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**(54) CLEANING COMPOSITIONS INCLUDING ENZYMES**

REINIGUNGSZUSAMMENSETZUNGEN MIT ENZYMEN

COMPOSITIONS DE NETTOYAGE COMPRENANT DES ENZYMES

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(56) References cited:  
**EP-A1- 2 363 455 WO-A1-2015/184526**  
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**Description**

## FIELD OF THE INVENTION

5 **[0001]** The present disclosure relates to cleaning compositions comprising a specific glycoside hydrolase enzyme. The present disclosure also relates to methods of making and using such cleaning compositions. The present disclosure also relates to the use of the glycoside hydrolase enzyme.

## BACKGROUND OF THE INVENTION

10 **[0002]** The detergent formulator is constantly aiming to improve the performance of detergent compositions. US 2010/125047, US2009/176680, EP2363455 and US2014/066353 all relate to laundry treatment compositions which may comprise glycosyl hydrolase enzymes from families 5, 12, 44, 45 or 74. WO2015/184526 relates to treating or preventing biofilm-related infection using a PelA glycosyl hydrolase enzyme. One particular challenge is the removal of certain soils of microbial origin from surfaces such as textiles. Such soils can be sticky and difficult to remove. Furthermore, because they are sticky they tend to adhere body soils and/or particulate soils to the surface, making soil removal difficult and having a tendency to build up over time. This may be particularly noticeable for example on collars and cuffs where incomplete cleaning may occur.

15 **[0003]** There is a need for improved cleaning compositions which provide cleaning of such soils. The present inventors have found that this problem may be ameliorated by cleaning compositions comprising certain glycoside hydrolases. Glycosyl hydrolases are enzymes that catalyze the hydrolysis of the glycosyl bond to release smaller sugars. There are over 100 classes of glycosyl hydrolase and many different enzymes fall within the class of glycosyl hydrolases, for example cellulases and xyloglucanases which can be used in cleaning compositions. Surprisingly, certain specific glycosyl hydrolases can provide particularly improved cleaning.

20 **[0004]** Glycoside hydrolases are described by Coutinho, P.M. and Henrissat, B., 1999, Carbohydrate-active enzymes: an integrated database approach, in "Recent Advances In Carbohydrate Bioengineering", H.J. Gilbert, G. Davies, B. Henrissat and B. Svensson eds., The Royal Society of Chemistry, Cambridge, pp. 3-12.

## SUMMARY OF THE INVENTION

25 **[0005]** The present invention provides a laundry and/or dishwashing cleaning and/or treatment composition comprising an amylase enzyme and an enzyme (i) having glycoside hydrolase activity, and (ii) said glycosyl hydrolase enzyme being selected from the endo-alpha-1,4-polygalactosminidase class (EC 3.2.1.109) of enzymes, wherein the glycoside hydrolase enzyme having glycoside hydrolase activity is a variant having at least 70% or at least 75% or at least 80% or at least 85% or at least 90% or at least 95% identity less than or up to 100% identity with SEQ ID NO:1.

30 **[0006]** Preferably the composition comprises from 1 to 80 wt% of a surfactant system, preferably comprising an anionic surfactant. The present invention provides a method of cleaning a surface, such as a textile, that comprises mixing a cleaning composition as described herein with water to form an aqueous liquor and contacting a surface with the aqueous liquor, in a laundering step. Preferably the glycoside hydrolase enzyme is present in the aqueous wash liquor in an amount of from 0.01 ppm to 1000 ppm enzyme, based on active protein.

35 **[0007]** The present invention also relates to the use of a composition comprising an amylase enzyme and an enzyme (i) having glycoside hydrolase activity; and (ii) selected from the endo-alpha-1,4-polygalactosminidase class (EC 3.2.1.109) of enzymes, having at least 70% or at least 75% or at least 80% or at least 85% or at least 90% or at least 95% identity to 100% identity with SEQ ID NO:1, to enhance soil and/or stain removal and/or for malodour reduction, in particular for body soil removal.

40 **[0008]** A preferred composition comprises a second glycosyl hydrolase enzyme selected from glycoside hydrolase family 39.

## DETAILED DESCRIPTION OF THE INVENTION

45 **[0009]** The components of the compositions and processes of the present disclosure are described in more detail below.

50 **[0010]** As used herein, the articles "a" and "an" when used in a claim, are understood to mean one or more of what is claimed or described. As used herein, the terms "include," "includes," and "including" are meant to be non-limiting. The compositions of the present disclosure can comprise, consist essentially of, or consist of, the components of the present disclosure.

55 **[0011]** The terms "substantially free of" or "substantially free from" may be used herein. This means that the indicated material is at the very minimum not deliberately added to the composition to form part of it, or, preferably, is not present at analytically detectable levels. It is meant to include compositions whereby the indicated material is present only as

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an impurity in one of the other materials deliberately included. The indicated material may be present, if at all, at a level of less than 1%, or less than 0.1%, or less than 0.01%, or even 0%, by weight of the composition.

**[0012]** As used herein, the term "etheramine" includes the term "polyetheramine" and includes amines that have one or more ether groups.

**[0013]** Unless otherwise noted, all component or composition levels are in reference to the active portion of that component or composition, and are exclusive of impurities, for example, residual solvents or by-products, which may be present in commercially available sources of such components or compositions.

**[0014]** All temperatures herein are in degrees Celsius (°C) unless otherwise indicated. Unless otherwise specified, all measurements herein are conducted at 20°C and under atmospheric pressure.

**[0015]** In all embodiments of the present disclosure, all percentages are by weight of the total composition, unless specifically stated otherwise. All ratios are weight ratios, unless specifically stated otherwise.

**[0016]** 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.

**[0017]** As used herein, the term "alkoxy" is intended to include C1-C8 alkoxy and C1-C8 alkoxy derivatives of polyols having repeating units such as butylene oxide, glycidol oxide, ethylene oxide or propylene oxide.

**[0018]** As used herein, unless otherwise specified, the terms "alkyl" and "alkyl capped" are intended to include C1-C18 alkyl groups, or even C1-C6 alkyl groups.

**[0019]** As used herein, unless otherwise specified, the term "aryl" is intended to include C3-12 aryl groups.

**[0020]** As used herein, unless otherwise specified, the term "arylalkyl" and "alkaryl" are equivalent and are each intended to include groups comprising an alkyl moiety bound to an aromatic moiety, typically having C1-C18 alkyl groups and, in one aspect, C1-C6 alkyl groups.

**[0021]** The terms "ethylene oxide," "propylene oxide" and "butylene oxide" may be shown herein by their typical designation of "EO," "PO" and "BO," respectively.

**[0022]** As used herein, the term "cleaning and/or treatment composition" includes, unless otherwise indicated, granular, powder, liquid, gel, paste, unit dose, bar form and/or flake type washing agents and/or fabric treatment compositions, including but not limited to products for laundering fabrics, fabric softening compositions, fabric enhancing compositions, fabric freshening compositions, and other products for the care and maintenance of fabrics, and combinations thereof. Such compositions may be pre-treatment compositions for use prior to a washing step or may be rinse added compositions, as well as cleaning auxiliaries, such as bleach additives and/or "stain-stick" or pre-treat compositions or substrate-laden products such as dryer added sheets.

**[0023]** As used herein, "cellulosic substrates" are intended to include any substrate which comprises cellulose, either 100% by weight cellulose or at least 20% by weight, or at least 30 % by weight or at least 40 or at least 50 % by weight or even at least 60 % by weight cellulose. Cellulose may be found in wood, cotton, linen, jute, and hemp. Cellulosic substrates may be in the form of powders, fibers, pulp and articles formed from powders, fibers and pulp. Cellulosic fibers, include, without limitation, cotton, rayon (regenerated cellulose), acetate (cellulose acetate), triacetate (cellulose triacetate), and mixtures thereof. Typically cellulosic substrates comprise cotton. Articles formed from cellulosic fibers include textile articles such as fabrics. Articles formed from pulp include paper.

**[0024]** As used herein, the term "maximum extinction coefficient" is intended to describe the molar extinction coefficient at the wavelength of maximum absorption (also referred to herein as the maximum wavelength), in the range of 400 nanometers to 750 nanometers.

**[0025]** As used herein "average molecular weight" is reported as a weight average molecular weight, as determined by its molecular weight distribution; as a consequence of their manufacturing process, polymers disclosed herein may contain a distribution of repeating units in their polymeric moiety.

**[0026]** As used herein the term "variant" refers to a polypeptide that contains an amino acid sequence that differs from a wild type or reference sequence. A variant polypeptide can differ from the wild type or reference sequence due to a deletion, insertion, or substitution of a nucleotide(s) relative to said reference or wild type nucleotide sequence. The reference or wild type sequence can be a full-length native polypeptide sequence or any other fragment of a full-length polypeptide sequence. A polypeptide variant generally has at least about 70% amino acid sequence identity with the reference sequence, but may include 75% amino acid sequence identity within the reference sequence, 80% amino acid sequence identity within the reference sequence, 85% amino acid sequence identity with the reference sequence, 86% amino acid sequence identity with the reference sequence, 87% amino acid sequence identity with the reference sequence, 88% amino acid sequence identity with the reference sequence, 89% amino acid sequence identity with the reference sequence, 90% amino acid sequence identity with the reference sequence, 91% amino acid sequence identity with the reference sequence, 92% amino acid sequence identity with the reference sequence, 93% amino acid sequence

identity with the reference sequence, 94% amino acid sequence identity with the reference sequence, 95% amino acid sequence identity with the reference sequence, 96% amino acid sequence identity with the reference sequence, 97% amino acid sequence identity with the reference sequence, 98% amino acid sequence identity with the reference sequence, 98.5% amino acid sequence identity with the reference sequence or 99% amino acid sequence identity with the reference sequence.

**[0027]** As used herein, the term "solid" includes granular, powder, bar and tablet product forms.

**[0028]** As used herein, the term "fluid" includes liquid, gel, paste, and gas product forms.

#### Cleaning Composition

**[0029]** The present disclosure relates to laundry and/or dish cleaning and/or treatment compositions. The cleaning composition may be selected from the group of light duty liquid detergents compositions, heavy duty liquid detergent compositions, solid, for example powder detergent, hard surface cleaning compositions, detergent gels commonly used for laundry, bleaching compositions, laundry additives, fabric enhancer compositions, and mixtures thereof. The cleaning composition may be a dishwashing composition or a laundry composition (such as a heavy duty liquid detergent composition).

**[0030]** The cleaning compositions may be in any suitable form. The composition can be selected from a liquid, solid, or combination thereof. As used herein, "liquid" includes free-flowing liquids, as well as pastes, gels, foams and mousses. Non-limiting examples of liquids include light duty and heavy duty liquid detergent compositions, fabric enhancers, detergent gels commonly used for laundry, bleach and laundry additives. Gases, e.g., suspended bubbles, or solids, e.g. particles, may be included within the liquids. A "solid" as used herein includes, but is not limited to, powders, agglomerates, and mixtures thereof. Non-limiting examples of solids include: granules, microcapsules, beads, noodles, and pearlised balls. Solid compositions may provide a technical benefit including, but not limited to, through-the-wash benefits, pre-treatment benefits, and/or aesthetic effects.

**[0031]** The cleaning composition may be in the form of a unitized dose article, such as a tablet or in the form of a pouch. Such pouches typically include a water-soluble film, such as a polyvinyl alcohol water-soluble film, that at least partially encapsulates a composition. Suitable films are available from MonoSol, LLC (Indiana, USA). The composition can be encapsulated in a single or multi-compartment pouch. A multi-compartment pouch may have at least two, at least three, or at least four compartments. A multi-compartmented pouch may include compartments that are side-by-side and/or superposed. The composition contained in the pouch may be liquid, solid (such as powders), or combinations thereof.

#### Glycoside Hydrolase Enzyme

**[0032]** The enzyme essential to the present invention comprises glycoside hydrolase activity belonging to the endo-alpha-1,4-polygalactosaminidase class (EC 3.2.1.109) of enzymes, having at least 70% or 75% or 80% or 85% or 90% or 95% up to 100% identity to SEQ ID NO:1.

**[0033]** Preferably, the glycoside hydrolase enzyme is a microbial enzyme. The glycoside hydrolase enzyme may be fungal or bacterial in origin. Bacterial glycoside hydrolases may be most preferred. Fungal glycoside hydrolases may be most preferred.

**[0034]** The glycoside hydrolase may be obtainable from *Pseudomonas*, such as a *Pseudomonas aeruginosa*. Suitable examples from class EC 3.2.1.109 are described in Baker et al., (2016) Sci Adv, 2, such as the mature polypeptide SEQ ID NO: 1 of the present invention from *Pseudomonas aeruginosa*. Preferably the glycoside hydrolase in the cleaning composition of the invention is PeIAh, optionally in addition to further glycoside hydrolases.

**[0035]** Preferably the glycoside hydrolase is an isolated glycoside hydrolase.

**[0036]** Preferably the glycoside hydrolase enzyme is present in the cleaning composition in an amount from 0.001 to 1 wt% based on active protein in the composition, or from 0.005 to 0.5 wt% or from 0.01 to 0.25 wt% based on weight of the composition.

**[0037]** Preferably the glycoside hydrolase enzyme is present in the laundering aqueous liquor in an amount of from 0.01ppm to 1000 ppm enzyme, based on active protein or from 0.05 or from 0.1ppm to 750 or 500ppm.

**[0038]** The glycoside hydrolases described herein may also give rise to biofilm-disrupting effects or soil anti-redeposition effects.

#### Amylase Enzyme

**[0039]** The composition comprises an amylase enzyme. Suitable alpha-amylases include those of bacterial or fungal origin. Chemically or genetically modified mutants (variants) are included. A preferred alkaline alpha-amylase is derived from a strain of *Bacillus*, such as *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus stearothermophilus*, *Bacillus*

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*subtilis*, or other *Bacillus* sp., such as *Bacillus* sp. NCIB 12289, NCIB 12512, NCIB 12513, DSM 9375 (USP 7,153,818) DSM 12368, DSMZ no. 12649, KSM AP1378 (WO 97/00324), KSM K36 or KSM K38 (EP 1,022,334). Preferred amylases include:

- 5 (a) the variants described in WO 94/02597, WO 94/18314, WO96/23874 and WO 97/43424, especially the variants with substitutions in one or more of the following positions versus the enzyme listed as SEQ ID No. 2 in WO 96/23874 (SEQ ID NO: 2 herein): 15, 23, 105, 106, 124, 128, 133, 154, 156, 181, 188, 190, 197, 202, 208, 209, 243, 264, 304, 305, 391, 408, and 444.
- (b) the variants described in USP 5,856,164 and WO99/23211, WO 96/23873, WO00/60060 and WO 06/002643, especially the variants with one or more substitutions in the following positions versus the AA560 enzyme listed as SEQ ID No. 12 in WO 06/002643 (SEQ ID NO: 3 herein):  
10 26, 30, 33, 82, 37, 106, 118, 128, 133, 149, 150, 160, 178, 182, 186, 193, 203, 214, 231, 256, 257, 258, 269, 270, 272, 283, 295, 296, 298, 299, 303, 304, 305, 311, 314, 315, 318, 319, 339, 345, 361, 378, 383, 419, 421, 437, 441, 444, 445, 446, 447, 450, 461, 471, 482, 484, preferably that also contain the deletions of D183\* and G184\*.
- 15 (c) variants exhibiting at least 90% identity with SEQ ID No. 4 in WO06/002643 (SEQ ID NO: 4 herein), the wild-type enzyme from *Bacillus* SP722, especially variants with deletions in the 183 and 184 positions and variants described in WO 00/60060.
- (d) variants exhibiting at least 95% identity with the wild-type enzyme from *Bacillus* sp.707 (SEQ ID NO:7 in US 6,093, 562) (SEQ ID NO: 5 herein), especially those comprising one or more of the following mutations M202, M208, S255, R172, and/or M261. Preferably said amylase comprises one or more of M202L, M202V, M202S, M202T, M202I, M202Q, M202W, S255N and/or R172Q. Particularly preferred are those comprising the M202L or M202T mutations.
- 20 (e) variants described in WO 09/149130, preferably those exhibiting at least 90% identity with SEQ ID NO: 1 or SEQ ID NO:2 in WO 09/149130 (SEQ ID NO:6 and SEQ ID NO: 7, respectively herein), the wild-type enzyme from
- 25 *Geobacillus Stearothermophilus* or a truncated version thereof;
- (f) variants as described in EP2540825 and EP2357220, EP2534233;
- (g) variants as described in WO2009100102 and WO2010115028;
- (h) variants exhibiting at least 89% identity with SEQ ID NO:1 in WO2016091688 (SEQ ID NO: 8 herein), especially those comprising deletions at positions H183+G184 and additionally one or more mutations at positions 405, 421, 422 and/or 428.
- 30 (i) variants exhibiting at least 60% amino acid sequence identity with the "PcuAmyl  $\alpha$ -amylase" from *Paenibacillus curdlanolyticus* YK9 (SEQ ID NO:3 in WO2014099523), (SEQ ID NO: 9 herein).
- (j) variants exhibiting at least 60% amino acid sequence identity with the "CspAmy2 amylase" from *Cytophaga* sp. (SEQ ID NO:1 in WO2014164777, (SEQ ID NO: 10 herein)).
- 35 (k) variants exhibiting at least 85% identity with AmyE from *Bacillus subtilis* (SEQ ID NO: 1 in WO2009149271, (SEQ ID NO: 11 herein)).
- (l) Variants exhibiting at least 90% identity variant with the wild-type amylase from *Bacillus* sp. KSM-K38 with accession number AB051102.

40 **[0040]** Suitable commercially available alpha-amylases include DURAMYL®, LIQUEZYME®, TERMAMYL®, TERMAMYL ULTRA®, NATALASE®, SUPRAMYL®, STAINZYME®, STAINZYME PLUS®, FUNGAMYL® and BAN® (Novozymes A/S, Bagsvaerd, Denmark), KEMZYM® AT 9000 Biozym Biotech Trading GmbH Wehlstrasse 27b A-1200 Wien Austria, RAPIDASE®, PURASTAR®, ENZYSIZE®, OPTISIZE HT PLUS®, POWERASE® and PURASTAR OX-AM® (Genencor International Inc., Palo Alto, California) and KAM® (Kao, 14-10 Nihonbashi Kayabacho, 1-chome, Chuo-ku Tokyo 103-8210, Japan). In one aspect, suitable amylases include NATALASE®, STAINZYME® and STAINZYME PLUS® and mixtures thereof. The amylase is preferably present in an amount from about 0.00001% to about 2%, from about 0.0001% to about 1% or even from about 0.001% to about 0.5% enzyme protein by weight of the composition.

### Optional Second Glycosyl Hydrolase Enzyme

50 **[0041]** A preferred composition comprises a second glycosyl hydrolase enzyme, preferably selected from GH family 39. A preferred second glycosyl hydrolase comprises glycoside hydrolase enzyme having at least 60% or at least 65% or at least 70% or at least 75% or at least 80% or at least 85% or at least 90% or at least 95%, and less than or up to 100% identity to SEQ ID NO: 13. Preferably, the second glycoside hydrolase enzyme comprises a microbial enzyme, which, may be fungal or bacterial in origin.

55 **[0042]** The second glycoside hydrolase may be obtainable from *Pseudomonas*, such as a *Pseudomonas aeruginosa*. Suitable examples are described in Baker et al., (2016) Sci Adv, 2, such as the mature polypeptide SEQ ID NO: 12 herein from *Pseudomonas aeruginosa*. A preferred second glycoside hydrolase in the cleaning composition of the

invention is PslGh. When present in the composition, the aforementioned second glycosyl hydrolase may be present at levels from about 0.00001% to about 2%, from about 0.0001% to about 1% or even from about 0.001% to about 0.5% enzyme protein by weight of the composition.

## 5 Adjuncts

**[0043]** The cleaning compositions described herein may optionally include other adjunct components, for example fabric care benefit agent; additional enzyme; surfactant system; fabric shading dye; deposition aid; rheology modifier; builder; chelant; bleach; bleach activator, bleaching agent; bleach precursor; bleach booster; bleach catalyst; perfume and/or perfume microcapsules; perfume loaded zeolite; starch encapsulated accord; polyglycerol esters; whitening agent; pearlescent agent; enzyme stabilizing systems; scavenging agents including fixing agents for anionic dyes, complexing agents for anionic surfactants, and mixtures thereof; optical brighteners or fluoescers; polymer including but not limited to soil release polymer and/or soil suspension polymer; dispersants; antifoam agents; non-aqueous solvent; fatty acid; suds suppressors, e.g., silicone suds suppressors; cationic starches; scum dispersants; substantive dyes; colorants; opacifier; antioxidant; hydrotropes such as toluenesulfonates, cumenesulfonates and naphthalenesulfonates; color speckles; colored beads, spheres or extrudates; clay softening agents; anti-bacterial agents, quaternary ammonium compounds. In particular quaternary ammonium compounds may be present in particular for fabric enhancer compositions, such as fabric softeners, and comprise quaternary ammonium cations that are positively charged polyatomic ions of the structure  $NR_4^+$ , where R is an alkyl group or an aryl group.

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## Additional Enzymes

**[0044]** Preferably the composition of the invention comprises additional enzyme, for example selected from lipases, proteases, nucleases, galactanases, mannanases, pectate lyases, cellulases, cutinases, and mixtures thereof. The cleaning compositions preferably comprise one or more additional enzymes from the group selected from nucleases, galactanases, mannanases and mixtures thereof. The cleaning composition preferably comprises one or more additional enzymes selected from the group nucleases, galactanases, mannanases and mixtures thereof. Preferably in addition, the cleaning compositions comprise one or more additional enzymes selected from proteases. Preferably the cleaning composition comprises one or more additional enzymes selected from lipases. The composition may also comprise hemicellulases, peroxidases, xylanases, pectinases, keratinases, reductases, oxidases, phenoloxidases, lipoxygenases, ligninases, pullulanases, tannases, pentosanases, malanases,  $\beta$ -glucanases, arabinosidases, hyaluronidase, chondroitinase, laccase and mixtures thereof. When present in the composition, the aforementioned additional enzymes may be present at levels from about 0.00001% to about 2%, from about 0.0001% to about 1% or even from about 0.001% to about 0.5% enzyme protein by weight of the composition.

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## Nucleases

**[0045]** In a preferred composition, the composition additionally comprises a nuclease enzyme. The nuclease enzyme is an enzyme capable of cleaving the phosphodiester bonds between the nucleotide sub-units of nucleic acids. Suitable nuclease enzymes may be deoxyribonuclease or ribonuclease enzyme or a functional fragment thereof. By functional fragment or part is meant the portion of the nuclease enzyme that catalyzes the cleavage of phosphodiester linkages in the DNA backbone and so is a region of said nuclease protein that retains catalytic activity. Thus it includes truncated, but functional versions, of the enzyme and/or variants and/or derivatives and/or homologues whose functionality is maintained.

**[0046]** Preferably the nuclease enzyme is a deoxyribonuclease, preferably selected from any of the classes E.C. 3.1.21.x, where x=1, 2, 3, 4, 5, 6, 7, 8 or 9, E.C. 3.1.22.y where y=1, 2, 4 or 5, E.C. 3.1.30.z where z= 1 or 2, E.C. 3.1.31.1 and mixtures thereof. Nuclease enzymes from class E.C. 3.1.21.x and especially where x=1 are particularly preferred. Nucleases in class E.C. 3.1.22.y cleave at the 5' hydroxyl to liberate 3' phosphomonoesters. Enzymes in class E.C. 3.1.30.z may be preferred as they act on both DNA and RNA and liberate 5'-phosphomonoesters. Suitable examples from class E.C. 3.1.31.2 are described in US2012/0135498A, such as SEQ ID NO:3 therein. Such enzymes are commercially available as DENARASE® enzyme from c-LECTA. Nuclease enzymes from class E.C. 3.1.31.1 produce 3'phosphomonoesters.

**[0047]** Preferably, the nuclease enzyme comprises a microbial enzyme. The nuclease enzyme may be fungal or bacterial in origin. Bacterial nucleases may be most preferred. Fungal nucleases may be most preferred.

**[0048]** The microbial nuclease is obtainable from *Bacillus*, such as a *Bacillus licheniformis* or *Bacillus subtilis* bacterial nucleases. A preferred nuclease is obtainable from *Bacillus licheniformis*, preferably from strain EI-34-6. A preferred deoxyribonuclease is a variant of *Bacillus licheniformis*, from strain EI-34-6 nucB deoxyribonuclease defined in SEQ ID NO:14 herein, or variant thereof, for example having at least 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%,

98%, 99% or 100% identical thereto. Other suitable nucleases are defined in SEQ ID NO:15 herein, or variant thereof, for example having at least 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto. Other suitable nucleases are defined in SEQ ID NO:16 herein, or variant thereof, for example having at least 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto.

**[0049]** A fungal nuclease is obtainable from *Aspergillus*, for example *Aspergillus oryzae*. A preferred nuclease is obtainable from *Aspergillus oryzae* defined in SEQ ID NO:17 herein, or variant thereof, for example having at least 60% or 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto.

**[0050]** Another suitable fungal nuclease is obtainable from *Trichoderma*, for example *Trichoderma harzianum*. A preferred nuclease is obtainable from *Trichoderma harzianum* defined in SEQ ID NO: 18 herein, or variant thereof, for example having at least 60% or 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto.

**[0051]** Other fungal nucleases include those encoded by the DNA sequences of *Aspergillus oryzae* RIB40, *Aspergillus oryzae* 3.042, *Aspergillus flavus* NRRL3357, *Aspergillus parasiticus* SU-1, *Aspergillus nomius* NRRL13137, *Trichoderma reesei* QM6a, *Trichoderma virens* Gv29-8, *Oidiodendron maius* Zn, *Metarhizium guizhouense* ARSEF 977, *Metarhizium majus* ARSEF 297, *Metarhizium robertsii* ARSEF 23, *Metarhizium acridum* CQMa 102, *Metarhizium brunneum* ARSEF 3297, *Metarhizium anisopliae*, *Colletotrichum florinae* PJ7, *Colletotrichum sublineola*, *Trichoderma atroviride* IMI 206040, *Tolyposcladium ophioglossoides* CBS 100239, *Beauveria bassiana* ARSEF 2860, *Colletotrichum higginsianum*, *Hirsutella minnesotensis* 3608, *Scedosporium apiospermum*, *Phaeoconiella chlamydospora*, *Fusarium verticillioides* 7600, *Fusarium oxysporum* f. sp. cubense race 4, *Colletotrichum graminicola* M1.001, *Fusarium oxysporum* FOSC 3-a, *Fusarium avenaceum*, *Fusarium langsethiae*, *Grosmannia clavigera* kw1407, *Claviceps purpurea* 20.1, *Verticillium longisporum*, *Fusarium oxysporum* f. sp. cubense race 1, *Magnaporthe oryzae* 70-15, *Beauveria bassiana* D1-5, *Fusarium pseudograminearum* CS3096, *Neonectria ditissima*, *Magnaportheopsis poae* ATCC 64411, *Cordyceps militaris* CM01, *Marssonina brunnea* f. sp. 'multigermtubi' MB\_m1, *Diaporthe ampelina*, *Metarhizium album* ARSEF 1941, *Colletotrichum gloeosporioides* Nara gc5, *Madurella mycetomatis*, *Metarhizium brunneum* ARSEF 3297, *Verticillium alfalfae* VaMs.102, *Gaeumannomyces graminis* var. tritici R3-111a-1, *Nectria haematococca* mpVI 77-13-4, *Verticillium longisporum*, *Verticillium dahliae* VdLs.17, *Torubiella hemipterigena*, *Verticillium longisporum*, *Verticillium dahliae* VdLs.17, *Botrytis cinerea* B05.10, *Chaetomium globosum* CBS 148.51, *Metarhizium anisopliae*, *Stemphylium lycopersici*, *Sclerotinia borealis* F-4157, *Metarhizium robertsii* ARSEF 23, *Myceliophthora thermophila* ATCC 42464, *Phaeosphaeria nodorum* SN15, *Phialophora attae*, *Ustilagoideia virens*, *Diplodia seriata*, *Ophiostoma piceae* UAMH 11346, *Pseudogymnoascus pannorum* VKM F-4515 (FW-2607), *Bipolaris oryzae* ATCC 44560, *Metarhizium guizhouense* ARSEF 977, *Chaetomium thermophilum* var. thermophilum DSM 1495, *Pestalotiopsis fici* W106-1, *Bipolaris zeicola* 26-R-13, *Setosphaeria turcica* Et28A, *Arthroderma otae* CBS 113480 and *Pyrenophora tritici-repentis* Pt-1C-BFP.

**[0052]** Preferably the nuclease is an isolated nuclease.

**[0053]** Preferably the nuclease enzyme is present in the aqueous solution in an amount from 0.01ppm to 1000 ppm of the nuclease enzyme, or from 0.05 or from 0.1ppm to 750 or 500ppm.

### Galactanases

**[0054]** Preferably as an additional enzyme, the composition comprises a galactanase. Particularly preferred are the endo-beta-1,6-galactanase extracellular polymer-degrading enzyme. The term "endo-beta-1,6-galactanase" or "a polypeptide having endo-beta-1,6-galactanase activity" means an endo-beta-1,6-galactanase (EC 3.2.1.164) from the glycoside hydrolase family 30 that catalyzes the hydrolytic cleavage of 1,6-3-D-galactooligosaccharides with a degree of polymerization (DP) higher than 3, and their acidic derivatives with 4-O-methylglucosyluronate or glucosyluronate groups at the non-reducing terminals. For purposes of the present disclosure, endo-beta-1,6-galactanase activity is determined according to the procedure described in WO 2015185689 in Assay I. Suitable examples from class EC 3.2.1.164 are described in WO 2015185689, such as the mature polypeptide SEQ ID NO: 2 described therein.

**[0055]** Preferably the galactanase enzyme is selected from Glycoside Hydrolase Family 30.

**[0056]** Preferably, the endo-beta-1,6-galactanase is a microbial enzyme. The endo-beta-1,6-galactanase may be fungal or bacterial in origin. Bacterial endo-beta-1,6-galactanase may be most preferred. Fungal endo-beta-1,6-galactanase may be most preferred.

**[0057]** A bacterial endo-beta-1,6-galactanase is obtainable from *Streptomyces*, for example *Streptomyces davawensis*. A preferred endo-beta-1,6-galactanase is obtainable from *Streptomyces davawensis* JCM 4913 defined in SEQ ID NO: 19 herein, or variant thereof, for example having at least 40% or 50% or 60% or 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto.

**[0058]** Other bacterial endo-beta-1,6-galactanase include those encoded by the DNA sequences of *Streptomyces avermitilis* MA-4680 with amino acid sequence defined in SEQ ID NO: 20 herein, or variant thereof, for example having at least 40% or 50% or 60% or 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto.

**[0059]** A fungal endo-beta-1,6-galactanase is obtainable from *Trichoderma*, for example *Trichoderma harzianum*. A preferred endo-beta-1,6-galactanase is obtainable from *Trichoderma harzianum* defined in SEQ ID NO: 21 herein, or

variant thereof, for example having at least 40% or 50% or 60% or 70% or 75% or 80% or 85% or 90% or 95%, 96%, 97%, 98%, 99% or 100% identical thereto.

**[0060]** Other fungal endo-beta-1,6-galactanase include those encoded by the DNA sequences of *Ceratocystis fimbriata* f. sp. Platani, *Muscodora strobilii* WG-2009a, *Oculimacula yallundae*, *Trichoderma viride* GD36A, *Thermomyces stellatus*, *Myceliophthora thermophila*.

Preferably the galactanase has an amino acid sequence having at least 60%, or at least 80%, or at least 90% or at least 95% identity with the amino acid sequence shown in SEQ ID NO: 19, SEQ ID NO: 20 or SEQ ID NO: 21.

**[0061]** Preferably the galactanase is an isolated galactanase.

**[0062]** Preferably the galactanase enzyme is present in the composition in an amount from 0.001 to 1 wt% based on active protein in the composition, or from 0.005 to 0.5 wt% or from 0.01 to 0.25 wt% based on the weight of the composition. Preferably the galactanase enzyme is present in the laundering aqueous solution in an amount of from 0.01 ppm to 1000 ppm of the galactanase enzyme, or from 0.05 or from 0.1 ppm to 750 or 500 ppm.

### Mannanases

**[0063]** Preferably the composition comprises a mannanase enzyme. Mannanase enzymes are polypeptides having mannan endo-1,4- beta-mannosidase activity (EC 3.2.1.78) from the glycoside hydrolase family 26 that catalyzes the hydrolysis of 1,4-3-D-mannosidic linkages in mannans, galactomannans and glucomannans. Alternative names of mannan endo-1,4-beta-mannosidase are 1,4-3-D-mannan mannanohydrolase; endo-1,4-3-mannanase; endo-  $\beta$ -1,4-mannanase;  $\beta$ -mannanase B; 3-1,4-mannan 4-mannanohydrolase; endo-3-mannanase; and  $\beta$ -D-mannanase. Preferred mannanases are members of the glycoside hydrolase family 26.

**[0064]** For purposes of the present disclosure, mannanase activity may be determined using the Reducing End Assay as described in the experimental section of WO 2015040159.

Suitable examples from class EC 3.2.1.78 are described in WO 2015040159, such as the mature polypeptide SEQ ID NO: 2 described therein.

**[0065]** Preferred mannanases are variants having at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 81 %, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 SEQ ID NO: 22 from *Ascobolus stictoides*;

**[0066]** Preferred mannanases are variants having at least 81 %, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 SEQ ID NO: 23 from *Chaetomium virescens*.

**[0067]** Preferred mannanases are variants having at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 SEQ ID NO: 24 from *Preussia aemulans*.

**[0068]** Preferred mannanases are variants having at least at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 SEQ ID NO: 25 from *Yunnania penicillata*.

**[0069]** Preferred mannanases are variants having at least at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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 SEQ ID NO: 26 from *Myrothecium roridum*.

**[0070]** Preferably the mannanase is an isolated mannanase.

**[0071]** Preferably the mannanase enzyme is present in the cleaning compositions in an amount from 0.001 to 1 wt% based on active protein in the composition, or from 0.005 to 0.5 wt% or from 0.01 to 0.25 wt%. Preferably the mannanase enzyme is present in a the laundering aqueous solution in an amount of from 0.01 ppm to 1000 ppm of the mannanase enzyme, or from 0.05 or from 0.1 ppm to 750 or 500 ppm.

**[0072]** The mannanases may also give rise to biofilm-disrupting effects.



Xanthan-degrading enzyme

**[0073]** The composition preferably comprises a xanthan-degrading enzyme. Xanthan gum is a polysaccharide secreted by the bacterium *Xanthomonas campestris*. Xanthan is composed of pentasaccharide subunits, forming a cellulose backbone with trisaccharide side chains composed of mannose-(beta 1, 4)-glucuronic-acid-(beta 1, 2)-mannose attached to alternate glucose residues in the backbone by alpha1,3 linkages. The cleaning composition preferably includes a xanthan degrading polypeptide having xanthan lyase activity and/or endo-beta-1,4-glucanase activity. Xanthan lyases are enzymes that cleave the beta-D-mannosylalpha-beta-D-1,4-glucuronosyl bond of xanthan, preferably xanthan lyases isolated from *Paenibacillus alginolyticus* XL-1. Preferred xanthan-degrading enzymes are selected from the glycosyl hydrolase family 5 (GH5).

Acetylglucosaminidases

**[0074]** In a preferred composition, the composition may additionally comprise an acetylglucosaminidase enzyme, preferably a  $\beta$ -N-acetylglucosaminidase enzyme from E.C. 3.2.1.52, preferably an enzyme having at least 70%, or at least 75% or at least 80% or at least 85% or at least 90% or at least 95% or at least 96% or at least 97% or at least 98% or at least 99% or at least or 100% identity to SEQ ID NO:27.

Proteases

**[0075]** Preferably the composition comprises one or more proteases. Suitable proteases include metalloproteases and serine proteases, including neutral or alkaline microbial serine proteases, such as subtilisins (EC 3.4.21.62). Suitable proteases include those of animal, vegetable or microbial origin. In one aspect, such suitable protease may be of microbial origin. The suitable proteases include chemically or genetically modified mutants of the aforementioned suitable proteases. In one aspect, the suitable protease may be a serine protease, such as an alkaline microbial protease or/and a trypsin-type protease. Examples of suitable neutral or alkaline proteases include:

(a) subtilisins (EC 3.4.21.62), preferably those derived from *Bacillus sp.*, such as *B. lentus*, *B. alkalophilus*, *B. subtilis*, *B. amyloliquefaciens*, *B. pumilus* and *B. gibsonii* and *B. akibaii* described in WO2004067737, WO2015091989, WO2015091990, WO2015024739, WO2015143360, US 6,312,936 B1, US 5,679,630, US 4,760,025, US7,262,042 and WO09/021867, DE102006022216A1, DE102006022224A1, WO2015089447, WO2015089441, WO2016066756, WO2016066757, WO2016069557, WO2016069563, WO2016069569.

(b) trypsin-type or chymotrypsin-type proteases, such as trypsin (e.g., of porcine or bovine origin), including the *Fusarium* protease described in WO 89/06270 and the chymotrypsin proteases derived from *Cellulomonas* described in WO 05/052161 and WO 05/052146.

(c) metalloproteases, preferably those derived from *Bacillus amyloliquefaciens* described in WO 07/044993A2; from *Bacillus*, *Brevibacillus*, *Thermoactinomyces*, *Geobacillus*, *Paenibacillus*, *Lysinibacillus* or *Streptomyces spp.* Described in WO2014194032, WO2014194054 and WO2014194117; from *Kribella alluminosa* described in WO2015193488; and from *Streptomyces* and *Lysobacter* described in WO2016075078.

(d) Protease having at least 90% identity to the subtilase from *Bacillus sp.* TY145, NCIMB 40339, described in WO92/17577 (Novozymes A/S), including the variants of this *Bacillus sp* TY145 subtilase described in WO2015024739, and WO2016066757.

**[0076]** Preferred proteases include those derived from *Bacillus gibsonii* or *Bacillus Lentus*.

**[0077]** Suitable commercially available protease enzymes include those sold under the trade names Alcalase®, Savinase®, Primase®, Durazym®, Polarzyme®, Kannase®, Liqueanase®, Liqueanase Ultra®, Savinase Ultra®, Ovozyme®, Neutrase®, Everlase® and Esperase® by Novozymes A/S (Denmark), those sold under the tradename Maxatase®, Maxacal®, Maxapem®, Properase®, Purafect®, Purafect Prime®, Purafect Ox®, FN3®, FN4®, Excellase® and Purafect OXP® by Genencor International, those sold under the tradename Opticlean® and Optimase® by Solvay Enzymes, those available from Henkel/ Kemira, namely BLAP (sequence shown in Figure 29 of US 5,352,604 with the following mutations S99D + S101 R + S103A + V104I + G159S, hereinafter referred to as BLAP), BLAP R (BLAP with S3T + V4I + V199M + V205I + L217D), BLAP X (BLAP with S3T + V4I + V205I) and BLAP F49 (BLAP with S3T + V4I + A194P + V199M + V205I + L217D) - all from Henkel/Kemira; and KAP (*Bacillus alkalophilus* subtilisin with mutations A230V + S256G + S259N) from Kao, or as disclosed in WO2009/149144, WO2009/149145, WO2010/56653, WO2010/56640, WO2011/072117, US2011/0237487, WO2011/140316, WO2012/151480, EP2510092, EP2566960 OR EP2705145.

Lipases

5 [0078] Preferably the composition comprises one or more lipases, including "first cycle lipases" such as those described in U.S. Patent 6,939,702 B1 and US PA 2009/0217464. Preferred lipases are first-wash lipases. In one embodiment of the invention the composition comprises a first wash lipase. First wash lipases includes a lipase which is a polypeptide having an amino acid sequence which: (a) has at least 90% identity with the wild-type lipase derived from *Humicola lanuginosa* strain DSM 4109; (b) compared to said wild-type lipase, comprises a substitution of an electrically neutral or negatively charged amino acid at the surface of the three-dimensional structure within 15A of E1 or Q249 with a positively charged amino acid; and (c) comprises a peptide addition at the C-terminal; and/or (d) comprises a peptide addition at the N-terminal and/or (e) meets the following limitations: i) comprises a negative amino acid in position E210 of said wild-type lipase; ii) comprises a negatively charged amino acid in the region corresponding to positions 90-101 of said wild-type lipase; and iii) comprises a neutral or negative amino acid at a position corresponding to N94 or said wild-type lipase and/or has a negative or neutral net electric charge in the region corresponding to positions 90-101 of said wild-type lipase. Preferred are variants of the wild-type lipase from *Thermomyces lanuginosus* comprising one or more of the T231R and N233R mutations. The wild-type sequence is the 269 amino acids (amino acids 23 - 291) of the Swissprot accession number Swiss-Prot O59952 (derived from *Thermomyces lanuginosus* (*Humicola lanuginosa*)). Preferred lipases would include those sold under the tradenames Lipex® and Lipolex® and Lipoclean®. Other suitable lipases include those described in European Patent Application No. 12001034.3 or EP2623586.

20 Endoglucanases

25 [0079] Other preferred enzymes include microbial-derived endoglucanases exhibiting endo-beta-1,4-glucanase activity (E.C. 3.2.1.4), including a bacterial polypeptide endogenous to a member of the genus *Bacillus* which has a sequence of at least 90%, 94%, 97% and even 99% identity to the amino acid sequence SEQ ID NO:2 in US7,141,403B2) and mixtures thereof. Suitable endoglucanases are sold under the tradenames Celluclean® and Whitezyme® (Novozymes A/S, Bagsvaerd, Denmark).

Pectate Lyases

30 [0080] Other preferred enzymes include pectate lyases sold under the tradenames Pectawash®, Pectaway®, Xpect® and mannanases sold under the tradenames Mannaway® (all from Novozymes A/S, Bagsvaerd, Denmark), and Purabrite® (Genencor International Inc., Palo Alto, California).

35 Surfactant system

[0081] The cleaning composition may comprise a surfactant system. The cleaning composition may comprise from about 1% to about 80%, or from 1% to about 60%, preferably from about 5% to about 50% more preferably from about 8% to about 40%, by weight of the cleaning composition, of a surfactant system.

[0082] Surfactants suitable for use in the surfactant system may be derived from natural and/or renewable sources.

40 [0083] The surfactant system may comprise an anionic surfactant, more preferably an anionic surfactant selected from the group consisting of alkyl benzene sulfonate, alkyl sulfate, alkyl alkoxy sulfate. Alkyl ethoxy sulfate, paraffin sulfonate and mixtures thereof may be preferred, however, alkyl benzene sulfonates are particularly preferred. The surfactant system may further comprise a surfactant selected from the group consisting of nonionic surfactant, cationic surfactant, amphoteric surfactant, zwitterionic surfactant, and mixtures thereof. The surfactant system preferably comprises a nonionic surfactant, for example an ethoxylated nonionic surfactant. The surfactant system may comprise an amphoteric surfactant, for example an amine oxide surfactant, such as an alkyl dimethyl amine oxide. The surfactant system may comprise a zwitterionic surfactant, such as a betaine.

45 [0084] The most preferred surfactant system for the detergent composition of the present invention comprises from 1% to 40%, preferably 6% to 35%, more preferably 8% to 30% weight of the total composition of an anionic surfactant, preferably comprising an alkyl benzene sulphonate. The preferred surfactant system may optionally in addition comprise an alkyl alkoxy sulfate surfactant, more preferably an alkyl ethoxy sulfate, optionally combined with 0.5% to 15%, preferably from 1% to 12%, more preferably from 2% to 10% by weight of the composition of amphoteric and/or zwitterionic surfactant, more preferably an amphoteric and even more preferably an amine oxide surfactant, especially an alkyl dimethyl amine oxide.

55 [0085] Most preferably the surfactant system comprises an anionic and a nonionic surfactant, preferably the weight ratio of the anionic to nonionic surfactant is from 25:1 to 1:2.

Anionic surfactant

**[0086]** Anionic surfactants may be in salt form or acid form, typically in the form of a water-soluble sodium, potassium, ammonium, magnesium or mono-, di- or tri- C2-C3 alkanolammonium salt, with the sodium cation being the usual one chosen.

Sulfonate Surfactant

**[0087]** Suitable anionic sulfonate surfactants for use herein include water-soluble salts of C8-C18 alkyl or hydroxyalkyl sulfonates; C11-C18 alkyl benzene sulfonates (LAS), modified alkylbenzene sulfonate (MLAS) as discussed in WO 99/05243, WO 99/05242, WO 99/05244, WO 99/05082, WO 99/05084, WO 99/05241, WO 99/07656, WO 00/23549, and WO 00/23548; methyl ester sulfonate (MES); and alpha-olefin sulfonate (AOS). Those also include the paraffin sulfonates may be monosulfonates and/or disulfonates, obtained by sulfonating paraffins of 10 to 20 carbon atoms. The sulfonate surfactant may also include the alkyl glyceryl sulfonate surfactants.

Sulfated anionic surfactant

**[0088]** Preferably the sulfated anionic surfactant is alkoxyated, more preferably, an alkoxyated branched sulfated anionic surfactant having an alkoxylation degree of from about 0.2 to about 4, even more preferably from about 0.3 to about 3, even more preferably from about 0.4 to about 1.5 and especially from about 0.4 to about 1. Preferably, the alkoxy group is ethoxy. When the sulfated anionic surfactant is a mixture of sulfated anionic surfactants, the alkoxylation degree is the weight average alkoxylation degree of all the components of the mixture (weight average alkoxylation degree). In the weight average alkoxylation degree calculation the weight of sulfated anionic surfactant components not having alkoxyated groups should also be included.

$$\text{Weight average alkoxylation degree} = (x_1 * \text{alkoxylation degree of surfactant 1} + x_2 * \text{alkoxylation degree of surfactant 2} + \dots) / (x_1 + x_2 + \dots)$$

wherein  $x_1, x_2, \dots$  are the weights in grams of each sulfated anionic surfactant of the mixture and alkoxylation degree is the number of alkoxy groups in each sulfated anionic surfactant.

**[0089]** Preferably, the branching group is an alkyl. Typically, the alkyl is selected from methyl, ethyl, propyl, butyl, pentyl, cyclic alkyl groups and mixtures thereof. Single or multiple alkyl branches could be present on the main hydrocarbyl chain of the starting alcohol(s) used to produce the sulfated anionic surfactant used in the detergent of the invention. Most preferably the branched sulfated anionic surfactant is selected from alkyl sulfates, alkyl ethoxy sulfates, and mixtures thereof.

**[0090]** The branched sulfated anionic surfactant can be a single anionic surfactant or a mixture of anionic surfactants. In the case of a single surfactant the percentage of branching refers to the weight percentage of the hydrocarbyl chains that are branched in the original alcohol from which the surfactant is derived.

**[0091]** In the case of a surfactant mixture the percentage of branching is the weight average and it is defined according to the following formula:

$$\text{Weight average of branching (\%)} = [(x_1 * \text{wt\% branched alcohol 1 in alcohol 1} + x_2 * \text{wt\% branched alcohol 2 in alcohol 2} + \dots) / (x_1 + x_2 + \dots)] * 100$$

wherein  $x_1, x_2, \dots$  are the weight in grams of each alcohol in the total alcohol mixture of the alcohols which were used as starting material for the anionic surfactant for the detergent of the invention. In the weight average branching degree calculation the weight of anionic surfactant components not having branched groups should also be included.

**[0092]** Suitable sulfate surfactants for use herein include water-soluble salts of C8-C18 alkyl or hydroxyalkyl, sulfate and/or ether sulfate. Suitable counterions include alkali metal cation or ammonium or substituted ammonium, but preferably sodium.

**[0093]** The sulfate surfactants may be selected from C8-C18 primary, branched chain and random alkyl sulfates (AS); C8-C18 secondary (2,3) alkyl sulfates; C8-C18 alkyl alkoxy sulfates (AExS) wherein preferably  $x$  is from 1-30 in which the alkoxy group could be selected from ethoxy, propoxy, butoxy or even higher alkoxy groups and mixtures thereof.

**[0094]** Alkyl sulfates and alkyl alkoxy sulfates are commercially available with a variety of chain lengths, ethoxylation and branching degrees. Commercially available sulfates include, those based on Neodol alcohols ex the Shell company, Lial - Isalchem and Safol ex the Sasol company, natural alcohols ex The Procter & Gamble Chemicals company.

**[0095]** Preferred alkyl sulfates are those in which the anionic surfactant is an alkyl ethoxy sulfate with a degree of ethoxylation of from about 0.2 to about 3, more preferably from about 0.3 to about 2, even more preferably from about 0.4 to about 1.5, and especially from about 0.4 to about 1. They are also preferred anionic surfactant having a level of branching of from about 5% to about 40%, even more preferably from about 10% to 35% and especially from about 20% to 30%.

#### Nonionic surfactant

**[0096]** Preferably the surfactant system comprises a nonionic surfactant, in an amount of from 0.1% to 40%, preferably 0.2% to 20%, most preferably 0.5% to 10% by weight of the composition. Suitable nonionic surfactants include the condensation products of aliphatic alcohols with from 1 to 25 moles of ethylene oxide. The alkyl chain of the aliphatic alcohol can either be straight or branched, primary or secondary, and generally contains from 8 to 22 carbon atoms. Particularly preferred are the condensation products of alcohols having an alkyl group containing from 10 to 18 carbon atoms, preferably from 10 to 15 carbon atoms with from 2 to 18 moles, preferably 2 to 15, more preferably 5-12 of ethylene oxide per mole of alcohol. Highly preferred nonionic surfactants are the condensation products of guerbet alcohols with from 2 to 18 moles, preferably 2 to 15, more preferably 5-12 of ethylene oxide per mole of alcohol.

**[0097]** Other suitable non-ionic surfactants for use herein include fatty alcohol polyglycol ethers, alkylpolyglucosides and fatty acid glucamides.

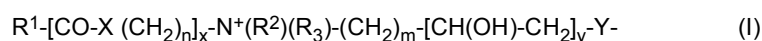
#### Amphoteric surfactant

**[0098]** The surfactant system may include amphoteric surfactant, such as amine oxide. Preferred amine oxides are alkyl dimethyl amine oxide or alkyl amido propyl dimethyl amine oxide, more preferably alkyl dimethyl amine oxide and especially coco dimethyl amino oxide. Amine oxide may have a linear or mid-branched alkyl moiety. Typical linear amine oxides include water-soluble amine oxides containing one R1 C8-18 alkyl moiety and 2 R2 and R3 moieties selected from the group consisting of C1-3 alkyl groups and C1-3 hydroxyalkyl groups. Preferably amine oxide is characterized by the formula  $R1 - N(R2)(R3) O$  wherein R1 is a C8-18 alkyl and R2 and R3 are selected from the group consisting of methyl, ethyl, propyl, isopropyl, 2-hydroxyethyl, 2-hydroxypropyl and 3-hydroxypropyl. The linear amine oxide surfactants in particular may include linear C10-C18 alkyl dimethyl amine oxides and linear C8-C12 alkoxy ethyl dihydroxy ethyl amine oxides. Preferred amine oxides include linear C10, linear C10-C12, and linear C12-C14 alkyl dimethyl amine oxides. As used herein "mid-branched" means that the amine oxide has one alkyl moiety having n1 carbon atoms with one alkyl branch on the alkyl moiety having n2 carbon atoms. The alkyl branch is located on the  $\alpha$  carbon from the nitrogen on the alkyl moiety. This type of branching for the amine oxide is also known in the art as an internal amine oxide. The total sum of n1 and n2 is from 10 to 24 carbon atoms, preferably from 12 to 20, and more preferably from 10 to 16. The number of carbon atoms for the one alkyl moiety (n1) should be approximately the same number of carbon atoms as the one alkyl branch (n2) such that the one alkyl moiety and the one alkyl branch are symmetric. As used herein "symmetric" means that  $|n1 - n2|$  is less than or equal to 5, preferably 4, most preferably from 0 to 4 carbon atoms in at least 50 wt%, more preferably at least 75 wt% to 100 wt% of the mid-branched amine oxides for use herein.

**[0099]** The amine oxide may further comprise two moieties, independently selected from a C1-3 alkyl, a C1-3 hydroxy-alkyl group, or a polyethylene oxide group containing an average of from about 1 to about 3 ethylene oxide groups. Preferably the two moieties are selected from a C1-3 alkyl, more preferably both are selected as a C1 alkyl.

#### Zwitterionic surfactant

**[0100]** Other suitable surfactants include betaines, such as alkyl betaines, alkylamidobetaine, amidazoliniumbetaine, sulfobetaine (INCI Sultaines) as well as the Phosphobetaine and preferably meets formula (I):



wherein

R<sup>1</sup> is a saturated or unsaturated C6-22 alkyl residue, preferably C8-18 alkyl residue, in particular a saturated C10-16 alkyl residue, for example a saturated C12-14 alkyl residue;

X is NH, NR<sup>4</sup> with C1-4 Alkyl residue R<sup>4</sup>, O or S,

n a number from 1 to 10, preferably 2 to 5, in particular 3,

x 0 or 1, preferably 1,

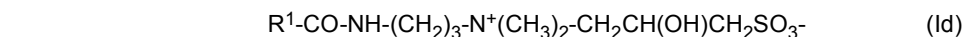
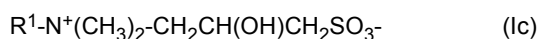
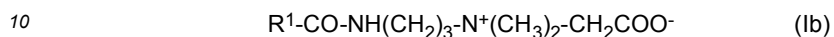
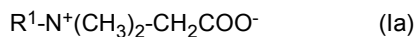
R<sup>2</sup>, R<sup>3</sup> are independently a C1-4 alkyl residue, potentially hydroxy substituted such as a hydroxyethyl, preferably a methyl.

m a number from 1 to 4, in particular 1, 2 or 3,

y 0 or 1 and

Y is COO, SO<sub>3</sub>, OPO(OR<sup>5</sup>)O or P(O)(OR<sup>5</sup>)O, whereby R<sup>5</sup> is a hydrogen atom H or a C1-4 alkyl residue.

5 **[0101]** Preferred betaines are the alkyl betaines of the formula (Ia), the alkyl amido propyl betaine of the formula (Ib), the Sulfo betaines of the formula (Ic) and the Amido sulfobetaine of the formula (Id);



in which R<sup>1</sup> has the same meaning as in formula I. Particularly preferred betaines are the Carbobetaine [wherein Y = COO<sup>-</sup>], in particular the Carbobetaine of the formula (Ia) and (Ib), more preferred are the Alkylamidobetaine of the formula (Ib).

20 **[0102]** Examples of suitable betaines and sulfobetaine are the following [designated in accordance with INCI]: Almondamidopropyl of betaines, Apricotamidopropyl betaines, Avocamidopropyl of betaines, Babassamidopropyl of betaines, Behenamidopropyl betaines, Behenyl of betaines, betaines, Canolamidopropyl betaines, Capryl/Capramidopropyl betaines, Carnitine, Cetyl of betaines, Cocamidoethyl of betaines, Cocamidopropyl betaines, Cocamidopropyl Hydroxysultaine, Coco betaines, Coco Hydroxysultaine, Coco/Oleamidopropyl betaines, Coco Sultaine, Decyl of betaines, Dihydroxyethyl Oleyl Glycinate, Dihydroxyethyl Soy Glycinate, Dihydroxyethyl Stearyl Glycinate, Dihydroxyethyl Tallow Glycinate, Dimethicone Propyl of PG-betaines, Erucamidopropyl Hydroxysultaine, Hydrogenated Tallow of betaines, Isostearamidopropyl betaines, Lauramidopropyl betaines, Lauryl of betaines, Lauryl Hydroxysultaine, Lauryl Sultaine, Milkamidopropyl betaines, Minkamidopropyl of betaines, Myristamidopropyl betaines, Myristyl of betaines, Oleamidopropyl betaines, Oleamidopropyl Hydroxysultaine, Oleyl of betaines, Olivamidopropyl of betaines, Palmamidopropyl betaines, Palm itamidopropyl betaines, Palmitoyl Carnitine, Palm Kernelamidopropyl betaines, Polytetrafluoroethylene Acetoxypromyl of betaines, Ricinoleamidopropyl betaines, Sesamidopropyl betaines, Soyamidopropyl betaines, Stearamidopropyl betaines, Stearyl of betaines, Tallowamidopropyl betaines, Tallowamidopropyl Hydroxysultaine, Tallow of betaines, Tallow Dihydroxyethyl of betaines, Undecylenamidopropyl betaines and Wheat Germamidopropyl betaines. A preferred betaine is, for example, Cocoamidopropylbetaine.

### 35 Fatty Acid

**[0103]** Especially when in liquid form, preferably, the detergent composition comprises between 1.5% and 20%, more preferably between 2% and 15%, even more preferably between 3% and 10%, most preferably between 4% and 8% by weight of the liquid detergent composition of soap, preferably a fatty acid salt, more preferably an amine neutralized fatty acid salt, wherein preferably the amine is an alkanolamine more preferably selected from monoethanolamine, diethanolamine, triethanolamine or a mixture thereof, more preferably monoethanolamine.

### Perfume

45 **[0104]** Preferred compositions of the invention comprise perfume. Typically the composition comprises a perfume that comprises one or more perfume raw materials, selected from the group as described in WO08/87497. However, any perfume useful in a detergent may be used. A preferred method of incorporating perfume into the compositions of the invention is via an encapsulated perfume particle comprising either a water-soluble hydroxylic compound or melamine-formaldehyde or modified polyvinyl alcohol. In one aspect the encapsulate comprises (a) an at least partially water-soluble solid matrix comprising one or more water-soluble hydroxylic compounds, preferably starch; and (b) a perfume oil encapsulated by the solid matrix. In a further aspect the perfume may be precomplexed with a polyamine, preferably a polyethylenimine so as to form a Schiff base.

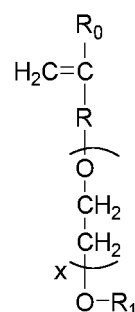
### Polymers

55 **[0105]** The detergent composition may comprise one or more polymers for example for cleaning and/or care. Examples are optionally modified carboxymethylcellulose, poly(ethylene glycol), poly(vinyl alcohol), polycarboxylates such as polyacrylates, maleic/acrylic acid copolymers and lauryl methacrylate/acrylic acid co-polymers and carboxylate polymers.

**[0106]** Suitable carboxylate polymers include maleate/acrylate random copolymer or polyacrylate homopolymer. The carboxylate polymer may be a polyacrylate homopolymer having a molecular weight of from 4,000 Da to 9,000 Da, or from 6,000 Da to 9,000 Da. Other suitable carboxylate polymers are co-polymers of maleic acid and acrylic acid, and may have a molecular weight in the range of from 4,000 Da to 90,000 Da.

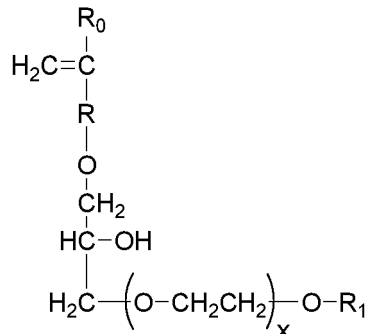
**[0107]** Other suitable carboxylate polymers are co-polymers comprising: (i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising carboxyl groups; (ii) from 1 to less than 49 wt% structural units derived from one or more monomers comprising sulfonate moieties; and (iii) from 1 to 49 wt% structural units derived from one or more types of monomers selected from ether bond-containing monomers represented by formulas (I) and (II):

formula (I):



wherein in formula (I),  $R_0$  represents a hydrogen atom or  $CH_3$  group, R represents a  $CH_2$  group,  $CH_2CH_2$  group or single bond, X represents a number 0-5 provided X represents a number 1-5 when R is a single bond, and  $R_1$  is a hydrogen atom or C1 to C20 organic group;

formula (II)



in formula (II),  $R_0$  represents a hydrogen atom or  $CH_3$  group, R represents a  $CH_2$  group,  $CH_2CH_2$  group or single bond, X represents a number 0-5, and  $R_1$  is a hydrogen atom or C1 to C20 organic group.

**[0108]** The composition may comprise one or more amphiphilic cleaning polymers such as the compound having the following general structure: bis(( $C_2H_5O$ )( $C_2H_4O$ ) $n$ )( $CH_3$ )- $N^+$ - $C_xH_{2x}$ - $N^+$ -( $CH_3$ )-bis(( $C_2H_5O$ )( $C_2H_4O$ ) $n$ ), wherein  $n$  = from 20 to 30, and  $x$  = from 3 to 8, or sulphated or sulphonated variants thereof. In one aspect, this polymer is sulphated or sulphonated to provide a zwitterionic soil suspension polymer.

**[0109]** The composition preferably comprises amphiphilic alkoxyated grease cleaning polymers which have balanced hydrophilic and properties such that they remove grease particles from fabrics and surfaces. Preferred amphiphilic alkoxyated grease cleaning polymers comprise a core structure and a plurality of alkoxyate groups attached to that core structure. These may comprise alkoxyated polyalkylenimines, preferably having an inner polyethylene oxide block and an outer polypropylene oxide block. Typically these may be incorporated into the compositions of the invention in amounts of from 0.005 to 10 wt%, generally from 0.5 to 8 wt%.

**[0110]** Alkoxyated polycarboxylates such as those prepared from polyacrylates are useful herein to provide additional grease removal performance. Such materials are described in WO 91/08281 and PCT 90/01815. Chemically, these materials comprise polyacrylates having one ethoxy side-chain per every 7-8 acrylate units. The side-chains are of the formula  $-(CH_2CH_2O)_m(CH_2)_nCH_3$  wherein  $m$  is 2-3 and  $n$  is 6-12. The side-chains are ester-linked to the polyacrylate

"backbone" to provide a "comb" polymer type structure. The molecular weight can vary, but is typically in the range of about 2000 to about 50,000. Such alkoxylated polycarboxylates can comprise from about 0.05% to about 10%, by weight, of the compositions herein.

**[0111]** The composition may comprise polyethylene glycol polymers and these may be particularly preferred in compositions comprising mixed surfactant systems. 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, C1-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.

**[0112]** Typically these polymers when present are each incorporated into the compositions of the invention in amounts from 0.005 to 10 wt%, more usually from 0.05 to 8 wt%.

**[0113]** Preferably the composition comprises one or more carboxylate polymer, such as a maleate/acrylate random copolymer or polyacrylate homopolymer. In one aspect, the carboxylate polymer is a polyacrylate homopolymer having a molecular weight of from 4,000 Da to 9,000 Da, or from 6,000 Da to 9,000 Da. Typically these are incorporated into the compositions of the invention in amounts from 0.005 to 10 wt%, or from 0.05 to 8 wt%.

**[0114]** Preferably the composition comprises one or more soil release polymers.

**[0115]** Suitable soil release polymers are polyester soil release polymers such as Repel-o-tex polymers, including Repel-o-tex SF, SF-2 and SRP6 supplied by Rhodia. Other suitable soil release polymers include Texcare polymers, including Texcare SRA100, SRA300, SRN100, SRN170, SRN240, SRN260, SRN300 and SRN325 supplied by Clariant. Other suitable soil release polymers are Marloquest polymers, such as Marloquest SL supplied by Sasol.

**[0116]** Preferably the composition comprises one or more cellulosic polymer, including those selected from alkyl cellulose, alkyl alkoxyalkyl cellulose, carboxyalkyl cellulose, alkyl carboxyalkyl cellulose. Preferred cellulosic polymers are selected from the group comprising carboxymethyl cellulose, methyl cellulose, methyl hydroxyethyl cellulose, methyl carboxymethyl cellulose, and mixtures thereof. In one aspect, the carboxymethyl cellulose has a degree of carboxymethyl substitution from 0.5 to 0.9 and a molecular weight from 100,000 Da to 300,000 Da.

**[0117]** The composition preferably comprises a cationically-modified polysaccharide polymer. Preferably, the cationic polysaccharide polymer is selected from cationically modified hydroxyethyl cellulose, cationically modified hydroxypropyl cellulose, cationically and hydrophobically modified hydroxyethyl cellulose, cationically and hydrophobically modified hydroxypropyl cellulose, or a mixture thereof, more preferably cationically modified hydroxyethyl cellulose, cationically and hydrophobically modified hydroxyethyl cellulose, or a mixture thereof.

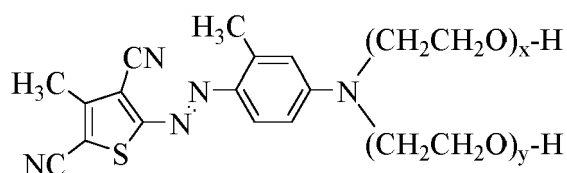
#### Amines

**[0118]** The cleaning compositions described herein may contain an amine. The cleaning compositions may include from about 0.1% to about 10%, or from about 0.2% to about 5%, or from about 0.5% to about 4%, or from about 0.1% to about 4%, or from about 0.1% to about 2%, by weight of the composition, of an amine. The amine can be subjected to protonation depending on the pH of the cleaning medium in which it is used. Non-limiting examples of amines include, but are not limited to, etheramines, cyclic amines, polyamines, oligoamines (e.g., triamines, diamines, pentamines, tetraamines), or combinations thereof. The compositions described herein may comprise an amine selected from the group consisting of oligoamines, etheramines, cyclic amines, and combinations thereof. In some aspects, the amine is not an alkanolamine. In some aspects, the amine is not a polyalkyleneimine. Examples of suitable oligoamines include tetraethylenepentamine, triethylenetetraamine, diethylenetriamine, and mixtures thereof. Etheramines and cyclic amines may be particularly preferred.

#### Fabric Shading Dye

**[0119]** The composition may comprise a fabric shading agent. Suitable fabric shading agents include dyes, dye-clay conjugates, and 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. Preferred dyes include alkoxylated azothiophenes, Solvent Violet 13, Acid Violet 50 and Direct Violet 9. Particularly preferred dyes are polymeric dyes, particularly comprising polyalkoxy, most preferably polyethoxy groups,

for example:



wherein the index values x and y are independently selected from 1 to 10.

#### Dye Transfer Inhibitors

**[0120]** Suitable dye transfer inhibitors include polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinylpyrrolidone, polyvinylloxazolidone, polyvinylimidazole and mixtures thereof. Preferred are poly(vinyl pyrrolidone), poly(vinylpyridine betaine), poly(vinylpyridine N-oxide), poly(vinyl pyrrolidone-vinyl imidazole) and mixtures thereof. Suitable commercially available dye transfer inhibitors include PVP-K15 and K30 (Ashland), Sokalan® HP165, HP50, HP53, HP59, HP56K, HP56, HP66 (BASF), Chromabond® S-400, S403E and S-100 (Ashland).

#### Chelant

**[0121]** The composition may comprise chelant for example selected from phosphonic, sulphonic, succinic and acetic chelants or mixtures thereof. Suitable examples include HEDP, DTPA, EDTA, MGDA, GLDA, EDDS and 4,5-dihydroxy-1,3-benzenedisulfonic acids and salts thereof.

#### Methods of Making the Composition

**[0122]** The present disclosure relates to methods of making the compositions described herein. The compositions of the invention may be solid (for example granules or tablets) or liquid form. It may be preferred for the compositions to be in liquid form. They may be made by any process chosen by the formulator, including by a batch process, a continuous loop process, or combinations thereof.

**[0123]** When in the form of a liquid, the compositions of the invention may be aqueous (typically above 2 wt% or even above 5 or 10 wt% total water, up to 90 or up to 80wt% or 70 wt% total water) or non-aqueous (typically below 2 wt% total water content). Typically the compositions of the invention will be in the form of an aqueous solution or uniform dispersion or suspension of optical brightener, DTI and optional additional adjunct materials, some of which may normally be in solid form, that have been combined with the normally liquid components of the composition, such as the liquid alcohol ethoxylate nonionic, the aqueous liquid carrier, and any other normally liquid optional ingredients. Such a solution, dispersion or suspension will be acceptably phase stable. When in the form of a liquid, the detergents of the invention preferably have viscosity from 1 to 1500 centipoises (1-1500 mPa\*s), more preferably from 100 to 1000 centipoises (100-1000 mPa\*s), and most preferably from 200 to 500 centipoises (200-500 mPa\*s) at 20s-1 and 21°C. Viscosity can be determined by conventional methods. Viscosity may be measured using an AR 550 rheometer from TA instruments using a plate steel spindle at 40 mm diameter and a gap size of 500 µm. The high shear viscosity at 20s-1 and low shear viscosity at 0.05-1 can be obtained from a logarithmic shear rate sweep from 0.1-1 to 25-1 in 3 minutes time at 21C. The preferred rheology described therein may be achieved using internal existing structuring with detergent ingredients or by employing an external rheology modifier. More preferably the detergents, such as detergent liquid compositions have a high shear rate viscosity of from about 100 centipoise to 1500 centipoise, more preferably from 100 to 1000 cps. Unit Dose detergents, such as detergent liquid compositions have high shear rate viscosity of from 400 to 1000cps. Detergents such as laundry softening compositions typically have high shear rate viscosity of from 10 to 1000, more preferably from 10 to 800 cps, most preferably from 10 to 500 cps. Hand dishwashing compositions have high shear rate viscosity of from 300 to 4000 cps, more preferably 300 to 1000 cps.

**[0124]** The cleaning and/or treatment compositions in the form of a liquid herein can be prepared by combining the components thereof in any convenient order and by mixing, e.g., agitating, the resulting component combination to form a phase stable liquid detergent composition. In a process for preparing such compositions, a liquid matrix is formed containing at least a major proportion, or even substantially all, of the liquid components, e.g., nonionic surfactant, the non-surface active liquid carriers and other optional liquid components, with the liquid components being thoroughly admixed by imparting shear agitation to this liquid combination. For example, rapid stirring with a mechanical stirrer may usefully be employed. While shear agitation is maintained, substantially all of any anionic surfactants and the solid form ingredients can be added. Agitation of the mixture is continued, and if necessary, can be increased at this point to form



a solution or a uniform dispersion of insoluble solid phase particulates within the liquid phase. After some or all of the solid-form materials have been added to this agitated mixture, particles of any enzyme material to be included, e.g., enzyme granulates, are incorporated. As a variation of the composition preparation procedure hereinbefore described, one or more of the solid components may be added to the agitated mixture as a solution or slurry of particles premixed with a minor portion of one or more of the liquid components. After addition of all of the composition components, agitation of the mixture is continued for a period of time sufficient to form compositions having the requisite viscosity and phase stability characteristics. Frequently this will involve agitation for a period of from about 30 to 60 minutes.

**[0125]** The adjunct ingredients in the compositions of this invention may be incorporated into the composition as the product of the synthesis generating such components, either with or without an intermediate purification step. Where there is no purification step, commonly the mixture used will comprise the desired component or mixtures thereof (and percentages given herein relate to the weight percent of the component itself unless otherwise specified) and in addition unreacted starting materials and impurities formed from side reactions and/or incomplete reaction. For example, for an ethoxylated or substituted component, the mixture will likely comprise different degrees of ethoxylation/substitution.

#### Method of Use

**[0126]** The present disclosure relates to a method of using the cleaning composition of the present disclosure to clean a surface, such as a textile. In general, the method includes mixing the cleaning composition as described herein with water to form an aqueous liquor and contacting a surface, preferably a textile, with the aqueous liquor in a laundering step. The target surface may include a greasy soil or body soil.

**[0127]** The present invention also provides use of a composition comprising an amylase enzyme and an enzyme having glycoside hydrolase activity belonging to the endo-alpha-1,4-polygalactosminidase class (EC 3.2.1.109) of enzymes for enhanced stain removal from a surface, preferably a fabric surface, particularly greasy stain or body soil removal and/or for reducing malodour. The glycoside hydrolase enzyme is a variant having at least 70% or 75% or 80% or 85% or 90% or 95% identity to 100% SEQ ID NO:1.

**[0128]** The compositions of this invention, typically prepared as hereinbefore described, can be used to form aqueous (washing/treatment) liquor for use in the laundering/treatment of fabrics and/or hard surfaces. Generally, an effective amount of such a composition is added to water, for example in a conventional fabric automatic washing machine, to form such aqueous liquor. The aqueous liquor so formed is then contacted, typically under agitation, with the fabrics to be laundered/treated therewith. An effective amount of the cleaning composition herein added to water to form aqueous liquor can comprise amounts sufficient to form from about 500 to 25,000 ppm, or from 500 to 15,000 ppm of composition in the aqueous liquor, or from about 1,000 to 3,000 ppm of the cleaning composition herein will be provided in aqueous liquor.

**[0129]** Typically, the aqueous liquor is formed by contacting the cleaning composition with wash water in such an amount so that the concentration of the anionic surfactant in the wash liquor is from above 0.1g/l to 5g/l, or from 1g/l, and to 4.5g/l, or to 4.0g/l, or to 3.5g/l, or to 3.0g/l, or to 2.5g/l, or even to 2.0g/l, or even to 1.5g/l. The method of laundering fabric or textile may be carried out in a top-loading or front-loading automatic washing machine, or can be used in a hand-wash laundry application. In these applications, the aqueous liquor formed and concentration of cleaning composition in the wash liquor is that of the main wash cycle. Any input of water during any optional rinsing step(s) is not included when determining the volume of the aqueous liquor.

**[0130]** The aqueous liquor may comprise 40 litres or less of water, or 30 litres or less, or 20 litres or less, or 10 litres or less, or 8 litres or less, or even 6 litres or less of water. The aqueous liquor may comprise from above 0 to 15 litres, or from 2 litres, and to 12 litres, or even to 8 litres of water. Typically from 0.01kg to 2kg of fabric per litre of aqueous liquor is dosed into said aqueous liquor. Typically from 0.01kg, or from 0.05kg, or from 0.07kg, or from 0.10kg, or from 0.15kg, or from 0.20kg, or from 0.25kg fabric per litre of aqueous liquor is dosed into said aqueous liquor. Optionally, 50g or less, or 45g or less, or 40g or less, or 35g or less, or 30g or less, or 25g or less, or 20g or less, or even 15g or less, or even 10g or less of the composition is contacted to water to form the aqueous liquor. Such compositions are typically employed at concentrations of from about 500 ppm to about 15,000 ppm in solution. The water temperature typically ranges from about 5 °C to about 90 °C for example from 20 °C to 60 °C, preferably up to 40 °C or 30 °C and, when laundering fabric, the water to fabric ratio is typically from about 1:1 to about 30:1. Typically the aqueous liquor comprising the cleaning composition of the invention has a pH of from 3 to 11.5, typically from 7 to 11, more usually 8 to 10.5.

**[0131]** In one aspect, such method comprises the steps of optionally washing and/or rinsing said surface or fabric, contacting said surface or fabric with any composition disclosed in this specification then optionally washing and/or rinsing said surface or fabric, with an optional drying step.

**[0132]** Drying of such surfaces or fabrics may be accomplished by any one of the common means employed either in domestic or industrial settings: machine drying or open-air drying. The fabric may comprise any fabric capable of being laundered in normal consumer or institutional use conditions, and the invention is particularly suitable for synthetic

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textiles such as polyester and nylon and especially for treatment of mixed fabrics and/or fibres comprising synthetic and cellulosic fabrics and/or fibres. As examples of synthetic fabrics are polyester, nylon, these may be present in mixtures with cellulosic fibres, for example, polycotton fabrics.

### 5 EXAMPLES

**[0133]** The following are illustrative examples of cleaning compositions according to the present disclosure and are not intended to be limiting.

#### 10 Examples 1 to 18: Unit Dose Compositions.

**[0134]** These examples provide various formulations for unit dose laundry detergents and comprise double compartment unit dose products comprising one powder and one liquid compartment. The film used to encapsulate the compositions in PVA. Each example is prepared by combining a liquid compartment composition selected from compositions A-E with a powder compartment composition selected from compositions F-K.

Example	<u>1</u>	<u>2</u>	<u>3</u>	<u>4</u>	<u>5</u>	<u>6</u>
Liquid composition	20g A	25g A	20g A	15g A	20g B	20g B
Solid composition	15g F	12g G	12g H	12g I	15g J	15g K

Example	<u>7</u>	<u>8</u>	<u>9</u>	<u>10</u>	<u>11</u>	<u>12</u>
Liquid composition	15g B	17g B	20g C	19g C	15g C	25g C
Solid composition	15g L	14g F	15g G	18g H	15g I	12g J

Example	<u>13</u>	<u>14</u>	<u>15</u>	<u>16</u>	<u>17</u>	<u>18</u>
Liquid composition	20g D	18g D	22g D	32g E	32g E	27g E
Solid composition	20g K	13g L	15g F	17g G	12g H	18g I

Ingredients	A	B	C	D	E
	% weight of compartment				
LAS	19.09	16.76	8.59	6.56	3.44
AE3S	1.91	0.74	0.18	0.46	0.07
AE7	14.00	17.50	26.33	28.08	31.59
Citric Acid	0.6	0.6	0.6	0.6	
C12-15 Fatty Acid	14.8	14.8	14.8	14.8	14.8
Polymer 3	4.0	4.0	4.0	4.0	
Chelant 2	1.2	1.2	1.2	1.2	
Optical Brightener 1	0.20	0.25	0.01	0.01	0.50
Optical Brightener 2	0.20	-	0.25	0.03	0.01
Optical Brightener 3	0.18	0.09	0.30	0.01	
DTI 1	0.10	-	0.20	0.01	0.05
DTI 2	-	0.10	0.20	0.25	0.05
Glycerol	6.1	6.1	6.1	6.1	

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(continued)

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Ingredients	A	B	C	D	E
	% weight of compartment				
Monoethanol amine	8.0	8.0	8.0	8.0	
Tri-isopropanol amine	-	-	2.0	-	
Tri-ethanol amine	-	2.0	-	-	
Cumene sulfonate	-	-	-	-	
Protease	0.80	0.60	0.07	1.00	1.50
Mannanase	0.07	0.05	0.05	0.10	0.01
Amylase 1	0.20	0.11	0.30	0.50	0.05
Amylase 2	0.11	0.20	0.10	-	0.50
Hydrolase of SEQ ID NO: 1 (active protein)	0.005	0.05	0.005	0.010	0.01
Second hydrolase of SEQ ID NO: 13 (active protein)	0.001	-	0.001	-	
Polishing enzyme	0.005	0.05	-	-	
Nuclease	0.005	-	-	-	0.005
Dispersin B	0.010	0.05	0.005	0.005	-
Cyclohexyl dimethanol	-	-	-	2.0	-
Acid violet 50	0.03	0.02			
Violet DD			0.01	0.05	0.02
Structurant	0.14	0.14	0.14	0.14	0.14
Perfume	1.9	1.9	1.9	1.9	1.9
Water, solvents and miscellaneous	To 100%				
pH	7.5-8.2				

35

40

45

Ingredient	F	G	H	I	J	K
	% weight					
Sodium carbonate	20.0	35.0	30.0	29.0	28.0	18.0
Carboxymethyl cellulose	2.0	1.0	-	-	2.5	0.6
Sodium silicate 2R	5.0	-	5.0	3.2	20.0	-
Tetraacetyl ethylenediamine	20.0	15.0	18.0	15.0	-	25.0
Sodium percarbonate	50.0	44.0	45.0	45.0	29.0	50.0
Polyetheramine	0.5	2	0.5	1	0.5	4
Sulfate/ Water & Miscellaneous	Balance					

50

**[0135]** Based on total cleaning and/or treatment composition/compartment weight. Enzyme levels are reported as raw material.

Examples 19 to 24

55

**[0136]** Granular laundry detergent compositions for hand washing or washing machines, typically top-loading washing machines.

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	<u>Ingredient</u>	19	20	21	22	23	24
		<u>% weight</u>					
5	LAS	11.33	10.81	7.04	4.20	3.92	2.29
	Quaternary ammonium	0.70	0.20	1.00	0.60	-	-
	AE3S	0.51	0.49	0.32	-	0.08	0.10
10	AE7	8.36	11.50	12.54	11.20	16.00	21.51
	Sodium Tripolyphosphate	5.0	-	4.0	9.0	2.0	-
	Zeolite A	-	1.0	-	1.0	4.0	1.0
	Sodium silicate 1.6R	7.0	5.0	2.0	3.0	3.0	5.0
15	Sodium carbonate	20.0	17.0	23.0	14.0	14.0	16.0
	Polyacrylate MW 4500	1.0	0.6	1.0	1.0	1.5	1.0
	Polymer 6	0.1	0.2	-	-	0.1	-
20	Carboxymethyl cellulose	1.0	0.3	1.0	1.0	1.0	1.0
	Acid Violet 50	0.05	-	0.02	-	0.04	-
	Violet DD	-	0.03	-	0.03	-	0.03
	Protease 2	0.10	0.10	0.10	0.10	-	0.10
25	Amylase	0.03	-	0.03	0.03	0.03	0.03
	Lipase	0.03	0.07	0.30	0.10	0.07	0.40
	Polishing enzyme	0.002	-	0.05	-	0.02	-
30	Hydrolase of SEQ ID NO:1 (active protein)	0.001	0.001	0.01	0.05	0.002	0.02
	Nuclease (as active protein)	0.001	-	-	-	0.001	-
	Dispersin B	0.001	0.001	0.05	-	0.001	-
	Optical Brightener 1	0.200	0.001	0.300	0.650	0.050	0.001
35	Optical Brightener 2	0.060	-	0.650	0.180	0.200	0.060
	Optical Brightener 3	0.100	0.060	0.050	-	0.030	0.300
	Chelant 1	0.60	0.80	0.60	0.25	0.60	0.60
40	DTI 1	0.32	0.15	0.15	-	0.10	0.10
	DTI 2	0.32	0.15	0.30	0.30	0.10	0.20
	Sodium Percarbonate	4.6	5.2	5.0	5.7	4.5	7.3
	Nonanoyloxybenzenesulfonate	1.9	0.0	1.66	0.0	0.33	0.75
45	Tetraacetythylenediamine	0.58	1.2	0.51	0.0	0.015	0.28
	Photo bleach	0.0030	0.0	0.0012	0.0030	0.0021	-
	S-ACMC	0.1	0.0	0.0	0.0	0.06	0.0
50	Polyetheramine	0.5	2	0.5	1	0.5	4
	Sulfate/Moisture	Balance					

Examples 25-30

55

**[0137]** Granular laundry detergent compositions typically for front-loading automatic washing machines.

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	Ingredient	25	26	27	28	29	30
		% weight					
5	LAS	6.08	5.05	4.27	3.24	2.30	1.09
	AE3S	-	0.90	0.21	0.18	-	0.06
	AS	0.34	-	-	-	-	-
10	AE7	4.28	5.95	6.72	7.98	9.20	10.35
	Quaternary ammonium	0.5	-	-	0.3	-	-
	Crystalline layered silicate	4.1	-	4.8	-	-	-
	Zeolite A	5.0	-	2.0	-	2.0	2.0
15	Citric acid	3.0	4.0	3.0	4.0	2.5	3.0
	Sodium carbonate	11.0	17.0	12.0	15.0	18.0	18.0
	Sodium silicate 2R	0.08	-	0.11	-	-	-
20	Optical Brightener 1	-	0.25	0.05	0.01	0.10	0.02
	Optical Brightener 2	-	-	0.25	0.20	0.01	0.08
	Optical Brightener 3	-	0.06	0.04	0.15	-	0.05
	DTI 1	0.08	-	0.04	-	0.10	0.01
25	DTI 2	0.08	-	0.04	0.10	0.10	0.02
	Soil release agent	0.75	0.72	0.71	0.72	-	-
	Acrylic /maleic acid copolymer	1.1	3.7	1.0	3.7	2.6	3.8
30	Carboxymethyl cellulose	0.2	1.4	0.2	1.4	1.0	0.5
	Protease 3	0.20	0.20	0.30	0.15	0.12	0.13
	Amylase 3	0.20	0.15	0.20	0.30	0.15	0.15
	Lipase	0.05	0.15	0.10	-	-	-
35	Amylase 2	0.03	0.07	-	-	0.05	0.05
	Cellulase 2	-	-	-	-	0.10	0.10
	Polishing enzyme	0.003	0.005	0.020	-	-	-
40	Hydrolase of SEQ ID NO:1 (active protein)	0.002	0.010	0.020	0.020	0.020	0.003
	Nuclease	-	-	-	-	0.005	0.005
	Dispersin B	0.002	-	0.020	0.020	-	-
45	Tetraacetylenehtylenediamine	3.6	4.0	3.6	4.0	2.2	1.4
	Sodium percarbonate	13.0	13.2	13.0	13.2	16.0	14.0
	Chelant 3	-	0.2	-	0.2	-	0.2
	Chelant 2	0.2	-	0.2	-	0.2	0.2
50	MgSO <sub>4</sub>	-	0.42	-	0.42	-	0.4
	Perfume	0.5	0.6	0.5	0.6	0.6	0.6
	Suds suppressor agglomerate	0.05	0.10	0.05	0.10	0.06	0.05
55	Soap	0.45	0.45	0.45	0.45	-	-
	Acid Violet 50	0.04	-	0.05	-	0.04	-
	Violet DD	-	0.04	-	0.05	-	0.04

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(continued)

Ingredient	25	26	27	28	29	30
	% weight					
S-ACMC	0.01	0.01	-	0.01	-	-
Direct Violet 9 (active)	-	-	0.0001	0.0001	-	-
Polyetheramine	0.5	2	0.5	1	0.5	4
Sulfate/ Water & Miscellaneous	Balance					

Examples 31-37: Heavy Duty Liquid laundry detergent compositions.

Ingredients	31	32	33	34	35	36	37
	% weight						
AE <sub>1,8</sub> S	6.77	5.16	1.36	1.30	-	-	-
AE <sub>3</sub> S	-	-	-	-	0.45	-	-
LAS	0.86	2.06	2.72	0.68	0.95	1.56	3.55
HSAS	1.85	2.63	1.02	-	-	-	-
AE9	6.32	9.85	10.20	7.92			
AE8							35.45
AE7					8.40	12.44	
C <sub>12-14</sub> dimethyl Amine Oxide	0.30	0.73	0.23	0.37	-	-	-
C <sub>12-18</sub> Fatty Acid	0.80	1.90	0.60	0.99	1.20	-	15.00
Citric Acid	2.50	3.96	1.88	1.98	0.90	2.50	0.60
Optical Brightener 1	1.00	0.80	0.10	0.30	0.05	0.50	0.001
Optical Brightener 3	0.001	0.05	0.01	0.20	0.50	-	1.00
Sodium formate	1.60	0.09	1.20	0.04	1.60	1.20	0.20
DTI 1	0.32	0.05	-	0.60	0.10	0.60	0.01
DTI 2	0.32	0.10	0.60	0.60	0.05	0.40	0.20
Sodium hydroxide	2.30	3.80	1.70	1.90	1.70	2.50	2.30
Monoethanolamine	1.40	1.49	1.00	0.70	-	-	-
Diethylene glycol	5.50	-	4.10	-	-	-	-
Chelant 1	0.15	0.15	0.11	0.07	0.50	0.11	0.80
4-formyl-phenylboronic acid	-	-	-	-	0.05	0.02	0.01
Sodium tetraborate	1.43	1.50	1.10	0.75	-	1.07	-
Ethanol	1.54	1.77	1.15	0.89	-	3.00	7.00
Polymer 1	0.10	-	-	-	-	-	2.00
Polymer 2	0.30	0.33	0.23	0.17	-	-	-
Polymer 3	-	-	-	-	-	-	0.80
Polymer 4	0.80	0.81	0.60	0.40	1.00	1.00	-
1,2-Propanediol	-	6.60	-	3.30	0.50	2.00	8.00
Structurant	0.10	-	-	-	-	-	0.10

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(continued)

Ingredients	31	32	33	34	35	36	37
	% weight						
Perfume	1.60	1.10	1.00	0.80	0.90	1.50	1.60
Perfume encapsulate	0.10	0.05	0.01	0.02	0.10	0.05	0.10
Protease	0.80	0.60	0.70	0.90	0.70	0.60	1.50
Hydrolase of SEQ ID: No 1 (active protein)	0.07	0.05	0.045	0.06	0.04	0.045	0.10
Amylase 1	0.30	-	0.30	0.10	-	0.40	0.10
Amylase 2	-	0.20	0.10	0.15	0.07	-	0.10
Xyloglucanase	0.20	0.10	-	-	0.05	0.05	0.20
Lipase	0.40	0.20	0.30	0.10	0.20	-	-
Polishing enzyme	-	0.04	-	-	-	0.004	-
Nuclease	0.05	0.03	0.01	0.03	0.03	0.003	0.003
Dispersin B	-	-	-	0.05	0.03	0.001	0.001
Acid Violet 50	0.05	-	-	-	-	-	0.005
Direct Violet 9	-	-	-	-	-	0.05	-
Violet DD	-	0.035	0.02	0.037	0.04	-	-
Water insoluble plant fiber	0.2	-	-	-	1.2	-	-
Dye control agent	-	0.3	-	0.5	-	0.3	-
Alkoxylated polyaryl/ polyalkyl phenol	-	-	1.2	-	-	-	3.1
Water, dyes & minors	Balance						
pH	8.2						

**[0138]** Based on total cleaning and/or treatment composition weight. Unless indicated otherwise, enzyme levels are reported as raw material.

- AE1.8S is C<sub>12-15</sub> alkyl ethoxy sulfate with an average degree of ethoxylation of 1.8
- AE3S is C<sub>12-15</sub> alkyl ethoxy sulfate with an av degree of ethoxylation of 3.0
- AE7 is C<sub>12-13</sub> alcohol ethoxylate, with an average degree of ethoxylation of 7
- AE8 is C<sub>12-13</sub> alcohol ethoxylate, with an average degree of ethoxylation of 8
- AE9 is C<sub>12-13</sub> alcohol ethoxylate, with an average degree of ethoxylation of 9
- Alkoxylated polyaryl / polyalkyl phenol is alkoxylated polyaryl/polyalkyl phenol for example Emulsogen® TS160, Hostapal® BV conc., Sapogenat® T110 or Sapogenat® T139, all from Clariant
- Amylase 1 is Stainzyme®, 15 mg active/g
- Amylase 2 is Natalase®, 29 mg active/g
- Amylase 3 is Stainzyme® Plus, 20 mg active/g,
- AS is C<sub>12-14</sub> alkylsulfate
- Cellulase 2 is Celluclean™, 15.6 mg active/g
- Xyloglucanase is Whitezyme®, 20mg active/g
- Chelant 1 is diethylene triamine pentaacetic acid
- Chelant 2 is 1-hydroxyethane 1,1-diphosphonic acid
- Chelant 3 is sodium salt of ethylenediamine-N,N'-disuccinic acid, (S,S) isomer (EDDS)
- Dispersin B is a glycoside hydrolase, reported as 1000mg active/g
- DTI 1 is poly(4-vinylpyridine-1-oxide) (such as Chromabond S-403E®),
- DTI 2 is poly(1-vinylpyrrolidone-co-1-vinylimidazole) (such as Sokalan HP56®).

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(continued)

	Dye Control Agent	is for example Suparex® O.IN (M1), Nylofixan® P (M2), Nylofixan® PM (M3), or Nylofixan® HF (M4)
5	HSAS	is mid-branched alkyl sulfate as disclosed in US 6,020,303 and US6,060,443
	LAS	is linear alkylbenzenesulfonate having an average aliphatic carbon chain length C <sub>9</sub> -C <sub>15</sub> (HLAS is acid form).
	Lipase	is Lipex®, 18 mg active/g
10	Mannanase	is Mannaway®, 25 mg active/g
	Nuclease	is a Phosphodiesterase according to any of SEQ ID NOs: 2 to 6, preferably SEQ ID NO: 2, 3 or 4, reported as active protein
	Optical Brightener 1	is disodium 4,4'-bis[[4-anilino-6-morpholino-s-triazin-2-yl]-amino]-2,2'-stilbenedisulfonate
15	Optical Brightener 2	is disodium 4,4'-bis-(2-sulfostyryl)biphenyl (sodium salt)
	Optical Brightener 3	is Optiblanc SPL10® from 3V Sigma
	Perfume encapsulate	is a core-shell melamine formaldehyde perfume microcapsules
	Photo bleach	is a sulfonated zinc phthalocyanine
	Polishing enzyme	is Para-nitrobenzyl esterase, reported as 1000mg active/g
20	Polyetheramine	as described in present disclosure.
	Polymer 1	is bis((C <sub>2</sub> H <sub>5</sub> O)(C <sub>2</sub> H <sub>4</sub> O) <sub>n</sub> )(CH <sub>3</sub> )-N <sup>+</sup> -C <sub>x</sub> H <sub>2x</sub> -N <sup>+</sup> -(CH <sub>3</sub> )-bis((C <sub>2</sub> H <sub>5</sub> O)(C <sub>2</sub> H <sub>4</sub> O) <sub>n</sub> ), wherein n = 20-30, x = 3 to 8 or sulphated or sulfonated variants thereof
	Polymer 2	is ethoxylated (EO <sub>15</sub> ) tetraethylene pentamine
25	Polymer 3	is ethoxylated polyethylenimine
	Polymer 4	is ethoxylated hexamethylene diamine
	Polymer 5	is Acusol 305, provided by Rohm&Haas
	Polymer 6	is a polyethylene glycol polymer grafted with vinyl acetate side chains, provided by BASF.
30	Protease 1	is Purafect Prime®, 40.6 mg active/g
	Protease 2	is Savinase®, 32.89 mg active/g
	Protease 3	is Purafect®, 84 mg active/g
	Quaternary ammonium	is C <sub>12-14</sub> Dimethylhydroxyethyl ammonium chloride
	S-ACMC	is Reactive Blue 19 Azo-CM-Cellulose provided by Megazyme
35	Soil release agent	is Repel-o-tex® SF2, supplied by Solvay
	Structurant	is Hydrogenated Castor Oil
	Violet DD	is a thiophene azo polymeric hueing dye provided by Milliken

40 **[0139]** The dimensions and values disclosed herein are not to be understood as being strictly limited to the exact numerical values recited. Instead, unless otherwise specified, each such dimension is intended to mean both the recited value and a functionally equivalent range surrounding that value. For example, a dimension disclosed as "40 mm" is intended to mean "about 40 mm."

### 45 SEQUENCE LISTING

#### **[0140]**

<110> P&G

50 <120> CLEANING COMPOSITIONS INCLUDING ENZYMES

<130> CM04645FM

55 <160> 32

<170> PatentIn version 3.5



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5

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				20					25					30		
20	Lys	Pro	Ala	Asp	Val	Gly	Tyr	Leu	Lys	Glu	Gln	Gly	Ser	Thr	Pro	Phe
			35					40					45			
25	Ala	Tyr	Leu	Ser	Val	Gly	Glu	Phe	Asp	Gly	Asp	Ala	Ala	Ala	Ile	Ala
		50					55					60				
30	Asp	Ser	Gly	Leu	Ala	Arg	Gly	Lys	Ser	Ala	Val	Arg	Asn	Gln	Ala	Trp
	65					70					75					80
35	Asn	Ser	Gln	Val	Met	Asp	Leu	Ala	Ala	Pro	Ser	Trp	Arg	Ala	His	Leu
					85					90					95	
40	Leu	Lys	Arg	Ala	Ala	Glu	Leu	Arg	Lys	Gln	Gly	Tyr	Ala	Gly	Leu	Phe
				100					105					110		
45	Leu	Asp	Thr	Leu	Asp	Ser	Phe	Gln	Leu	Gln	Ala	Glu	Glu	Arg	Arg	Glu
			115					120					125			
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5 Arg Asp Trp Leu Lys Gly His Leu Asp Ala Leu Arg Ala Gln Gly Met  
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10 Pro Ile Val Ala Ile Asp Tyr Leu Pro Pro Glu Arg Arg Asp Glu Ala  
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 Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr  
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 Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala  
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 Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu  
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 Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu  
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 Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His  
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 Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg  
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 Lys Leu Leu Asn Gly Thr Trp Ser Lys His Pro Leu Lys Ser Val Thr  
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 Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr  
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 Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys  
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 Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro  
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Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr  
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5 Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser  
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10 Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly  
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40 Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp  
 35 40 45

45 Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
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50 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly  
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 Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val  
 275 280 285

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

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 Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala  
 340 345 350

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 Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
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75  
 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser  
 370 375 380

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Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg  
 385 390 395 400  
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 Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu  
 405 410 415  
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 Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
 420 425 430  
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 Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly  
 435 440 445  
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 Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile  
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 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp  
 35 40 45  
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 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
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 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
 65 70 75 80  
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 Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly  
 85 90 95  
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 Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
 100 105 110

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Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn  
115 120 125

5 Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp  
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10 Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr  
145 150 155 160

15 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg  
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190

20 Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205

25 Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr  
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240

30 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala  
245 250 255

35 Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

40 Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val  
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
290 295 300

45 Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys  
305 310 315 320

50 His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala  
340 345 350

55 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr

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	355					360					365					
5	Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Ser	Val	Pro	Ala	Met	Lys	Ala
		370					375					380				
10	Lys	Ile	Asp	Pro	Ile	Leu	Glu	Ala	Arg	Gln	Asn	Phe	Ala	Tyr	Gly	Thr
	385					390					395					400
15	Gln	His	Asp	Tyr	Phe	Asp	His	His	Asn	Ile	Ile	Gly	Trp	Thr	Arg	Glu
					405					410					415	
20	Gly	Asn	Thr	Thr	His	Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asp
				420					425					430		
25	Gly	Pro	Gly	Gly	Glu	Lys	Trp	Met	Tyr	Val	Gly	Gln	Asn	Lys	Ala	Gly
			435					440					445			
30	Gln	Val	Trp	His	Asp	Ile	Thr	Gly	Asn	Lys	Pro	Gly	Thr	Val	Thr	Ile
		450					455					460				
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<211> 484

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<213> Bacillus sp.

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5	Leu	Pro	Asn	Asp	Gly	Asn	His	Trp	Asn	Arg	Leu	Asn	Ser	Asp	Ala	Ser
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10	Asn	Leu	Lys	Ser	Lys	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Trp
			35					40					45			
15	Lys	Gly	Ala	Ser	Gln	Asn	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr
		50					55					60				
20	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly
	65					70					75					80
25	Thr	Arg	Ser	Gln	Leu	Gln	Ala	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly
30																
35																
40																
45																
50																
55																

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5	Ile	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp
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10	Ala	Thr	Glu	Met	Val	Arg	Ala	Val	Glu	Val	Asn	Pro	Asn	Asn	Arg	Asn
			115					120					125			
15	Gln	Glu	Val	Thr	Gly	Glu	Tyr	Thr	Ile	Glu	Ala	Trp	Thr	Arg	Phe	Asp
		130					135					140				
20	Phe	Pro	Gly	Arg	Gly	Asn	Thr	His	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr
	145					150					155					160
25	His	Phe	Asp	Gly	Val	Asp	Trp	Asp	Gln	Ser	Arg	Arg	Leu	Asn	Asn	Arg
				165						170					175	
30	Ile	Tyr	Lys	Phe	Arg	Gly	His	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp
				180					185					190		
35	Thr	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Met
			195					200					205			
40	Asp	His	Pro	Glu	Val	Val	Asn	Glu	Leu	Arg	Asn	Trp	Gly	Val	Trp	Tyr
		210					215					220				
45	Thr	Asn	Thr	Leu	Gly	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His
	225					230					235					240
50	Ile	Lys	Tyr	Ser	Phe	Thr	Arg	Asp	Trp	Ile	Asn	His	Val	Arg	Ser	Ala
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55	Thr	Gly	Lys	Asn	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu
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60	Gly	Ala	Ile	Glu	Asn	Tyr	Leu	Gln	Lys	Thr	Asn	Trp	Asn	His	Ser	Val
			275					280					285			
65	Phe	Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Lys	Ser	Gly
		290					295					300				
70	Gly	Asn	Tyr	Asp	Met	Arg	Asn	Ile	Phe	Asn	Gly	Thr	Val	Val	Gln	Arg
	305					310					315					320
75	His	Pro	Ser	His	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Ser	Gln	Pro
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Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala  
 340 345 350  
 5 Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
 355 360 365  
 10 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser  
 370 375 380  
 15 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys  
 385 390 395 400  
 20 Gln Asn Asp Tyr Leu Asp His His Asn Ile Gly Trp Thr Arg Glu Gly  
 405 410 415  
 25 Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp Gly  
 420 425 430  
 30 Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly Gln  
 435 440 445  
 35 Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile Asn  
 450 455 460  
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 Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp  
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Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr  
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 5 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met  
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 10 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly  
 100 105 110  
 15 Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln  
 115 120 125  
 20 Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe  
 130 135 140  
 25 Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His  
 145 150 155 160  
 30 Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr  
 165 170 175  
 35 Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu  
 180 185 190  
 40 Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His  
 195 200 205  
 45 Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn  
 210 215 220  
 50 Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys  
 225 230 235 240  
 55 Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly  
 245 250 255  
 60 Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys  
 260 265 270  
 65 Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Thr Met Ser Leu Phe Asp  
 275 280 285  
 70 Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala  
 290 295 300  
 75 Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro  
 305 310 315 320

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Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln  
 325 330 335  
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 Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala  
 340 345 350  
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 Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp  
 355 360 365  
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 Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile  
 370 375 380  
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 Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His  
 385 390 395 400  
 25  
 Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val  
 405 410 415  
 30  
 Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro  
 420 425 430  
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 Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val  
 435 440 445  
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 Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser  
 450 455 460  
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 Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp  
 465 470 475 480  
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 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr  
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Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn  
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 5 Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys  
 35 40 45  
 10 Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp  
 50 55 60  
 15 Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr  
 65 70 75 80  
 20 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met  
 85 90 95  
 25 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly  
 100 105 110  
 30 Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln  
 115 120 125  
 35 Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe  
 130 135 140  
 40 Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His  
 145 150 155 160  
 45 Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr  
 165 170 175  
 50 Lys Phe Arg Gly Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Asn  
 180 185 190  
 55 Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His Pro  
 195 200 205  
 60 Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn Thr  
 210 215 220  
 65 Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe  
 225 230 235 240  
 70 Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly Lys  
 245 250 255  
 75 Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys Leu  
 260 265 270

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His Asn Tyr Ile Thr Lys Thr Asn Gly Thr Met Ser Leu Phe Asp Ala  
 275 280 285  
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 Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala Phe  
 290 295 300  
 10  
 Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro Thr  
 305 310 315 320  
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 Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln Ala  
 325 330 335  
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 Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe  
 340 345 350  
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 Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr  
 355 360 365  
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 Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile Asp  
 370 375 380  
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 Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His Asp  
 385 390 395 400  
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 Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val Thr  
 405 410 415  
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 Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly  
 420 425 430  
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 Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val Phe  
 435 440 445  
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 Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser Asp  
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 Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp Val  
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 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser  
 20 25 30  
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 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Ala Trp  
 35 40 45  
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 Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
 50 55 60  
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 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
 65 70 75 80  
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 Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly  
 85 90 95  
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 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
 100 105 110  
 35  
 Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn  
 115 120 125  
 40  
 Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp  
 130 135 140  
 45  
 Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr  
 145 150 155 160  
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 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg  
 165 170 175  
 55  
 Ile Tyr Lys Phe Arg Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu  
 180 185 190  
 Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met Asp His  
 195 200 205  
 Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr Thr Asn  
 210 215 220  
 Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His Ile Lys  
 225 230 235 240

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Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala Thr Gly  
 245 250 255  
 5 Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu Gly Ala  
 260 265 270  
 10 Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val Phe Asp  
 275 280 285  
 15 Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly Gly Asn  
 290 295 300  
 20 Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg His Pro  
 305 310 315 320  
 25 Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro Glu Glu  
 325 330 335  
 30 Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala Tyr Ala  
 340 345 350  
 35 Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr Gly Asp  
 355 360 365  
 40 Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser Lys Ile  
 370 375 380  
 45 Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Pro Gln His  
 385 390 395 400  
 50 Asp Tyr Leu Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp  
 405 410 415  
 55 Ser Ser His Pro Lys Ser Gly Leu Ala Thr Leu Ile Thr Asp Gly Pro  
 420 425 430  
 60 Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr  
 435 440 445  
 65 Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser  
 450 455 460  
 70 Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr  
 465 470 475 480  
 75 Val Gln Lys

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<400> 9

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15	Asn	Val	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Gly
			35					40					45			
20	Ser	Ser	Ala	Asp	Val	Gly	Tyr	Gly	Val	Tyr	Asp	Thr	Tyr	Asp	Leu	Gly
		50					55					60				
	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser
25	65					70					75					80
	Glu	Leu	Ile	Ser	Ala	Val	Asn	Asn	Leu	His	Ala	Lys	Gly	Ile	Ala	Val
					85					90					95	
30	Tyr	Gly	Asp	Val	Val	Leu	Asn	His	Arg	Met	Asn	Ala	Asp	Ala	Thr	Glu
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	Leu	Val	Asp	Ala	Val	Glu	Val	Asp	Pro	Asn	Asn	Arg	Asn	Val	Glu	Thr
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	Thr	Ser	Thr	Tyr	Gln	Ile	Gln	Ala	Trp	Thr	Gln	Tyr	Asp	Phe	Pro	Gly
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	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr	His	Phe	Asp
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45	Gly	Val	Asp	Trp	Asp	Gln	Ser	Arg	Gly	Leu	Asn	Arg	Ile	Tyr	Lys	Leu
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	Arg	Gly	Asp	Gly	Lys	Asp	Trp	Asp	Trp	Glu	Val	Asp	Ser	Glu	Tyr	Gly
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	Asn	Tyr	Asp	Tyr	Leu	Met	Gly	Ala	Asp	Leu	Asp	Phe	Asn	His	Pro	Asp
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	Val	Val	Asn	Glu	Thr	Lys	Thr	Trp	Gly	Lys	Trp	Phe	Val	Asn	Thr	Val

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	210		215		220											
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10	Phe	Met	Arg	Asp	Trp 245	Val	Asn	Asn	Val	Arg 250	Ser	Thr	Thr	Gly	Lys 255	Asn
15	Leu	Phe	Ala	Val 260	Gly	Glu	Tyr	Trp	His 265	Tyr	Asp	Val	Asn	Lys 270	Leu	Asn
20	Ser	Tyr	Ile	Thr	Lys	Thr	Asn	Gly 280	Thr	Met	Ser	Leu	Phe	Asp 285	Val	Pro
25	Leu	His 290	Phe	Arg	Phe	Tyr	Asp 295	Ala	Ser	Asn	Gly	Gly 300	Gly	Gly	Tyr	Asp
30	Met	Arg	Asn	Leu	Leu	Asn 310	Asn	Thr	Leu	Met	Ser 315	Ser	Asn	Pro	Met	Lys 320
35	Ala	Val	Thr	Phe	Val 325	Glu	Asn	His	Asp	Thr 330	Gln	Pro	Thr	Gln	Ala	Leu 335
40	Gln	Ser	Thr	Val 340	Gln	Ser	Trp	Phe	Lys 345	Pro	Leu	Ala	Tyr	Ala 350	Thr	Ile
45	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Cys 360	Val	Phe	Tyr	Gly 365	Asp	Tyr	Tyr
50	Gly	Thr	Ser	Asp	Gly	Lys	Ile 375	Ser	Ser	Tyr	Lys	Pro 380	Ile	Met	Asp	Lys
55	Leu	Leu	Asn	Ala	Arg	Lys 390	Val	Tyr	Ala	Tyr	Gly 395	Thr	Gln	Arg	Asp	Tyr 400
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65	His	Ala	Gly	Ser	Gly 420	Leu	Ala	Thr	Leu	Ile 425	Thr	Asp	Gly	Pro 430	Gly	Gly
70	Ser	Lys	Trp	Met	Tyr	Val	Gly	Thr 440	Ser	Lys	Ala	Gly	Gln 445	Val	Trp	Thr
75	Asp	Lys 450	Thr	Gly	Asn	Arg	Ser 455	Gly	Thr	Val	Thr	Ile	Asp 460	Ala	Asn	Gly

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Trp Gly Asn Phe Trp Val Asn Gly Gly Ser Val Ser Val Trp Ala Lys  
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Ser Ser Val Gly Ile Thr Ala Val Trp Thr Pro Pro Ala Tyr Lys Gly  
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Thr Ser Gln Ala Asp Val Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu  
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Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys  
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Gly Glu Leu Lys Ser Ala Val Asn Thr Leu His Ser Asn Gly Ile Gln  
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Val Tyr Gly Asp Val Val Met Asn His Lys Ala Gly Ala Asp Tyr Thr  
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Glu Asn Val Thr Ala Val Glu Val Asn Pro Ser Asn Arg Asn Gln Glu  
 115 120 125

Thr Ser Gly Glu Tyr Asn Ile Gln Ala Trp Thr Gly Phe Asn Phe Pro  
 130 135 140

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Gly Arg Gly Thr Thr Tyr Ser Asn Phe Lys Trp Gln Trp Phe His Phe  
 145 150 155 160

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Asp Gly Thr Asp Trp Asp Gln Ser Arg Ser Leu Ser Arg Ile Phe Lys  
 165 170 175

Phe Thr Gly Lys Ala Trp Asp Trp Pro Val Ser Ser Glu Asn Gly Asn  
 180 185 190

55

Tyr Asp Tyr Leu Met Tyr Ala Asp Tyr Asp Tyr Asp His Pro Asp Val  
 195 200 205

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Val Asn Glu Met Lys Lys Trp Gly Val Trp Tyr Ala Asn Glu Val Gly  
 210 215 220

5 Leu Asp Gly Tyr Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe  
 225 230 235 240

10 Leu Lys Asp Trp Val Asp Asn Ala Arg Ala Ala Thr Gly Lys Glu Met  
 245 250 255

15 Phe Thr Val Gly Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Asn Asn  
 260 265 270

20 Tyr Leu Ala Lys Val Asn Tyr Asn Gln Ser Leu Phe Asp Ala Pro Leu  
 275 280 285

25 His Tyr Asn Phe Tyr Ala Ala Ser Thr Gly Gly Gly Tyr Tyr Asp Met  
 290 295 300

30 Arg Asn Ile Leu Asn Asn Thr Leu Val Ala Ser Asn Pro Thr Lys Ala  
 305 310 315 320

35 Val Thr Leu Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu  
 325 330 335

40 Ser Thr Val Gln Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu  
 340 345 350

45 Thr Arg Ser Gly Gly Tyr Pro Ser Val Phe Tyr Gly Asp Met Tyr Gly  
 355 360 365

50 Thr Lys Gly Thr Thr Thr Arg Glu Ile Pro Ala Leu Lys Ser Lys Ile  
 370 375 380

55 Glu Pro Leu Leu Lys Ala Arg Lys Asp Tyr Ala Tyr Gly Thr Gln Arg  
 385 390 395 400

Asp Tyr Ile Asp Asn Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp  
 405 410 415

Ser Thr Lys Ala Lys Ser Gly Leu Ala Thr Val Ile Thr Asp Gly Pro  
 420 425 430

Gly Gly Ser Lys Arg Met Tyr Val Gly Thr Ser Asn Ala Gly Glu Ile  
 435 440 445

Trp Tyr Asp Leu Thr Gly Asn Asn Ser Thr Lys Ile Thr Ile Gly Ser  
 450 455 460

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Asp Gly Tyr Ala Thr Phe Pro Val Asn Lys Gly Ser Val Ser Val Trp  
 465 470 475 480

5 Val Gln Gln

<210> 11

<211> 618

<212> PRT

10 <213> Bacillus subtilis

<400> 11

15 Leu Thr Ala Pro Ser Ile Lys Ser Gly Thr Ile Leu His Ala Trp Asn  
 1 5 10 15

20 Trp Ser Phe Asn Thr Leu Lys His Asn Met Lys Asp Ile His Asp Ala  
 20 25 30

25 Gly Tyr Thr Ala Ile Gln Thr Ser Pro Ile Asn Gln Val Lys Glu Gly  
 35 40 45

30 Asn Gln Gly Asp Lys Ser Met Ser Asn Trp Tyr Trp Leu Tyr Gln Pro  
 50 55 60

35 Thr Ser Tyr Gln Ile Gly Asn Arg Tyr Leu Gly Thr Glu Gln Glu Phe  
 65 70 75 80

40 Lys Glu Met Cys Ala Ala Ala Glu Glu Tyr Gly Ile Lys Val Ile Val  
 85 90 95

45 Asp Ala Val Ile Asn His Thr Thr Ser Asp Tyr Ala Ala Ile Ser Asn  
 100 105 110

50 Glu Val Lys Ser Ile Pro Asn Trp Thr His Gly Asn Thr Gln Ile Lys  
 115 120 125

55 Asn Trp Ser Asp Arg Trp Asp Val Thr Gln Asn Ser Leu Leu Gly Leu  
 130 135 140

60 Tyr Asp Trp Asn Thr Gln Asn Thr Gln Val Gln Ser Tyr Leu Lys Arg  
 145 150 155 160

65 Phe Leu Asp Arg Ala Leu Asn Asp Gly Ala Asp Gly Phe Arg Phe Asp  
 165 170 175

70 Ala Ala Lys His Ile Glu Leu Pro Asp Asp Gly Ser Tyr Gly Ser Gln  
 180 185 190

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Phe Trp Pro Asn Ile Thr Asn Thr Ser Ala Glu Phe Gln Tyr Gly Glu  
 195 200 205  
 5  
 Ile Leu Gln Asp Ser Ala Ser Arg Asp Ala Ala Tyr Ala Asn Tyr Met  
 210 215 220  
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 Asp Val Thr Ala Ser Asn Tyr Gly His Ser Ile Arg Ser Ala Leu Lys  
 225 230 235 240  
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 Asn Arg Asn Leu Gly Val Ser Asn Ile Ser His Tyr Ala Ser Asp Val  
 245 250 255  
 20  
 Ser Ala Asp Lys Leu Val Thr Trp Val Glu Ser His Asp Thr Tyr Ala  
 260 265 270  
 25  
 Asn Asp Asp Glu Glu Ser Thr Trp Met Ser Asp Asp Asp Ile Arg Leu  
 275 280 285  
 Gly Trp Ala Val Ile Ala Ser Arg Ser Gly Ser Thr Pro Leu Phe Phe  
 290 295 300  
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 Ser Arg Pro Glu Gly Gly Gly Asn Gly Val Arg Phe Pro Gly Lys Ser  
 305 310 315 320  
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 Gln Ile Gly Asp Arg Gly Ser Ala Leu Phe Glu Asp Gln Ala Ile Thr  
 325 330 335  
 Ala Val Asn Arg Phe His Asn Val Met Ala Gly Gln Pro Glu Glu Leu  
 340 345 350  
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 Ser Asn Pro Asn Gly Asn Asn Gln Ile Phe Met Asn Gln Arg Gly Ser  
 355 360 365  
 45  
 His Gly Val Val Leu Ala Asn Ala Gly Ser Ser Ser Val Ser Ile Asn  
 370 375 380  
 50  
 Thr Ala Thr Lys Leu Pro Asp Gly Arg Tyr Asp Asn Lys Ala Gly Ala  
 385 390 395 400  
 Gly Ser Phe Gln Val Asn Asp Gly Lys Leu Thr Gly Thr Ile Asn Ala  
 405 410 415  
 55  
 Arg Ser Val Ala Val Leu Tyr Pro Asp Asp Ile Ala Lys Ala Pro His  
 420 425 430  
 Val Phe Leu Glu Asn Tyr Lys Thr Gly Val Thr His Ser Phe Asn Asp  
 435 440 445



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Gln Leu Thr Ile Thr Leu Arg Ala Asp Ala Asn Thr Thr Lys Ala Val  
450 455 460

5 Tyr Gln Ile Asn Asn Gly Pro Glu Thr Ala Phe Lys Asp Gly Asp Gln  
465 470 475 480

10 Phe Thr Ile Gly Lys Gly Asp Pro Phe Gly Lys Thr Tyr Thr Ile Met  
485 490 495

15 Leu Lys Gly Thr Asn Ser Asp Gly Val Thr Arg Thr Glu Lys Tyr Ser  
500 505 510

Phe Val Lys Arg Asp Pro Ala Ser Ala Lys Thr Ile Gly Tyr Gln Asn  
515 520 525

20 Pro Asn His Trp Ser Gln Val Asn Ala Tyr Ile Tyr Lys His Asp Gly  
530 535 540

25 Ser Arg Val Ile Glu Leu Thr Gly Ser Trp Pro Gly Lys Pro Met Thr  
545 550 555 560

Lys Asn Ala Asp Gly Ile Tyr Thr Leu Thr Leu Pro Ala Asp Thr Asp  
565 570 575

30 Thr Thr Asn Ala Lys Val Ile Phe Asn Asn Gly Ser Ala Gln Val Pro  
580 585 590

35 Gly Gln Asn Gln Pro Gly Phe Asp Tyr Val Leu Asn Gly Leu Tyr Asn  
595 600 605

40 Asp Ser Gly Leu Ser Gly Ser Leu Pro His  
610 615

<210> 12  
<211> 480  
<212> PRT  
45 <213> Bacillus sp.

<400> 12

50 Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu  
1 5 10 15

Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu  
20 25 30

55 Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly  
35 40 45

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Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu  
50 55 60

5 Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys  
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn  
10 85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr  
100 105 110

15 Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp  
115 120 125

20 Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser  
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe  
25 145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg  
165 170 175

30 Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn  
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val  
35 195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp  
40 210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr  
225 230 235 240

45 Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu  
245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe  
50 260 265 270

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

55 Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met

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	290		295		300												
5	Arg 305	Asn	Ile	Leu	Arg	Gly 310	Ser	Leu	Val	Glu	Ala 315	His	Pro	Met	His	Ala 320	
10	Val	Thr	Phe	Val	Asp 325	Asn	His	Asp	Thr	Gln 330	Pro	Gly	Glu	Ser	Leu 335	Glu	
15	Ser	Trp	Val	Ala 340	Asp	Trp	Phe	Lys	Pro 345	Leu	Ala	Tyr	Ala	Thr	Ile	Leu	
20	Thr	Arg	Glu 355	Gly	Gly	Tyr	Pro	Asn 360	Val	Phe	Tyr	Gly	Asp 365	Tyr	Tyr	Gly	
25	Ile	Pro 370	Asn	Asp	Asn	Ile	Ser 375	Ala	Lys	Lys	Asp	Met 380	Ile	Asp	Glu	Leu	
30	Leu 385	Asp	Ala	Arg	Gln	Asn 390	Tyr	Ala	Tyr	Gly	Thr 395	Gln	His	Asp	Tyr	Phe 400	
35	Asp	His	Trp	Asp	Val 405	Val	Gly	Trp	Thr	Arg 410	Glu	Gly	Ser	Ser	Ser	Arg 415	
40	Pro	Asn	Ser	Gly 420	Leu	Ala	Thr	Ile	Met 425	Ser	Asn	Gly	Pro	Gly 430	Gly	Ser	
45	Lys	Trp	Met 435	Tyr	Val	Gly	Arg	Gln 440	Asn	Ala	Gly	Gln	Thr 445	Trp	Thr	Asp	
50	Leu	Thr 450	Gly	Asn	Asn	Gly	Ala 455	Ser	Val	Thr	Ile	Asn 460	Gly	Asp	Gly	Trp	
55	Gly 465	Glu	Phe	Phe	Thr	Asn 470	Gly	Gly	Ser	Val	Ser 475	Val	Tyr	Val	Asn	Gln 480	

<210> 13  
 <211> 412  
 <212> PRT  
 <213> Pseudomonas aeruginosa

<400> 13

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Glu Ile Gln Val Leu Lys Ala Pro Arg Ala Val Val Trp Lys Asp Phe  
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5           Leu Gly Val Asn Ala Gln Phe Leu Trp Phe Ser Pro Glu Arg Tyr Asn  
                  20                   25                   30

10           Lys Gln Ile Asp Arg Leu Gln Asp Leu Gly Leu Glu Trp Val Arg Leu

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

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Phe Thr Leu Ser Asp Leu Asp Gln Arg Ala Ser Val Arg Asp Arg Asp  
 290 295 300

5

Tyr Gly Leu Leu Asp Leu Asp Ala Asn Pro Lys Pro Val Tyr Leu Ala  
 305 310 315 320

10

Leu Gln Arg Phe Leu Lys Val Thr Gly Pro Lys Leu Arg Pro Ala Asp  
 325 330 335

15

Pro Pro Val Thr Glu Asp Leu Pro Asp Gly Ser Phe Ser Ile Gly Trp  
 340 345 350

20

Thr Arg Glu Asp Gly Arg Asn Val Trp Leu Phe Trp Ser Ala Arg Gly  
 355 360 365

25

Gly Asn Val Arg Leu Pro Lys Leu Lys Glu Ala Thr Leu His Asp Pro  
 370 375 380

Leu Ser Gly Lys Val Thr Pro Leu Ser Gly Ser Asp Gly Leu Glu Val  
 385 390 395 400

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Pro Val Lys Ser Ser Leu Gln Met Leu Val Trp Glu  
 405 410

<210> 14  
 <211> 109  
 <212> PRT  
 <213> Bacillus licheniformis

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<400> 14

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Ala Arg Tyr Asp Asp Val Leu Tyr Phe Pro Ala Ser Arg Tyr Pro Glu  
 1 5 10 15

45

Thr Gly Ala His Ile Ser Asp Ala Ile Lys Ala Gly His Ala Asp Val  
 20 25 30

50

Cys Thr Ile Glu Arg Ser Gly Ala Asp Lys Arg Arg Gln Glu Ser Leu  
 35 40 45

55

Lys Gly Ile Pro Thr Lys Pro Gly Phe Asp Arg Asp Glu Trp Pro Met  
 50 55 60

Ala Met Cys Glu Glu Gly Gly Lys Gly Ala Ser Val Arg Tyr Val Ser  
 65 70 75 80

Ser Ser Asp Asn Arg Gly Ala Gly Ser Trp Val Gly Asn Arg Leu Asn  
 85 90 95

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Gly Tyr Ala Asp Gly Thr Arg Ile Leu Phe Ile Val Gln  
 100 105

5 <210> 15  
 <211> 109  
 <212> PRT  
 <213> Bacillus subtilis

10 <400> 15

Ala Ser Ser Tyr Asp Lys Val Leu Tyr Phe Pro Leu Ser Arg Tyr Pro  
 1 5 10 15

15 Glu Thr Gly Ser His Ile Arg Asp Ala Ile Ala Glu Gly His Pro Asp  
 20 25 30

20 Ile Cys Thr Ile Asp Asp Gly Ala Asp Lys Arg Arg Glu Glu Ser Leu  
 35 40 45

25 Lys Gly Ile Pro Thr Lys Pro Gly Tyr Asp Arg Asp Glu Trp Pro Met  
 50 55 60

Ala Val Cys Glu Glu Gly Gly Ala Gly Ala Asp Val Arg Tyr Val Thr  
 65 70 75 80

30 Pro Ser Asp Asn Arg Gly Ala Gly Ser Trp Val Gly Asn Gln Met Ser  
 85 90 95

35 Ser Tyr Pro Asp Gly Thr Arg Val Leu Phe Ile Val Gln  
 100 105

40 <210> 16  
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 <212> PRT  
 <213> Bacillus licheniformis

<400> 16

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Ala Arg Tyr Asp Asp Ile Leu Tyr Phe Pro Ala Ser Arg Tyr Pro Glu  
 1 5 10 15

5 Thr Gly Ala His Ile Ser Asp Ala Ile Lys Ala Gly His Ser Asp Val  
 20 25 30

10 Cys Thr Ile Glu Arg Ser Gly Ala Asp Lys Arg Arg Gln Glu Ser Leu  
 35 40 45

15 Lys Gly Ile Pro Thr Lys Pro Gly Phe Asp Arg Asp Glu Trp Pro Met  
 50 55 60

Ala Met Cys Glu Glu Gly Gly Lys Gly Ala Ser Val Arg Tyr Val Ser  
 65 70 75 80

20 Ser Ser Asp Asn Arg Gly Ala Gly Ser Trp Val Gly Asn Arg Leu Ser  
 85 90 95

25 Gly Phe Ala Asp Gly Thr Arg Ile Leu Phe Ile Val Gln  
 100 105

30 <210> 17  
 <211> 204  
 <212> PRT  
 <213> Aspergillus oryzae

35 <400> 17

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1 Lys Thr Gly Ser Gly Asp Ser Gln Ser Asp Pro Ile Lys Ala Asp Leu  
 5 5 10 15  
 5 Glu Val Lys Gly Gln Ser Ala Leu Pro Phe Asp Val Asp Cys Trp Ala  
 20 25 30  
 10 Ile Leu Cys Lys Gly Ala Pro Asn Val Leu Gln Arg Val Asn Glu Lys  
 35 40 45  
 15 Thr Lys Asn Ser Asn Arg Asp Arg Ser Gly Ala Asn Lys Gly Pro Phe  
 50 55 60  
 20 Lys Asp Pro Gln Lys Trp Gly Ile Lys Ala Leu Pro Pro Lys Asn Pro  
 65 70 75 80  
 25 Ser Trp Ser Ala Gln Asp Phe Lys Ser Pro Glu Glu Tyr Ala Phe Ala  
 85 90 95  
 30 Ser Ser Leu Gln Gly Gly Thr Asn Ala Ile Leu Ala Pro Val Asn Leu  
 100 105 110  
 35 Ala Ser Gln Asn Ser Gln Gly Gly Val Leu Asn Gly Phe Tyr Ser Ala  
 115 120 125  
 40 Asn Lys Val Ala Gln Phe Asp Pro Ser Lys Pro Gln Gln Thr Lys Gly  
 130 135 140  
 45 Thr Trp Phe Gln Ile Thr Lys Phe Thr Gly Ala Ala Gly Pro Tyr Cys  
 145 150 155 160  
 50 Lys Ala Leu Gly Ser Asn Asp Lys Ser Val Cys Asp Lys Asn Lys Asn  
 165 170 175  
 55 Ile Ala Gly Asp Trp Gly Phe Asp Pro Ala Lys Trp Ala Tyr Gln Tyr  
 180 185 190  
 Asp Glu Lys Asn Asn Lys Phe Asn Tyr Val Gly Lys  
 195 200

<210> 18

<211> 188

<212> PRT

<213> Trichoderma harzianum

<400> 18

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Ala Pro Ala Pro Met Pro Thr Pro Pro Gly Ile Pro Thr Glu Ser Ser  
 1 5 10 15

5 Ala Arg Thr Gln Leu Ala Gly Leu Thr Val Ala Val Ala Gly Ser Gly  
 20 25 30

10 Thr Gly Tyr Ser Arg Asp Leu Phe Pro Thr Trp Asp Ala Ile Ser Gly  
 35 40 45

15 Asn Cys Asn Ala Arg Glu Tyr Val Leu Lys Arg Asp Gly Glu Gly Val  
 50 55 60

Gln Val Asn Asn Ala Cys Glu Ser Gln Ser Gly Thr Trp Ile Ser Pro  
 65 70 75 80

20 Tyr Asp Asn Ala Ser Phe Thr Asn Ala Ser Ser Leu Asp Ile Asp His  
 85 90 95

25 Met Val Pro Leu Lys Asn Ala Trp Ile Ser Gly Ala Ser Ser Trp Thr  
 100 105 110

30 Thr Ala Gln Arg Glu Ala Leu Ala Asn Asp Val Ser Arg Pro Gln Leu  
 115 120 125

Trp Ala Val Ser Ala Ser Ala Asn Arg Ser Lys Gly Asp Arg Ser Pro  
 130 135 140

35 Asp Gln Trp Lys Pro Pro Leu Thr Ser Phe Tyr Cys Thr Tyr Ala Lys  
 145 150 155 160

40 Ser Trp Ile Asp Val Lys Ser Phe Tyr Lys Leu Thr Ile Thr Ser Ala  
 165 170 175

Glu Lys Thr Ala Leu Ser Ser Met Leu Asp Thr Cys  
 180 185

45 <210> 19  
 <211> 458  
 <212> PRT  
 <213> Trichoderma harzianum

50 <400> 19

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Asp Thr Thr Leu Ser Ile Asp Pro Thr Ser Asn Trp Gly Thr Trp Glu  
 1 5 10 15  
 Gly Trp Gly Val Ser Leu Ala Trp Trp Ala Lys Ala Phe Gly Asn Arg  
 5 20 25 30  
 Asp Asp Leu Ala Asn Val Phe Phe Thr Arg Asn Asn Gln Val Ile Asn  
 10 35 40 45  
 Gly Gln Asn Leu Pro Gly Leu Gly Phe Asn Ile Ala Arg Tyr Asn Ala  
 15 50 55 60  
 Gly Ala Cys Ser Thr Asn Thr Tyr Asn Gly Ser Ser Met Val Val Ser  
 65 70 75 80  
 Ser Ser Ile Lys Pro Ser Arg Gln Val Asp Gly Tyr Trp Leu Asp Trp  
 20 85 90 95  
 Ala Ser Thr Asp Pro Ala Ser Ser Ser Trp Asn Trp Asn Val Asp Ala  
 25 100 105 110  
 Asn Gln Arg Ala Met Leu Gln Lys Ala Lys Ala Asn Gly Ala Asn Ile  
 30 115 120 125  
 Phe Glu Leu Phe Ser Asn Ser Pro Met Trp Trp Met Cys Leu Asn His  
 130 135 140  
 Asn Pro Ser Gly Ser Gly Ser Ser Asp Asn Leu Gln Ser Trp Asn Tyr  
 35 145 150 155 160  
 Gln Asn His Ala Val Tyr Leu Ala Asn Ile Ala Gln His Ala Gln Gln  
 40 165 170 175  
 Asn Trp Gly Ile Gln Phe Gln Ser Val Glu Ala Phe Asn Glu Pro Ser  
 180 185 190  
 Ser Gly Trp Gly Pro Thr Gly Thr Gln Glu Gly Cys His Phe Ala Val  
 195 200 205  
 Ser Thr Met Ala Thr Val Ile Gly Tyr Leu Asn Thr Glu Leu Ala Gln  
 210 215 220  
 Arg Gly Leu Ser Ser Phe Ile Ser Ala Ser Asp Glu Thr Ser Tyr Asp  
 55

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	225					230						235				240
5	Leu	Ala	Ile	Ser	Thr	Trp	Gln	Gly	Leu	Gly	Ser	Ser	Ala	Gln	Asn	Ala
					245					250					255	
10	Val	Lys	Arg	Val	Asn	Val	His	Gly	Tyr	Gln	Gly	Gly	Gly	Gly	Arg	Arg
				260					265					270		
15	Asp	Thr	Leu	Tyr	Ser	Leu	Val	Ser	Gln	Ala	Gly	Lys	Arg	Leu	Trp	Asn
			275					280					285			
20	Ser	Glu	Tyr	Gly	Asp	Ala	Asp	Ala	Ser	Gly	Lys	Ser	Met	Tyr	Thr	Asn
		290					295					300				
25	Leu	Leu	Leu	Asp	Phe	Thr	Trp	Leu	His	Pro	Thr	Ala	Trp	Val	Tyr	Trp
	305					310					315					320
30	Gln	Ala	Ile	Asp	Gly	Ser	Gly	Trp	Gly	Leu	Ile	Val	Gly	Asp	Asn	Asp
				325						330					335	
35	Gln	Leu	Thr	Leu	Ser	Ser	Ala	Ser	Thr	Lys	Tyr	Phe	Val	Leu	Ala	Gln
			340						345					350		
40	Leu	Thr	Arg	His	Ile	Arg	Pro	Gly	Met	Gln	Ile	Leu	Thr	Thr	Pro	Asp
			355					360					365			
45	Gly	Asn	Thr	Val	Ala	Ala	Tyr	Asp	Ser	Gly	Ser	Gln	Lys	Leu	Val	Ile
		370					375					380				
50	Val	Ala	Ala	Asn	Trp	Gly	Ser	Ala	Gln	Thr	Ile	Thr	Phe	Asp	Leu	Thr
	385					390					395					400
55	Arg	Ala	Lys	Thr	Ala	Gly	Ser	Asn	Gly	Ala	Thr	Val	Pro	Arg	Trp	Ser
				405						410					415	
60	Thr	Gln	Thr	Ser	Gly	Gly	Asp	Gln	Tyr	Lys	Ser	Tyr	Ser	Asp	Thr	Lys
				420					425					430		
65	Ile	Asn	Asn	Gly	Lys	Phe	Ser	Val	Ser	Phe	Ser	Thr	Gly	Gln	Val	Gln
			435					440					445			
70	Thr	Phe	Glu	Ile	Ser	Gly	Val	Val	Leu	Lys						
	450						455									

<210> 20  
 <211> 463  
 <212> PRT

<213> Streptomyces davawensis

<400> 20

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Asp Ala Thr Ile Val Ile Asn Pro Gly Thr Arg Tyr Gly Thr Trp Glu  
 1 5 10 15  
 Gly Trp Gly Thr Ser Leu Ala Trp Trp Gly Asn Val Phe Gly Thr Arg  
 5 20 25 30  
 Asp Asp Phe Ala Asp Leu Phe Phe Thr Thr Lys Ser Val Thr Tyr Asn  
 10 35 40 45  
 Gly Thr Ser Leu Pro Gly Leu Gly Leu Asn Ile Ala Arg Tyr Asn Leu  
 15 50 55 60  
 Gly Ala Cys Ser Trp Asn Ala Val Asn Gly Glu Thr Met Val Lys Ser  
 65 70 75 80  
 Pro Asn Ile Pro Ala Phe Lys Gln Ile Glu Gly Phe Trp Gln Asp Trp  
 20 85 90 95  
 Asn Asn Glu Asp Pro Thr Ser Ser Ala Trp Asp Trp Thr Ala Asp Ala  
 25 100 105 110  
 Thr Gln Arg Ala Met Leu Val Lys Ala Thr Gln Arg Gly Ala Val Thr  
 30 115 120 125  
 Glu Leu Phe Ala Asn Ser Pro Met Trp Trp Met Cys Tyr Asn His Asn  
 130 135 140  
 Pro Ser Gly Ala Ala Asp Gly Gly Asn Asn Leu Gln Thr Trp Asn Tyr  
 35 145 150 155 160  
 Arg Gln His Ala Ser His Leu Ala Ala Val Ala Leu Tyr Ala Arg Thr  
 40 165 170 175  
 Asn Trp Gly Val Asn Phe Ala Thr Val Asp Pro Phe Asn Glu Pro Ala  
 180 185 190  
 Ser Ser Trp Trp Thr Ala Ser Gly Thr Gln Glu Gly Cys His Leu Asp  
 195 200 205  
 Pro Ala Val Gln Ala Ala Val Leu Pro Tyr Met Arg Ser Glu Leu Asp  
 210 215 220  
 Lys Arg Gly Leu Thr Gly Val Arg Ile Ser Ala Ser Asp Glu Thr Asn  
 225 230 235 240

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Tyr Asp Thr Ala Arg Ser Thr Trp Ser Ser Phe Gly Ser Ala Thr Lys  
 245 250 255  
 5  
 Ala Leu Val Ser Gln Val Asn Val His Gly Tyr Gln Gly Thr Gly Gly  
 260 265 270  
 10  
 Arg Arg Asp Leu Leu Tyr Thr Asp Val Val Thr Thr Ser Gly Lys Lys  
 275 280 285  
 15  
 Leu Trp Asn Ser Glu Thr Gly Asp Ser Asp Gly Thr Gly Leu Ser Met  
 290 295 300  
 20  
 Ala Arg Asn Leu Cys Tyr Asp Phe Arg Trp Leu His Pro Thr Ala Trp  
 305 310 315 320  
 25  
 Cys Tyr Trp Gln Val Met Asp Pro Ser Thr Gly Trp Ala Met Ile Ala  
 325 330 335  
 30  
 Tyr Asp Ala Asn Thr Leu Gln Pro Thr Thr Val Gln Pro Lys Tyr Tyr  
 340 345 350  
 35  
 Val Met Ala Gln Phe Ser Arg His Ile Arg Pro Gly Met Thr Ile Leu  
 355 360 365  
 40  
 Asp Thr Gly Val Ser Phe Ala Ala Ala Tyr Asp Ala Ser Ala Arg  
 370 375 380  
 45  
 Arg Leu Val Leu Val Ala Val Asn Thr Ser Thr Ser Pro Gln Thr Phe  
 385 390 395 400  
 50  
 Thr Phe Asp Leu Ser Arg Phe Thr Thr Val Thr Gly Gly Ser Gly Gly  
 405 410 415  
 55  
 Leu Val Pro Arg Trp Asn Thr Val Thr Gly Gly Gly Asp Met Tyr Arg  
 420 425 430  
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 Ala Tyr Thr Asn Thr Tyr Val Thr Gly Lys Ser Val Ser Ala Thr Phe  
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 Ala Ala Gly Ser Val Gln Thr Leu Gln Val Asp Gly Val Thr Thr  
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<210> 21

<211> 464

55 <212> PRT

<213> Streptomyces avermitilis

<400> 21

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 Gly Trp Gly Thr Ser Leu Ala Trp Trp Ala Asn Val Phe Gly Ala Arg  
 5 20 25 30  
 Asp Asp Phe Ala Asp Leu Phe Phe Thr Thr Lys Ser Val Thr Tyr Asn  
 10 35 40 45  
 Gly Arg Thr Leu Pro Gly Leu Gly Leu Asn Ile Ala Arg Tyr Asn Leu  
 50 55 60  
 Gly Ala Cys Ser Trp Asn Ser Val Ser Gly Glu Ser Met Val Ala Ser  
 15 65 70 75 80  
 Ala Asn Ile Pro Ala Phe Lys Gln Ile Glu Gly Tyr Trp Gln Asp Trp  
 20 85 90 95  
 Asn Asn Glu Asp Pro Thr Ser Ser Ala Trp Lys Trp Thr Ala Asp Ala  
 25 100 105 110  
 Ala Gln Arg Thr Met Leu Val Lys Ala Thr Ala Arg Gly Ala Thr Thr  
 115 120 125  
 Glu Leu Phe Ala Asn Ser Pro Met Trp Trp Met Cys Leu Asn His Asn  
 30 130 135 140  
 Pro Ser Gly Ala Ser Gly Gly Gly Asn Asn Leu Gln Ser Trp Asn Tyr  
 35 145 150 155 160  
 Arg Gln His Ala Ser His Leu Ala Ala Val Ala Leu Tyr Ala Lys Ser  
 165 170 175  
 Asn Trp Gly Val Asn Phe Ala Thr Val Asp Pro Phe Asn Glu Pro Ser  
 180 185 190  
 Ser Ser Trp Trp Thr Ala Thr Gly Thr Gln Glu Gly Cys His Met Asp  
 45 195 200 205  
 Ala Ser Val Gln Ala Ala Val Leu Pro Tyr Leu Arg Ser Glu Leu Asp  
 50 210 215 220  
 Arg Arg Gly Leu Thr Gly Thr Lys Ile Ser Ala Ser Asp Glu Thr Ser  
 225 230 235 240  
 Tyr Asp Leu Ala Arg Thr Thr Trp Gly Ser Phe Gly Ser Ser Thr Lys  
 55 245 250 255



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Ala Leu Val Asn Arg Val Asn Val His Gly Tyr Gln Gly Ser Gly Gly  
 260 265 270

5 Arg Arg Asp Leu Leu Tyr Thr Asp Val Val Thr Thr Ala Gly Lys Ala  
 275 280 285

10 Leu Trp Asn Ser Glu Thr Gly Asp Ser Asp Gly Thr Gly Leu Thr Leu  
 290 295 300

15 Ala Ser Asn Leu Cys Leu Asp Phe Arg Trp Leu His Pro Thr Ala Trp  
 305 310 315 320

20 Val Tyr Trp Gln Val Met Asp Pro Ser Ser Gly Trp Ala Met Ile Ala  
 325 330 335

25 Tyr Asp Ala Ser Thr Leu Gln Pro Gly Ala Val Gln Thr Lys Tyr Tyr  
 340 345 350

Val Met Ala Gln Phe Ser Arg His Ile Arg Ala Gly Met Thr Ile Val  
 355 360 365

30 Asp Thr Gly Val Gly Tyr Ala Ala Ala Ala Tyr Asp Ala Thr Ala Arg  
 370 375 380

Arg Leu Val Ile Val Ala Val Asn Thr Ser Thr Ser Ala Gln Thr Leu  
 385 390 395 400

35 Thr Phe Asp Leu Ser Arg Phe Ser Thr Val Thr Gly Gly Thr Gly Gly  
 405 410 415

40 Leu Val Arg Arg Trp Asn Thr Val Thr Gly Gly Gly Gly Asp Leu Tyr  
 420 425 430

45 Ala Ala His Ser Asp Thr Tyr Leu Ser Gly Lys Ser Leu Ser Val Pro  
 435 440 445

Phe Ala Ala Gly Ala Val Gln Thr Leu Glu Val Asp Gly Val Thr Val  
 450 455 460

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 <211> 458  
 <212> PRT  
 <213> Trichoderma harzianum

<400> 22

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

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Asp Thr Leu Tyr Ser Leu Val Ser Gln Ala Gly Lys Arg Leu Trp Asn  
 275 280 285  
 5 Ser Glu Tyr Gly Asp Ala Asp Ala Ser Gly Lys Ser Met Tyr Thr Asn  
 290 295 300  
 10 Leu Leu Leu Asp Phe Thr Trp Leu His Pro Thr Ala Trp Val Tyr Trp  
 305 310 315 320  
 15 Gln Ala Ile Asp Gly Ser Gly Trp Gly Leu Ile Val Gly Asp Asn Asp  
 325 330 335  
 20 Gln Leu Thr Leu Ser Ser Ala Ser Thr Lys Tyr Phe Val Leu Ala Gln  
 340 345 350  
 25 Leu Thr Arg His Ile Arg Pro Gly Met Gln Ile Leu Thr Thr Pro Asp  
 355 360 365  
 30 Gly Asn Thr Val Ala Ala Tyr Asp Ser Gly Ser Gln Lys Leu Val Ile  
 370 375 380  
 35 Val Ala Ala Asn Trp Gly Ser Ala Gln Thr Ile Thr Phe Asp Leu Thr  
 385 390 395 400  
 40 Arg Ala Lys Thr Ala Gly Ser Asn Gly Ala Thr Val Pro Arg Trp Ser  
 405 410 415  
 45 Thr Gln Thr Ser Gly Gly Asp Gln Tyr Lys Ser Tyr Ser Asp Thr Lys  
 420 425 430  
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 Thr Phe Glu Ile Ser Gly Val Val Leu Lys  
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 <213> Streptomyces davawensis  
 <400> 23  
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EP 3 330 348 B1

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

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		275				280						285				
5	Leu	Trp	Asn	Ser	Glu	Thr	Gly	Asp	Ser	Asp	Gly	Thr	Gly	Leu	Ser	Met
		290					295					300				
10	Ala	Arg	Asn	Leu	Cys	Tyr	Asp	Phe	Arg	Trp	Leu	His	Pro	Thr	Ala	Trp
	305					310					315					320
15	Cys	Tyr	Trp	Gln	Val	Met	Asp	Pro	Ser	Thr	Gly	Trp	Ala	Met	Ile	Ala
					325					330					335	
20	Tyr	Asp	Ala	Asn	Thr	Leu	Gln	Pro	Thr	Thr	Val	Gln	Pro	Lys	Tyr	Tyr
				340					345					350		
25	Val	Met	Ala	Gln	Phe	Ser	Arg	His	Ile	Arg	Pro	Gly	Met	Thr	Ile	Leu
			355					360					365			
30	Asp	Thr	Gly	Val	Ser	Phe	Ala	Ala	Ala	Ala	Tyr	Asp	Ala	Ser	Ala	Arg
		370					375					380				
35	Arg	Leu	Val	Leu	Val	Ala	Val	Asn	Thr	Ser	Thr	Ser	Pro	Gln	Thr	Phe
	385					390					395					400
40	Thr	Phe	Asp	Leu	Ser	Arg	Phe	Thr	Thr	Val	Thr	Gly	Gly	Ser	Gly	Gly
					405					410					415	
45	Leu	Val	Pro	Arg	Trp	Asn	Thr	Val	Thr	Gly	Gly	Gly	Asp	Met	Tyr	Arg
				420					425					430		
50	Ala	Tyr	Thr	Asn	Thr	Tyr	Val	Thr	Gly	Lys	Ser	Val	Ser	Ala	Thr	Phe
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<400> 24

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5 Gly Trp Gly Thr Ser Leu Ala Trp Trp Ala Asn Val Phe Gly Ala Arg  
20 25 30

10 Asp Asp Phe Ala Asp Leu Phe Phe Thr Thr Lys Ser Val Thr Tyr Asn

15

20

25

30

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45

50

55

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

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Leu Trp Asn Ser Glu Thr Gly Asp Ser Asp Gly Thr Gly Leu Thr Leu  
 290 295 300  
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 Ala Ser Asn Leu Cys Leu Asp Phe Arg Trp Leu His Pro Thr Ala Trp  
 305 310 315 320  
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 Val Tyr Trp Gln Val Met Asp Pro Ser Ser Gly Trp Ala Met Ile Ala  
 325 330 335  
 Tyr Asp Ala Ser Thr Leu Gln Pro Gly Ala Val Gln Thr Lys Tyr Tyr  
 340 345 350  
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 Val Met Ala Gln Phe Ser Arg His Ile Arg Ala Gly Met Thr Ile Val  
 355 360 365  
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 Asp Thr Gly Val Gly Tyr Ala Ala Ala Ala Tyr Asp Ala Thr Ala Arg  
 370 375 380  
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 Arg Leu Val Ile Val Ala Val Asn Thr Ser Thr Ser Ala Gln Thr Leu  
 385 390 395 400  
 Thr Phe Asp Leu Ser Arg Phe Ser Thr Val Thr Gly Gly Thr Gly Gly  
 405 410 415  
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 Leu Val Arg Arg Trp Asn Thr Val Thr Gly Gly Gly Gly Asp Leu Tyr  
 420 425 430  
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 Ala Ala His Ser Asp Thr Tyr Leu Ser Gly Lys Ser Leu Ser Val Pro  
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 Phe Ala Ala Gly Ala Val Gln Thr Leu Glu Val Asp Gly Val Thr Val  
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 45 <213> Trichoderma harzianum  
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 Asp Asp Leu Ala Asn Val Phe Phe Thr Arg Asn Asn Gln Val Ile Asn  
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Gly Gln Asn Leu Pro Gly Leu Gly Phe Asn Ile Ala Arg Tyr Asn Ala  
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5 Gly Ala Cys Ser Thr Asn Thr Tyr Asn Gly Ser Ser Met Val Val Ser  
 65 70 75 80

10 Ser Ser Ile Lys Pro Ser Arg Gln Val Asp Gly Tyr Trp Leu Asp Trp  
 85 90 95

15 Ala Ser Thr Asp Pro Ala Ser Ser Ser Trp Asn Trp Asn Val Asp Ala  
 100 105 110

20 Asn Gln Arg Ala Met Leu Gln Lys Ala Lys Ala Asn Gly Ala Asn Ile  
 115 120 125

25 Phe Glu Leu Phe Ser Asn Ser Pro Met Trp Trp Met Cys Leu Asn His  
 130 135 140

30 Asn Pro Ser Gly Ser Gly Ser Ser Asp Asn Leu Gln Ser Trp Asn Tyr  
 145 150 155 160

35 Gln Asn His Ala Val Tyr Leu Ala Asn Ile Ala Gln His Ala Gln Gln  
 165 170 175

40 Asn Trp Gly Ile Gln Phe Gln Ser Val Glu Ala Phe Asn Glu Pro Ser  
 180 185 190

45 Ser Gly Trp Gly Pro Thr Gly Thr Gln Glu Gly Cys His Phe Ala Val  
 195 200 205

50 Ser Thr Met Ala Thr Val Ile Gly Tyr Leu Asn Thr Glu Leu Ala Gln  
 210 215 220

55 Arg Gly Leu Ser Ser Phe Ile Ser Ala Ser Asp Glu Thr Ser Tyr Asp  
 225 230 235 240

60 Leu Ala Ile Ser Thr Trp Gln Gly Leu Gly Ser Ser Ala Gln Asn Ala  
 245 250 255

65 Val Lys Arg Val Asn Val His Gly Tyr Gln Gly Gly Gly Gly Arg Arg  
 260 265 270

70 Asp Thr Leu Tyr Ser Leu Val Ser Gln Ala Gly Lys Arg Leu Trp Asn  
 275 280 285

75 Ser Glu Tyr Gly Asp Ala Asp Ala Ser Gly Lys Ser Met Tyr Thr Asn  
 290 295 300

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Leu Leu Leu Asp Phe Thr Trp Leu His Pro Thr Ala Trp Val Tyr Trp  
 305 310 315 320  
 5  
 Gln Ala Ile Asp Gly Ser Gly Trp Gly Leu Ile Val Gly Asp Asn Asp  
 325 330 335  
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 Gln Leu Thr Leu Ser Ser Ala Ser Thr Lys Tyr Phe Val Leu Ala Gln  
 340 345 350  
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 Leu Thr Arg His Ile Arg Pro Gly Met Gln Ile Leu Thr Thr Pro Asp  
 355 360 365  
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 Gly Asn Thr Val Ala Ala Tyr Asp Ser Gly Ser Gln Lys Leu Val Ile  
 370 375 380  
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 Val Ala Ala Asn Trp Gly Ser Ala Gln Thr Ile Thr Phe Asp Leu Thr  
 385 390 395 400  
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 Arg Ala Lys Thr Ala Gly Ser Asn Gly Ala Thr Val Pro Arg Trp Ser  
 405 410 415  
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 Thr Gln Thr Ser Gly Gly Asp Gln Tyr Lys Ser Tyr Ser Asp Thr Lys  
 420 425 430  
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 Ile Asn Asn Gly Lys Phe Ser Val Ser Phe Ser Thr Gly Gln Val Gln  
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 Thr Phe Glu Ile Ser Gly Val Val Leu Lys  
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 40 <212> PRT  
 <213> Ascobolus stictoides  
 <400> 26  
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 Val Met Asn Glu Ile Ala Gly Phe Ser Gly Thr Gly Tyr Val Gly Gly  
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 Trp Asp Glu Asp Ala Asp Thr Val Ser Leu Thr Phe Thr Ser Asp Ala  
 35 40 45  
 Thr Lys Leu Tyr Asp Val Lys Ile Arg Tyr Ser Gly Pro Tyr Gly Ser  
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Lys Tyr Thr Arg Ile Ser Tyr Asn Gly Ala Thr Gly Gly Asp Ile Ser  
 65 70 75 80  
 5 Leu Pro Glu Thr Thr Glu Trp Ala Thr Val Asn Ala Gly Gln Ala Leu  
 85 90 95  
 10 Leu Asn Ala Gly Ser Asn Thr Ile Lys Leu His Asn Asn Trp Gly Trp  
 100 105 110  
 Tyr Leu Ile Asp Ala Val Ile Leu Thr Pro Ser Val Pro Arg Pro Pro  
 115 120 125  
 15 His Gln Val Thr Asp Ala Leu Val Asn Thr Asn Ser Asn Ala Val Thr  
 130 135 140  
 20 Lys Gln Leu Met Lys Phe Leu Val Ser Lys Tyr His Lys Ala Tyr Ile  
 145 150 155 160  
 Thr Gly Gln Gln Glu Leu His Ala His Gln Trp Val Glu Lys Asn Val  
 165 170 175  
 25 Gly Lys Ser Pro Ala Ile Leu Gly Leu Asp Phe Met Asp Tyr Ser Pro  
 180 185 190  
 30 Ser Arg Val Glu Phe Gly Thr Thr Ser Gln Ala Val Glu Gln Ala Ile  
 195 200 205  
 35 Asp Phe Asp Lys Arg Gly Gly Ile Val Thr Phe Ala Trp His Trp Asn  
 210 215 220  
 Ala Pro Ser Gly Leu Ile Asn Thr Pro Gly Ser Glu Trp Trp Arg Gly  
 225 230 235 240  
 40 Phe Tyr Thr Glu His Thr Thr Phe Asp Val Ala Ala Ala Leu Gln Asn  
 245 250 255  
 45 Thr Thr Asn Ala Asn Tyr Asn Leu Leu Ile Arg Asp Ile Asp Ala Ile  
 260 265 270  
 Ala Val Gln Leu Lys Arg Leu Gln Thr Ala Gly Val Pro Val Leu Trp  
 275 280 285  
 50 Arg Pro Leu His Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys  
 290 295 300  
 55 Gly Pro Glu Pro Ala Lys Lys Leu Tyr Lys Ile Leu Tyr Asp Arg Leu  
 305 310 315 320

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Thr Asn Tyr His Lys Leu Asn Asn Leu Ile Trp Val Trp Asn Ser Val  
 325 330 335  
 5  
 Ala Lys Asp Trp Tyr Pro Gly Asp Glu Ile Val Asp Val Leu Ser Phe  
 340 345 350  
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 Asp Ser Tyr Pro Ala Gln Pro Gly Asp His Gly Pro Val Ser Ala Gln  
 355 360 365  
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 Tyr Asn Ala Leu Val Glu Leu Gly Lys Asp Lys Lys Leu Ile Ala Ala  
 370 375 380  
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 Thr Glu Val Gly Thr Ile Pro Asp Pro Asp Leu Met Gln Leu Tyr Glu  
 385 390 395 400  
 25  
 Ser Tyr Trp Ser Phe Phe Val Thr Trp Glu Gly Glu Phe Ile Glu Asn  
 405 410 415  
 30  
 Gly Val His Asn Ser Leu Glu Phe Leu Lys Lys Leu Tyr Asn Asn Ser  
 420 425 430  
 35  
 Phe Val Leu Asn Leu Asp Thr Ile Gln Gly Trp Lys Asn Gly Ala Gly  
 435 440 445  
 40  
 Ser Ser Thr Thr Thr Val Lys Ser Thr Thr Thr Thr Pro Thr Thr Thr  
 450 455 460  
 45  
 Ile Lys Ser Thr Thr Thr Thr Pro Val Thr Thr Pro Thr Thr Val Lys  
 465 470 475 480  
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 Thr Thr Thr Thr Pro Thr Thr Thr Ala Thr Thr Val Lys Ser Thr Thr  
 485 490 495  
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 Thr Thr Ala Gly Pro Thr Pro Thr Ala Val Ala Gly Arg Trp Gln Gln  
 500 505 510  
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 Cys Gly Gly Ile Gly Phe Thr Gly Pro Thr Thr Cys Glu Ala Gly Thr  
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 Thr Cys Asn Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu  
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<210> 27

<211> 541

55 <212> PRT

<213> *Ascobolus stictoides*

<400> 27



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10	Ala	Val	Gln	Leu	Lys	Arg	Leu	Gln	Thr	Ala	Gly	Val	Pro	Val	Leu	Trp
			275					280					285			
15	Arg	Pro	Leu	His	Glu	Ala	Glu	Gly	Gly	Trp	Phe	Trp	Trp	Gly	Ala	Lys
		290					295					300				
20	Gly	Pro	Glu	Pro	Ala	Lys	Lys	Leu	Tyr	Lys	Ile	Leu	Tyr	Asp	Arg	Leu
	305					310					315					320
25	Thr	Asn	Tyr	His	Lys	Leu	Asn	Asn	Leu	Ile	Trp	Val	Trp	Asn	Ser	Val
				325						330					335	
30	Ala	Lys	Asp	Trp	Tyr	Pro	Gly	Asp	Glu	Ile	Val	Asp	Val	Leu	Ser	Phe
				340					345					350		
35	Asp	Ser	Tyr	Pro	Ala	Gln	Pro	Gly	Asp	His	Gly	Pro	Val	Ser	Ala	Gln
			355					360					365			
40	Tyr	Asn	Ala	Leu	Val	Glu	Leu	Gly	Lys	Asp	Lys	Lys	Leu	Ile	Ala	Ala
		370					375					380				
45	Thr	Glu	Val	Gly	Thr	Ile	Pro	Asp	Pro	Asp	Leu	Met	Gln	Leu	Tyr	Glu
	385					390					395					400
50	Ser	Tyr	Trp	Ser	Phe	Phe	Val	Thr	Trp	Glu	Gly	Glu	Phe	Ile	Glu	Asn
				405						410					415	
55	Gly	Val	His	Asn	Ser	Leu	Glu	Phe	Leu	Lys	Lys	Leu	Tyr	Asn	Asn	Ser
				420					425					430		
60	Phe	Val	Leu	Asn	Leu	Asp	Thr	Ile	Gln	Gly	Trp	Lys	Asn	Gly	Ala	Gly
			435					440					445			
65	Ser	Ser	Thr	Thr	Thr	Val	Lys	Ser	Thr	Thr	Thr	Thr	Pro	Thr	Thr	Thr
		450					455						460			
70	Ile	Lys	Ser	Thr	Thr	Thr	Thr	Pro	Val	Thr	Thr	Pro	Thr	Thr	Val	Lys
	465					470					475					480
75	Thr	Thr	Thr	Thr	Pro	Thr	Thr	Thr	Ala	Thr	Thr	Val	Lys	Ser	Thr	Thr
				485						490					495	

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Thr Thr Ala Gly Pro Thr Pro Thr Ala Val Ala Gly Arg Trp Gln Gln  
 500 505 510  
 5  
 Cys Gly Gly Ile Gly Phe Thr Gly Pro Thr Thr Cys Glu Ala Gly Thr  
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 Thr Cys Asn Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu  
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 15 <213> Chaetomium virescens  
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 35 40 45  
 30 Thr Val Asp Ser Ala Ser Thr Glu Leu Tyr Asp Leu Ser Ile Arg Val  
 50 55 60  
 35 Ala Ala Ile Tyr Gly Asp Lys Arg Thr Ser Val Val Leu Asn Gly Gly  
 65 70 75 80  
 40 Ala Ser Ser Glu Val Tyr Phe Pro Ala Gly Glu Thr Trp Thr Asn Val  
 85 90 95  
 45 Ala Ala Gly Gln Leu Leu Leu Asn Gln Gly Ser Asn Thr Ile Asp Ile  
 100 105 110  
 50 Val Ser Asn Trp Gly Trp Tyr Leu Ile Asp Ser Ile Thr Leu Thr Pro  
 115 120 125  
 55 Ser Thr Pro Arg Pro Ala His Gln Ile Asn Glu Ala Pro Val Asn Ala  
 130 135 140  
 Ala Ala Asp Lys Asn Ala Lys Ala Leu Tyr Ser Tyr Leu Arg Ser Ile  
 145 150 155 160  
 Tyr Gly Lys Lys Ile Leu Ser Gly Gln Gln Glu Leu Ser Leu Ser Asn  
 165 170 175

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Trp Ile Ala Gln Gln Thr Gly Lys Thr Pro Ala Leu Val Ser Val Asp  
180 185 190

5 Leu Met Asp Tyr Ser Pro Ser Arg Val Glu Arg Gly Thr Val Gly Thr  
195 200 205

10 Ala Val Glu Glu Ala Ile Gln His His Asn Arg Gly Gly Ile Val Ser  
210 215 220

Val Leu Trp His Trp Asn Ala Pro Thr Gly Leu Tyr Asp Thr Glu Glu  
225 230 235 240

15 His Arg Trp Trp Ser Gly Phe Tyr Thr Ser Ala Thr Asp Phe Asp Val  
245 250 255

20 Ala Ala Ala Leu Ser Ser Thr Thr Asn Ala Asn Tyr Thr Leu Leu Ile  
260 265 270

Arg Asp Ile Asp Ala Ile Ala Val Gln Leu Lys Arg Leu Gln Ser Ala  
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Claims

1. A laundry or dish-washing cleaning composition comprising an amylase enzyme and an enzyme: (i) having glycoside hydrolase activity; and (ii) being selected from the endo-alpha-1,4-polygalactosaminidase class (EC 3.2.1.109) of enzymes, wherein the glycoside hydrolase enzyme having glycoside hydrolase activity is a variant having at least 70%, more preferably at least 80% identity to SEQ ID NO:1.
2. A laundry or dish-washing cleaning composition according to claim 1 wherein the glycoside hydrolase comprises PelAh.
3. A laundry or dish-washing cleaning composition according to claim 1 or 2 wherein the glycoside hydrolase enzyme is obtainable from *Pseudomonas*, preferably from *Pseudomonas aeruginosa*.



4. A laundry or dish-washing cleaning composition according to any preceding claim wherein the glycoside hydrolase enzyme is an isolated glycoside hydrolase.
- 5 5. A laundry or dish-washing cleaning composition according to any preceding claim wherein the composition further comprises additional enzyme selected from galactanases, mannanases, nucleases, and mixtures thereof.
6. A laundry or dish-washing cleaning composition according to claim 5 wherein the composition additionally comprises a nuclease enzyme, preferably a deoxyribonuclease enzyme.
- 10 7. A laundry or dish-washing cleaning composition according to any preceding claim wherein the composition further comprises one, preferably two or three or more additional enzymes selected from lipases, proteases, pectate lyases, cellulases, cutinases, and mixtures thereof.
- 15 8. A laundry or dish-washing cleaning composition according to any preceding claim wherein the composition further comprises a  $\beta$ -N-acetylglucosaminidase enzyme from E.C. 3.2.1.52, preferably an enzyme having at least 70% identity to SEQ ID NO:12.
- 20 9. A laundry or dish-washing cleaning composition according to any preceding claim wherein the cleaning composition further comprises from 1% to 80 wt%, preferably from 5 to 80 wt% of the cleaning composition, of a surfactant system, preferably comprising an anionic surfactant.
10. A laundry or dish-washing cleaning composition according to claim 9 wherein the surfactant system additionally comprises a nonionic surfactant, and preferably the weight ratio of the anionic to nonionic surfactant is from 25:1 to 1:2.
- 25 11. A laundry or dish-washing cleaning composition according to claim 9 or claim 10 wherein the anionic surfactant is selected from alkyl benzene sulphonates and (optionally alkoxyated) alkyl sulfates and mixtures thereof, preferably the anionic surfactant comprising at least 50 wt% alkyl benzene sulphonate surfactant.
- 30 12. A method of laundry or dish-cleaning, preferably a textile, comprising mixing the laundry or dish-washing cleaning composition according to any preceding claim with water to form an aqueous liquor and contacting the laundry or dish surface, preferably a textile, with the aqueous liquor in a laundering step, preferably wherein the glycoside hydrolase enzyme is present in the aqueous liquor in an amount of from 0.01ppm to 1000 ppm enzyme, based on active protein or from 0.05 or from 0.1ppm to 750 or 500ppm.
- 35 13. Use of a composition comprising an amylase enzyme and an enzyme having glycoside hydrolase activity and belonging to the endo-alpha-1,4-polygalactosminidase class (EC 3.2.1.109) of enzymes, to enhance stain removal from a laundry or dish surface, preferably a fabric surface, particularly greasy-stain removal, body soil removal and/or for reduction of malodour from the surface, wherein the glycoside hydrolase enzyme having glycoside hydrolase activity is a variant having at least 70%, more preferably at least 80% identity to SEQ ID NO:1.
- 40

#### Patentansprüche

- 45 1. Wäschewasch- oder Geschirrspülreinigungszusammensetzung, umfassend ein Amylase-Enzym und ein Enzym: (i) mit Glycosidhydrolaseaktivität; und (ii) ausgewählt aus der Endo-alpha-1,4-polygalactosminidase-Klasse (EC 3.2.1.109) von Enzymen, wobei das Glycosidhydrolase-Enzym mit Glycosidhydrolaseaktivität eine Variante mit mindestens 70 %, mehr bevorzugt mindestens 80 % Identität mit SEQ ID NO:1 ist.
- 50 2. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach Anspruch 1, wobei die Glycosidhydrolase PeIAh umfasst.
3. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach Anspruch 1 oder 2, wobei das Glycosidhydrolase-Enzym aus *Pseudomonas*, vorzugsweise aus *Pseudomonas aeruginosa*, erhältlich ist.
- 55 4. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach einem der vorstehenden Ansprüche, wobei das Glycosidhydrolase-Enzym eine isolierte Glycosidhydrolase ist.
5. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach einem der vorstehenden Ansprüche, wobei

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die Zusammensetzung ferner zusätzliches Enzym umfasst, ausgewählt aus Galactanasen, Mannanasen, Nukleasen und Mischungen davon.

- 5 6. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach Anspruch 5, wobei die Zusammensetzung zusätzlich ein Nuklease-Enzym, vorzugsweise ein Desoxyribonuklease-Enzym, umfasst.
7. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach einem der vorstehenden Ansprüche, wobei die Zusammensetzung ferner ein, vorzugsweise zwei oder drei oder mehr zusätzliche Enzyme umfasst, ausgewählt aus Lipasen, Proteasen, Pektatlyasen, Cellulasen, Cutinasen und Mischungen davon.
- 10 8. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach einem der vorstehenden Ansprüche, wobei die Zusammensetzung ferner ein  $\beta$ -N-Acetylglucosaminidase-Enzym aus E.C. 3.2.1.52 umfasst, vorzugsweise ein Enzym mit mindestens 70 % Identität mit SEQ ID NO:12.
- 15 9. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach einem der vorstehenden Ansprüche, wobei die Reinigungszusammensetzung ferner zu 1 Gew.-% bis 80 Gew.-%, vorzugsweise zu 5 Gew.-% bis 80 Gew.-% der Reinigungszusammensetzung ein Tensidsystem umfasst, das vorzugsweise ein anionisches Tensid umfasst.
- 20 10. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach Anspruch 9, wobei das Tensidsystem zusätzlich ein nichtionisches Tensid umfasst und das Gewichtsverhältnis des anionischen zu dem nichtionischen Tensid vorzugsweise 25:1 bis 1:2 beträgt.
- 25 11. Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach Anspruch 9 oder Anspruch 10, wobei das anionische Tensid ausgewählt ist aus Alkylbenzolsulfonaten und (wahlweise alkoxylierten) Alkylsulfaten und Mischungen davon, wobei das anionische Tensid vorzugsweise mindestens 50 Gew.-% Alkylbenzolsulfonattensid umfasst.
- 30 12. Verfahren zum Wäschewaschen oder Geschirrspülen, vorzugsweise eines Textils, umfassend das Mischen der Wäschewasch- oder Geschirrspülreinigungszusammensetzung nach einem der vorstehenden Ansprüche mit Wasser, um eine wässrige Flotte zu bilden, und Inkontaktbringen der Wäsche- oder Geschirroberfläche, vorzugsweise eines Textils, mit der wässrigen Flotte in einem Waschschrift, wobei das Glycosidhydrolase-Enzym vorzugsweise in der wässrigen Flotte in einer Menge von 0,01 ppm bis 1000 ppm Enzym, bezogen auf aktives Protein, oder von 0,05 oder von 0,1 ppm bis 750 oder 500 ppm vorliegt.
- 35 13. Verwendung einer Zusammensetzung, die ein Amylase-Enzym und ein Enzym mit Glycosidhydrolaseaktivität umfasst und zur Endo-alpha-1,4-polygalactosaminidase-Klasse (EC 3.2.1.109) von Enzymen gehört, um die Fleckenentfernung von einer Wäsche- oder Geschirroberfläche, vorzugsweise einer Textiloberfläche zu verbessern, insbesondere Fettfleckenentfernung, Körperschmutzentfernung und/oder zur Verringerung von schlechtem Geruch von der Oberfläche, wobei das Glycosidhydrolase-Enzym mit Glycosidhydrolaseaktivität eine Variante mit mindestens 70 %, mehr bevorzugt mindestens 80 % Identität mit SEQ ID NO:1 ist.
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### Revendications

- 45 1. Composition de nettoyage pour le lavage du linge ou de la vaisselle comprenant une enzyme amylase et une enzyme : (i) ayant une activité de glycoside hydrolase ; et (ii) étant choisie parmi la classe endo-alpha-1,4-polygalactosaminidase (EC 3.2.1.109) d'enzymes, dans laquelle l'enzyme glycoside hydrolase ayant une activité de glycoside hydrolase est un variant ayant au moins 70 %, plus préférablement au moins 80 % d'identité par rapport à SEQ ID NO:1.
- 50 2. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon la revendication 1 dans laquelle la glycoside hydrolase comprend PelAh.
- 55 3. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon la revendication 1 ou 2 dans laquelle l'enzyme glycoside hydrolase peut être obtenue à partir de *Pseudomonas*, de préférence à partir de *Pseudomonas aeruginosa*.
4. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon une quelconque revendication précédente

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dans laquelle l'enzyme glycoside hydrolase est une glycoside hydrolase isolée.

- 5 5. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon une quelconque revendication précédente dans laquelle la composition comprend en outre une enzyme supplémentaire choisie parmi galactanases, mannanases, nucléases, et des mélanges de celles-ci.
- 10 6. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon la revendication 5 dans laquelle la composition comprend en outre une enzyme nucléase, de préférence une enzyme désoxyribonucléase.
- 15 7. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon une quelconque revendication précédente dans laquelle la composition comprend en outre une, de préférence deux ou trois enzymes supplémentaires ou plus choisies parmi lipases, protéases, pectate lyases, cellulases, cutinases, et des mélanges de celles-ci.
- 20 8. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon une quelconque revendication précédente dans laquelle la composition comprend en outre une enzyme  $\beta$ -N-acétylglucosaminidase de E.C. 3.2.1.52, de préférence une enzyme ayant au moins 70 % d'identité par rapport à SEQ ID NO:12.
- 25 9. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon une quelconque revendication précédente dans laquelle la composition de nettoyage comprend en outre de 1 % à 80 % en poids, de préférence de 5 à 80 % en poids de la composition de nettoyage, d'un système tensioactif, comprenant de préférence un agent tensioactif anionique.
- 30 10. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon la revendication 9 dans laquelle le système tensioactif comprend en outre un agent tensioactif non ionique, et de préférence le rapport pondéral de l'agent tensioactif anionique au non ionique va de 25:1 à 1:2.
- 35 11. Composition de nettoyage pour le lavage du linge ou de la vaisselle selon la revendication 9 ou la revendication 10 dans laquelle l'agent tensioactif anionique est choisi parmi des sulfonates d'alkylbenzène et des sulfates d'alkyle (facultativement alcoxylés) et des mélanges de ceux-ci, de préférence l'agent tensioactif anionique comprenant au moins 50 % en poids d'agent tensioactif sulfonate d'alkylbenzène.
- 40 12. Procédé de lavage du linge ou de la vaisselle, de préférence un textile, comprenant le mélange de la composition de nettoyage pour le lavage du linge ou de la vaisselle selon une quelconque revendication précédente avec de l'eau pour former une liqueur aqueuse et la mise en contact de la surface de linge ou de vaisselle, de préférence un textile, avec la liqueur aqueuse dans une étape de lavage du linge, de préférence dans lequel l'enzyme glycoside hydrolase est présente dans la liqueur aqueuse en une quantité allant de 0,01 ppm à 1000 ppm d'enzyme, sur une base de protéine active ou de 0,05 ou de 0,1 ppm à 750 ou 500 ppm.
- 45 13. Utilisation d'une composition comprenant une enzyme amylase et une enzyme ayant une activité de glycoside hydrolase et appartenant à la classe endo-alpha-1,4-polygalactosminidase (EC 3.2.1.109) d'enzymes, pour améliorer l'élimination des salissures d'une surface de linge ou de vaisselle, de préférence une surface textile, particulièrement une élimination de salissures grasses, une élimination de salissures corporelles et/ou pour la réduction d'une mauvaise odeur de la surface, dans laquelle l'enzyme glycoside hydrolase ayant une activité de glycoside hydrolase est un variant ayant au moins 70 %, plus préférentiellement au moins 80 % d'identité par rapport à SEQ ID NO:1.

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