hydrolase or a composition comprising a glycosyl hydrolase; wherein glycosyl hydrolase is selected from the group consisting of;

(a) a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 70;

(w) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(y) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(z) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(aa) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(bb) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(cc) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(dd) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(ee) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95;

(ff) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

e. completing at least one wash cycle; and

f. optionally rinsing the item,

wherein the item is a textile.

A preferred embodiment relates to a method for laundering an item comprising the steps of:

a. exposing an item to a wash liquor comprising the Glyco_hydro_114 glycosyl hydrolase or a composition comprising a Glyco_hydro_114 glycosyl hydrolase, wherein the Glyco_hydro_114 glycosyl hydrolase is selected from the group consisting of;

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100%sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(w) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(y) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(z) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(aa) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(bb) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(cc) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(dd) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96

b. completing at least one wash cycle; and

c. optionally rinsing the item,

wherein the item is a textile.

The invention is further summarized in the following paragraphs:

1. Use of a polypeptide comprising one or more of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) for deep cleaning of an item, wherein the item is a textile.
2. Use according to paragraph 1 for preventing, reducing or removing stickiness of the item.
3. Use according to any of paragraphs 1 or 2 for pre-treating stains on the item.
4. Use according to any of paragraphs 1-3 for preventing, reducing or removing re-deposition of soil during a wash cycle.
5. Use according to any of paragraphs 1-4 for preventing, reducing or removing adherence of soil to the item.
6. Use according to any of the preceding paragraphs for maintaining or improving the whiteness of the item.
7. Use according to any of the preceding paragraphs, wherein a malodor is reduced or removed from the item.
8. Use according to any of the preceding composition paragraphs, wherein the surface is a textile surface.
9. Use according to any of the preceding composition paragraphs, wherein the textile is made of cotton, Cotton/Polyester, Polyester, Polyamide, Polyacryl and/or silk.
10. Use according to any of the preceding paragraphs, wherein the polypeptide is a polypeptide of paragraphs 68-108.
11. A composition comprising a polypeptide comprising one or more of the motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) and a cleaning or an adjunct ingredient.
12. Composition according to paragraph 11, wherein the polypeptide is the polypeptide of

paragraphs 68- 108.

13. Composition according to any of the preceding composition paragraphs, wherein the detergent adjunct ingredient is selected from the group consisting of surfactants, builders, flocculating aid, chelating agents, dye transfer inhibitors, enzymes, enzyme stabilizers, enzyme inhibitors, catalytic materials, bleach activators, hydrogen peroxide, sources of hydrogen peroxide, preformed peracids, polymeric dispersing agents, clay soil removal/anti-redeposition agents, brighteners, suds suppressors, dyes, perfumes, structure elasticizing agents, fabric softeners, carriers, hydrotropes, builders and co-builders, fabric huing agents, anti-foaming agents, dispersants, processing aids, and/or pigments.

14. Composition according to any of the preceding composition paragraphs wherein the composition comprises from about 5 wt % to about 50 wt %, from about 5 wt % to about 40 wt % , from about 5 wt % to about 30 wt % , from about 5 wt % to about 20 wt % , from about 5 wt % to about 10 wt % anionic surfactant, preferably selected from linear alkylbenzenesulfonates (LAS), isomers of LAS, branched alkylbenzenesulfonates (BABS), phenylalkanesulfonates, alpha-olefinsulfonates (AOS), olefin sulfonates, alkene sulfonates, alkane-2,3-diylbis(sulfates), hydroxyalkanesulfonates and disulfonates, alkyl sulfates (AS) such as sodium dodecyl sulfate (SDS), fatty alcohol sulfates (FAS), primary alcohol sulfates (PAS), alcohol ethersulfates (AES or AEOS or FES), secondary alkanesulfonates (SAS), paraffin sulfonates (PS), ester sulfonates, sulfonated fatty acid glycerol esters, alpha-sulfo fatty acid methyl esters (alpha-SFMe or SES) including methyl ester sulfonate (MES), alkyl- or alkenylsuccinic acid, dodecenyl/tetradecenyl succinic acid (DTSA), fatty acid derivatives of amino acids, diesters and monoesters of sulfo-succinic acid or salt of fatty acids (soap), and combinations thereof.

15. Composition according to any of the preceding composition paragraphs wherein the composition comprises from about 10 wt% to about 50 wt % of at least one builder, preferably selected from citric acid, methylglycine-N,N-diacetic acid (MGDA) and/or glutamic acid-N,N-diacetic acid (GLDA) and mixtures thereof.

16. Composition according to any of the proceeding paragraphs comprising from about 5 wt % to about 40 wt % nonionic surfactants, and from about 0 wt % to about 5 wt % anionic surfactants.

17. Composition according to paragraph 16, wherein the nonionic surfactant is selected from alcohol ethoxylates (AE or AEO), alcohol propoxylates, propoxylated fatty alcohols (PFA), alkoxylated fatty acid alkyl esters, such as ethoxylated and/or propoxylated fatty acid alkyl esters, alkylphenol ethoxylates (APE), nonylphenol ethoxylates (NPE), alkylpolyglycosides (APG), alkoxylated amines, fatty acid monoethanolamides (FAM), fatty acid diethanolamides (FADA), ethoxylated fatty acid monoethanolamides (EFAM), propoxylated fatty acid monoethanolamides (PFAM), polyhydroxyalkyl fatty acid amides, or N-acyl N-alkyl derivatives of glucosamine (glucamides, GA, or fatty acid glucamides, FAGA) and

combinations thereof.

18. Composition according to any of the preceding composition paragraphs, wherein the composition further comprises one or more enzymes selected from the group consisting of proteases, lipases, cutinases, amylases, carbohydrases, cellulases, pectinases, mannanases, arabinases, galactanases, xylanases and oxidases.

19. Composition according to any of the preceding composition paragraphs, wherein the composition is a bar, a homogenous tablet, a tablet having two or more layers, a pouch having one or more compartments, a regular or compact powder, a granule, a paste, a gel, or a regular, compact or concentrated liquid.

20. Composition according to any of the preceding composition paragraphs, wherein the composition is a cleaning composition selected from liquid detergent, powder detergent and granule detergent compositions.

21. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprises one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104) and wherein the polypeptide is selected from the group consisting of polypeptides having the amino acid sequence of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 and polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

22. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 3 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

23. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34),

AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 6 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

24. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 9 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

25. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 12 or polypeptides having at least 60%, 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%, at least 99% or 100%sequence identity hereto.

26. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 15 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

27. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 18 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

28. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 21 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

29. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 24 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

30. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 27 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

31. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 30 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

32. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 33 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

33. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 40 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

34. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises

the amino acid sequence shown SEQ ID NO 43 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

35. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 46 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

36. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 49 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

37. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 52 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

38. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 55 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

39. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 58 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity

hereto.

40. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 61 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

41. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 64 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

42. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 67 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

43. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 70 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

44. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 73 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

45. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34),

AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 76 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

46. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 79 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

47. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 82 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

48. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 85 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

49. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 88 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

50. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 91 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

51. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 94 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

52. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 95 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

53. Composition according to any of the preceding composition paragraphs wherein the polypeptide comprising one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97) and comprises the amino acid sequence shown SEQ ID NO 96 or polypeptides having at least 60%, 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%, at least 99% or 100% sequence identity hereto.

54. A laundering method for laundering an item comprising the steps of:

    a. Exposing an item to a wash liquor comprising a polypeptide of paragraphs 68-108 or a composition according to any of paragraphs 11-53;
    b. Completing at least one wash cycle; and
    c. Optionally rinsing the item,

wherein the item is a textile.

55. A method of treating an item, wherein the item is preferably a textile, said method comprising the steps of:

    a. Exposing an item to a polypeptide selected from the group consisting of a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the mature polypeptide of SEQ ID NO 2, SEQ ID NO5, SEQ ID NO 8, SEQ ID NO 11, SEQ ID NO 14, SEQ ID NO 17, SEQ ID NO 20, SEQ ID NO 23, SEQ ID NO 26, SEQ ID NO 29,SEQ ID NO 32, SEQ ID NO 39, SEQ ID NO 42, SEQ ID NO 45, SEQ ID NO 48, SEQ ID

NO 51, SEQ ID NO 54, SEQ ID NO 57, SEQ ID NO 60, SEQ ID NO 63, SEQ ID NO 66, SEQ ID NO 69, SEQ ID NO 72, SEQ ID NO 75, SEQ ID NO 78, SEQ ID NO 81, SEQ ID NO 84, SEQ ID NO 87, SEQ ID NO 90, SEQ ID NO 93, SEQ ID NO 95 and SEQ ID NO 96; a wash liquor comprising said polypeptide or a composition according to any proceeding paragraphs.

56. Method according to any proceeding paragraphs, wherein the pH of the wash liquor is in the range of 1 to 11.

57. Method according to any of the preceding method paragraphs, wherein the pH of the wash liquor is in the range 5.5 to 11, such as in the range of 7 to 9, in the range of 7 to 8 or in the range of 7 to 8.5.

58. Method according to any of the preceding method paragraphs, wherein the temperature of the wash liquor is in the range of 5°C to 95°C, or in the range of 10°C to 80°C, in the range of 10°C to 70°C, in the range of 10°C to 60°C, in the range of 10°C to 50°C, in the range of 15°C to 40°C, in the range of 20°C to 40°C, in the range of 15°C to 30°C or in the range of 20°C to 30°C.

59. Method according to any of the preceding method paragraphs, wherein the temperature of the wash liquor is from about 20°C to about 40°C.

60. Method according to any of the preceding method paragraphs, wherein the temperature of the wash liquor is from about 15°C to about 30°C.

61. Method according to any of the preceding method paragraphs, wherein stains present on the item is pre-treated with a polypeptide of paragraphs 68-108 or a detergent composition according to any of paragraphs 11-53.

62. Method according to any of the preceding method paragraphs, wherein stickiness of the item is reduced.

63. Method according to any of the preceding method paragraphs, wherein redeposition of soil is reduced.

64. Method according to any of the preceding method paragraphs, wherein adherence of soil to the item is reduced or removed.

65. Method according to any of the preceding method paragraphs, wherein whiteness of the item is maintained or improved.

66. Method according to any of the preceding method paragraphs, wherein malodor is reduced or removed from the item.

67. Method according to any of the preceding method paragraphs, wherein the concentration of the polypeptide having hydrolytic and/or deacetylase activity in the wash liquor is in the range 0.002 mg/L to 2 mg/L, such as 0.02 mg/L to 2 mg/L, such as 0.2 mg/L to 2 mg/L or in the range of 0.0001 mg/L to 10 mg/L or in the range of in the range of 0.001 mg/L to 10 mg/L, or in the range of 0.01 mg/L to 10 mg/L, or in in the range of 0.1 mg/L to 10 mg/L per liter of wash liquor, optionally the concentration of the polypeptide of the invention is

0.0001% to 2 wt %, such as 0.001 to 0.1 wt%, such as 0.005 to 0.1 wt%, such as 0.01 to 0.1 wt%, such as 0.01 to 0.5 wt% or most preferred 0.002 to 0.09 wt% in the total detergent concentration.

68. A polypeptide having hydrolytic and/or deacetylase activity, selected from the group consisting of:

a. a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the mature polypeptide of SEQ ID NO 2, SEQ ID NO5, SEQ ID NO 8, SEQ ID NO 11, SEQ ID NO 14, SEQ ID NO 17, SEQ ID NO 20, SEQ ID NO 23, SEQ ID NO 26, SEQ ID NO 29,SEQ ID NO 32, SEQ ID NO 39, SEQ ID NO 42, SEQ ID NO 45, SEQ ID NO 48, SEQ ID NO 51, SEQ ID NO 54, SEQ ID NO 57, SEQ ID NO 60, SEQ ID NO 63, SEQ ID NO 66, SEQ ID NO 69, SEQ ID NO 72, SEQ ID NO 75, SEQ ID NO 78, SEQ ID NO 81, SEQ ID NO 84, SEQ ID NO 87, SEQ ID NO 90, SEQ ID NO 93 or a polypeptide having at least 60%, 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%, at least 99% or 100%sequence identity to the mature polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33 SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 or SEQ ID NO 96;

b. a polypeptide encoded by a polynucleotide that hybridizes under low stringency conditions with

i. the mature polypeptide coding sequence of SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28, SEQ ID NO 31, SEQ ID NO 38, SEQ ID NO 41, SEQ ID NO 44, SEQ ID NO 47, SEQ ID NO 50, SEQ ID NO 53, SEQ ID NO 56, SEQ ID NO 59, SEQ ID NO 62, SEQ ID NO 65, SEQ ID NO 68, SEQ ID NO 71, SEQ ID NO 74, SEQ ID NO 77, SEQ ID NO 80, SEQ ID NO 83, SEQ ID NO 86, SEQ ID NO 89, SEQ ID NO 92;

ii. the cDNA sequence thereof, or

iii. the full-length complement of (i) or (ii);

c. a polypeptide encoded by a polynucleotide having at least 60% sequence identity to the mature polypeptide coding sequence of SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28, SEQ ID NO 31, SEQ ID NO 38, SEQ ID NO 41, SEQ ID NO 44, SEQ ID NO 47, SEQ ID NO 50, SEQ ID NO 53, SEQ ID NO 56, SEQ ID NO 59, SEQ ID NO 62, SEQ ID NO 65, SEQ ID NO 68, SEQ ID NO 71, SEQ ID NO 74, SEQ ID NO 77, SEQ ID NO 80, SEQ ID NO 83, SEQ ID NO 86, SEQ ID NO 89, SEQ ID NO 92 or the cDNA sequence thereof;

d. a variant of the mature polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 and SEQ ID NO 96 comprising a substitution, deletion, and/or insertion at one or more positions; and

e. a fragment of the polypeptide of (a), (b), (c), or (d) that comprises one or more motif(s) GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100) or DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101) or one or more of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), ([SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) or [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

69. The polypeptide of paragraph 68, having at least 60%, 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 mature polypeptide of SEQ ID NO 2, SEQ ID NO5, SEQ ID NO 8, SEQ ID NO 11, SEQ ID NO 14, SEQ ID NO 17, SEQ ID NO 20, SEQ ID NO 23, SEQ ID NO 26, SEQ ID NO 29,SEQ ID NO 32, SEQ ID NO 39, SEQ ID NO 42, SEQ ID NO 45, SEQ ID NO 48, SEQ ID NO 51, SEQ ID NO 54, SEQ ID NO 57, SEQ ID NO 60, SEQ ID NO 63, SEQ ID NO 66, SEQ ID NO 69, SEQ ID NO 72, SEQ ID NO 75, SEQ ID NO 78, SEQ ID NO 81, SEQ ID NO 84, SEQ ID NO 87, SEQ ID NO 90, SEQ ID NO 93 or to the mature polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID

NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95 and SEQ ID NO 96.

70. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 2 or to the mature polypeptide shown in SEQ ID NO 3.

71. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 5 or to the mature polypeptide shown in SEQ ID NO 6.

72. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 8 or to the mature polypeptide shown in SEQ ID NO 9.

73. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 11 or to the mature polypeptide shown in SEQ ID NO 12.

74. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 14 or to the mature polypeptide shown in SEQ ID NO 15.

75. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 17 or to the mature polypeptide shown in SEQ ID NO 18.

76. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 20 or to the mature polypeptide shown in SEQ ID NO 21.

77. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 23 or to the mature polypeptide shown in SEQ ID NO 24.

78. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 26 or to the mature polypeptide shown in SEQ ID NO 27.

79. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 29 or to the mature polypeptide shown in SEQ ID NO 30.

80. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 32 or to the mature polypeptide shown in SEQ ID NO 33.

81. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 39 or to the mature polypeptide shown in SEQ ID NO 40.

82. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 42 or to the mature polypeptide shown in SEQ ID NO 43.

83. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 45 or to the mature polypeptide shown in SEQ ID NO 46.

84. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 48 or to the mature polypeptide shown in SEQ ID NO 49.

85. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 51 or to the mature polypeptide shown in SEQ ID NO 52.

86. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 54 or to the mature polypeptide shown in SEQ ID NO 55.

87. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 57 or to the mature polypeptide shown in SEQ ID NO 58.

88. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 60 or to the mature polypeptide shown in SEQ ID NO 61.

89. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 63 or to the mature polypeptide shown in SEQ ID NO 64.

90. v The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 66 or to the mature polypeptide shown in SEQ ID NO 67.

91. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 69 or to the mature polypeptide shown in SEQ ID NO 70.

92. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 72 or to the mature polypeptide shown in SEQ ID NO 73.

93. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 75 or to the mature polypeptide shown in SEQ ID NO 76.

94. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 78 or to the mature polypeptide shown in SEQ ID NO 79.

95. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 81 or to the mature polypeptide shown in SEQ ID NO 82.

96. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 84 or to the mature polypeptide shown in SEQ ID NO 85.

97. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 87 or to the mature polypeptide shown in SEQ ID NO 88.

98. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 90 or to the mature polypeptide shown in SEQ ID NO 91.

99. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide of SEQ ID NO 93 or to the mature

polypeptide shown in SEQ ID NO 94.

100. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide shown in SEQ ID NO 95.

101. The polypeptide of paragraph 68 or 69, having at least 60%, 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 mature polypeptide shown in SEQ ID NO 96.

102. The polypeptide according to any of paragraphs 68 to 101, which is encoded by a polynucleotide that hybridizes under low stringency conditions, low-medium stringency conditions, medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with

i. the mature polypeptide coding sequence of SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28,SEQ ID NO 31 SEQ ID NO 38, SEQ ID NO 41, SEQ ID NO 44, SEQ ID NO 47, SEQ ID NO 50, SEQ ID NO 53, SEQ ID NO 56, SEQ ID NO 59, SEQ ID NO 62, SEQ ID NO 65, SEQ ID NO 68, SEQ ID NO 71, SEQ ID NO 74, SEQ ID NO 77, SEQ ID NO 80, SEQ ID NO 83, SEQ ID NO 86, SEQ ID NO 89, SEQ ID NO 92;

ii. the cDNA sequence thereof, or

iii. the full-length complement of (i) or (ii).

103. The polypeptide according to any of paragraphs 68 to 102, which is encoded by a polynucleotide having at least 60%, 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 mature polypeptide coding sequence of SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28,SEQ ID NO 31, SEQ ID NO 38, SEQ ID NO 41, SEQ ID NO 44, SEQ ID NO 47, SEQ ID NO 50, SEQ ID NO 53, SEQ ID NO 56, SEQ ID NO 59, SEQ ID NO 62, SEQ ID NO 65, SEQ ID NO 68, SEQ ID NO 71, SEQ ID NO 74, SEQ ID NO 77, SEQ ID NO 80, SEQ ID NO 83, SEQ ID NO 86, SEQ ID NO 89, SEQ ID NO 92 or the cDNA sequence thereof.

104. The polypeptide according to any of paragraphs 68 to 103, comprising or consisting of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID

NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96 or the mature polypeptide of SEQ ID NO 2, SEQ ID NO 5, SEQ ID NO 8, SEQ ID NO 11, SEQ ID NO 14, SEQ ID NO 17, SEQ ID NO 20, SEQ ID NO 23, SEQ ID NO 26, SEQ ID NO 29, SEQ ID NO 32, SEQ ID NO 39, SEQ ID NO 42, SEQ ID NO 45, SEQ ID NO 48, SEQ ID NO 51, SEQ ID NO 54, SEQ ID NO 57, SEQ ID NO 60, SEQ ID NO 63, SEQ ID NO 66, SEQ ID NO 69, SEQ ID NO 72, SEQ ID NO 75, SEQ ID NO 78, SEQ ID NO 81, SEQ ID NO 84, SEQ ID NO 87, SEQ ID NO 90, SEQ ID NO 93.

105. The polypeptide according to any of paragraphs 68 to 104, which is a variant of the any of the polypeptides with SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91, SEQ ID NO 94, SEQ ID NO 95, SEQ ID NO 96, comprising a substitution, deletion, and/or insertion at one or more positions.

106. The polypeptide according to any of paragraphs 68 to 105 for use as a medicament.

107. The polypeptide according to any of paragraphs 68 to 106 for use in treatment or prevention of a bacterial infection, preferably said bacterial infection is an infection caused by Gram-positive or Gram-negative bacteria, further preferably said bacterial infection is selected from a group consisting of: *Staphylococcus spp. (e.g., Staphylococcus epidermidis, S. aureus), Enterococcus spp. (e.g., Enterococcus faecalis),* Escherichia spp. (e.g., *Escherichia coli), Listeria spp. (e.g., Listeria monocytogenes), Pseudomonas spp. (e.g., Pseudomonas aeruginosa), Bacillus spp., Salmonella spp., Coagulase-negative Staphylococci, Klebsiella spp. (e.g., Klebsiella pneumoniae)* infections.

108. The polypeptide according to any of paragraphs 68 to 107 for use in treatment or prevention of a disease selected from the group consisting of: Cystic fibrosis pneumonia (e.g., caused by Pseudomonas aeruginosa and/or Burkholderia cepacia), Meloidosis (e.g., caused by Pseudomonas pseudomallei), Necrotizing fasciitis (e.g., caused by Group A streptococci), Musculoskeletal infections (e.g., caused by Staphylococci and other Gram-positive cocci), Otitis media (e.g., caused by Haemophilus influenzae), Biliary tract infection (e.g., caused by E. coli and other enteric bacteria), Urinary catheter cystitis (e.g., caused by E. coli and other Gram-negative rods), Bacterial prostatitis (e.g., E. coli and other Gram-negative bacteria), Periodontitis (e.g., caused by Gram negative anaerobic oral bacteria), Dental caries (e.g., caused by Streptococcus spp. and other acidogenic Gram positive cocci).

109. A polynucleotide encoding the polypeptide according to any of paragraphs 68-108.

110. A nucleic acid construct or expression vector comprising the polynucleotide of paragraph 109 operably linked to one or more control sequences that direct the production of the

polypeptide in an expression host.

111. A recombinant host cell comprising the polynucleotide of paragraph 109 operably linked to one or more control sequences that direct the production of the polypeptide.
112. A method of producing the polypeptide of any of paragraphs 68-108, comprising cultivating a cell, which in its wild-type form produces the polypeptide, under conditions conducive for production of the polypeptide.
113. The method of paragraph 112, further comprising recovering the polypeptide.
114. A method of producing a polypeptide according to any of paragraphs 68-108, comprising cultivating the host cell of paragraph 111 under conditions conducive for production of the polypeptide.
115. The method of paragraph 114, further comprising recovering the polypeptide.
116. A nucleic acid construct or expression vector comprising a gene encoding a protein operably linked to the polynucleotide of paragraph 109, wherein the gene is foreign to the polynucleotide encoding the signal peptide.
117. A recombinant host cell comprising a gene encoding a protein operably linked to the polynucleotide of paragraph 109, wherein the gene is foreign to the polynucleotide encoding the signal peptide.
118. A method of producing a protein, comprising cultivating a recombinant host cell comprising a gene encoding a protein operably linked to the polynucleotide of paragraph 109, wherein the gene is foreign to the polynucleotide encoding the signal peptide, under conditions conducive for production of the protein.
119. The method of paragraph 118, further comprising recovering the protein.
120. Item laundered according to the method of any of paragraphs 54-67.

The invention is further described in the following paragraphs

Paragraph 1 A composition comprising at least 0.01 mg of active polypeptide per gram of composition, wherein the polypeptide comprises a Glyco_hydro_114 domain and at least one adjunct ingredient.

Paragraph 2 The composition according to paragraph 1, wherein the polypeptide further comprises a CE4 domain.

Paragraph 3 The composition according to any of the proceeding paragraphs, wherein the polypeptide is of the FLD sub family and comprising one or more of the motif(s) [GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97).

Paragraph 4 The composition of paragraph 1 or 2, wherein the polypeptide has at least 60%, 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 mature polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, 1 SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30 or SEQ ID NO 33.

Paragraph 5 The composition of any of paragraphs 1 or 3,
(a) comprising or consisting of SEQ ID NO 3 or the mature polypeptide of SEQ ID NO 2;
(b) comprising or consisting of SEQ ID NO 6 or the mature polypeptide of SEQ ID NO 5;
(c) comprising or consisting of SEQ ID NO 9 or the mature polypeptide of SEQ ID NO 8;
(d) comprising or consisting of SEQ ID NO 12 or the mature polypeptide of SEQ ID NO 11;
(e) comprising or consisting of SEQ ID NO 15 or the mature polypeptide of SEQ ID NO 14;
(f) comprising or consisting of SEQ ID NO 18 or the mature polypeptide of SEQ ID NO 17;
(g) comprising or consisting of SEQ ID NO 21 or the mature polypeptide of SEQ ID NO 20;
(h) comprising or consisting of SEQ ID NO 24 or the mature polypeptide of SEQ ID NO 23;
(i) comprising or consisting of SEQ ID NO 27 or the mature polypeptide of SEQ ID NO 26;
(j) comprising or consisting of SEQ ID NO 30 or the mature polypeptide of SEQ ID NO 29; or
(k) comprising or consisting of SEQ ID NO 33 or the mature polypeptide of SEQ ID NO 32;

Paragraph 6 The composition according to any of paragraphs 1 to 5, wherein the composition is a cleaning composition such as a laundry or dish wash composition

Paragraph 7 The composition according to paragraph 6, wherein the adjunct ingredient is selected from the group consisting of,

a) at least one builder,
b) at least one surfactant, and
c) at least one bleach component.

Paragraph 8 A polypeptide having hydrolytic and/or deacetyl activity, wherein the polypeptide is of the FLD sub family, comprising one or more of the motif(s) [GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) or GXXGX[FY][LYFI]D (SEQ ID NO 97), wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a variant of the polypeptide selected from the group consisting of SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, wherein the variant has hydrolytic and/or deacetylase activity and comprises one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 positions;

(m) a polypeptide comprising the polypeptide of (a) to (l) and a N-terminal and/or C-terminal His-tag and/or HQ-tag;

(n) a polypeptide comprising the polypeptide of (a) to (l) and a N-terminal and/or C-terminal extension of between 1 and 10 amino acids; and

(o) a fragment of the polypeptide of (a) to (l) having hydrolytic and/or deacetylase activity and having at least 90% of the length of the mature polypeptide.

Paragraph 9 The polypeptide of paragraph 8, having at least 60%, 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 polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, or SEQ ID NO 33.

Paragraph 10 The polypeptide of any of paragraphs 8 to 9, which is encoded by a polynucleotide having at least 60%, 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 mature polypeptide coding sequence of SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28 or SEQ ID NO 31.

Paragraph 11 The polypeptide of any of paragraphs 8 to 10 selected from the group consisting of polypeptides:

(a) comprising or consisting of SEQ ID NO 3 or the mature polypeptide of SEQ ID NO 2;
(b) comprising or consisting of SEQ ID NO 6 or the mature polypeptide of SEQ ID NO 5;
(c) comprising or consisting of SEQ ID NO 9 or the mature polypeptide of SEQ ID NO 8;
(d) comprising or consisting of SEQ ID NO 12 or the mature polypeptide of SEQ ID NO 11;
(e) comprising or consisting of SEQ ID NO 15 or the mature polypeptide of SEQ ID NO 14.
(f) comprising or consisting of SEQ ID NO 18 or the mature polypeptide of SEQ ID NO 17;
(g) comprising or consisting of SEQ ID NO 21 or the mature polypeptide of SEQ ID NO 20;
(h) comprising or consisting of SEQ ID NO 24 or the mature polypeptide of SEQ ID NO 23;
(i) comprising or consisting of SEQ ID NO 27 or the mature polypeptide of SEQ ID NO 26;
(j) comprising or consisting of SEQ ID NO 30 or the mature polypeptide of SEQ ID NO 29; and
(k) comprising or consisting of SEQ ID NO 33 or the mature polypeptide of SEQ ID NO 32.

Paragraph 12 A method for laundering an item comprising the steps of:

a. exposing an item to a wash liquor comprising the polypeptide according to any

of paragraphs 8 to 11 or the composition according to any of paragraphs 1 to 7;

b. completing at least one wash cycle; and

c. optionally rinsing the item,

wherein the item is a textile.

Paragraph 13 Use of a polypeptide comprising a Glyco_hydro_114 domain, preferably a polypeptide comprising a Glyco_hydro_114 domain and a CE4 domain in a cleaning process, such as laundry and/or dish wash.

Paragraph 14 Use of a polypeptide comprising a Glyco_hydro_114 domain, preferably a polypeptide comprising a Glyco_hydro_114 domain and a CE4 domain

i. for preventing, reducing or removing stickiness of the item;
ii. for pretreating stains on the item;
iii. for preventing, reducing or removing redeposition of soil during a wash cycle;
iv. for preventing, reducing or removing adherence of soil to the item;
v. for maintaining or improving whiteness of the item;
vi. for preventing, reducing or removal malodor from the item,

wherein the item is a textile.

Paragraph 15 Use according to any of the preceding paragraphs, wherein the polypeptide is selected from the group consisting of polypeptides having at least 60% sequence identity to the polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30 or SEQ ID NO 33.

Paragraph 16 Use according to paragraph 14, wherein the polypeptide has at least 60%, 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 polypeptide shown in SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30 or SEQ ID NO 33.

Paragraph 17 Use of a polypeptide according to any of paragraphs 8 to 11 for deep cleaning of an item, wherein item is a textile.

It should be understood that every maximum numerical limitation given throughout this specification includes every lower numerical limitation, as if such lower numerical limitations were

expressly written herein. Every minimum numerical limitation given throughout this specification will include every higher numerical limitation, as if such higher numerical limitations were expressly written herein. Every numerical range given throughout this specification will include every narrower numerical range that falls within such broader numerical range, as if such narrower numerical ranges were all expressly written herein.

Examples

Model Detergents

Model detergent A wash liquor (100%) was prepared by dissolving 3.33 g/l of model detergent A containing 12% LAS, 1.1% AEO Biosoft N25-7 (NI), 7% AEOS (SLES), 6% MPG, 3% ethanol, 3% TEA (triethanolamine), 2.75% cocoa soap, 2.75% soya soap, 2% glycerol, 2% sodium hydroxide, 2% sodium citrate, 1% sodium formiate, 0.2% DTMPA and 0.2% PCA (all percentages are w/w (weight volume) in water with hardness 15 dH.

Triple-20 Nonionic Model Detergent (60% surfactant) was prepared by dissolving 3.33 g/l non-ionic detergent containing NaOH 0.87%, MPG (Monopropylenglycol) 6%, Glycerol 2%, Soap-soy 2.75%, Soap-coco 2.75%, PCA (Sokalon CP-5) 0.2%, AEO Biosoft N25-7(NI) 16%, Sodium formiate 1%, Sodium Citrate 2%, DTMPA 0.2%, Ethanol (96%) 3 %, adjustment of pH with NaOH or Citric acid ass water to 100% (all percentages are w/w (weight volume) in water with hardness 15 dH.

Model Detergent MC: A medical cleaning model detergent (model detergent MC) was prepared containing 5% MPG (propylene glycol), 5% Pluronic PE 4300 (PO/EO block polymer; 70%/30%, approx. 1750 g/mol), 2% Plurafac LF 305 (fatty alcohol alkoxylate; C6-10 + EO/PO), 1% MGDA (methyl glycine diacetic acid, 1% TEA (triethanolamine) (all percentages are w/w). The pH was adjusted to 8.7 with phosphoric acid.

Assays

The activity of the Glyco_hydro_114 glycosyl hydrolases of the invention may be measured in a pNP-acetate assay as described in Marmont et.al. (2017) “PelA and PelB proteins form a modification and secretion complex essential for Pel polysaccharide-dependent biofilm formation in *Pseudomonas aeruginosa*”, J. Biol.Chem. 292, 19411-19422 or as described by Colvin, K. M., et.al (2013) “PelA deacetylase activity is required for Pel polysaccharide synthesis in *Pseudomonas aeruginosa*”. J. Bacteriol. 195, 2329–2339.

Wash assay

Mini Launder-O-Meter (MiniLOM) Model Wash System

MiniLOM is a modified mini wash system of the Launder-O-Meter (LOM), which is a

medium scale model wash system that can be applied to test up to 20 different wash conditions simultaneously. A LOM is basically a large temperature controlled water bath with 20 closed metal beakers rotating inside it. Each beaker constitutes one small washing machine and during an experiment, each will contain a solution of a specific detergent/enzyme system to be tested along with the soiled and unsoiled fabrics it is tested on. Mechanical stress is achieved by the beakers being rotated in the water bath and by including metal balls in the beaker.

The LOM model wash system is mainly used in medium scale testing of detergents and enzymes at European wash conditions. In a LOM experiment, factors such as the ballast to soil ratio and the fabric to wash liquor ratio can be varied. Therefore, the LOM provides the link between small scale experiments, such as AMSA and mini-wash, and the more time consuming full scale experiments in front loader washing machines. In miniLOM, washes are performed in 50 ml test tubes placed in Stuart rotator.

Example 1 cloning and expression of polypeptides

The DNA encoding the gene of SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28, SEQ ID NO 31, SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 9, SEQ ID NO 12, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, SEQ ID NO 24, SEQ ID NO 27, SEQ ID NO 30, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52, SEQ ID NO 55, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 73, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 85, SEQ ID NO 88, SEQ ID NO 91 and SEQ ID NO 94, were isolated from bacterial strains and environmental bacterial communities isolated from soil samples collected in different countries (see table 1).Chromosomal DNA from the different strains and bacterial communities was subjected to full genome sequencing using Illumina technology. The genome sequence was analyzed for protein sequences that that had glycosyl hydrolase domains (according to the CAZY definition). 11 sequences containing a Glyco_hydro_114 domain, as defined in PFAM (PF03537, Pfam version 31.0 Finn (2016). Nucleic Acids Research, Database Issue 44:D279-D285) were identified in the genomes.

Table 1:

enzyme	Donor	country of origin
SEQ ID NO 3	*Pseudomonas sp-62208*	United States
SEQ ID NO 6	*Enviromental bacterial community* A	United States
SEQ ID NO 9	*Thermus rehai*	China
SEQ ID NO 15	*Burkholderia sp-63093*	Denmark
SEQ ID NO 18	*Myxococcus macrosporus*	Denmark
SEQ ID NO 12	*Enviromental bacterial community* E	Denmark
SEQ ID NO 21	*Gallaecimonas pentaromativorans*	Denmark

SEQ ID NO 24	*Nonomuraea coxensis*	Philippines
SEQ ID NO 27	*Glycomyces rutgersensis*	China
SEQ ID NO 30	*Enviromental bacterial community E*	Denmark
SEQ ID NO 33	*Paraburkholderia phenazinium*	Denmark
SEQ ID NO 40	*Environmental bacterial community LA*	Denmark
SEQ ID NO 43	*Myxococcus virescens*	Germany
SEQ ID NO 46	*Myxococcus fulvus*	Denmark
SEQ ID NO 49	*Myxococcus macrosporus*	Denmark
SEQ ID NO 52	*Myxococcus stipitatus*	Denmark
SEQ ID NO 55	*Myxococcus macrosporus*	Denmark
SEQ ID NO 58	*Pseudomonas seleniipraecipitans*	United States
SEQ ID NO 61	*Pseudomonas migulae*	United States
SEQ ID NO 64	*Pseudomonas corrugate*	United States
SEQ ID NO 67	*Pseudomonas pelagia*	United States
SEQ ID NO 70	*Pseudomonas aeruginosa*	United States
SEQ ID NO 73	*Streptomyces griseofuscus*	Spain
SEQ ID NO 76	*Lysinibacillus xylanilyticus*	Denmark
SEQ ID NO 79	*Tumebacillus ginsengisoli*	Denmark
SEQ ID NO 82	*Lysinibacillus boronitolerans*	United States
SEQ ID NO 85	*Microbulbifer hydrolyticus*	United States
SEQ ID NO 88	*Carnobacterium inhibens subsp. gilichinskyi*	Denmark
SEQ ID NO 91	*Environmental bacterial community PA*	Denmark
SEQ ID NO 94	*Pseudomonas composti*	Denmark
SEQ ID NO 95	*Paraburkholderia phenazinium*	Denmark
SEQ ID NO 96	*Burkholderia sp-63093*	Denmark

Example 2: Cloning and expression of polypeptides of the invention

The DNA encoding the mature peptide of Glyco_hydro_114 genes SEQ ID NO 1, SEQ ID NO 4, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 13, SEQ ID NO 16, SEQ ID NO 19, SEQ ID NO 22, SEQ ID NO 25, SEQ ID NO 28, SEQ ID NO 31, SEQ ID NO 38, SEQ ID NO 41, SEQ ID NO 44, SEQ ID NO 47, SEQ ID NO 50, SEQ ID NO 53, SEQ ID NO 56, SEQ ID NO 59, SEQ ID NO 62, SEQ ID NO 65, SEQ ID NO 68, SEQ ID NO 71, SEQ ID NO 74, SEQ ID NO 77, SEQ ID NO 80, SEQ ID NO 83, SEQ ID NO 86, SEQ ID NO 89, SEQ ID NO 92, were amplified from the genomic DNA of the corresponding bacterial strains by standard PCR techniques using specific primers containing an overhang to cloning vector. The amplified PCR fragments were inserted into a *Bacillus* expression vector as described in WO12/025577. Briefly, the DNA encoding the mature peptide of the gene was cloned in frame to a *Bacillus clausii* secretion signal (BcSP; with

the following amino acid sequence: MKKPLGKIVASTALLISVAFSSSIASA (SEQ ID NO36). BcSP replaced the native secretion signal in the gene. Downstream of the BcSP sequence, an affinity tag sequence was introduced to ease the purification process (His-tag; with the following amino acid sequence: HHHHHHPR (SEQ ID NO 37) The gene that was expressed therefore comprised the BcSP sequence followed by the His-tag sequence followed by the mature wild type Glyco_hydro_114 gene sequence. The final expression plasmid (BcSP-His-tag-Glyco_hydro_114) was transformed into a *Bacillus subtilis* expression host. The Glyco_hydro_114 BcSP-fusion gene was integrated by homologous recombination into the *Bacillus subtilis* host cell genome upon transformation. The gene construct was expressed under the control of a triple promoter system (as described in WO 99/43835). The gene coding for chloramphenicol acetyltransferase was used as maker (as described in (Diderichsen *et al*., 1993, *Plasmid* 30: 312-315)). Transformants were selected on LB media agar supplemented with 6 microgram of chloramphenicol per ml. One recombinant *Bacillus subtilis* clone containing the Glyco_hydro_114 expression construct was selected and was cultivated on a rotary shaking table in 500 ml baffled Erlenmeyer flasks each containing 100 ml yeast extract-based media. After 3-5 days' cultivation time at 30 °C to 37°C, the enzyme containing supernatant was harvested by centrifugation and the enzymes was purified by His-tag purification.

Example 3: His tag purification method

The His-tagged Glyco_hydro_114 enzymes were purified by immobilized metal chromatography (IMAC) using Ni^{2+} as the metal ion on 5 mL HisTrap Excel columns (GE Healthcare Life Sciences). The purification took place at pH 7 and the bound protein was eluted with imidazole. The purity of the purified enzymes was checked by SDS-PAGE and the concentration of the enzyme determined by Absorbance 280 nm after a buffer exchange in 50mM HEPES, 100mM NaCl pH7.0

Example 4. MiniLOM Deep-cleaning in liquid model detergent on Pel swatches

A crude extract of the biofilm extracellular polymer Pel was prepared from *Pseudomonas aeruginosa* (DSM 19882) as follows; The strain was restreaked on LB Agar (pH 7.3) and incubated for 3 days at ambient temperature. 500 mL of T-broth (10 g/L Bacto™ Tryptone (211705, BD), 5g/L sodium chloride (31434, Sigma-Aldrich)) was then inoculated and incubated statically for 6 days at ambient temperature. The biofilm pellicle was carefully removed from the flask, and pelleted by centrifugation (10 min, 16000 g, 25°C). The pellet was then resuspended in 3M NaCl, vortexed vigorously and incubated for 15min at ambient temperature to extract the surface-associated polymer. The cells were then re-pelleted (10 min, 16000g, 25°C) and the Pel-containing supernatant was retrieved. The supernatant was then diluted three times with sterile MilliQ water. The extract was stored at -20^{0}C until further use (termed Pel extract). Wash performance was determined as follows; 50ul aliquots of the crude Pel extract were spotted on sterile textile swatches (WFK20A, 65% polyester/35% cotton) and incubated for 15 min at

ambient temperature. The swatches (sterile or with the extract) were placed in 50 mL test tubes and 10 mL of wash liquor (15^0dH water with 0.2 g/L iron(III) oxide nano-powder (544884; Sigma-Aldrich) with 3.33 g/L liquid model A or non-ionic model detergent) and the 5 µg/ml enzyme(s) (when appropriate) was added to each tube. Washes without enzyme were included as controls. The test tubes were placed in a Stuart rotator and incubated for 1 hour at 30°C and 20 rpm. The wash liquor was then removed, and the swatches were rinsed twice with 15^0dH water and dried on filter paper over night.

The color difference (L) values were measured using a Handheld Minolta CR-300, and are displayed in table 2. Delta values ($L_{(\text{swatch washed with enzyme})} - L_{(\text{swatch washed without enzyme})}$) are also indicated.

Table 2. Deep-cleaning effects of the PelA homologues in non-ionic model detergent and in model A detergent

Enzyme	**Enzyme concentration (ppm)**	**L values, non-ionic model detergent**	**ΔL non-ionic model detergent**	**L values, model A detergent**	**ΔL model A detergent**
No enzyme	0.0	67.1		64.7	
SEQ ID NO 3	5.0	87.8	20.7	85.6	20.9
SEQ ID NO 6	5.0	75.4	8.3	69.2	4.6
SEQ ID NO 9	5.0	69.9	2.8	67.5	2.9
SEQ ID NO 12	5.0	79.8	12.7	84.1	19.4
SEQ ID NO 15	5.0	73.6	6.5	78.1	13.4
SEQ ID NO 18	5.0	80.0	12.9	85.2	20.6
SEQ ID NO 21	5.0	70.5	3.4	68.9	4.3
SEQ ID NO 24	5.0	76.5	9.4	67.3	2.6
SEQ ID NO 27	5.0	78.0	10.9	78.9	14.2
SEQ ID NO 30	5.0	79.5	12.5	73.0	8.3
SEQ ID NO 33	5.0	75.0	8.0	67.4	2.8

Example 5: Construction of clades and phylogenetic trees

The polypeptides of the invention having hydrolase activity and comprises the Glyco_hydro_114 domain as well as clusters such as the clades. A phylogenetic tree was constructed, of polypeptide sequences containing a Glyco_hydro_114 domain, as defined in PFAM (PF03537,

Pfam version 31.0 Finn (2016). Nucleic Acids Research, Database Issue 44: D279-D285). The phylogenetic tree was constructed from a multiple alignment of mature polypeptide sequences containing at least one Glyco_hydro_114 domain. The sequences were aligned using the MUSCLE algorithm version 3.8.31 (Edgar, 2004. *Nucleic Acids Research* 32(5): 1792-1797), and the trees were constructed using FastTree version 2.1.8 (Price et al., 2010, *PloS one* 5(3)) and visualized using iTOL (Letunic & Bork, 2007. *Bioinformatics* 23(1): 127-128). The polypeptide comprises of the Glyco_hydro_114 domain comprises several motifs. One example is GX[FY][LYF]D (SEQ ID NO 34) situated in positions corresponding to positions 113 to 117 in *Pseudomonas sp-62208* (SEQ ID NO 3), where D at position 117 is part of the substrate binding pocket, and one of the two putative catalytic site residues. Another motif which may be comprised by the polypeptides of the invention is AYX[SET]XX[EAS] (SEQ ID NO 35) situated in positions corresponding to positions 53 to 58 in *Pseudomonas sp-62208* (SEQ ID NO 3). The polypeptides containing a Glyco_hydro_114 domain can be separated into distinct sub-clusters. The sub-clusters are defined by one or more short sequence motifs, as well as containing a Glyco_hydro_114 domain as defined in PFAM (PF03537, Pfam version 31.0). We denoted one sub-cluster comprising the motif GXXGX[FY][LYFI]D (SEQ ID NO 97) as the FLD clade. All polypeptide sequences containing a Glyco_hydro_114 domain as well as the motif will be denoted as belonging to the FLD clade.

The polypeptides in the FLD clade can be further separated into multiple distinct sub-clusters, or clades, where we denoted the clades listed below. The distinct motifs for each clade are described in detail below.

Generation of FLD clade

A phylogenetic tree was constructed, of polypeptide sequences containing a Glyco_hydro_114 domain, as defined above. The phylogenetic tree was constructed from a multiple alignment of mature polypeptide sequences containing at least one Glyco_hydro_114 domain. The sequences were aligned using the MUSCLE algorithm version 3.8.31 (Edgar, 2004. *Nucleic Acids Research* 32(5): 1792-1797), and the tree was constructed using FastTree version 2.1.8 (Price et al., 2010, *PloS one* 5(3)) and visualized using iTOL (Letunic & Bork, 2007. *Bioinformatics* 23(1): 127-128). Using the phylogenetic tree, the polypeptides in Glyco_hydro_114 can be separated into distinct sub-clusters, one which we denoted FLD.

A characteristic motif for this sub-cluster is the motif GXXGX[FY][LYFI]D (SEQ ID NO 97), corresponding to amino acids GYAGLFLD at positions 110 to 117 in SEQ ID NO 3, where D at position 117 is part of the substrate binding pocket and one of the two putative catalytic site residues of the PelA. The other catalytic site residue is located at position 175 in SEQ ID NO 3. An additional motif of the FLD clade is GX[FY][LYF]D (SEQ ID NO 34), corresponding to amino acid 113 to 117 in the reference polypeptide (SEQ ID NO 3).

Generation of NRG clade

The NRG clade comprises polypeptides of bacterial origin, containing a Glyco_hydro_114 domain and belonging to the FLD clade, having hydrolase activity. The polypeptides of the clade comprise the motif example [ILFQV]N[RW]G[FL] (SEQ ID NO 98), corresponding to amino acids FNRGF at positions 155 to 159 of SEQ ID NO 3 where N and G (corresponding to position 156 and 158 of SEQ ID NO 3) is fully conserved in NRG clade.

Examples of polypeptides of the NRG clade includes SEQ ID NO 3, SEQ ID NO 9, SEQ ID NO 15, SEQ ID NO 21, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 76, SEQ ID NO 79, SEQ ID NO 82, SEQ ID NO 94, SEQ ID NO 95, and SEQ ID NO 96.

Generation of DTLDS clade

The DTLDS clade comprises polypeptides of bacterial origin, containing a Glyco_hydro_114 domain and belonging to the NRG clade, having hydrolase activity. The polypeptides of the clade comprise the motif example DTLDS[YF] (SEQ ID NO 99), corresponding to amino acids DTLDSF positions 117 to 122 of SEQ ID NO 3 where DTLDS (corresponding to positions 117 and 121 of SEQ ID NO 3) is fully conserved in DTLDS clade, and D at position 117 is part of the substrate binding pocket and one of the two putative catalytic site residues.

Examples of polypeptides of the DTLDS clade includes SEQ ID NO 3, SEQ ID NO 15, SEQ ID NO 21, SEQ ID NO 33, SEQ ID NO 40, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, SEQ ID NO 94, SEQ ID NO 95, and SEQ ID NO 96.

Generation of GVFLD clade

The GVFLD clade comprises polypeptides of bacterial origin, containing a Glyco_hydro_114 domain and belonging to the DTLDS clade, having hydrolase activity. The polypeptides of the clade comprise the motif example G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), corresponding to amino acids GLFLDTLDSFQLL positions 113 to 125 of SEQ ID NO 3 where D (corresponding to position 117 of SEQ ID NO 3) is fully conserved in GVFLD clade, part of the substrate binding pocket, and one of the two putative catalytic site residues.

Examples of polypeptides of the GVFLD clade includes SEQ ID NO 3, SEQ ID NO 40, SEQ ID NO 58, SEQ ID NO 61, SEQ ID NO 64, SEQ ID NO 67, SEQ ID NO 70, and SEQ ID NO 94.

Generation of DTVG clade

The DTVG clade comprises polypeptides of bacterial origin, containing a Glyco_hydro_114 domain and belonging to the NRG clade, having hydrolase activity. The polypeptides of the clade comprise the motif example DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), corresponding to amino acids DTVGNIN in SEQ ID NO 76 at positions 134 to 140 of SEQ ID NO 76, where D and T (corresponding to position 134 and 135 of SEQ ID NO 76) is fully conserved in the DTVG clade.

Examples of polypeptides of the DTVG clade is SEQ ID NO 76 and SEQ ID NO 82.

Generation of IGEAE clade

The IGEAE clade comprises polypeptides of bacterial origin, containing a Glyco_hydro_114 domain and belonging to the FLD clade, having hydrolase activity. The polypeptides of the clade comprise the motif example [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), corresponding to amino acids EIGAIEEY at positions 262 to 269 of SEQ ID NO 12 where G and E (corresponding to position 264 and 267 of SEQ ID NO 12) are fully conserved in IGEAE clade. Residue A at position 265 is part of the substrate binding pocket.

Examples of polypeptides of the IGEAE clade is SEQ ID NO 6, SEQ ID NO 12, SEQ ID NO 18, SEQ ID NO 30, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52 and SEQ ID NO 55.

Generation of QNSPEL clade

The QNSPEL clade comprises polypeptides of bacterial origin, containing a Glyco_hydro_114 domain and belonging to the IGEAE clade, having hydrolase activity. The polypeptides of the clade comprise the motif example [QL]N[AS]PEL (SEQ ID NO 103), corresponding to amino acids QNSPEL at positions 370 to 375 of SEQ ID NO 12 where P, E and L (corresponding to position 373 to 375 of SEQ ID NO 12) are fully conserved in QNSPEL clade. Another conserved motif of this clade is [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104), located at positions 366 to 374 in SEQ ID NO 12, and corresponding to peptide KVVPQNSPE in SEQ ID NO 12. Examples of polypeptides of the QNSPEL clade is SEQ ID NO 12, SEQ ID NO 18, SEQ ID NO 30, SEQ ID NO 43, SEQ ID NO 46, SEQ ID NO 49, SEQ ID NO 52 and SEQ ID NO 55.

An alignment of some of the polypeptides of the invention comprised in the clade is shown in Figure 1.

A phylogenetic tree of the polypeptides in the clades is shown in Figure 2, Figur 3 and Figur 4.

Example 6 Biofilm removal activity

The Pel-producing *Pseudomonas aeruginosa* strain DSM19882 was used as a model microorganism in the present example. The strain was restreaked on LB agar and incubated at 30°C. An overnight culture was inoculated in 10 mL LB and the culture was incubated for 16 hours at 37°C under shaking conditions. The culture was subsequently diluted (1:100) in LBNS, added to 96-well microtiter plates (150 µL per well, Thermo Scientific, cat # 167008) and Peg lids were inserted (NUNC-TSP, Thermo Scientific, cat # 445497). The microtiter plates were incubated for 24 hours at 26°C under static conditions. After incubation, the peg lids were rinsed in MTP plates with 5°dH water hardness, and transferred to treatments plate with LBNS containing no enzyme (control) or 20 µg/mL enzyme for 1 hour at 26°C. The lids were subsequently rinsed in water hardness and stained with 0.095% crystal violet (Sigma-Aldrich, cat # V5265) for 15 min. Following the staining, the peg lids were rinsed twice, moved to clean microtiter plates and the

remaining dye was dissolved with 30% acetic acid. The absorbance was measured at 595 nm. The results are displayed in table 3

Table 3: Biofilm reducing properties of Glyco_hydro_114 glycosyl hydrolases

Enzyme	Conc	% remaining biofilm
no enzyme	0	100,0
SEQ ID NO 3	20	2,9
SEQ ID NO 6	20	31,4
SEQ ID NO 15	20	37,8
SEQ ID NO 18	20	35,0
SEQ ID NO 12	20	7,2
SEQ ID NO 24	20	54,9
SEQ ID NO 27	20	39,9
SEQ ID NO 30	20	25,7
SEQ ID NO 33	20	52,6
SEQ ID NO 40	20	54,6
SEQ ID NO 43	20	15,8
SEQ ID NO 46	20	8,3
SEQ ID NO 49	20	13,4
SEQ ID NO 52	20	10,2
SEQ ID NO 55	20	16,3
SEQ ID NO 61	20	41,4
SEQ ID NO 64	20	2,6
SEQ ID NO 70	20	3,5
SEQ ID NO 76	20	2,3
SEQ ID NO 79	20	49,0
SEQ ID NO 82	20	1,8
SEQ ID NO 91	20	1,9

All tested Glyco_hydro_114 glycosyl hydrolases showed biofilm reducing properties on the Pel-producing *Pseudomonas aeruginosa* strain DSM19882.

Example 7 Deep-cleaning in liquid model detergent A on Pel swatches

A crude extract of the biofilm extracellular polymer Pel was prepared from *Pseudomonas aeruginosa* PA14 (DSM 19882) as described above. The wash performance was determined as follows; 50ul aliquots of the crude Pel extract were spotted on sterile textile swatches (WFK20A) and incubated for 15 min at ambient temperature. Control swatches were spotted with 3M NaCl.

The swatches (sterile or with the extract) were placed in 50 mL test tubes and 10 mL of wash liquor (15^0dH water with 0.2 g/L iron(III) oxide nano-powder (544884; Sigma-Aldrich) with 3.33g/L liquid model A detergent) and the 2 µg/ml enzyme was added to each tube. Washes without enzyme were included as controls. The test tubes were placed in a Stuart rotator and incubated for 1 hour at 30°C and 20rpm. The wash liquor was then removed, and the swatches were rinsed twice with 15^0dH water and dried on filter paper over night. The color difference (L) values were measured using a Handheld Minolta CR-300, and are displayed in table 4. Wash performance (WP) values ($L_{(\text{swatch washed with enzyme})} - L_{(\text{swatch washed without enzyme})}$) are also indicated.

Table 4. Cleaning effects of the PelA homologues (Glyco_hydro_114 glycosyl hydrolases) in model A detergent

Swatch/Enzyme	Enzyme conc. (µg/ml)	Average L values	WP (ΔL)
wfk20A, no EPS	0.0	88,1	
Wfk20A, EPS, no enzyme	2	82,2	
Wfk20A, EPS, SEQ ID NO 43	2	91,1	8,9
Wfk20A, EPS, SEQ ID NO 46	2	90,3	8,1
Wfk20A, EPS, SEQ ID NO 49	2	91,4	9,2
Wfk20A, EPS, SEQ ID NO 52	2	90,5	8,3
Wfk20A, EPS, SEQ ID NO 55	2	90,6	8,4
Wfk20A, EPS, SEQ ID NO 58	2	87,8	5,6
Wfk20A, EPS, SEQ ID NO 64	2	86,8	4,6

All tested Glyco_hydro_114 glycosyl hydrolases showed Wash performance and capability to remove pel stains from textile.

Example 8. Cleaning in liquid model detergent NI on Pel swatches

A crude extract of the biofilm extracellular polymer Pel was prepared from *Pseudomonas aeruginosa* PA14 (DSM 19882) as mentioned above. Wash performance was determined as follows; 50ul aliquots of the crude Pel extract were spotted on sterile textile swatches (WFK20A)

and incubated for 15 min at ambient temperature. Control swatches without EPS were used as controls. The swatches (sterile or with the extract) were placed in 50 mL test tubes and 10 mL of wash liquor (15^0dH water with 0.2 g/L iron(III) oxide nano-powder (544884; Sigma-Aldrich) with 3.33g/L liquid model NI detergent) and the 10 µg/ml enzyme was added to each tube. Washes without enzyme were included as controls. The test tubes were placed in a Stuart rotator and incubated for 1 hour at 30°C and 20rpm. The wash liquor was then removed, and the swatches were rinsed twice with 15^0dH water and dried on filter paper over night. The tristimulus light intensity (Y) values were measured using a Handheld Minolta CR-300, and are displayed in table 5. Wash performance, WP ($\Delta Y = Y_{(\text{swatches washed with enzyme})} - Y_{(\text{swatches washed without enzyme})}$) are also indicated.

Table 5. Cleaning effects of the PelA homologues (Glyco_hydro_114 glycosyl hydrolases) in model NI detergent

Swatch	Enzyme	Enzyme concentration (µg/ml)	Average Y values	WP(ΔY)
Wfk20A, no EPS	No enzyme	0	74,9	
Wfk20A, Pel EPS swatch	No enzyme	0	64,1	
Wfk20A, Pel EPS swatch	SEQ ID NO 40	10	70,0	5,9
Wfk20A, Pel EPS swatch	SEQ ID NO 61	10	72,2	8,1
Wfk20A, Pel EPS swatch	SEQ ID NO 73	10	68,5	4,4
Wfk20A, Pel EPS swatch	SEQ ID NO 76	10	73,3	9,2
Wfk20A, Pel EPS swatch	SEQ ID NO 79	10	68,6	4,5
Wfk20A, Pel EPS swatch	SEQ ID NO 82	10	76,1	12,0
Wfk20A, Pel EPS swatch	SEQ ID NO 91	10	77,4	13,3
Wfk20A, Pel EPS swatch	SEQ ID NO 67	10	72,4	8,2
Wfk20A, Pel EPS swatch	SEQ ID NO 85	10	71,3	7,2
Wfk20A, Pel EPS swatch	SEQ ID NO 94	10	66,9	2,8
Wfk20A, Pel EPS swatch	SEQ ID NO 88	10	67,7	3,6
Wfk20A, Pel EPS swatch	SEQ ID NO 70	10	75,1	11,0

Example: 9 Effect of PelA homologues (Glyco_hydro_114 glycosyl hydrolases) on *P. aeruginosa* biofilm

Two different clinical isolates of *P. aeruginosa* were for formation of medical biofilms in the example. One biofilm was produced by *P. aeruginosa* PA14 (DSM19882) and another one by *P. aeruginosa* PA01 (DSM22644). The bacteria were re-streaked on TSA plates and incubated for

three days at 30°C. After three days of incubation, 8 mL of Tryptic Soy Broth (TSB) was inoculated with one colony of *P. aeruginosa* PA14 (DSM19882), and 8 mL of TSB was inoculated with *P. aeruginosa* PA01 (DSM22644). The inoculated TSB tubes were incubated overnight at 30°C, 200 rpm, and diluted in TSB to a specific optical density (OD). 150 µl of diluted overnight culture was added to each well in Thermo Scientific™ Nunc™ MicroWell™ 96-Well Microplates (sterile, non-treated). Two plates with *P. aeruginosa* PA14 (DSM19882) were prepared. One plate with *P. aeruginosa* PA01 (DSM22644) was prepared. The plates were incubated at 30°C for 24 hours. After 24 hours of incubation, the microtiter plates containing biofilm were removed from the incubator and emptied for media using VacusafeTM Vacuum Aspiration System (INTEGRA Biosciences). Each well was rinsed twice with 200 µl 0.9% NaCl solution. To each well, 200 µl of model detergent liquor with 20 µg/ml enzyme was added. Treatment without enzyme was included as controls. Each treatment was tested in quadruplicates. After addition of detergent liquor +/- enzyme, the microtiter plates were incubated static for 60 minutes at 30°C. After 60 minutes of incubation, the treatment liquor was removed using the vacuum system. Each well was rinsed twice with 200 µl 0.9% NaCl solution, and 200 µl of 0.095% crystal violet solution was added to each well. The plates were incubated for 15 minutes at ambient temperature. The crystal violet solution was removed using the vacuum system, and each well was rinsed twice with 200 µl 0.9% NaCl solution. 150 µl of 30% acetic acid was added to each well. The plates were incubated for 10 minutes at ambient temperature, where after the absorbance at 595 nm was measured using a spectrophotometer (SpectraMax M3, Molecular Devices). The plates were shaked for 10 seconds before absorbance measurements were performed.

The % remaining biofilm after enzymatic treatment was calculated as

$ABS_{595(\text{biofilm treated with model detergent+enzyme})}/ABS_{595(\text{biofilm treated with model detergent})}$ x 100%.

For *P. aeruginosa* PA14 (DSM19882) and average of two plates was calculated. The results are displayed in Table 6.

Table 6: %remaining biofilm after treatment with PelA homologues in model detergent

Enzyme	Concentration (µg/mL)	%remaining biofilm	
		PA14 (DSM19882)	PA01 (DSM22644)
No enzyme	0	100.0	100.0
SEQ ID NO 64	20	50.3	57.7
SEQ ID NO 3	20	39.6	52.9
SEQ ID NO 12	20	45.3	61.5
SEQ ID NO 52	20	55.5	54.5
SEQ ID NO 43	20	49.0	46.0

Example 10 Endoscope cleaning in liquid model detergent

Endoscope biofilms were established using *P.aeruginosa* PA14 (DSM19882): The strain was inoculated into 10 mL LB and incubated at 37°C for 16 hours with shaking (200 rpm). After propagation, the culture was diluted (1:100) in LBNS and the bacterial suspension was added to 96-well microtiter plates (Thermo Scientific, cat # 167008) containing sterile pieces (1cm) of endoscope tubing (4.7mm diameter, Fluoroelastomer/Viton®, USP Class VI, Endoscopy Development Company, LLC). Sterile medium was added to control wells. After 24h at 26°C (static incubation), the endoscope tubes were treated with a model cleaning solution (5 g/L Model detergent MC in 5°dH water hardness) containing no enzyme (control) or 20 µg/mL enzyme for 1 hour at 26°C. The endoscope pieces were subsequently rinsed with 5^0dH water and stained with 0.095% crystal violet (SIGMA V5265) for 15 min. After additional rinses, the endoscope pieces were blotted on absorbent paper and the remaining dye was dissolved using 30% acetic acid. 200 µl aliquots of the suspensions were transferred to a 96-well microtiter plate and the absorbance was measured at 595nm. The results are displayed in table 7 as percentages of remaining biofilm after enzymatic treatment as compared to the control (endoscope biofilm treated without enzyme).

Table 7. Endoscope cleaning properties in medical cleaning model detergent MC

Enzyme	Enzyme dosage (µg/ml)	Remaining biofilm (% of untreated control)
No enzyme	0	100.0
SEQ ID NO 12	20	23,3
SEQ ID NO 3	20	47,1
SEQ ID NO 70	20	66,7

The results show that the polypeptides of the invention have endoscope cleaning properties i.e. disrupt and/or remove the biofilm or components of the biofilm tested when compared to samples comprising no enzyme.

Claims

1. A Glyco_hydro_114 glycosyl hydrolase comprising one, two or all three of the motifs GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35) and GXXGX[FY][LYFI]D (SEQ ID NO 97), wherein the Glyco_hydro_114 glycosyl hydrolase has hydrolytic activity, and wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(c) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(d) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(g) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(h) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 24;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 27;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(l) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(n) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(o) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52;

(q) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55;

(r) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(s) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(t) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(u) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(v) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 73;

(w) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(x) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(y) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(z) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 85;

(aa) a polypeptide having at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 88;

(bb) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 91;

(cc) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(dd) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(ee) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

2. A Glyco_hydro_114 glycosyl hydrolase according to claim 1, comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98), wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 9;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(d) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(e) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(f) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(g) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(h) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(i) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(j) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(k) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76;

(l) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 79;

(m) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82;

(n) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(o) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(p) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

3. A Glyco_hydro_114 glycosyl hydrolase according to claim 1 or 2 comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98) and/or the motif DTLDS[YF] (SEQ ID NO 99), wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 15;

(c) a polypeptide having at least 60%, 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 21;

(d) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 33;

(e) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(f) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(g) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(h) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(i) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67;

(j) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94;

(k) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 95; and

(l) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 96.

4. A Glyco_hydro_114 glycosyl hydrolase according to claim 3 comprising the motifs [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and/or G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 40;

(c) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(e) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(f) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67; and

(g) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94.

5. A Glyco_hydro_114 glycosyl hydrolase according to claim 2, comprising the motif [ILFQV]N[RW]G[FL] (SEQ ID NO 98) and/or the motif DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 76; and

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 82.

6. A Glyco_hydro_114 glycosyl hydrolase, according to claim 1 comprising the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102), wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 6;

(b) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(d) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(f) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(g) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(h) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(i) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

7. A Glyco_hydro_114 glycosyl hydrolase according to claim 6 comprising the motif [SETC]IG[EQA][ALI]EXY (SEQ ID NO 102) and/or one or both motifs [QL]N[AS]PEL (SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104), wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 12;

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(c) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 30;

(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(e) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(g) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(h) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

8. A Glyco_hydro_114 glycosyl hydrolase according to any of claims 1 to 4, wherein the Glyco_hydro_114 glycosyl hydrolase is obtained from *Pseudomonas*, preferably *Pseudomonas sp-62208, Pseudomonas seleniipraecipitans*, *Pseudomonas migulae*, *Pseudomonas corrugate*, *Pseudomonas pelagia*, *Pseudomonas aeruginosa* or *Pseudomonas composti*, and wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 3;

(b) a polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 58;

(c) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 61;

(d) a polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 64;

(e) a polypeptide having 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%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 67; and

(f) a polypeptide having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 94.

9. The Glyco_hydro_114 glycosyl hydrolase according to claim 8, wherein the Glyco_hydro_114 glycosyl comprises four, five or six of the motifs selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35),

GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100).

10. The Glyco_hydro_114 glycosyl hydrolase according to any of claims 8 to 9, wherein the Glyco_hydro_114 glycosyl comprises five or six of the motifs selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100).

11. The Glyco_hydro_114 glycosyl hydrolase according to any of claims 8 to 10, wherein the Glyco_hydro_114 glycosyl comprises all six motifs: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99) and G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100).

12. A Glyco_hydro_114 glycosyl hydrolase according to claims 6 or 7, wherein the Glyco_hydro_114 glycosyl hydrolase is obtained from *Myxococcus*, preferably *Myxococcus macrosporus, Myxococcus virescens*, *Myxococcus fulvus* or *Myxococcus stipitatus*, wherein the Glyco_hydro_114 glycosyl hydrolase comprises or consist of a polypeptide selected from the group consisting of:

(a) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 18;

(b) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 43;

(c) a polypeptide having 100% sequence identity to the polypeptide of SEQ ID NO 46;

(d) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 49;

(e) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 52; and

(f) a polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO 55.

13. The Glyco_hydro_114 glycosyl hydrolase according to claim 12, wherein the Glyco_hydro_114 glycosyl comprises four, five or six of the motifs selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

14. The Glyco_hydro_114 glycosyl hydrolase according to any of claims 12 or 13, wherein the Glyco_hydro_114 glycosyl comprises five or six of the motifs selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

15. The Glyco_hydro_114 glycosyl hydrolase according to any of claims 12 to 14, wherein the Glyco_hydro_114 glycosyl comprises all six motifs: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103), [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

16. A granule comprising;
(a) a core comprising a Glyco_hydro_114 glycosyl hydrolase according to any of claims 1 to 15, and
(b) optionally a coating consisting of one or more layer(s) surrounding the core.

17. A cleaning composition comprising:
(a) at least 0.001 ppm of at least one Glyco_hydro_114 glycosyl hydrolase according to any of claims 1 to 15;
(b) one or more cleaning composition components, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

18. A method for laundering an item comprising the steps of:
(a) exposing an item to a wash liquor comprising the Glyco_hydro_114 glycosyl hydrolase according to any of claims 1 to 15 or the composition according to claim 17;
(b) completing at least one wash cycle; and
(c) optionally rinsing the item,
wherein the item is a textile.

19. Use of a Glyco_hydro_114 glycosyl hydrolase in a cleaning process, such as laundry and/or dish wash.

20. Use of a Glyco_hydro_114 glycosyl hydrolase,
i. for preventing, reducing or removing stickiness of the item;
ii. for preventing, reducing or removing biofilm or biofilm components
iii. for reducing or removing pel stains on the item;

iv. for preventing, reducing or removing redeposition of soil during a wash cycle;

v. for preventing, reducing or removing adherence of soil to the item;

vi. for maintaining or improving whiteness of the item;

vii. for preventing, reducing or removing malodor from the item,

wherein the item is a textile.

21. Use according to any of claims 19 or 20, wherein Glyco_hydro_114 glycosyl hydrolase comprising one or more of the motif(s) selected from the group consisting of: GX[FY][LYF]D (SEQ ID NO 34), AYX[SET]XX[EAS] (SEQ ID NO 35), GXXGX[FY][LYFI]D (SEQ ID NO 97), [ILFQV]N[RW]G[FL] (SEQ ID NO 98), DTLDS[YF] (SEQ ID NO 99), G[VL]FLDTLDSF[QTH]L[LMQ] (SEQ ID NO 100), DT[VIMA][GD][DNW][VIL][DEN] (SEQ ID NO 101), [SETC]IG[EQA][ALI]EXY(SEQ ID NO 102), [QL]N[AS]PEL(SEQ ID NO 103) and [KLYMQ]XX[PV]QN[SA]PE (SEQ ID NO 104).

22. Use according to any of claims 19 to 21, wherein the polypeptide is selected from any of the Glyco_hydro_114 glycosyl hydrolase of claims 1 to 15.

```
SEQ ID NO 3 Pseudomonas sp-62208                  ........................................
SEQ ID NO 18 Myxococcus macrosporus               ..................AERSGDAAVLADARTLTCASLQ
SEQ ID NO 12 Environmental bacterial community LE ..................DDFDTGQDAILPDARTLPCTTLQ
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      ........................................
SEQ ID NO 9 Thermus rehai                         QVDPSHVAQAVRRTIQIGGGLEQWSGLPQYPVVLSNTFPA
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


SEQ ID NO 3 Pseudomonas sp-62208                  ........................................
SEQ ID NO 18 Myxococcus macrosporus               VASGYIGSGQTVQGLHTQTLSGTQDRWAEYVEFSPGTSAT
SEQ ID NO 12 Environmental bacterial community LE FERGALPSGQSVQGLNTQTLSGTQDRWAEYVEFAPNSSAT
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      ........................................
SEQ ID NO 9 Thermus rehai                         KPVTHGGYFSVAWDDRHLYILGVFEQKAETVKAALPEEHP
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


SEQ ID NO 3 Pseudomonas sp-62208                  ........................................
SEQ ID NO 18 Myxococcus macrosporus               CTYALPADVGAADVVAAEVGINYRGPHKSQMRWLFEAWDY
SEQ ID NO 12 Environmental bacterial community LE CTYPLPTGVSADSVVAAEVGVNYRGPTKAQMRWVIEAWDY
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      ........................................
SEQ ID NO 9 Thermus rehai                         EWWNDDTMEVFLKPDPKGVEVIHLAANPKGTRFKAYTFTT
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


SEQ ID NO 3 Pseudomonas sp-62208                  ........................................
SEQ ID NO 18 Myxococcus macrosporus               EGGAWVLVGDNTFAQSWTWTATSLALTSPQRFVSGGPVKL
SEQ ID NO 12 Environmental bacterial community LE STNSWALVGDNTFAQSWRWTATSLALPTPARFLSGGPVKL
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      ........................................
SEQ ID NO 9 Thermus rehai                         DYATSGRVEASRWVLEWAIPFASLKTSPPEPGAIWAMKVG
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


SEQ ID NO 3 Pseudomonas sp-62208                  ........................................
SEQ ID NO 18 Myxococcus macrosporus               RYRTTSTADASLLDLLVVRIQVAASDAGTPGDAGTPGDAG
SEQ ID NO 12 Environmental bacterial community LE RYRTDSTADASLLDLLVVRVQVAASDAGTPTDAGTPTDAG
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      ........................................
SEQ ID NO 9 Thermus rehai                         REHQAAQEYPLWPMGGDYHAPTNFGYLVFVEKLEDPQALA
SEQ ID NO 33 Paraburkholderia phenazinium         ..............................QTAADAA
SEQ ID NO 24 Nonomuraea coxensis                  ........................................
```

Figure 1

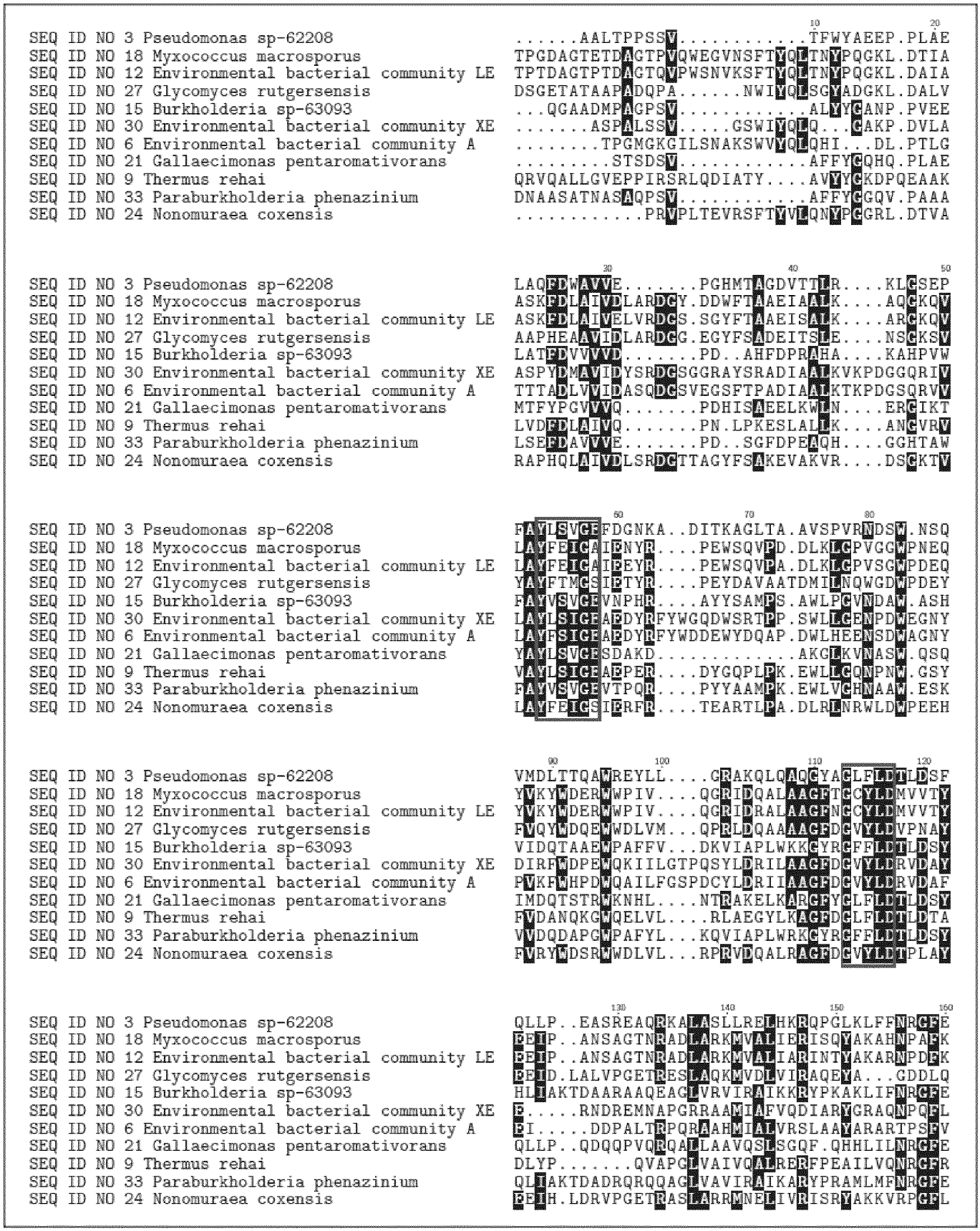


Figure 1 continued

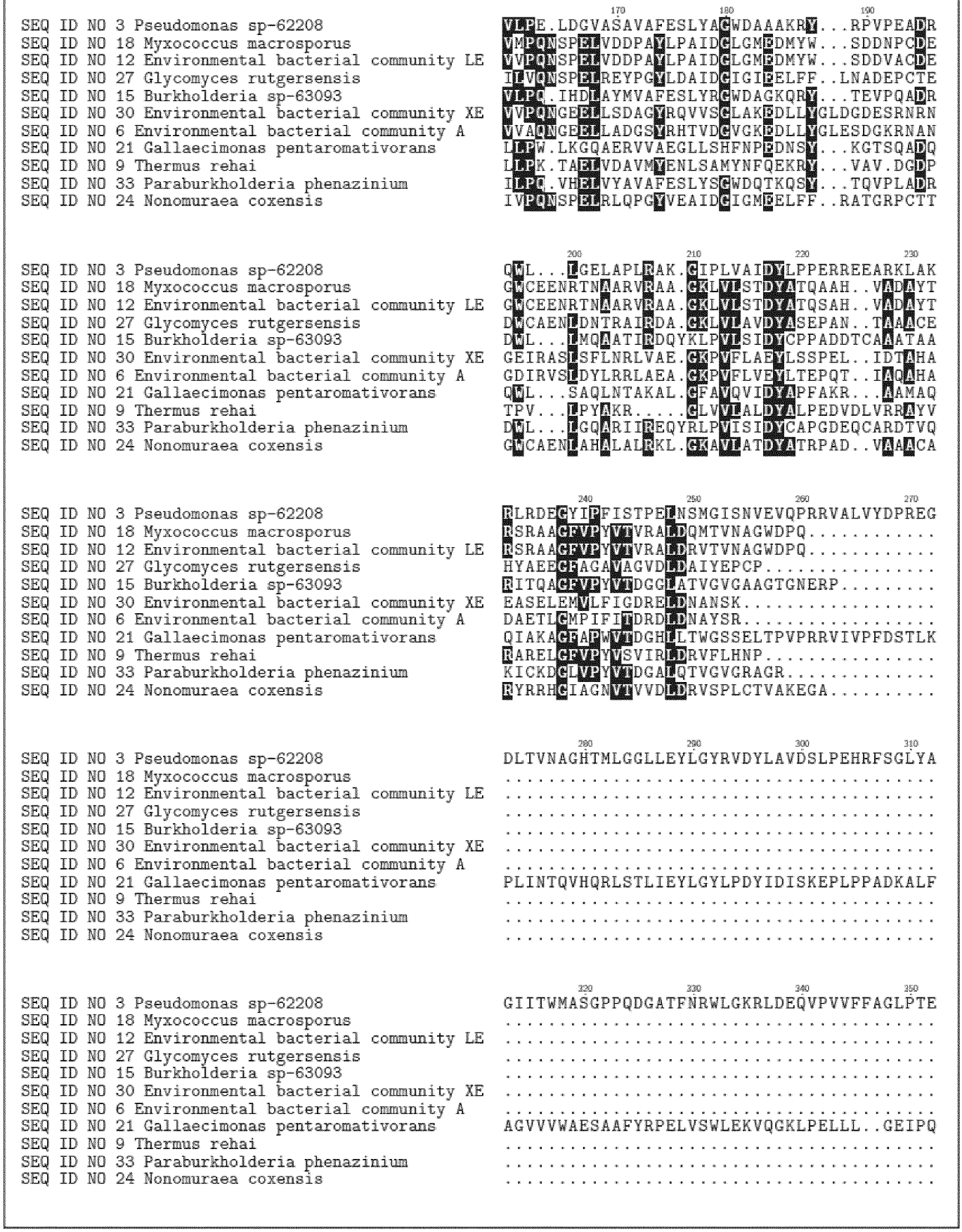


Figure 1 continued

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                                                  360        370        380        390
SEQ ID NO 3 Pseudomonas sp-62208                  DKVLLKRLGLNLMAPAGTQPLTISYQDKALIGAFEAPVQP
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      SPALLAGLGLNLQSLSPKGPFSQTEMASWLKGETALSLKN
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


                                                  400        410        420        430
SEQ ID NO 3 Pseudomonas sp-62208                  RSRELTAVSLLPQGPKAALLLTGKDGQTFAPVATAKWGGL
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      LEPYSAT...LAEGAEALISIKAGNGEPVLQGARTDKGAV
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


                                                  440        450        460        470
SEQ ID NO 3 Pseudomonas sp-62208                  ALAPYVLET.NNERSRWILDPFAFLQASLQLPAQPRPDTT
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      VLSPWLIDALPLEENRWLINPVALLQKGLGLPPIPAPDVT
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


                                                  480        490        500        510
SEQ ID NO 3 Pseudomonas sp-62208                  TENGRRIATVHIDGDGFPSRAEVRGSPYAGKQVLNDFIQP
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      TESGRRLFTLHIDGDAFPSRARFPGQPFAGEVMEKQIIEH
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................


                                                  520        530        540        550
SEQ ID NO 3 Pseudomonas sp-62208                  NPFLTSVSIIEGEISPRGMYPHLARELEPIARELFANPKV
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      YQLPITVSVIQGEVGPTGMYPKQSPQLEAIARDIFTKPYV
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................
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Figure 1 continued

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                                                    560       570       580       590
SEQ ID NO 3 Pseudomonas sp-62208                    EVATHTFSHPFY.MQPELAEKDEDFSAEYGLKMAIPGYDK
SEQ ID NO 18 Myxococcus macrosporus                 ........................................
SEQ ID NO 12 Environmental bacterial community LE   ........................................
SEQ ID NO 27 Glycomyces rutgersensis                ........................................
SEQ ID NO 15 Burkholderia sp-63093                  ........................................
SEQ ID NO 30 Environmental bacterial community XE   ........................................
SEQ ID NO 6 Environmental bacterial community A     ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans        EIASHTYSHPFFWSQIAGREKLTEQDTEYGFHLNIPGYNK
SEQ ID NO 9 Thermus rehai                           ........................................
SEQ ID NO 33 Paraburkholderia phenazinium           ........................................
SEQ ID NO 24 Nonomuraea coxensis                    ........................................

                                                        600       610       620       630
SEQ ID NO 3 Pseudomonas sp-62208                    IDFKREIFGSRDYINQQLTTPEKPVKMVFWPGDALPSAAT
SEQ ID NO 18 Myxococcus macrosporus                 ........................................
SEQ ID NO 12 Environmental bacterial community LE   ........................................
SEQ ID NO 27 Glycomyces rutgersensis                ........................................
SEQ ID NO 15 Burkholderia sp-63093                  ........................................
SEQ ID NO 30 Environmental bacterial community XE   ........................................
SEQ ID NO 6 Environmental bacterial community A     ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans        IDLTKEIDGSIDYINERLAPKDKKVVMMLWSGDAAPGPVA
SEQ ID NO 9 Thermus rehai                           ........................................
SEQ ID NO 33 Paraburkholderia phenazinium           ........................................
SEQ ID NO 24 Nonomuraea coxensis                    ........................................

                                                    640       650       660       670
SEQ ID NO 3 Pseudomonas sp-62208                    IKLAYDAGLKNVNGASTMLTKARPSLTGLNPLLRPTEGGL
SEQ ID NO 18 Myxococcus macrosporus                 ........................................
SEQ ID NO 12 Environmental bacterial community LE   ........................................
SEQ ID NO 27 Glycomyces rutgersensis                ........................................
SEQ ID NO 15 Burkholderia sp-63093                  ........................................
SEQ ID NO 30 Environmental bacterial community XE   ........................................
SEQ ID NO 6 Environmental bacterial community A     ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans        LAHARKMGVLNVNGGNTVMTRDNPSLSEIWPIGRPEGDLL
SEQ ID NO 9 Thermus rehai                           ........................................
SEQ ID NO 33 Paraburkholderia phenazinium           ........................................
SEQ ID NO 24 Nonomuraea coxensis                    ........................................

                                                        680       690       700
SEQ ID NO 3 Pseudomonas sp-62208                    .QYYAPVINENVYTNLWKGPYYGFRDVIDTYELTDSPRRL
SEQ ID NO 18 Myxococcus macrosporus                 ........................................
SEQ ID NO 12 Environmental bacterial community LE   ........................................
SEQ ID NO 27 Glycomyces rutgersensis                ........................................
SEQ ID NO 15 Burkholderia sp-63093                  ........................................
SEQ ID NO 30 Environmental bacterial community XE   ........................................
SEQ ID NO 6 Environmental bacterial community A     ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans        YQVYAPIMNENVYTDLWHGPYFGFRRVRETFDITGHPYRL
SEQ ID NO 9 Thermus rehai                           ........................................
SEQ ID NO 33 Paraburkholderia phenazinium           ........................................
SEQ ID NO 24 Nonomuraea coxensis                    ........................................

                                                    710       720       730       740
SEQ ID NO 3 Pseudomonas sp-62208                    RGIHLYYHFYSATKQASIKAMGEIYGYMREQHPMSLWMSD
SEQ ID NO 18 Myxococcus macrosporus                 ........................................
SEQ ID NO 12 Environmental bacterial community LE   ........................................
SEQ ID NO 27 Glycomyces rutgersensis                ........................................
SEQ ID NO 15 Burkholderia sp-63093                  ........................................
SEQ ID NO 30 Environmental bacterial community XE   ........................................
SEQ ID NO 6 Environmental bacterial community A     ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans        KPFGLYFHFYSATNPAGLQALRDDIGYVLGRPNTPAHLSH
SEQ ID NO 9 Thermus rehai                           ........................................
SEQ ID NO 33 Paraburkholderia phenazinium           ........................................
SEQ ID NO 24 Nonomuraea coxensis                    ........................................
```

Figure 1 continued

```
                                                  750        760        770        780
SEQ ID NO 3 Pseudomonas sp-62208                  YLDRLHGLYQASLARTADGAWQIRGMDALRTVRLDPQMGW
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      YARMAKDFYFSALARDAKGDWLLSS.KYLRTLRLPKALGY
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................

                                                  790        800        810        820
SEQ ID NO 3 Pseudomonas sp-62208                  PDLLRSQGIAGVRDLPQGRYVHLSSDRALLVLRPDRDDR.
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      AQLDASQGLAGATE..DGRYLHVVNGDARFALAASASPRK
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................

                                                  830        840        850        860
SEQ ID NO 3 Pseudomonas sp-62208                  PALEEANVPLTDWRYLDDRRVSFAFAGQFDVTFSVRSASA
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      PYLVSANVLLKSWQLPGK....VAFKAWQKADLILANAEG
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................

                                                  870        880        890        900
SEQ ID NO 3 Pseudomonas sp-62208                  CRVEVDGQRFAGKSSAGLWTFQLPMKQVSNGQLLCN...
SEQ ID NO 18 Myxococcus macrosporus               ........................................
SEQ ID NO 12 Environmental bacterial community LE ........................................
SEQ ID NO 27 Glycomyces rutgersensis              ........................................
SEQ ID NO 15 Burkholderia sp-63093                ........................................
SEQ ID NO 30 Environmental bacterial community XE ........................................
SEQ ID NO 6 Environmental bacterial community A   ........................................
SEQ ID NO 21 Gallaecimonas pentaromativorans      CRFVSDQGPSYGGQQKGRLTEFSLPEGDFAGHLACGTQQ
SEQ ID NO 9 Thermus rehai                         ........................................
SEQ ID NO 33 Paraburkholderia phenazinium         ........................................
SEQ ID NO 24 Nonomuraea coxensis                  ........................................
```

Figure 1 continued

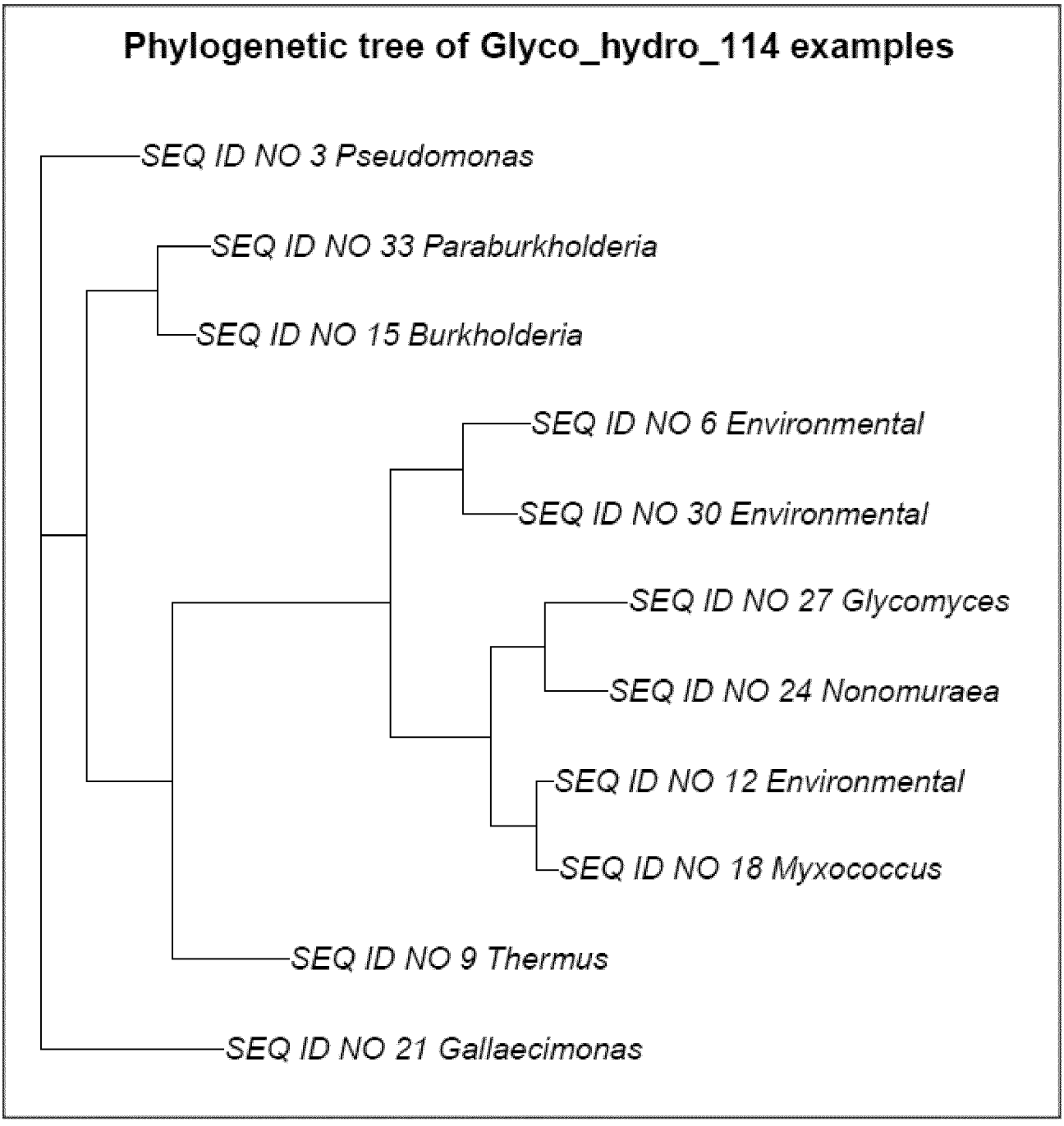
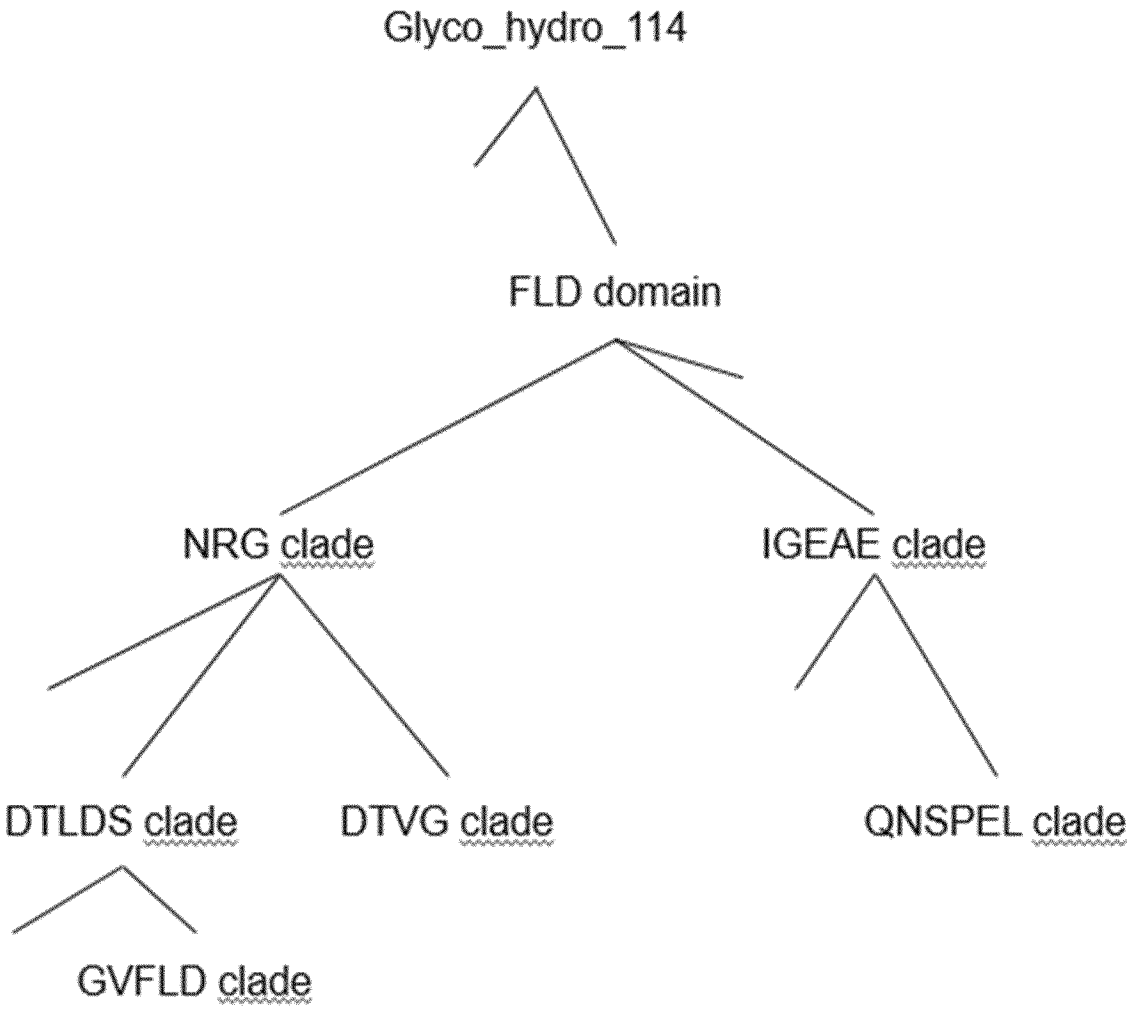
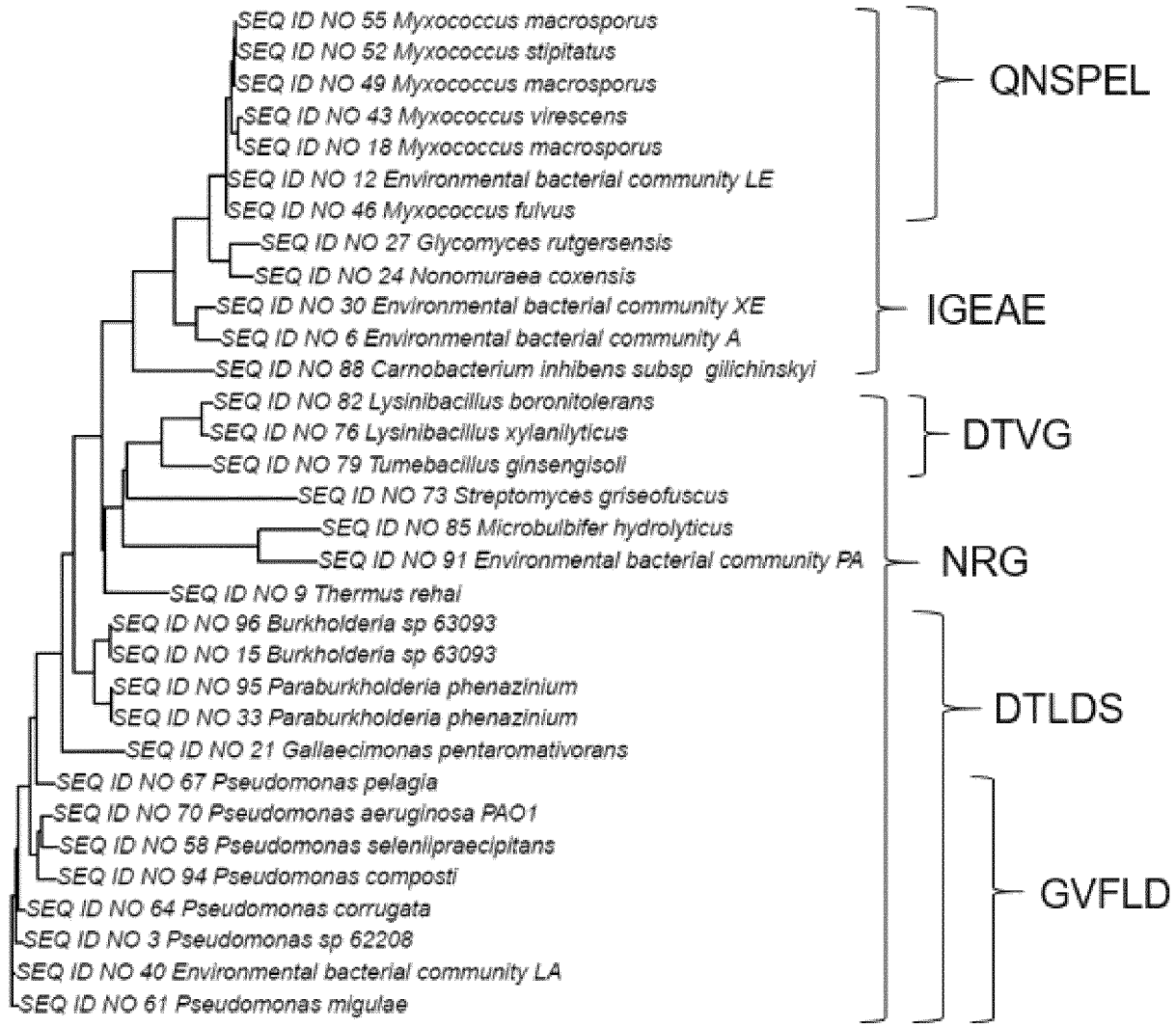

Phylogenetic tree of Glyco_hydro_114 examples
SEQ ID NO 3 Pseudomonas
SEQ ID NO 33 Paraburkholderia
SEQ ID NO 15 Burkholderia
SEQ ID NO 6 Environmental
SEQ ID NO 30 Environmental
SEQ ID NO 27 Glycomyces
SEQ ID NO 24 Nonomuraea
SEQ ID NO 12 Environmental
SEQ ID NO 18 Myxococcus
SEQ ID NO 9 Thermus
SEQ ID NO 21 Gallaecimonas

Figure 2


Glyco_hydro_114
FLD domain
NRG clade
IGEAE clade
DTLDS clade
DTVG clade
QNSPEL clade
GVFLD clade

Phylogenetic tree of Glyco_hydro_114 examples



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2018/058639

A. CLASSIFICATION OF SUBJECT MATTER
INV. C11D3/386 C12N9/24
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C11D C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2015/184526 A1 (HOSPITAL FOR SICK CHILDREN) 10 December 2015 (2015-12-10) paragraph [00322]; claims 1-78; examples 21, 32 -----	1-4, 8-11, 16-22
X	WO 2014/059541 A1 (UNIV CONCORDIA [CA]) 24 April 2014 (2014-04-24) Psehe2p4_007114; page 98, paragraphs 1-3,212,224; claims 1-57; sequences 1647,2171,2695 ----- -/--	1-4, 8-11, 16-22

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18 July 2018	17/09/2018

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	van Klompenburg, Wim

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Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE UniProt [Online] 11 November 2015 (2015-11-11), "SubName: Full=PbsX family transcriptional regulator {ECO:0000313|EMBL:AKV06550.1};", XP002773919, retrieved from EBI accession no. UNIPROT:A0A0K1QM56 Database accession no. A0A0K1QM56 87% identity; sequence -----	1-4, 8-11, 16-22
X	US 2007/020624 A1 (RUBENFIELD MARC J [US] ET AL) 25 January 2007 (2007-01-25) SEQ ID 28773: 67% identical A.A. to SEQ ID 3; sequence 28773 -----	1-4, 8-11, 16-22
A	B. L. CANTAREL ET AL: "The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics", NUCLEIC ACIDS RESEARCH, vol. 37, no. Database, 1 January 2009 (2009-01-01), pages D233-D238, XP055048251, ISSN: 0305-1048, DOI: 10.1093/nar/gkn663 the whole document -----	1-4, 8-11, 16-22

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2018/058639

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-4, 8-11, 16-22(all partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-4, 8-11, 16-22(all partially)

Polypeptide with at least 90% identity to SEQ ID NO:3. A granule comprising a core with said polypeptide, a cleaning composition comprising said polypeptide. A method of laundering an item, use of said polypeptide in cleaning.

2-31. claims: 5-7, 12-15(completely); 1-4, 8-11, 16-22(partially)

Polypeptides, granules, cleaning compositions, methods and uses as in subject 1, but wherein invention subject 2 is characterized by a (percentage) identity to SEQ ID 6, invention 3 by SEQ ID 9, invention 4 by SEQ ID 12, invention 5 by SEQ ID 15, invention 6 by SEQ ID 18, invention 7 by SEQ ID 21, invention 8 by SEQ ID 24, invention 9 by SEQ ID 27, invention 10 by SEQ ID 30, invention 11 by SEQ ID 33, invention 12 by SEQ ID 40, invention 13 by SEQ ID 43, invention 14 by SEQ ID 46, invention 15 by SEQ ID 49, invention 16 by SEQ ID 52, invention 17 by SEQ ID 55, invention 18 by SEQ ID 58, invention 19 by SEQ ID 61, invention 20 by SEQ ID 64, invention 21 by SEQ ID 67, invention 22 by SEQ ID 73, invention 23 by SEQ ID 76, invention 24 by SEQ ID 79, invention 25 by SEQ ID 82, invention 26 by SEQ ID 85, invention 27 by SEQ ID 88, invention 28 by SEQ ID 91, invention 29 by SEQ ID 94, invention 30 by SEQ ID 95, invention 31 by SEQ ID 96.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2018/058639

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2015184526 A1	10-12-2015	AU 2015271666 A1	19-01-2017
		CA 2951152 A1	10-12-2015
		EP 3152303 A1	12-04-2017
		JP 2017524344 A	31-08-2017
		US 2017216410 A1	03-08-2017
		WO 2015184526 A1	10-12-2015
WO 2014059541 A1	24-04-2014	NONE	
US 2007020624 A1	25-01-2007	US 6551795 B1	22-04-2003
		US 2007020624 A1	25-01-2007