(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) **EP 3 301 150 A1**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
04.04.2018 Bulletin 2018/14

(21) Application number: **16192078.0**

(22) Date of filing: **03.10.2016**

(51) Int Cl.:
C11D 1/02 *(2006.01)* ***C11D 3/20*** *(2006.01)*
C11D 11/00 *(2006.01)* ***C11D 17/06*** *(2006.01)*

(84) Designated Contracting States:
AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR
Designated Extension States:
BA ME
Designated Validation States:
MA MD

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(54) **LOW PH LAUNDRY DETERGENT COMPOSITION**

(57) The present invention relates to the use of a solid free flowing particulate laundry detergent composition, wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 9.0, to provide improved fabric cleaning performance during a laundering process, wherein the laundering process has a wash time of 30 minutes or less, and wherein the laundering process has a wash bath temperature of 30°C or less.

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Description

FIELD OF THE INVENTION

[0001] The present invention relates to a solid free flowing particulate laundry detergent composition having a low pH profile. The compositions of the present invention provide good solubility profile, good cleaning profile, good stability profile and good fabric care profile.

BACKGROUND OF THE INVENTION

[0002] Laundry detergent powder manufacturers seek to provide solid free-flowing particulate laundry detergent compositons that have good solubility profile, good cleaning profile, good stability profile and good fabric care profile. Typically, a performance balance is required between the chosen formulation to ensure that these profile requriements are met.

[0003] The pH profile of a typical laundry detergent powder is quite high, around pH 10.5 and sometimes even higher. This pH profile ensures the good performance of historic cleaning mechanisms: such as grease saponification mechanisms and/or fabric fibre swelling mechanisms. However, this high pH profile also means that the detergent formulators are having to address problems with improving the fabric care profile, and ensuring fabric appearance performance and/or fabric shape retention performance is still adequate.

[0004] The inventors have found that an alternative approach to this historic dichotomy of formulating high pH detergent powders to ensure good cleaning performance whilst needing to balance the formulation so as to also provide good fabric care performance, is to formulate the solid detergent powder at a lower pH and then to balance the formulation so as to also provide good cleaning performance.

[0005] This low pH laundry deterent powder formulation approach ensures good fabric appearance and good fabric care profiles, but careful attention is needed to ensure good cleaning performance, and especially to address any undesirable cleaning performance skews that result due to the low pH profile.

[0006] In particular, the inventors have found that a good cleaning performance is achieved by a low pH solid laundry detergent powder when used in a laundering process having a cold wash bath temperature and a short wash time.

SUMMARY OF THE INVENTION

[0007] The present invention relates to the use of a solid free flowing particulate laundry detergent composition, wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 9.0, to provide improved fabric cleaning performance during a laundering process, wherein the laundering process has a wash time of 30 minutes or less, and wherein the laundering process has a wash bath temperature of 30°C or less.

DETAILED DESCRIPTION OF THE INVENTION

[0008] The present invention relates to the use of a solid free flowing particulate laundry detergent composition, wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 9.0, to provide improved fabric cleaning performance during a laundering process, wherein the laundering process has a wash time of 30 minutes or less, and wherein the laundering process has a wash bath temperature of 30°C or less.

[0009] The solid free flowing particulate laundry detergent composition typically comprises:

(a) anionic detersive surfactant;
(b) from 0wt% to 8wt% zeolite builder;
(c) from 0wt% to 4wt% phosphate builder;
(d) from 0wt% to 8wt% sodium carbonate;
(e) from 0wt% to 8wt% sodium silicate; and
(f) from 4wt% to 20wt% organic acid,

wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 9.0, preferably from 6.5 to 8.0,
wherein the composition typically comprises from 30wt% to 90wt% base detergent particle, wherein the base detergent particle comprising (by weight of the base detergent particle):

(a) from 4wt% to 35wt% anionic detersive surfactant;
(b) optionally, from 1wt% to 8wt% zeolite builder;
(c) from 0wt% to 4wt% phosphate builder;

(d) from 0wt% to 8wt% sodium carbonate;
(e) from 0wt% to 8wt% sodium silicate;
(f) from 1wt% to 16wt% organic acid; and
(g) optionally, from 1wt% to 10wt% magnesium sulphate.

[0010] Solid free-flowing particulate laundry detergent composition: Typically, the solid free-flowing particulate laundry detergent composition is a fully formulated laundry detergent composition, not a portion thereof such as a spray-dried, extruded or agglomerate particle that only forms part of the laundry detergent composition. Typically, the solid composition comprises a plurality of chemically different particles, such as spray-dried base detergent particles and/or agglomerated base detergent particles and/or extruded base detergent particles, in combination with one or more, typically two or more, or five or more, or even ten or more particles selected from: surfactant particles, including surfactant agglomerates, surfactant extrudates, surfactant needles, surfactant noodles, surfactant flakes; phosphate particles; zeolite particles; polymer particles such as carboxylate polymer particles, cellulosic polymer particles, starch particles, polyester particles, polyamine particles, terephthalate polymer particles, polyethylene glycol particles; aesthetic particles such as coloured noodles, needles, lamellae particles and ring particles; enzyme particles such as protease granulates, amylase granulates, lipase granulates, cellulase granulates, mannanase granulates, pectate lyase granulates, xyloglucanase granulates, bleaching enzyme granulates and co- granulates of any of these enzymes, preferably these enzyme granulates comprise sodium sulphate; bleach particles, such as percarbonate particles, especially coated percarbonate particles, such as percarbonate coated with carbonate salt, sulphate salt, silicate salt, borosilicate salt, or any combination thereof, perborate particles, bleach activator particles such as tetra acetyl ethylene diamine particles and/or alkyl oxybenzene sulphonate particles, bleach catalyst particles such as transition metal catalyst particles, and/or isoquinolinium bleach catalyst particles, pre-formed peracid particles, especially coated pre-formed peracid particles; filler particles such as sulphate salt particles and chloride particles; clay particles such as montmorillonite particles and particles of clay and silicone; flocculant particles such as polyethylene oxide particles; wax particles such as wax agglomerates; silicone particles, brightener particles; dye transfer inhibition particles; dye fixative particles; perfume particles such as perfume microcapsules and starch encapsulated perfume accord particles, or pro-perfume particles such as Schiff base reaction product particles; hueing dye particles; chelant particles such as chelant agglomerates; and any combination thereof.

[0011] Typically, the solid free flowing particulate laundry detergent composition comprises:

(a) anionic detersive surfactant;
(b) from 0wt% to 8wt% zeolite builder;
(c) from 0wt% to 4wt% phosphate builder;
(d) from 0wt% to 8wt% sodium carbonate;
(e) from 0wt% to 8wt% sodium silicate; and (f) from 4wt% to 20wt% organic acid.

[0012] Typically, the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 9.0, preferably from 6.5 to 8.5, more preferably from 7.0 to 8.0.

[0013] Typically, the composition at 1wt% dilution in deionized water at 20°C, has a reserve alkalinity to pH 7.0 of less than 4.0gNaOH/100g, preferably less than 3.0gNaOH/100g, or even less than 2.0gNaOH/100g.

[0014] As used herein, the term "reserve alkalinity" is a measure of the buffering capacity of the detergent composition (g/NaOH/100g detergent composition) determined by titrating a 1% (w/v) solution of detergent composition with hydrochloric acid to pH 7.0 i.e. in order to calculate Reserve Alkalinity as defined herein:

$$\text{Reserve Alkalinity (to pH 7.0) as \% alkali in g NaOH/100 g product} = \frac{T \times M \times 40 \times Vol}{10 \times Wt \times Aliquot}$$

T = titre (ml) to pH 7.0
M = Molarity of HCl = 0.2
40 = Molecular weight of NaOH
Vol = Total volume (ie. 1000 ml)
W = Weight of product (10 g)
Aliquot = (100 ml)

[0015] Obtain a 10g sample accurately weighed to two decimal places, of fully formulated detergent composition. The sample should be obtained using a Pascall sampler in a dust cabinet. Add the 10g sample to a plastic beaker and add 200 ml of carbon dioxide-free de-ionised water. Agitate using a magnetic stirrer on a stirring plate at 150 rpm until fully

dissolved and for at least 15 minutes. Transfer the contents of the beaker to a l litre volumetric flask and make up to 1 litre with deionised water. Mix well and take a 100 mls ± 1 ml aliquot using a 100 mls pipette immediately. Measure and record the pH and temperature of the sample using a pH meter capable of reading to ±0.01pH units, with stirring, ensuring temperature is 21°C +/- 2°C. Titrate whilst stirring with 0.2M hydrochloric acid until pH measures exactly 7.0. Note the millilitres of hydrochloric acid used. Take the average titre of three identical repeats. Carry out the calculation described above to calculate the reserve alkalinity to pH 7.0.

[0016] Typically, the composition comprises from 30wt% to 90wt% base detergent particle, wherein the base detergent particle comprising (by weight of the base detergent particle): (a) from 4wt% to 35wt% anionic detersive surfactant; (b) optionally, from 1wt% to 8wt% zeolite builder; (c) from 0wt% to 4wt% phosphate builder; (d) from 0wt% to 8wt%, preferably from 0wt% to 4wt%, sodium carbonate; (e) from 0wt% to 8wt%, preferably from 0wt% to 4wt%, sodium silicate; (f) from 1wt% to 10wt% organic acid; and (g) optionally, from 1wt% to 10wt% magnesium sulphate. Typically, the base detergent particle is in the form of a spray-dried particle.

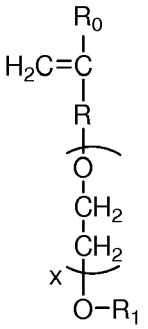
[0017] Typically, the organic acid comprises citric acid and the base detergent particle comprises from 1wt% to 10wt% citric acid.

[0018] The organic acid may be at least partially coated, or even completely coated, by a water-dispersible material. Water-dispersible material also typically includes water-soluble material. A suitable water-dispersible material is wax. A suitable water-soluble material is citrate.

[0019] Typically, the anionic detersive surfactant comprises alkyl benzene sulphonate and wherein the base detergent particle comprises from 4wt% to 35wt% alkyl benzene sulphonate.

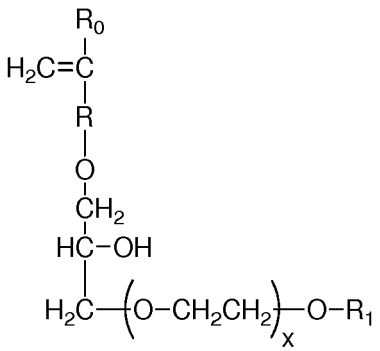
[0020] Typically, the base detergent particle comprises from 0.5wt% to 5wt% carboxylate co-polymer, wherein the carboxylate co-polymer comprises: (i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising carboxyl groups; (ii) from 1 to less than 49 wt% structural units 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 C_1 to C_{20} organic group;

formula (II)



wherein 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 C_1 to C_{20} organic group.

[0021] Typically, the base detergent particle comprises from 30wt% to 70wt% sodium sulphate.

[0022] Typically, the composition comprises from 1wt% to 20wt% co-surfactant particle, wherein the co-surfactant particle comprises: (a) from 25wt% to 60wt% co-surfactant; (b) from 10wt% to 50wt% carbonate salt; and (c) from 1wt% to 30wt% silica. Typically, the co-surfactant particle is in the form of an agglomerate.

[0023] Typically, the co-surfactant comprises alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.5, and wherein the co-surfactant particle comprises from 25wt% to 60wt% alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.5.

[0024] The co-surfactant particle may comprise linear alkyl benzene sulphonate and alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.5.

[0025] The composition at 1wt% dilution in deionized water at 20°C, may have an equilibrium pH in the range of from 6.5 to 8.5.

[0026] The composition may have a reserve alkalinity to pH 7.5 of less than 3.0gNaOH/100g.

[0027] The composition may comprise from 0wt% to 6wt%, preferably from 0wt% to 4wt%, sodium bicarbonate.

[0028] The composition may comprise from 0wt% to 4wt% sodium carbonate.

[0029] The composition may comprise from 0wt% to 4wt% sodium silicate.

[0030] The composition may comprise from 0wt% to 4wt% phosphate builder.

[0031] The composition is preferably substantially free of phosphate builder.

[0032] The composition may be substantially free of sodium carbonate.

[0033] The composition may be substantially free of sodium bicarbonate.

[0034] The composition may be substantially free of sodium silicate.

[0035] By "substantially free" it is typically meant herein to mean: "comprises no deliberately added".

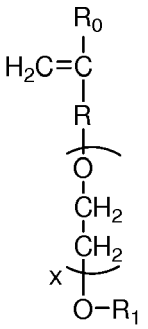
[0036] The composition may comprise the combination of lipase enzyme and soil release polymer.

[0037] Preferably, the composition comprises alkyl benzene sulphonate, wherein the alkyl benzene sulphonate comprises at least 25wt% of the 2-phenyl isomer. A suitable alkyl benzene sulphonate having this feature is obtained by DETAL synthesis.

[0038] The composition may comprises alkyl amine oxide.

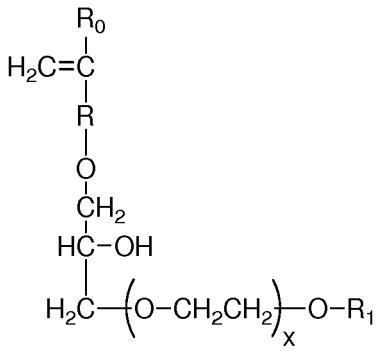
[0039] The composition may comprises from 0.5wt% to 8wt% carboxylate co-polymer, wherein the carboxylate co-polymer comprises: (i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising carboxyl groups;
(ii) from 1 to less than 49 wt% structural units derived from one 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 C_1 to C_{20} organic group;

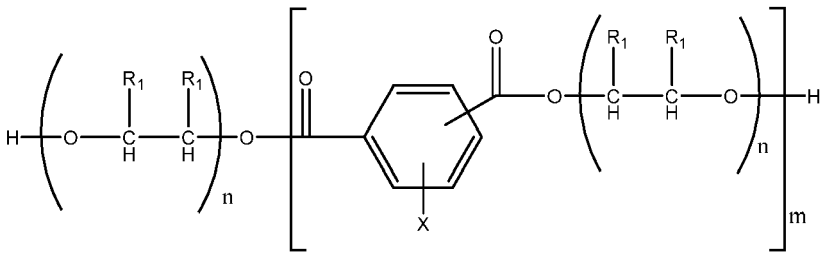
formula (II)



wherein 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 C_1 to C_{20} organic group.

The composition may comprise polyethylene glycol polymer, wherein the polyethylene glycol polymer comprises a polyethylene glycol backbone with grafted polyvinyl acetate side chains.

[0040] The composition may comprise a polyester soil release polymer having the structure:



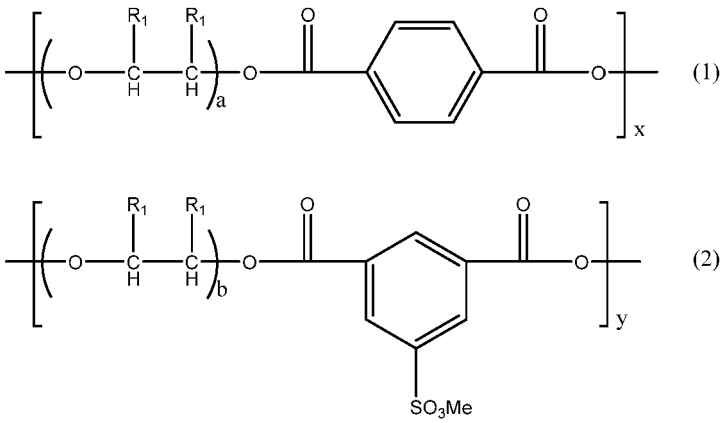
wherein n is from 1 to 10; m is from 1 to 15 ;

X is H or SO_3Me;

wherein Me is H, Na^+, Li^+, K^+, Mg^{2+}, Ca^{2+}, Al^{3+}, ammonium, mono-, di-, tri-, or tetraalkylammonium; wherein the alkyl groups are C_1-C_{18} alkyl or C_2-C_{10} hydroxyalkyl, or any mixture thereof;

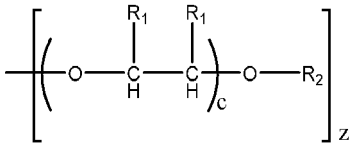
R1 are independently selected from H or C_1-C_{18} n- or iso-alkyl.

[0041] The composition may comprise a polyester soil release polymer consisting of structure units (1) to (3):



(1)

(2)



(3)

wherein:

a, b and c are from 1 to 10;
x, y is from 1 to 10;
z is from 0.1 to 10;
Me is H, Na^+, Li^+, K^+, Mg^{2+}, Ca^{2+}, Al^{3+}, ammonium, mono-, di-, tri-, or tetraalkylammonium wherein the alkyl groups are C_1-C_{18} alkyl or C_2-C_{10} hydroxyalkyl, or any mixture thereof;
R_1, are independently selected from H or C_1-C_{18} n- or iso-alkyl;
R_2 is a linear or branched C_1-C_{18} alkyl, or a linear or branched C_2-C_{30} alkenyl, or a cycloalkyl group with 5 to 9 carbon atoms, or a C_6-C_{30} aryl group, or a C_6-C_{30} arylalkyl group.

[0042] The composition may comprise carboxymethyl cellulose having a degree of substitution greater than 0.65 and a degree of blockiness greater than 0.45.

[0043] The composition may comprise an alkoxylated polyalkyleneimine, wherein said alkoxylated polyalkyleneimine has a polyalkyleneimine core with one or more side chains bonded to at least one nitrogen atom in the polyalkyleneimine core, wherein said alkoxylated polyalkyleneimine has an empirical formula (I) of $(PEI)_a$-$(EO)_b$-R_1, wherein a is the average number-average molecular weight (MW_{PEI}) of the polyalkyleneimine core of the alkoxylated polyalkyleneimine and is in the range of from 100 to 100,000 Daltons, wherein b is the average degree of ethoxylation in said one or more side chains of the alkoxylated polyalkyleneimine and is in the range of from 5 to 40, and wherein R_1 is independently selected from the group consisting of hydrogen, C_1-C_4 alkyls, and combinations thereof.

[0044] The composition may comprise an alkoxylated polyalkyleneimine, wherein said alkoxylated polyalkyleneimine has a polyalkyleneimine core with one or more side chains bonded to at least one nitrogen atom in the polyalkyleneimine core, wherein the alkoxylated polyalkyleneimine has an empirical formula (II) of $(PEI)_o$-$(EO)_m(PO)_n$-R_2 or $(PEI)_o$-$(PO)_n(EO)_m$-R_2, wherein o is the average number-average molecular weight (MW_{PEI}) of the polyalkyleneimine core of the alkoxylated polyalkyleneimine and is in the range of from 100 to 100,000 Daltons, wherein m is the average degree of ethoxylation in said one or more side chains of the alkoxylated polyalkyleneimine which ranges from 10 to 50, wherein *n* is the average degree of propoxylation in said one or more side chains of the alkoxylated polyalkyleneimine which ranges from 1 to 50, and wherein R_2 is independently selected from the group consisting of hydrogen, C_1-C_4 alkyls, and combinations thereof.

[0045] The composition may comprise the combination of a non-ionic soil release polymer and an anionic soil release polymer.

[0046] Highly preferably, the composition is substantially free of pre-formed peracid.

[0047] The composition may comprise:

(a) from 1wt% to 20wt% sodium percarbonate;
(b) from 0.5wt% to 5wt% bleach activator; and
(c) from 0.5wt% to 5wt% chelant.

[0048] The bleach activator may comprise sodium tetraacetylethylenediamine, and wherein the composition may comprise from 0.5wt% to 5wt% sodium tetraacetylethylenediamine.

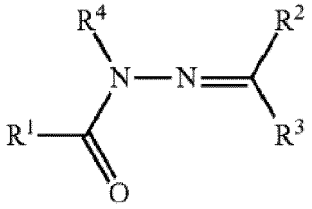
[0049] The chelant may comprise sodium salt of methylglycine diacetic acid (MGDA), and wherein the composition may comprise from 0.5wt% to 5wt% sodium salt of methylglycine diacetic acid (MGDA).

[0050] The chelant may comprise ethylenediamine disuccinic acid (EDDS), and wherein the composition may comprise from 0.5wt% to 5wt% ethylenediamine disuccinic acid (EDDS).

[0051] The chelant may comprise disodium 4,5-dihydroxy-1,3-benzenedisulfonate, and wherein the composition may comprise from 0.5wt% to 5wt% disodium 4,5-dihydroxy-1,3-benzenedisulfonate.

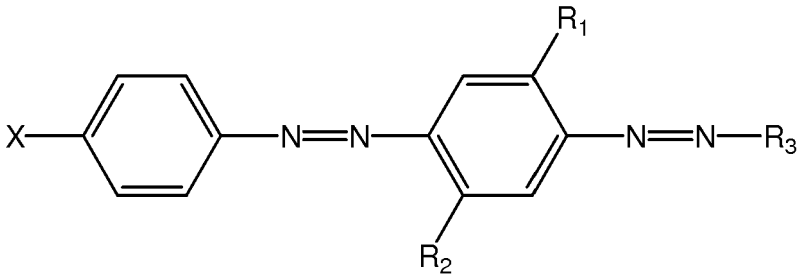
[0052] The composition may comprises 4,4'-bis-(triazinylamino)-stilbene-2,2'-disulfonic acid brightener and/or 4,4'-distyryl biphenyl brightener.

[0053] The composition may comprises an acyl hydrazone bleach catalyst, wherein the acyl hydrazone bleach catalyst has the formula I:



wherein, R^1 is selected from the groups comprising CF_3, C_{1-28} alkyl, C_{2-28} alkenyl, C_{2-22} alkynyl, C_{3-12} cycloalkyl, C_{3-12} cycloalkenyl, phenyl, naphthyl, C_{7-9} aralkyl, C_{3-20} heteroalkyl, C_{3-12} cycloheteroalkyl or a mixture thereof;
R^2 and R^3 are independently selected from the group comprising hydrogen, substituted C_{1-28} alkyl, C_{2-28} alkenyl, C_{2-22} alkynyl, C_{3-12} cycloalkyl, C_{3-12} cycloalkenyl, C_{7-9} aralkyl, C_{3-28} heteroalkyl, C_{3-12} cycloheteroalkyl, C_{5-16} heteroaralkyl, phenyl, naphthyl, heteroaryl or a mixture thereof;
or R^2 and R^3 are linked to form a substituted 5-, 6-, 7-, 8- or 9-membered ring that optionally comprises heteroatoms;
and R^4 is selected from the groups comprising hydrogen, C_{1-28} alkyl, C_{2-28} alkenyl, C_{2-22} alkynyl, C_{3-12} cycloalkyl, C_{3-12} cycloalkenyl, C_{7-9} aralkyl, C_{3-20} heteroalkyl, C_{3-12} cycloheteroalkyl, C_{5-16} heteroaralkyl, substituted phenyl, naphthyl, heteroaryl or a mixture thereof.

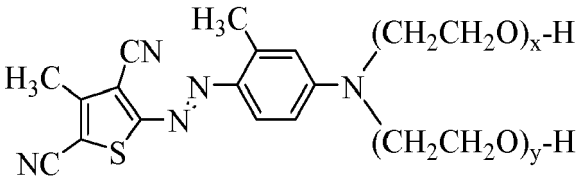
[0054] The composition may comprise a hueing agent having the following structure:



wherein:

R1 and R2 are independently selected from the group consisting of: H; alkyl; alkoxy; alkyleneoxy; alkyl capped alkyleneoxy; urea; and amido;
R3 is a substituted aryl group;
X is a substituted group comprising sulfonamide moiety and optionally an alkyl and/or aryl moiety, and wherein the substituent group comprises at least one alkyleneoxy chain that comprises an average molar distribution of at least four alkyleneoxy moieties.

[0055] The composition may comprise a hueing agent having the following structure:



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

[0056] The composition may comprise a hueing agent selected from Acid Violet 50, Direct Violet 9, 66 and 99, Solvent Violet 13 and any combination thereof.

[0057] The composition may comprise a protease having at least 90% identity to the amino acid sequence of *Bacillus amyloliquefaciens* as shown in SEQ ID NO:9

[0058] The composition may comprise a protease having at least 90% identity to the amino acid sequence of *Bacillus amyloliquefaciens BPN'* as shown in SEQ ID NO: 10, and which comprises one or more mutations selected from group consisting of V4I, S9R, A15T, S24G, S33T, S53G, V68A, N76D, S78N, S101M/N, Y167F, and Y217Q.

[0059] The composition may comprise a protease having at least 90% identity to the amino acid sequence of *Bacillus thermoproteolyticus* as shown in SEQ ID NO:11.

[0060] The composition may comprise a protease having at least 90% identity to the amino acid sequence of *Bacillus lentus* as shown in SEQ IS NO:12, and which comprises one or mutations selected from the group consisting of S3T, V4I, A194P, V199M, V205I, and L217D.

[0061] The composition may comprise a protease having at least 90% identity to the amino acid sequence of *Bacillus sp. TY145* as shown in SEQ ID NO:13.

[0062] The composition may comprises a protease having at least 90% identity to the amino acid sequence of *Bacillus sp. KSM-KP43* as shown in SEQ ID NO:14.

[0063] The composition may comprise a variant of the wild-type amylase from *Bacillus sp.* which has at least 90% identity for amino acid sequence SEQ ID NO:5, and which comprises one or more mutations at positions N195, G477, G304, W140, W189, D134, V206, Y243, E260, F262, W284, W347, W439, W469 and/or G476, and optionally which comprises the deletions of D183* and/or G184*.

[0064] The composition may comprise a variant of the wild-type amylase from *Bacillus sp.* which has at least 90% identity for amino acid sequence SEQ ID NO:6, and which comprises one or more mutations at positions 9, 26, 30, 33, 82, 37, 106, 118, 128, 133, 149, 150, 160, 178, 182, 186, 193, 195, 202, 214, 231, 256, 257, 258, 269, 270, 272, 283, 295, 296, 298, 299, 303, 304, 305, 311, 314, 315, 318, 319, 320, 323, 339, 345, 361, 378, 383, 419, 421, 437, 441, 444, 445, 446, 447, 450, 458, 461, 471, 482 and/or 484, preferably that also contain the deletions of D183* and G184*.

[0065] The composition may comprise a variant of the wild-type amylase from *Bacillus sp. KSM-K38* which has at least 90% identity for amino acid sequence SEQ ID NO:7.

[0066] The composition may comprise a variant of the wild-type amylase from *Cytophaga sp.* which has at least 60% identity for amino acid sequence SEQ ID NO:8.

[0067] The composition may comprise a variant of the wild-type lipase from *Thermomyces lanuginosus* which has at least 90% identity for amino acid sequence SEQ ID NO:1.

[0068] The composition may comprise a variant of the wild-type lipase from *Thermomyces lanuginosus* which has at least 90% identity for amino acid sequence SEQ ID NO:1, and which comprises T231R and/or N233R mutations.

[0069] The composition may comprise a variant of the wild-type lipase from *Thermomyces lanuginosus* which has at least 90% identity for amino acid sequence SEQ ID NO:1, and which comprises G91A, D96G, G225R, T231R and/or N233R mutations.

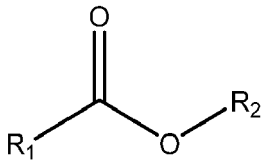
the composition may comprise a cellulase that is a wild-type or variant of a microbially-derived endoglucanase endogenous to *Bacillus* sp. exhibiting endo-beta-1,4-glucanase activity (E.C. 3.2.1.4) which has at least 90% identity to the amino acid sequence SEQ ID NO:2.

[0070] The composition may comprise cellulase that is a wild-type or variant of a microbially-derived endoglucanase endogenous to *Paenibacillus polymyxa* exhibiting endo-beta-1,4-glucanase activity (E.C. 3.2.1.4) which has at least 90% identity to amino acid sequence SEQ ID NO:3.

[0071] The composition may comprise a cellulase that is a hybrid fusion endoglucanase comprising a Glycosyl Hydrolase Family 45 catalytic domain that is a wild-type or variant of a microbially-derived endoglucanase endogenous to *Melanocarpus albomyces,* and a carbohydrate binding module that is a wild-type or variant of a carbohydrate binding module endogenous to *Trichoderma reesei,* and which has at least 90% identity to amino acid sequence SEQ ID NO:4.

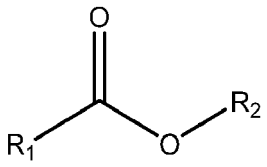
[0072] The composition may comprise an enzyme selected from mannanase, pectate lyase, laccase, polyesterase, galactanase, acyltransferase, and any combination thereof.

[0073] The composition may comprise a perfume, wherein the perfume comprises from 60wt% to 85wt% ester perfume raw materials having the structure:



wherein R1 and R2 are independently selected from C1 to C30 linear or branched, cyclic or non-cyclic, aromatic or non-aromatic, saturated or un-saturated, substituted or unsubstituted alkyl.

[0074] The composition may comprise: (a) alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.0; (b) perfume, wherein the perfume comprises from 60wt% to 85wt% ester perfume raw materials having the structure:



wherein R1 and R2 are independently selected from C1 to C30 linear or branched, cyclic or non-cyclic, aromatic or non-aromatic, saturated or un-saturated, substituted or unsubstituted alkyl.

[0075] The composition may comprise polyvinyl N oxide polymer.

[0076] The composition may comprise: silicate salt particles, especially sodium silicate particles; and/or carbonate salt particles, especially sodium bicarbonate particles. However it may be preferred for the composition to be free of silicate salt particles, especially free of sodium silicate particles. It may also be preferred for the composition to be free of carbonate salt particles, especially free of sodium carbonate particles.

[0077] Preferably, the composition comprises from 1wt% to 10wt% dry-added acid particles, preferably from 2wt% to 8wt% dry-added acid particles. A suitable dry-added acid is an organic acid, preferably a carboxylic acid, preferably cirtric acid.

[0078] Base detergent particle: The solid free-flowing particulate laundry detergent composition typically comprises a base detergent particle. The base detergent particle may be in the form of spray-dried particle, or an agglomerate, preferably the base particle is in the form of a spray-dried particle. Typically, the composition comprises from 30wt% to 90wt% base detergent particle, preferably from 40wt% to 80wt%, more preferably from 50wt% to 70wt% base detergent particle.

[0079] The base detergent particle typically comprises from 1wt% to 10wt% organic acid, preferably from 2wt% to 8wt%, or from 3wt% to 7wt% organic acid. A preferred organic acid is a carboxylic acid, preferably citric acid.

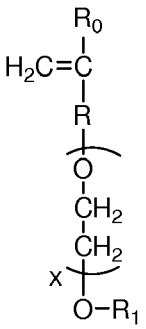
[0080] The base detergent particle typically comprises from 1wt% to 10wt% magnesium sulphate, preferably from 2wt% to 8wt%, or from 3wt% to 6wt% magnesium sulphate.

[0081] The base detergent particle typically comprises from 1wt% to 8wt%, preferably from 2wt% to 6wt% or from 2wt% to 4wt% zeolite. A preferred zeolite is zeolite A, especially zeolite 4A.

[0082] The base detergent particle typically comprises from 5wt% to 40wt%, preferably from 10wt% to 30wt% anionic detersive surfactant. A preferred anionic detersive surfactant is alkyl benzene sulphonate.

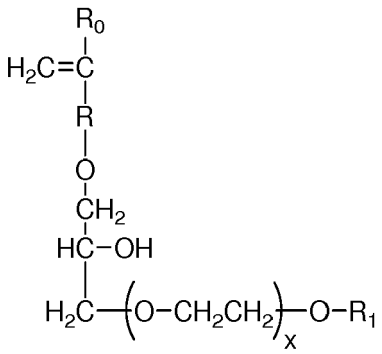
[0083] The base detergent particle typically comprises from 0.5wt% to 5wt% polymer, preferably from 1wt% to 3wt% polymer. A preferred polymer is a carboxylate polymer, more preferably a co-polymer that comprises: (i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising 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 C_1 to C_{20} organic group;

formula (II)



wherein 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 C_1 to C_{20} organic group.

It may be preferred that the polymer has a weight average molecular weight of at least 50kDa, or even at least 70kDa.

[0084] Typically, the base detergent particle comprises from 30wt% to 70wt%, or from 40wt% to 70wt% sodium sulphate.

[0085] Co-surfactant particle: Typically, the detergent composition comprises a co-surfactant particle. Typically, the composition comprises from 1wt% to 20wt%, or from 2wt% to 15wt%, or from 3wt% to 10wt% co-surfactant particle. Typically, the co-surfactant particle is in the form of an agglomerate, extrudate, needle, noodle, flake or any combination thereof. Preferably, the co-surfactant particle is in the form of an agglomerate.

[0086] The co-surfactant particle typically comprises from 25wt% to 60wt% co-surfactant, preferably from 30wt% to 50wt% co-surfactant. A preferred co-surfactant is alkyl alkoxy sulphate, preferably a C_{10}-C_{20} alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.0.

[0087] Typically, the co-surfactant particle comprises from 10wt% to 50wt% carbonate salt. A preferred carbonate salt is sodium carbonate and/or sodium bicarbonate. However, it may be preferred for the co-surfactant particle to be free of carbonate salt, especially free of sodium carbonate.

[0088] Typically, the co-surfactant particle comprises from 1wt% to 30wt% silica, preferably from 5wt% to 20wt% silica.

[0089] Detergent Ingredients: Suitable laundry detergent compositions comprise a detergent ingredient selected from: detersive surfactant, such as anionic detersive surfactants, non-ionic detersive surfactants, cationic detersive surfactants, zwitterionic detersive surfactants and amphoteric detersive surfactants; polymers, such as carboxylate polymers, soil release polymer, anti-redeposition polymers, cellulosic polymers and care polymers; bleach, such as sources of hydrogen peroxide, bleach activators, bleach catalysts and pre-formed peracids; photobleach, such as such as zinc and/or aluminium sulphonated phthalocyanine; enzymes, such as proteases, amylases, cellulases, lipases; zeolite builder; phosphate builder; co-builders, such as citric acid and citrate; sulphate salt, such as sodium sulphate; chloride salt, such as sodium chloride; brighteners; chelants; hueing agents; dye transfer inhibitors; dye fixative agents; perfume; silicone; fabric softening agents, such as clay; flocculants, such as polyethyleneoxide; suds supressors; and any combination thereof.

[0090] The composition may comprise: silicate salt, especially sodium silicate; and/or carbonate salt, especially sodium bicarbonate and/or sodium carbonate. However it may be preferred for the composition to be free of silicate salt, especially free of sodium silicate. It may also be preferred for the composition to be free of carbonate salt, especially free of sodium carbonate and/or sodium bicarbonate.

[0091] The composition may have a pH profile such that upon dilution in de-ionized water at a concentration of 1g/L at a temperature of 20oC, the composition has a pH in the range of from 6.5 to 8.5, preferably from 7.0 to 8.0.

[0092] Suitable laundry detergent compositions may have a low buffering capacity. Such laundry detergent compositions typically have a reserve alkalinity to pH 7.5 of less than 5.0gNaOH/100g, preferably less than 3.0gNaOH/100g.

[0093] The composition is preferably substantially free of pre-formed peracid. The composition is prerferably substantially free of phthalimido-peroxycaproic acid. Substantially free means no deliberately added.

[0094] Detersive Surfactant: Suitable detersive surfactants include anionic detersive surfactants, non-ionic detersive surfactant, cationic detersive surfactants, zwitterionic detersive surfactants and amphoteric detersive surfactants. Suitable detersive surfactants may be linear or branched, substituted or un-substituted, and may be derived from petrochemical material or biomaterial.

[0095] Anionic detersive surfactant: Suitable anionic detersive surfactants include sulphonate and sulphate detersive surfactants.

[0096] Suitable sulphonate detersive surfactants include methyl ester sulphonates, alpha olefin sulphonates, alkyl benzene sulphonates, especially alkyl benzene sulphonates, preferably C_{10-13} alkyl benzene sulphonate. Suitable alkyl benzene sulphonate (LAS) is obtainable, preferably obtained, by sulphonating commercially available linear alkyl ben-

zene (LAB); suitable LAB includes low 2-phenyl LAB, other suitable LAB include high 2-phenyl LAB, such as those supplied by Sasol under the tradename Hyblene®.

[0097] Suitable sulphate detersive surfactants include alkyl sulphate, preferably C_{8-18} alkyl sulphate, or predominantly C_{12} alkyl sulphate.

[0098] A preferred sulphate detersive surfactant is alkyl alkoxylated sulphate, preferably alkyl ethoxylated sulphate, preferably a C_{8-18} alkyl alkoxylated sulphate, preferably a C_{8-18} alkyl ethoxylated sulphate, preferably the alkyl alkoxylated sulphate has an average degree of alkoxylation of from 0.5 to 20, preferably from 0.5 to 10, preferably the alkyl alkoxylated sulphate is a C_{8-18} alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 10, preferably from 0.5 to 5, more preferably from 0.5 to 3 and most preferably from 0.5 to 1.5.

[0099] The alkyl sulphate, alkyl alkoxylated sulphate and alkyl benzene sulphonates may be linear or branched, substituted or un-substituted, and may be derived from petrochemical material or biomaterial.

[0100] Other suitable anionic detersive surfactants include alkyl ether carboxylates.

[0101] Suitable anionic detersive surfactants may be in salt form, suitable counter-ions include sodium, calcium, magnesium, amino alcohols, and any combination thereof. A preferred counter-ion is sodium.

[0102] Non-ionic detersive surfactant: Suitable non-ionic detersive surfactants are selected from the group consisting of: C_8-C_{18} alkyl ethoxylates, such as, NEODOL® non-ionic surfactants from Shell; C_6-C_{12} alkyl phenol alkoxylates wherein preferably the alkoxylate units are ethyleneoxy units, propyleneoxy units or a mixture thereof; C_{12}-C_{18} alcohol and C_6-C_{12} alkyl phenol condensates with ethylene oxide/propylene oxide block polymers such as Pluronic® from BASF; alkylpolysaccharides, preferably alkylpolyglycosides; methyl ester ethoxylates; polyhydroxy fatty acid amides; ether capped poly(oxyalkylated) alcohol surfactants; and mixtures thereof.

[0103] Suitable non-ionic detersive surfactants are alkylpolyglucoside and/or an alkyl alkoxylated alcohol.

[0104] Suitable non-ionic detersive surfactants include alkyl alkoxylated alcohols, preferably C_{8-18} alkyl alkoxylated alcohol, preferably a C_{8-18} alkyl ethoxylated alcohol, preferably the alkyl alkoxylated alcohol has an average degree of alkoxylation of from 1 to 50, preferably from 1 to 30, or from 1 to 20, or from 1 to 10, preferably the alkyl alkoxylated alcohol is a C_{8-18} alkyl ethoxylated alcohol having an average degree of ethoxylation of from 1 to 10, preferably from 1 to 7, more preferably from 1 to 5 and most preferably from 3 to 7. The alkyl alkoxylated alcohol can be linear or branched, and substituted or un-substituted.

[0105] Suitable nonionic detersive surfactants include secondary alcohol-based detersive surfactants.

[0106] Cationic detersive surfactant: Suitable cationic detersive surfactants include alkyl pyridinium compounds, alkyl quaternary ammonium compounds, alkyl quaternary phosphonium compounds, alkyl ternary sulphonium compounds, and mixtures thereof.

[0107] Preferred cationic detersive surfactants are quaternary ammonium compounds having the general formula:

$$(R)(R_1)(R_2)(R_3)N^+ X^-$$

wherein, R is a linear or branched, substituted or unsubstituted C_{6-18} alkyl or alkenyl moiety, R_1 and R_2 are independently selected from methyl or ethyl moieties, R_3 is a hydroxyl, hydroxymethyl or a hydroxyethyl moiety, X is an anion which provides charge neutrality, preferred anions include: halides, preferably chloride; sulphate; and sulphonate.

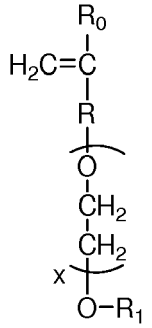
[0108] Zwitterionic detersive surfactant: Suitable zwitterionic detersive surfactants include amine oxides and/or betaines.

[0109] Polymer: Suitable polymers include carboxylate polymers, soil release polymers, anti-redeposition polymers, cellulosic polymers, care polymers and any combination thereof.

[0110] Carboxylate polymer: The composition may comprise a carboxylate polymer, such as a maleate/acrylate random copolymer or polyacrylate homopolymer. Suitable carboxylate polymers include: polyacrylate homopolymers having a molecular weight of from 4,000 Da to 9,000 Da; maleate/acrylate random copolymers having a molecular weight of from 50,000 Da to 100,000 Da, or from 60,000 Da to 80,000 Da.

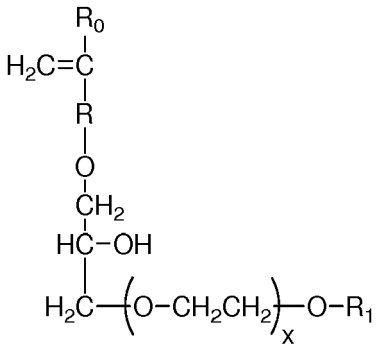
[0111] Another suitable carboxylate polymer is a co-polymer that comprises: (i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising carboxyl groups; (ii) from 1 to less than 49 wt% structural units derived from one or more monomers comprising sulfonate moieties; 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 C_1 to C_{20} organic group;

formula (II)



wherein 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 C_1 to C_{20} organic group.
It may be preferred that the polymer has a weight average molecular weight of at least 50kDa, or even at least 70kDa.

[0112] Soil release polymer: The composition may comprise a soil release polymer. A suitable soil release polymer has a structure as defined by one of the following structures (I), (II) or (III):

(I) $-[(OCHR^1\text{-}CHR^2)_a\text{-}O\text{-}OC\text{-}Ar\text{-}CO\text{-}]_d$

(II) $-[(OCHR^3\text{-}CHR^4)_b\text{-}O\text{-}OC\text{-}sAr\text{-}CO\text{-}]_e$

(III) $-[(OCHR^5\text{-}CHR^6)_c\text{-}OR^7]_f$

wherein:

a, b and c are from 1 to 200;
d, e and f are from 1 to 50;
Ar is a 1,4-substituted phenylene;
sAr is 1,3-substituted phenylene substituted in position 5 with SO_3Me;
Me is Li, K, Mg/2, Ca/2, Al/3, ammonium, mono-, di-, tri-, or tetraalkylammonium wherein the alkyl groups are C_1-C_{18} alkyl or C_2-C_{10} hydroxyalkyl, or mixtures thereof;
R^1, R^2, R^3, R^4, R^5 and R^6 are independently selected from H or C_1-C_{18} n- or iso-alkyl; and
R^7 is a linear or branched C_1-C_{18} alkyl, or a linear or branched C_2-C_{30} alkenyl, or a cycloalkyl group with 5 to 9 carbon atoms, or a C_8-C_{30} aryl group, or a C_6-C_{30} arylalkyl group.

[0113] Suitable soil release polymers are sold by Clariant under the TexCare® series of polymers, e.g. TexCare® SRN240 and TexCare® SRA300. Other suitable soil release polymers are sold by Solvay under the Repel-o-Tex® series of polymers, e.g. Repel-o-Tex® SF2 and Repel-o-Tex® Crystal.

[0114] Anti-redeposition polymer: Suitable anti-redeposition polymers include polyethylene glycol polymers and/or polyethyleneimine polymers.

[0115] Suitable polyethylene glycol polymers include random graft co-polymers comprising: (i) hydrophilic backbone comprising polyethylene glycol; and (ii) hydrophobic side chain(s) selected from the group consisting of: C_4-C_{25} alkyl group, polypropylene, polybutylene, vinyl ester of a saturated C_1-C_6 mono-carboxylic acid, C_1-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. Suitable polyethylene glycol polymers are described in WO08/007320.

[0116] Cellulosic polymer: Suitable cellulosic polymers are selected from alkyl cellulose, alkyl alkoxyalkyl cellulose, carboxyalkyl cellulose, alkyl carboxyalkyl cellulose, sulphoalkyl cellulose, more preferably selected from carboxymethyl cellulose, methyl cellulose, methyl hydroxyethyl cellulose, methyl carboxymethyl cellulose, and mixures thereof.

[0117] Suitable carboxymethyl celluloses have a degree of carboxymethyl substitution from 0.5 to 0.9 and a molecular weight from 100,000 Da to 300,000 Da.

Suitable carboxymethyl celluloses have a degree of substitution greater than 0.65 and a degree of blockiness greater than 0.45, e.g. as described in WO09/154933.

[0118] Care polymers: Suitable care polymers include cellulosic polymers that are cationically modified or hydrophobically modified. Such modified cellulosic polymers can provide anti-abrasion benefits and dye lock benefits to fabric during the laundering cycle. Suitable cellulosic polymers include cationically modified hydroxyethyl cellulose.

[0119] Other suitable care polymers include dye lock polymers, for example the condensation oligomer produced by the condensation of imidazole and epichlorhydrin, preferably in ratio of 1:4:1. A suitable commercially available dye lock polymer is Polyquart® FDI (Cognis).

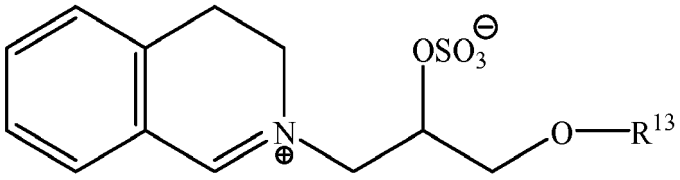
[0120] Other suitable care polymers include amino-silicone, which can provide fabric feel benefits and fabric shape retention benefits.

[0121] Bleach: Suitable bleach includes sources of hydrogen peroxide, bleach activators, bleach catalysts, pre-formed peracids and any combination thereof. A particularly suitable bleach includes a combination of a source of hydrogen peroxide with a bleach activator and/or a bleach catalyst.

[0122] Source of hydrogen peroxide: Suitable sources of hydrogen peroxide include sodium perborate and/or sodium percarbonate.

[0123] Bleach activator: Suitable bleach activators include tetra acetyl ethylene diamine and/or alkyl oxybenzene sulphonate.

[0124] Bleach catalyst: The composition may comprise a bleach catalyst. Suitable bleach catalysts include oxaziridinium bleach catalysts, transistion metal bleach catalysts, especially manganese and iron bleach catalysts. A suitable bleach catalyst has a structure corresponding to general formula below:



wherein R^{13} is selected from the group consisting of 2-ethylhexyl, 2-propylheptyl, 2-butyloctyl, 2-pentylnonyl, 2-hexyldecyl, n-dodecyl, n-tetradecyl, n-hexadecyl, n-octadecyl, iso-nonyl, isodecyl, iso-tridecyl and iso-pentadecyl.

[0125] Pre-formed peracid: Suitable pre-form peracids include phthalimido-peroxycaproic acid. However, it is preferred that the composition is substantially free of pre-formed peracid. By: "substantially free" it is meant: "no deliberately added".

[0126] Enzymes: Suitable enzymes include lipases, proteases, cellulases, amylases and any combination thereof.

[0127] Protease: Suitable proteases include metalloproteases and/or serine proteases. Examples of suitable neutral or alkaline proteases include: subtilisins (EC 3.4.21.62); trypsin-type or chymotrypsin-type proteases; and metalloproteases. The suitable proteases include chemically or genetically modified mutants of the aforementioned suitable proteases.

[0128] Suitable commercially available protease enzymes include those sold under the trade names Alcalase®, Savinase®, Primase®, Durazym®, Polarzyme®, Kannase®, Liquanase®, Liquanase Ultra®, Savinase Ultra®, Ovozyme®, Neutrase®, Everlase® and Esperase® by Novozymes A/S (Denmark), those sold under the tradename Maxatase®, Maxacal®, Maxapem®, Preferenz P® series of proteases including Preferenz® P280, Preferenz® P281, Preferenz® P2018-C, Preferenz® P2081-WE, Preferenz® P2082-EE and Preferenz® P2083-A/J, Properase®, Purafect®, Purafect Prime®, Purafect Ox®, FN3®, FN4®, Excellase® and Purafect OXP® by DuPont, 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 folowing 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.

[0129] A suitable protease is described in WO11/140316 and WO11/072117.

[0130] Amylase: Suitable amylases are derived from AA560 alpha amylase endogenous to Bacillus sp. DSM 12649, preferably having the following mutations: R118K, D183*, G184*, N195F, R320K, and/or R458K. Suitable commercially available amylases include Stainzyme®, Stainzyme® Plus, Natalase, Termamyl®, Termamyl® Ultra, Liquezyme® SZ, Duramyl®, Everest® (all Novozymes) and Spezyme® AA, Preferenz S® series of amylases, Purastar® and Purastar® Ox Am, Optisize® HT Plus (all Du Pont).

A suitable amylase is described in WO06/002643.

[0131] Cellulase: Suitable cellulases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are also suitable. Suitable cellulases include cellulases from the genera *Bacillus, Pseudomonas, Humicola, Fusarium, Thielavia, Acremonium,* e.g., the fungal cellulases produced from *Humicola insolens, Myceliophthora thermophila* and *Fusarium oxysporum*.

[0132] Commercially available cellulases include Celluzyme®, Carezyme®, and Carezyme® Premium, Celluclean® and Whitezyme® (Novozymes A/S), Revitalenz® series of enzymes (Du Pont), and Biotouch® series of enzymes (AB Enzymes). Suitable commercially available cellulases include Carezyme® Premium, Celluclean® Classic. Suitable cellulases are described in WO07/144857 and WO10/056652.

[0133] Lipase: Suitable lipases include those of bacterial, fungal or synthetic origin, and variants thereof. Chemically modified or protein engineered mutants are also suitable. Examples of suitable lipases include lipases from *Humicola* (synonym *Thermomyces*), e.g., from *H. lanuginosa* (*T. lanuginosus*).

[0134] The lipase may be a "first cycle lipase", e.g. such as those described in WO06/090335 and WO13/116261. In one aspect, the lipase is a first-wash lipase, preferably a variant of the wild-type lipase from Thermomyces lanuginosus comprising T231R and/or N233R mutations. Preferred lipases include those sold under the tradenames Lipex®, Lipolex® and Lipoclean® by Novozymes, Bagsvaerd, Denmark.

[0135] Other suitable lipases include: Liprl 139, e.g. as described in WO2013/171241; and TfuLip2, e.g. as described in WO2011/084412 and WO2013/033318.

[0136] Other enzymes: Other suitable enzymes are bleaching enzymes, such as peroxidases/oxidases, which include those of plant, bacterial or fungal origin and variants thereof. Commercially available peroxidases include Guardzyme® (Novozymes A/S). Other suitable enzymes include choline oxidases and perhydrolases such as those used in Gentle Power Bleach™.

[0137] Other suitable enzymes include pectate lyases sold under the tradenames X-Pect®, Pectaway® (from Novozymes A/S, Bagsvaerd, Denmark) and PrimaGreen® (DuPont) and mannanases sold under the tradenames Mannaway® (Novozymes A/S, Bagsvaerd, Denmark), and Mannastar® (Du Pont).

[0138] Identity: When used herein identity or sequence identity refers to the relatedness between two amino acid sequences.

[0139] For purposes of the present invention, the degree of sequence identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, J. Mol. Biol. 48: 443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, Trends Genet. 16: 276-277), preferably version 3.0.0 or later. The optional parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix. The output of Needle labeled "longest identity" (obtained using the -nobrief option) is used as the percent identity and is calculated as follows:

$$\text{(Identical Residues x 100)/(Length of Alignment – Total Number of Gaps in Alignment)}$$

[0140] Zeolite builder: The composition may comprise zeolite builder. The composition may comprise from 0wt% to 5wt% zeolite builder, or 3wt% zeolite builder. The composition may even be substantially free of zeolite builder; substantially free means "no deliberately added". Typical zeolite builders include zeolite A, zeolite P and zeolite MAP.

[0141] Phosphate builder: The composition may comprise phosphate builder. The composition may comprise from 0wt% to 5wt% phosphate builder, or to 3wt%, phosphate builder. The composition may even be substantially free of phosphate builder; substantially free means "no deliberately added". A typical phosphate builder is sodium tri-polyphosphate.

[0142] Carbonate salt: The composition may comprise carbonate salt. The composition may comprise from 0wt% to 5wt% carbonate salt. The composition may even be substantially free of carbonate salt; substantially free means "no deliberately added". Suitable carbonate salts include sodium carbonate and sodium bicarbonate.

[0143] Silicate salt: The composition may comprise silicate salt. The composition may comprise from 0wt% to 5wt% silicate salt. The composition may even be substantially free of silicate salt; substantially free means "no deliberately added". A preferred silicate salt is sodium silicate, especially preferred are sodium silicates having a $Na_2O:SiO_2$ ratio of from 1.0 to 2.8, preferably from 1.6 to 2.0.

[0144] Sulphate salt: A suitable sulphate salt is sodium sulphate.

[0145] Brightener: Suitable fluorescent brighteners include: di-styryl biphenyl compounds, e.g. Tinopal® CBS-X, diamino stilbene di-sulfonic acid compounds, e.g. Tinopal® DMS pure Xtra and Blankophor® HRH, and Pyrazoline compounds, e.g. Blankophor® SN, and coumarin compounds, e.g. Tinopal® SWN.
Preferred brighteners are: sodium 2 (4-styryl-3-sulfophenyl)-2H-napthol[1,2-d]triazole, disodium 4,4'-bis{[(4-anilino-6-(N methyl-N-2 hydroxyethyl)amino 1 ,3,5- triazin-2-yl)]amino}stilbene-2-2' disulfonate, disodium 4,4'-bis{[(4-anilino-6-morpholino-1,3,5-triazin-2-yl)]amino} stilbene-2-2' disulfonate, and disodium 4,4'- bis(2-sulfostyryl)biphenyl. A suitable fluorescent brightener is C.I. Fluorescent Brightener 260, which may be used in its beta or alpha crystalline forms, or a mixture of these forms.

[0146] Chelant: The composition may also comprise a chelant selected from: diethylene triamine pentaacetate, diethylene triamine penta(methyl phosphonic acid), ethylene diamine-N'N'-disuccinic acid, ethylene diamine tetraacetate, ethylene diamine tetra(methylene phosphonic acid) and hydroxyethane di(methylene phosphonic acid). A preferred chelant is ethylene diamine-N'N'-disuccinic acid (EDDS) and/or hydroxyethane diphosphonic acid (HEDP). The composition preferably comprises ethylene diamine-N'N'- disuccinic acid or salt thereof. Preferably the ethylene diamine-N'N'-disuccinic acid is in S,S enantiomeric form. Preferably the composition comprises 4,5-dihydroxy-m-benzenedisulfonic acid disodium salt. Preferred chelants may also function as calcium carbonate crystal growth inhibitors such as: 1-hydroxyethanediphosphonic acid (HEDP) and salt thereof; N,N-dicarboxymethyl-2-aminopentane-1,5-dioic acid and salt thereof; 2-phosphonobutane-1,2,4-tricarboxylic acid and salt thereof; and combination thereof.

[0147] Hueing agent: Suitable hueing agents include small molecule dyes, typically falling into the Colour Index (C.I.) classifications of Acid, Direct, Basic, Reactive (including hydrolysed forms thereof) or Solvent or Disperse dyes, for example classified as Blue, Violet, Red, Green or Black, and provide the desired shade either alone or in combination. Preferred such hueing agents include Acid Violet 50, Direct Violet 9, 66 and 99, Solvent Violet 13 and any combination thereof.

[0148] Many hueing agents are known and described in the art which may be suitable for the present invention, such as hueing agents described in WO2014/089386.

[0149] Suitable hueing agents include phthalocyanine and azo dye conjugates, such as described in WO2009/069077.

[0150] Suitable hueing agents may be alkoxylated. Such alkoxylated compounds may be produced by organic synthesis that may produce a mixture of molecules having different degrees of alkoxylation. Such mixtures may be used directly to provide the hueing agent, or may undergo a purification step to increase the proportion of the target molecule. Suitable hueing agents include alkoxylated bis-azo dyes, such as described in WO2012/054835, and/or alkoxylated thiophene azo dyes, such as described in WO2008/087497 and WO2012/166768.

[0151] The hueing agent may be incorporated into the detergent composition as part of a reaction mixture which is the result of the organic synthesis for a dye molecule, with optional purification step(s). Such reaction mixtures generally comprise the dye molecule itself and in addition may comprise un-reacted starting materials and/or by-products of the organic synthesis route. Suitable hueing agents can be incorporated into hueing dye particles, such as described in WO 2009/069077.

[0152] Dye transfer inhibitors: Suitable dye transfer inhibitors include polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinylpyrrolidone, polyvinyloxazolidone, 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).

[0153] Perfume: Suitable perfumes comprise perfume materials selected from the group: (a) perfume materials having a ClogP of less than 3.0 and a boiling point of less than 250°C (quadrant 1 perfume materials); (b) perfume materials having a ClogP of less than 3.0 and a boiling point of 250°C or greater (quadrant 2 perfume materials); (c) perfume materials having a ClogP of 3.0 or greater and a boiling point of less than 250°C (quadrant 3 perfume materials); (d) perfume materials having a ClogP of 3.0 or greater and a boiling point of 250°C or greater (quadrant 4 perfume materials);

and (e) mixtures thereof.

[0154] It may be preferred for the perfume to be in the form of a perfume delivery technology. Such delivery technologies further stabilize and enhance the deposition and release of perfume materials from the laundered fabric. Such perfume delivery technologies can also be used to further increase the longevity of perfume release from the laundered fabric. Suitable perfume delivery technologies include: perfume microcapsules, pro-perfumes, polymer assisted deliveries, molecule assisted deliveries, fiber assisted deliveries, amine assisted deliveries, cyclodextrin, starch encapsulated accord, zeolite and other inorganic carriers, and any mixture thereof. A suitable perfume microcapsule is described in WO2009/101593.

[0155] Silicone: Suitable silicones include polydimethylsiloxane and amino-silicones. Suitable silicones are described in WO05075616.

[0156] Process for making the solid composition: Typically, the particles of the composition can be prepared by any suitable method. For example: spray-drying, agglomeration, extrusion and any combination thereof.

[0157] Typically, a suitable spray-drying process comprises the step of forming an aqueous slurry mixture, transferring it through at least one pump, preferably two pumps, to a pressure nozzle. Atomizing the aqueous slurry mixture into a spray-drying tower and drying the aqueous slurry mixture to form spray-dried particles. Preferably, the spray-drying tower is a counter-current spray-drying tower, although a co-current spray-drying tower may also be suitable.

[0158] Typically, the spray-dried powder is subjected to cooling, for example an air lift. Typically, the spray-drying powder is subjected to particle size classification, for example a sieve, to obtain the desired particle size distribution. Preferably, the spray-dried powder has a particle size distribution such that weight average particle size is in the range of from 300 micrometers to 500 micrometers, and less than 10wt% of the spray-dried particles have a particle size greater than 2360 micrometers.

[0159] It may be preferred to heat the aqueous slurry mixture to elevated temperatures prior to atomization into the spray-drying tower, such as described in WO2009/158162.

[0160] It may be preferred for anionic surfactant, such as linear alkyl benzene sulphonate, to be introduced into the spray-drying process after the step of forming the aqueous slurry mixture: for example, introducing an acid precursor to the aqueous slurry mixture after the pump, such as described in WO 09/158449.

[0161] It may be preferred for a gas, such as air, to be introduced into the spray-drying process after the step of forming the aqueous slurry, such as described in WO2013/181205.

[0162] It may be preferred for any inorganic ingredients, such as sodium sulphate and sodium carbonate, if present in the aqueous slurry mixture, to be micronized to a small particle size such as described in WO2012/134969.

[0163] Typically, a suitable agglomeration process comprises the step of contacting a detersive ingredient, such as a detersive surfactant, e.g. linear alkyl benzene sulphonate (LAS) and/or alkyl alkoxylated sulphate, with an inorganic material, such as sodium carbonate and/or silica, in a mixer. The agglomeration process may also be an in-situ neutralization agglomeration process wherein an acid precursor of a detersive surfactant, such as LAS, is contacted with an alkaline material, such as carbonate and/or sodium hydroxide, in a mixer, and wherein the acid precursor of a detersive surfactant is neutralized by the alkaline material to form a detersive surfactant during the agglomeration process.

[0164] Other suitable detergent ingredients that may be agglomerated include polymers, chelants, bleach activators, silicones and any combination thereof.

[0165] The agglomeration process may be a high, medium or low shear agglomeration process, wherein a high shear, medium shear or low shear mixer is used accordingly. The agglomeration process may be a multi-step agglomeration process wherein two or more mixers are used, such as a high shear mixer in combination with a medium or low shear mixer. The agglomeration process can be a continuous process or a batch process.

[0166] It may be preferred for the agglomerates to be subjected to a drying step, for example to a fluid bed drying step. It may also be preferred for the agglomerates to be subjected to a cooling step, for example a fluid bed cooling step.

[0167] Typically, the agglomerates are subjected to particle size classification, for example a fluid bed elutriation and/or a sieve, to obtain the desired particle size distribution. Preferably, the agglomerates have a particle size distribution such that weight average particle size is in the range of from 300 micrometers to 800 micrometers, and less than 10wt% of the agglomerates have a particle size less than 150 micrometers and less than 10wt% of the agglomerates have a particle size greater than 1200 micrometers.

[0168] It may be preferred for fines and over-sized agglomerates to be recycled back into the agglomeration process. Typically, over-sized particles are subjected to a size reduction step, such as grinding, and recycled back into an appropriate place in the agglomeration process, such as the mixer. Typically, fines are recycled back into an appropriate place in the agglomeration process, such as the mixer.

[0169] It may be preferred for ingredients such as polymer and/or non-ionic detersive surfactant and/or perfume to be sprayed onto base detergent particles, such as spray-dried base detergent particles and/or agglomerated base detergent particles. Typically, this spray-on step is carried out in a tumbling drum mixer.

[0170] Method of laundering fabric: The method of laundering fabric comprises the step of contacting the solid composition to water to form a wash liquor, and laundering fabric in said wash liquor. Typically, the wash liquor has a

temperature of above 0°C to 90°C, or to 60°C, or to 40°C, or to 30°C, or to 20°C. The fabric may be contacted to the water prior to, or after, or simultaneous with, contacting the solid composition with water. Typically, the wash liquor is formed by contacting the laundry detergent to water in such an amount so that the concentration of laundry detergent composition in the wash liquor is from 0.2g/l to 20g/l, or from 0.5g/l to 10g/l, or to 5.0g/l. The method of laundering fabric can be carried out in a front-loading automatic washing machine, top loading automatic washing machines, including high efficiency automatic washing machines, or suitable hand-wash vessels._Typically, the wash liquor comprises 90 litres or less, or 60 litres or less, or 15 litres or less, or 10 litres or less of water. Typically, 200g or less, or 150g or less, or 100g or less, or 50g or less of laundry detergent composition is contacted to water to form the wash liquor.

Solid free-flowing particulate laundry detergent composition illustrative examples:

Ingredient	Amount (in wt%)
Anionic detersive surfactant (such as alkyl benzene sulphonate, alkyl ethoxylated sulphate and mixtures thereof)	from 8wt% to 15wt%
Non-ionic detersive surfactant (such as alkyl ethoxylated alcohol)	from 0.1wt% to 4wt%
Cationic detersive surfactant (such as quaternary ammonium compounds)	from 0wt% to 4wt%
Other detersive surfactant (such as zwiterionic detersive surfactants, amphoteric surfactants and mixtures thereof)	from 0wt% to 4wt%
Carboxylate polymer (such as co-polymers of maleic acid and acrylic acid and/or carboxylate polymers comprising ether moieties and sulfonate moieties)	from 0.1wt% to 4wt%
Polyethylene glycol polymer (such as a polyethylene glycol polymer comprising polyvinyl acetate side chains)	from 0wt% to 4wt%
Polyester soil release polymer (such as Repel-o-tex and/or Texcare polymers)	from 0wt% to 2wt%
Cellulosic polymer (such as carboxymethyl cellulose, methyl cellulose and combinations thereof)	from 0.5wt% to 2wt%
Other polymer (such as care polymers)	from 0wt% to 4wt%
Zeolite builder and phosphate builder (such as zeolite 4A and/or sodium tripolyphosphate)	from 0wt% to 4wt%
Other co-builder (such as sodium citrate and/or citric acid)	from 0wt% to 3wt%
Citric Acid	from 4wt% to 16wt%
Magnesium Sulphate	from 1wt% to 4wt%
Carbonate salt (such as sodium carbonate and/or sodium bicarbonate)	from 0wt% to 4wt%
Silicate salt (such as sodium silicate)	from 0wt% to 4wt%
Filler (such as sodium sulphate and/or bio-fillers)	from 10wt% to 70wt%
Source of hydrogen peroxide (such as sodium percarbonate)	from 0wt% to 20wt%
Bleach activator (such as tetraacetylethylene diamine (TAED) and/or nonanoyloxybenzenesulphonate (NOBS))	from 0wt% to 8wt%
Bleach catalyst (such as oxaziridinium-based bleach catalyst and/or transition metal bleach catalyst)	from 0wt% to 0.1wt%
Other bleach (such as reducing bleach and/or pre-formed peracid)	from 0wt% to 10wt%
Photobleach (such as zinc and/or aluminium sulphonated phthalocyanine)	from 0wt% to 0.1wt%
Chelant (such as ethylenediamine-N'N'-disuccinic acid (EDDS) and/or hydroxyethane diphosphonic acid (HEDP))	from 0.2wt% to 1wt%

(continued)

Ingredient	Amount (in wt%)
Hueing agent (such as direct violet 9, 66, 99, acid red 50, solvent violet 13 and any combination thereof)	from 0wt% to 1wt%
Brightener (C.I. fluorescent brightener 260 or C.I. fluorescent brightener 351)	from 0.1wt% to 0.4wt%
Protease (such as Savinase, Savinase Ultra, Purafect, FN3, FN4 and any combination thereof)	from 0.1wt% to 0.4wt%
Amylase (such as Termamyl, Termamyl ultra, Natalase, Optisize, Stainzyme, Stainzyme Plus and any combination thereof)	from 0wt% to 0.2wt%
Cellulase (such as Carezyme and/or Celluclean)	from 0wt% to 0.2wt%
Lipase (such as Lipex, Lipolex, Lipoclean and any combination thereof)	from 0wt% to 1wt%
Other enzyme (such as xyloglucanase, cutinase, pectate lyase, mannanase, bleaching enzyme)	from 0wt% to 2wt%
Fabric softener (such as montmorillonite clay and/or polydimethylsiloxane (PDMS))	from 0wt% to 15wt%
Flocculant (such as polyethylene oxide)	from 0wt% to 1wt%
Suds suppressor (such as silicone and/or fatty acid)	from 0wt% to 4wt%
Perfume (such as perfume microcapsule, spray-on perfume, starch encapsulated perfume accords, perfume loaded zeolite, and any combination thereof)	from 0.1wt% to 1wt%
Aesthetics (such as coloured soap rings and/or coloured speckles/noodles)	from 0wt% to 1wt%
Miscellaneous	balance to 100wt%

EXAMPLES

Example 1 - Low pH formulation (embodiment of the present invention)

[0171] A low pH base powder was prepared by mixing the ingredients together. The composition of the base powder was:

Ingredient	Amount (wt% of base powder)
Alkyl benzene sulphonate anionic detersive surfactant	17.1
Sodium sulphate	69.3
Citric acid	12.4
Water & miscellaneous	to 100wt%

[0172] 143g Sodium sulphate, 18g sodium carbonate, 18g sodium silicate, 45g sodium percarbonate, 12.5g tetraacetyl ethylene diamine (TAED), and 4.1g tri sodium salt of methylglycine diacetic acid (MGDA) were added to the 342.5g base powder to form 583.1g of solid free-flowing particulate laundry detergent composition (in accordance with the present invention) having the following formulation:

Ingredient	Amount (wt% of composition)
Alkyl benzene sulphonate anionic detersive surfactant	10.0
Sodium sulphate	65.2
Citric acid	7.3

(continued)

Ingredient	Amount (wt% of composition)
Sodium carbonate	3.1
Sodium silicate	3.1
Sodium percarbonate	7.7
TAED	2.1
MGDA	0.7
Water & miscellaneous	to 100wt%

[0173] The composition had an equilibrium pH at 1wt% dilution in deionized water at 20°C of 7.0.

[0174] The compositon had a reserve alkalinity to pH 7 at 1wt% dilution in deionized water at 20°C of 2.0.

Example 2 - High pH formulation (comparative example)

[0175] A high pH base powder was prepared by mixing the ingredients together. The composition of the base powder was:

Ingredient	Amount (wt% of base powder)
Alkyl benzene sulphonate anionic detersive surfactant	18.0
Sodium sulphate	73.1
Citric acid	7.7
Water & miscellaneous	to 100wt%

[0176] 50g Sodium sulphate, 100g sodium carbonate, 50g sodium silicate, 45g sodium percarbonate, 12.5g tetraacetyl ethylene diamine (TAED) and 4.1g tri sodium salt of methylglycine diacetic acid (MGDA) were added to the 325g base powder to form 586.6g of solid free-flowing particulate laundry detergent composition (in accordance with the present invention) having the following formulation:

Ingredient	Amount (wt% of composition)
Alkyl benzene sulphonate anionic detersive surfactant	10.0
Sodium sulphate	49.0
Citric acid	4.3
Sodium carbonate	17.0
Sodium silicate	8.5
Sodium percarbonate	7.7
TAED	2.1
MGDA	0.7
Water & miscellaneous	to 100wt%

[0177] The composition had an equilibrium pH at 1wt% dilution in deionized water at 20°C of 10.5.

[0178] The compositon had a reserve alkalinity to pH 7 at 1wt% dilution in deionized water at 20°C of 9.6.

Washing method: The following method demonstrates the ability of Samples 1 and 2 to remove stains during the wash process. The above samples were added separately into the pots of a tergotometer (quantity of sample = 1% of the bulk preparation as described in the Examples, sampled-down uniformly to give a representative sample). The volume of each pot was 1 L. The wash temperature was set to 20 °C or 30 °C (as stated in the results). Throughout the procedure, 21 gpg water was used. The products were agitated for 2 minutes before addition of fabrics (4 internal replicates of each

stain (wine on polycotton (CFT)), and 15 g of WfK SBL 2004 soil sheets per pot with additional knitted cotton ballast to make the total fabric weight up to 35 g). Once the fabrics were added, the wash solution was agitated for 15 minutes or 30 minutes in total (as stated in the results). After 15 minutes, two of the stains were removed from the wash and put in a cool drier for 20 minutes (no heating, to drive off excess water and halt any further cleaning). The remaining stains were washed to 30 minutes in total and dried in the same fashion. Both sets of stains were then placed in a ventilated drying cabinet overnight before being analysed to measure the stain removal from the fabric. This procedure wash repeated a further two times to give a total of three external replicates.

Stain Removal Analysis: The fabrics were analysed using commercially available DigiEye software for L, a, b values. SRI values were then calculated from the L, a, b values using the formula shown. The higher the SRI, the better the stain removal.

$$\%SRI\ (stain\ removal) = 100*((\Delta E_b - \Delta E_a)/\Delta E_b)$$

$$\Delta E_b = \sqrt{((L_c\text{-}L_b)^2 + (a_c\text{-}a_b)^2 + b_c\text{-}b_b)^2)}$$

$$\Delta E_a = \sqrt{((L_c\text{-}L_a)^2 + (a_c\text{-}a_a)^2 + b_c\text{-}b_a)^2)}$$

Subscript 'b' denotes data for the stain before washing
Subscript 'a' denotes data for the stain after washing
Subscript 'c' denotes data for the unstained fabric

[0179] Thus, L*a*b* values are taken of the unstained fabric, of the stained fabric before washing and of the stained fabric after washing.

At a wash bath temperature of 30°C

	%SRI Wash time of 30 mins	%SRI Wash time of 15mins
Sample 1: low pH (invention)	78.51	71.01
Sample 2: high pH (comparative)	69.79	67.42

At a wash bath temperature of 20°C

	%SRI Wash time of 30 mins	%SRI Wash time of 15mins
Sample 1: low pH (invention)	72.43	68.12
Sample 2: high pH (comparative)	64.21	64.16

[0180] 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".

SEQUENCE LISTING

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Gly Phe Leu Ala Leu Asp Asn Thr Asn Lys Leu Ile Val Leu Ser Phe
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His Ser Leu Gly Gly Ala Leu Ala Thr Val Ala Gly Ala Asp Leu Arg
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Gly Asn Gly Tyr Asp Ile Asp Val Phe Ser Tyr Gly Ala Pro Arg Val
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Gly Thr Leu Val Pro Val Thr Arg Asn Asp Ile Val Lys Ile Glu Gly
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Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
        35                  40                  45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
    50                  55                  60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65                  70                  75                  80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
                85                  90                  95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
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Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
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Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
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Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asn
    210                 215                 220

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

Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
        515                 520                 525

Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
    530                 535                 540

Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
545                 550                 555                 560

Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
                565                 570                 575

Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
            580                 585                 590

Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
        595                 600                 605

Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
    610                 615                 620

Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
625                 630                 635                 640
```

Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
645 650 655

Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
660 665 670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
675 680 685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
690 695 700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe
705 710 715 720

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
725 730 735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
740 745 750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
755 760 765

Glu Glu Lys Glu Glu
770

<210> 3
<211> 524
<212> PRT
<213> Paenibacillus polymyxa

<400> 3

Val Val His Gly Gln Thr Ala Lys Thr Ile Thr Ile Lys Val Asp Thr
1 5 10 15

Phe Lys Asp Arg Lys Pro Ile Ser Pro Tyr Ile Tyr Gly Thr Asn Gln
20 25 30

Asp Leu Ala Gly Asp Glu Asn Met Ala Ala Arg Arg Leu Gly Gly Asn
35 40 45

Arg Met Thr Gly Tyr Asn Trp Glu Asn Asn Met Ser Asn Ala Gly Ser
50 55 60

Asp Trp Gln Gln Ser Ser Asp Asn Tyr Leu Cys Ser Asn Gly Gly Leu
65 70 75 80

```
Thr Gln Ala Glu Cys Glu Lys Pro Gly Ala Val Thr Thr Ser Phe His
                85                  90                  95

Asp Gln Ser Leu Lys Leu Gly Thr Tyr Ser Leu Val Thr Leu Pro Met
            100                 105                 110

Ala Gly Tyr Val Ala Lys Asp Gly Asn Gly Ser Val Gln Glu Ser Glu
        115                 120                 125

Lys Ala Pro Ser Ala Arg Trp Asn Gln Val Val Asn Ala Lys Asn Ala
    130                 135                 140

Pro Phe Gln Leu Gln Pro Asp Leu Asn Asp Asn Arg Val Tyr Val Asp
145                 150                 155                 160

Glu Phe Val His Phe Leu Val Asn Lys Tyr Gly Thr Ala Ser Thr Lys
                165                 170                 175

Ala Gly Val Lys Gly Tyr Ala Leu Asp Asn Glu Pro Ala Leu Trp Ser
            180                 185                 190

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

Val Asp Arg Ser Val Ser Leu Ser Lys Ala Val Lys Ala Ile Asp Ala
    210                 215                 220

Gly Ala Glu Val Phe Gly Pro Val Leu Tyr Gly Phe Gly Ala Tyr Lys
225                 230                 235                 240

Asp Leu Gln Thr Ala Pro Asp Trp Asp Ser Val Lys Gly Asn Tyr Ser
                245                 250                 255

Trp Phe Val Asp Tyr Tyr Leu Asp Gln Met Arg Leu Ser Ser Gln Val
            260                 265                 270

Glu Gly Lys Arg Leu Leu Asp Val Phe Asp Val His Trp Tyr Pro Glu
        275                 280                 285

Ala Met Gly Gly Gly Ile Arg Ile Thr Asn Glu Val Gly Asn Asp Glu
    290                 295                 300

Thr Lys Lys Ala Arg Met Gln Ala Pro Arg Thr Leu Trp Asp Pro Thr
305                 310                 315                 320

Tyr Lys Glu Asp Ser Trp Ile Ala Gln Trp Asn Ser Glu Phe Leu Pro
```

325 330 335

Ile Leu Pro Arg Leu Lys Gln Ser Val Asp Lys Tyr Tyr Pro Gly Thr
340 345 350

Lys Leu Ala Met Thr Glu Tyr Ser Tyr Gly Gly Glu Asn Asp Ile Ser
355 360 365

Gly Gly Ile Ala Met Thr Asp Val Leu Gly Ile Leu Gly Lys Asn Asp
370 375 380

Val Tyr Met Ala Asn Tyr Trp Lys Leu Lys Asp Gly Val Asn Asn Tyr
385 390 395 400

Val Ser Ala Ala Tyr Lys Leu Tyr Arg Asn Tyr Asp Gly Lys Asn Ser
405 410 415

Thr Phe Gly Asp Thr Ser Val Ser Ala Gln Thr Ser Asp Ile Val Asn
420 425 430

Ser Ser Val His Ala Ser Val Thr Asn Ala Ser Asp Lys Glu Leu His
435 440 445

Leu Val Val Met Asn Lys Ser Met Asp Ser Ala Phe Asp Ala Gln Phe
450 455 460

Asp Leu Ser Gly Ala Lys Thr Tyr Ile Ser Gly Lys Val Trp Gly Phe
465 470 475 480

Asp Lys Asn Ser Ser Gln Ile Lys Glu Ala Ala Pro Ile Thr Gln Ile
485 490 495

Ser Gly Asn Arg Phe Thr Tyr Thr Val Pro Pro Leu Thr Ala Tyr His
500 505 510

Ile Val Leu Thr Thr Gly Asn Asp Thr Ser Pro Val
515 520

<210> 4
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid protein containing fragments originating from proteins endogenous to Melanocarpus albomyces and Trichoderma reesei

<400> 4

Ala Asn Gly Gln Ser Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys

```
1               5                   10                  15

Gly Trp Arg Gly Lys Gly Pro Val Asn Gln Pro Val Tyr Ser Cys Asp
            20                  25                  30

Ala Asn Phe Gln Arg Ile His Asp Phe Asp Ala Val Ser Gly Cys Glu
        35                  40                  45

Gly Gly Pro Ala Phe Ser Cys Ala Asp His Ser Pro Trp Ala Ile Asn
    50                  55                  60

Asp Asn Leu Ser Tyr Gly Phe Ala Ala Thr Ala Leu Ser Gly Gln Thr
65                  70                  75                  80

Glu Glu Ser Trp Cys Cys Ala Cys Tyr Ala Leu Thr Phe Thr Ser Gly
                85                  90                  95

Pro Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Ser Thr Gly Gly
            100                 105                 110

Asp Leu Gly Ser Asn His Phe Asp Leu Asn Ile Pro Gly Gly Gly Val
        115                 120                 125

Gly Leu Phe Asp Gly Cys Thr Pro Gln Phe Gly Gly Leu Pro Gly Ala
    130                 135                 140

Arg Tyr Gly Gly Ile Ser Ser Arg Gln Glu Cys Asp Ser Phe Pro Glu
145                 150                 155                 160

Pro Leu Lys Pro Gly Cys Gln Trp Arg Phe Asp Trp Phe Gln Asn Ala
                165                 170                 175

Asp Asn Pro Ser Phe Thr Phe Glu Arg Val Gln Cys Pro Glu Glu Leu
            180                 185                 190

Val Ala Arg Thr Gly Cys Arg Arg His Asp Asp Gly Gly Phe Pro Ala
        195                 200                 205

Val Gln Ile Pro Ser Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro Pro
    210                 215                 220

Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr
225                 230                 235                 240

Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys Gly
                245                 250                 255
```

```
Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr Cys
            260                 265                 270

Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
        275                 280
```

<210> 5
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 5

```
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1               5                   10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
            20                  25                  30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
        35                  40                  45

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

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

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
                85                  90                  95

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

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

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
145                 150                 155                 160

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
```

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

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

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

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

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

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

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

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
    370                 375                 380

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

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
                405                 410                 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
        435                 440                 445
```

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Lys Arg
485

<210> 6
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 6

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
20 25 30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

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

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

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

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

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

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

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

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
        195                 200                 205

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

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

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

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

Gly Ala Ile 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 Lys Ser Gly
    290                 295                 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
305                 310                 315                 320

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

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

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
    370                 375                 380

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

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
                405                 410                 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430
```

```
Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
        435                 440                 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
    450                 455                 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

Ile Trp Val Asn Lys
                485
```

<210> 7
<211> 480
<212> PRT
<213> Bacillus sp. KSM-K38

<400> 7

```
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

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

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

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
                85                  90                  95

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

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

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
145                 150                 155                 160
```

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

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
        195                 200                 205

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

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

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
            260                 265                 270

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

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
    290                 295                 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305                 310                 315                 320

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

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

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
        355                 360                 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
    370                 375                 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385                 390                 395                 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
```

405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465 470 475 480

<210> 8
<211> 483
<212> PRT
<213> Cytophaga sp.

<400> 8

Ala Ala Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Val Pro
1 5 10 15

Asn Asp Gly Gln Gln Trp Asn Arg Leu Arg Thr Asp Ala Pro Tyr Leu
20 25 30

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

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

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

Gly Glu Leu Lys Ser Ala Val Asn Thr Leu His Ser Asn Gly Ile Gln
85 90 95

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

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

Gly Arg Gly Thr Thr Tyr Ser Asn Phe Lys Trp Gln Trp Phe His Phe

```
145                 150                 155                 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Gln Gln
```

<210> 9
<211> 300
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 9

```
Ala Ala Thr Thr Gly Thr Gly Thr Thr Leu Lys Gly Lys Thr Val Ser
1               5                   10                  15

Leu Asn Ile Ser Ser Glu Ser Gly Lys Tyr Val Leu Arg Asp Leu Ser
            20                  25                  30

Lys Pro Thr Gly Thr Gln Ile Ile Thr Tyr Asp Leu Gln Asn Arg Glu
        35                  40                  45

Tyr Asn Leu Pro Gly Thr Leu Val Ser Ser Thr Thr Asn Gln Phe Thr
    50                  55                  60

Thr Ser Ser Gln Arg Ala Ala Val Asp Ala His Tyr Asn Leu Gly Lys
65                  70                  75                  80

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

Lys Gly Gly Lys Ile Val Ser Ser Val His Tyr Gly Ser Arg Tyr Asn
            100                 105                 110

Asn Ala Ala Trp Ile Gly Asp Gln Met Ile Tyr Gly Asp Gly Asp Gly
        115                 120                 125
```

```
Ser Phe Phe Ser Pro Leu Ser Gly Ser Met Asp Val Thr Ala His Glu
    130                 135                 140

Met Thr His Gly Val Thr Gln Glu Thr Ala Asn Leu Asn Tyr Glu Asn
145                 150                 155                 160

Gln Pro Gly Ala Leu Asn Glu Ser Phe Ser Asp Val Phe Gly Tyr Phe
                165                 170                 175

Asn Asp Thr Glu Asp Trp Asp Ile Gly Glu Asp Ile Thr Val Ser Gln
            180                 185                 190

Pro Ala Leu Arg Ser Leu Ser Asn Pro Thr Lys Tyr Gly Gln Pro Asp
        195                 200                 205

Asn Phe Lys Asn Tyr Lys Asn Leu Pro Asn Thr Asp Ala Gly Asp Tyr
    210                 215                 220

Gly Gly Val His Thr Asn Ser Gly Ile Pro Asn Lys Ala Ala Tyr Asn
225                 230                 235                 240

Thr Ile Thr Lys Ile Gly Val Asn Lys Ala Glu Gln Ile Tyr Tyr Arg
                245                 250                 255

Ala Leu Thr Val Tyr Leu Thr Pro Ser Ser Thr Phe Lys Asp Ala Lys
            260                 265                 270

Ala Ala Leu Ile Gln Ser Ala Arg Asp Leu Tyr Gly Ser Gln Asp Ala
        275                 280                 285

Ala Ser Val Glu Ala Ala Trp Asn Ala Val Gly Leu
    290                 295                 300
```

<210> 10
<211> 275
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 10

```
Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
1               5                   10                  15

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

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
        35                  40                  45
```

```
Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
    50                  55                  60

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

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
                85                  90                  95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
            100                 105                 110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
        115                 120                 125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
    130                 135                 140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145                 150                 155                 160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
                165                 170                 175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
            180                 185                 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
        195                 200                 205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
    210                 215                 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
225                 230                 235                 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
                245                 250                 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
            260                 265                 270

Ala Ala Gln
        275
```

<210> 11
<211> 316
<212> PRT

<213> Bacillus thermoproteolyticus

<400> 11

```
Ile Thr Gly Thr Ser Thr Val Gly Val Gly Arg Gly Val Leu Gly Asp
1               5                  10                  15

Gln Lys Asn Ile Asn Thr Thr Tyr Ser Thr Tyr Tyr Tyr Leu Gln Asp
            20                  25                  30

Asn Thr Arg Gly Asn Gly Ile Phe Thr Tyr Asp Ala Lys Tyr Arg Thr
        35                  40                  45

Thr Leu Pro Gly Ser Leu Trp Ala Asp Ala Asp Asn Gln Phe Phe Ala
    50                  55                  60

Ser Tyr Asp Ala Pro Ala Val Asp Ala His Tyr Tyr Ala Gly Val Thr
65                  70                  75                  80

Tyr Asp Tyr Tyr Lys Asn Val His Asn Arg Leu Ser Tyr Asp Gly Asn
                85                  90                  95

Asn Ala Ala Ile Arg Ser Ser Val His Tyr Ser Gln Gly Tyr Asn Asn
            100                 105                 110

Ala Phe Trp Asn Gly Ser Gln Met Val Tyr Gly Asp Gly Asp Gly Gln
        115                 120                 125

Thr Phe Ile Pro Leu Ser Gly Gly Ile Asp Val Val Ala His Glu Leu
    130                 135                 140

Thr His Ala Val Thr Asp Tyr Thr Ala Gly Leu Ile Tyr Gln Asn Glu
145                 150                 155                 160

Ser Gly Ala Ile Asn Glu Ala Ile Ser Asp Ile Phe Gly Thr Leu Val
                165                 170                 175

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

Tyr Thr Pro Gly Ile Ser Gly Asp Ser Leu Arg Ser Met Ser Asp Pro
        195                 200                 205

Ala Lys Tyr Gly Asp Pro Asp His Tyr Ser Lys Arg Tyr Thr Gly Thr
    210                 215                 220

Gln Asp Asn Gly Gly Val His Ile Asn Ser Gly Ile Ile Asn Lys Ala
225                 230                 235                 240
```

```
Ala Tyr Leu Ile Ser Gln Gly Gly Thr His Tyr Gly Val Ser Val Val
                245                 250                 255

Gly Ile Gly Arg Asp Lys Leu Gly Lys Ile Phe Tyr Arg Ala Leu Thr
            260                 265                 270

Gln Tyr Leu Thr Pro Thr Ser Asn Phe Ser Gln Leu Arg Ala Ala Ala
        275                 280                 285

Val Gln Ser Ala Thr Asp Leu Tyr Gly Ser Thr Ser Gln Glu Val Ala
    290                 295                 300

Ser Val Lys Gln Ala Phe Asp Ala Val Gly Val Lys
305                 310                 315
```

<210> 12
<211> 269
<212> PRT
<213> Bacillus lentus

<400> 12

```
Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
1               5                   10                  15

His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
            20                  25                  30

Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
        35                  40                  45

Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
    50                  55                  60

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

Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
                85                  90                  95

Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
            100                 105                 110

Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
        115                 120                 125

Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
    130                 135                 140
```

```
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
145                 150                 155                 160

Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
                165                 170                 175

Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
            180                 185                 190

Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
        195                 200                 205

Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
    210                 215                 220

Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225                 230                 235                 240

Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
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Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
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Asp Gln Ser Ile Thr Lys Thr Thr Gly Gly Ser Gly Ile Lys Val Ala
            20                  25                  30

Val Leu Asp Thr Gly Val Tyr Thr Ser His Leu Asp Leu Ala Gly Ser
        35                  40                  45

Ala Glu Gln Cys Lys Asp Phe Thr Gln Ser Asn Pro Leu Val Asp Gly
    50                  55                  60

Ser Cys Thr Asp Arg Gln Gly His Gly Thr His Val Ala Gly Thr Val
65                  70                  75                  80

Leu Ala His Gly Gly Ser Asn Gly Gln Gly Val Tyr Gly Val Ala Pro
                85                  90                  95
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Gln Ala Lys Leu Trp Ala Tyr Lys Val Leu Gly Asp Asn Gly Ser Gly
            100                 105                 110

Tyr Ser Asp Asp Ile Ala Ala Ala Ile Arg His Val Ala Asp Glu Ala
        115                 120                 125

Ser Arg Thr Gly Ser Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser
    130                 135                 140

Ala Lys Asp Ser Leu Ile Ala Ser Ala Val Asp Tyr Ala Tyr Gly Lys
145                 150                 155                 160

Gly Val Leu Ile Val Ala Ala Ala Gly Asn Ser Gly Ser Gly Ser Asn
                165                 170                 175

Thr Ile Gly Phe Pro Gly Gly Leu Val Asn Ala Val Ala Val Ala Ala
            180                 185                 190

Leu Glu Asn Val Gln Gln Asn Gly Thr Tyr Arg Val Ala Asp Phe Ser
        195                 200                 205

Ser Arg Gly Asn Pro Ala Thr Ala Gly Asp Tyr Ile Ile Gln Glu Arg
    210                 215                 220

Asp Ile Glu Val Ser Ala Pro Gly Ala Ser Val Glu Ser Thr Trp Tyr
225                 230                 235                 240

Thr Gly Gly Tyr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His
                245                 250                 255

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

His Ser Gln Leu Arg Thr Glu Leu Gln Asn Arg Ala Lys Val Tyr Asp
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Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
            20                  25                  30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
        35                  40                  45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
    50                  55                  60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65                  70                  75                  80

Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
                85                  90                  95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
            100                 105                 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
        115                 120                 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
    130                 135                 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
145                 150                 155                 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
                165                 170                 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
            180                 185                 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
        195                 200                 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
    210                 215                 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
225                 230                 235                 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
                245                 250                 255
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Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
            260                 265                 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
        275                 280                 285

Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn
    290                 295                 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
305                 310                 315                 320

Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
                325                 330                 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
            340                 345                 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
        355                 360                 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
    370                 375                 380

Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu
385                 390                 395                 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
                405                 410                 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile
            420                 425                 430

Val Asn
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Claims

1. Use of a solid free flowing particulate laundry detergent composition, wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 9.0, to provide improved fabric cleaning performance during a laundering process, wherein the laundering process has a wash time of 30 minutes or less, and wherein the laundering process has a wash bath temperature of 30°C or less.

2. Use according to claim 1, wherein the laundering process has a wash time of 20 minutes or less, and wherein the laundering process has a wash bath temperature of 20°C or less.

3. Use according to any preceding claim, wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 8.0.

4. Use according to any preceding claim, wherein the solid free flowing particulate laundry detergent composition comprises:

(a) anionic detersive surfactant;
(b) from 0wt% to 8wt% zeolite builder;
(c) from 0wt% to 4wt% phosphate builder;
(d) from 0wt% to 8wt% sodium carbonate;
(e) from 0wt% to 8wt% sodium silicate; and
(f) from 4wt% to 20wt% organic acid,

wherein the composition comprises from 30wt% to 90wt% base detergent particle,
wherein the base detergent particle comprising (by weight of the base detergent particle):

(a) from 4wt% to 35wt% anionic detersive surfactant;
(b) optionally, from 1wt% to 8wt% zeolite builder;
(c) from 0wt% to 4wt% phosphate builder;
(d) from 0wt% to 8wt% sodium carbonate;
(e) from 0wt% to 8wt% sodium silicate;
(f) from 1wt% to 16wt% organic acid; and
(g) optionally, from 1wt% to 10wt% magnesium sulphate.

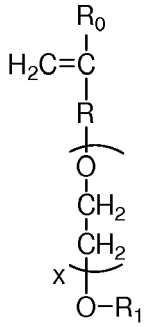
5. Use according to any preceding claim, wherein the organic acid comprises citric acid, and wherein the base detergent particle comprises from 1wt% to 10wt% citric acid, and wherein optionally the organic acid is at least partially coated with a water-dispersible material.

6. Use according to any preceding claim, wherein:

(a) the anionic detersive surfactant comprises alkyl benzene sulphonate and wherein the base detergent particle comprises from 4wt% to 35wt% alkyl benzene sulphonate; and/or
(b) the base detergent particle comprises from 0.5wt% to 5wt% carboxylate co-polymer, wherein the carboxylate co-polymer comprises:

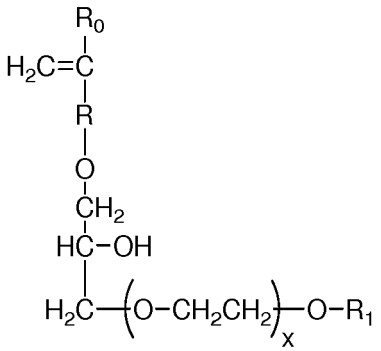
(i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising carboxyl groups;
(ii) from 1 to less than 49 wt% structural units derived from one or more monomers comprising sulfonate moieties; and
(iii) from 1 to 49 wt% structural units derived from one or more types of 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 C_1 to C_{20} organic group;

formula (II)



wherein 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 C_1 to C_{20} organic group; and/or
(c) wherein the base detergent particle comprises from 30wt% to 70wt% sodium sulphate.

7. Use according to any preceding claim, wherein the composition comprises from 1wt% to 20wt% co-surfactant particle, wherein the co-surfactant particle comprises:

(a) from 25wt% to 60wt% co-surfactant;
(b) from 10wt% to 50wt% carbonate salt; and
(c) from 1wt% to 30wt% silica,

and wherein optionally:

(a) the co-surfactant particle is in the form of an agglomerate; and/or
(b) the co-surfactant comprises alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.5, and wherein the co-surfactant particle comprises from 25wt% to 60wt% alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.5; and/or
(c) the co-surfactant particle comprises linear alkyl benzene sulphonate and alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.5.

8. Use according to any preceding claim wherein the composition at 1wt% dilution in deionized water at 20°C, has an equilibrium pH in the range of from 6.5 to 8.5, and wherein optionally the composition has a reserve alkalinity to pH 7.0 of less than 3.0gNaOH/100g.

9. Use according to any preceding claim, wherein the composition comprises:

(a) from 0wt% to 6wt% sodium bicarbonate;
(b) from 0wt% to 4wt% sodium carbonate;
(c) from 0wt% to 4wt% sodium silicate; and
(d) from 0wt% to 4wt% phosphate builder,

and optionally wherein the composition is substantially free of phosphate builder,
and optionally wherein the composition is substantially free of sodium carbonate,
and optionally wherein the composition is substantially free of sodium bicarbonate,
and optionally wherein the composition is substantially free of sodium silicate.

10. Use according to any preceding claim, wherein the composition comprises the combination of a lipase enzyme and soil release polymer.

11. Use according to any preceding claim wherein the composition comprises:

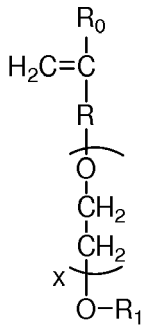
(a) alkyl benzene sulphonate, wherein the alkyl benzene sulphonate comprises at least 25wt% of the combined total of 2-phenyl isomer and 3-phenyl isomer; and/or
(b) alkyl amine oxide.

12. Use according to any preceding claim, wherein the composition comprises:

(a) from 0.5wt% to 8wt% carboxylate co-polymer, wherein the carboxylate co-polymer comprises:

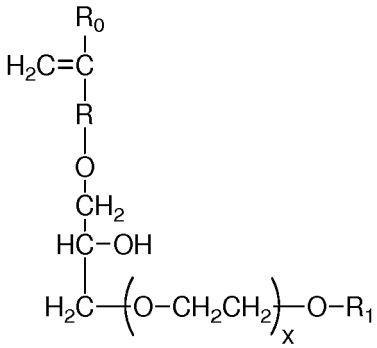
(i) from 50 to less than 98 wt% structural units derived from one or more monomers comprising carboxyl groups;
(ii) from 1 to less than 49 wt% structural units derived from one or more monomers comprising sulfonate moieties; and
(iii) from 1 to 49 wt% structural units derived from one or more types of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

formula (I):

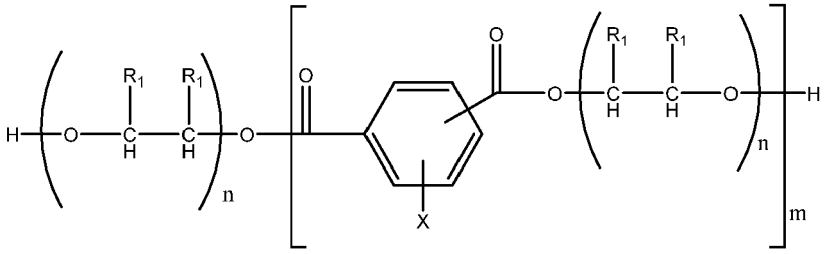


wherein in formula (I), R_0 represents a hydrogen atom or CH_3 group, R represents a CH_2 group, CH_2CH_2 group or single bond, X represents a number 0-5 provided X represents a number 1-5 when R is a single bond, and R_1 is a hydrogen atom or C_1 to C_{20} organic group;

formula (II)

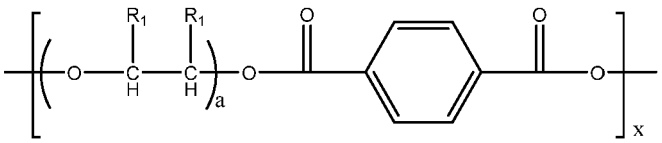


wherein in formula (II), R_0 represents a hydrogen atom or CH_3 group, R represents a CH_2 group, CH_2CH_2 group or single bond, X represents a number 0-5, and R_1 is a hydrogen atom or C_1 to C_{20} organic group; and/or
(b) polyethylene glycol polymer, wherein the polyethylene glycol polymer comprises a polyethylene glycol backbone with grafted polyvinyl acetate side chains; and/or
(c) polyester soil release polymer having the structure:

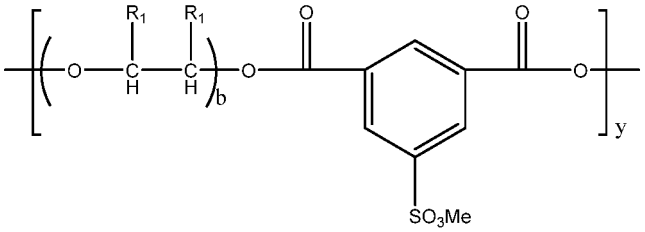


wherein n is from 1 to 10; m is from 1 to 15 ;
X is H or SO_3Me;
wherein Me is H, Na^+, Li^+, K^+, Mg^{2+}, Ca^{2+}, Al^{3+}, ammonium, mono-, di-, tri-, or tetraalkylammonium; wherein the alkyl groups are C_1-C_{18} alkyl or C_2-C_{10} hydroxyalkyl, or any mixture thereof;
R1 are independently selected from H or C_1-C_{18} n- or iso-alkyl; and/or

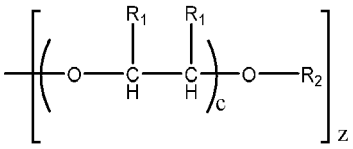
(d) polyester soil release polymer consisting of structure units (1) to (3):



(1)



(2)



(3)

wherein:

a, b and c are from 1 to 10;
x, y is from 1 to 10;
z is from 0.1 to 10;
Me is H, Na^+, Li^+, K^+, Mg^{2+}, Ca^{2+}, Al^{3+}, ammonium, mono-, di-, tri-, or tetraalkylammonium wherein the alkyl groups are C_1-C_{18} alkyl or C_2-C_{10} hydroxyalkyl, or any mixture thereof;
R_1, are independently selected from H or C_1-C_{18} n- or iso-alkyl;
R_2 is a linear or branched C_1-C_{18} alkyl, or a linear or branched C_2-C_{30} alkenyl, or a cycloalkyl group with 5 to 9 carbon atoms, or a C_6-C_{30} aryl group, or a C_6-C_{30} arylalkyl group; and/or

(e) carboxymethyl cellulose having a degree of substitution greater than 0.65 and a degree of blockiness greater than 0.45; and/or
(f) alkoxylated polyalkyleneimine, wherein said alkoxylated polyalkyleneimine has a polyalkyleneimine core with one or more side chains bonded to at least one nitrogen atom in the polyalkyleneimine core, wherein said alkoxylated polyalkyleneimine has an empirical formula (I) of $(PEI)_a$-$(EO)_b$-R_1, wherein a is the average number-average molecular weight (MW_{PEI}) of the polyalkyleneimine core of the alkoxylated polyalkyleneimine and is in the range of from 100 to 100,000 Daltons, wherein b is the average degree of ethoxylation in said one or more side chains of the alkoxylated polyalkyleneimine and is in the range of from 5 to 40, and wherein R_1 is inde-

pendently selected from the group consisting of hydrogen, C_1-C_4 alkyls, and combinations thereof; and/or
(g) alkoxylated polyalkyleneimine, wherein said alkoxylated polyalkyleneimine has a polyalkyleneimine core with one or more side chains bonded to at least one nitrogen atom in the polyalkyleneimine core, wherein the alkoxylated polyalkyleneimine has an empirical formula (II) of $(PEI)_o$-$(EO)_m(PO)_n$-R_2 or $(PEI)_o$-$(PO)_n(EO)_m$-R_2, wherein o is the average number-average molecular weight (MW_{PEI}) of the polyalkyleneimine core of the alkoxylated polyalkyleneimine and is in the range of from 100 to 100,000 Daltons, wherein *m* is the average degree of ethoxylation in said one or more side chains of the alkoxylated polyalkyleneimine which ranges from 10 to 50, wherein *n* is the average degree of propoxylation in said one or more side chains of the alkoxylated polyalkyleneimine which ranges from 1 to 50, and wherein R_2 is independently selected from the group consisting of hydrogen, C_1-C_4 alkyls, and combinations thereof; and/or
(h) the combination of a non-ionic soil release polymer and an anionic soil release polymer.

13. Use according to any preceding claim, wherein the composition is substantially free of pre-formed peracid.

14. Use according to any preceding claim, wherein the composition comprises:

(a) from 1wt% to 20wt% sodium percarbonate;
(b) from 0.5wt% to 5wt% bleach activator; and
(c) from 0.5wt% to 5wt% chelant.

15. Use according to any preceding claim, wherein the composition comprises from 0.5wt% to 5wt% sodium tetraacetylethylenediamine.

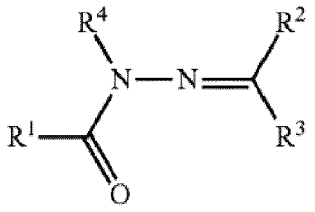
16. Use according to any preceding claim, wherein the composition comprises:

(a) from 0.5wt% to 5wt% tri sodium salt of methylglycine diacetic acid (MGDA); and/or
(b) from 0.5wt% to 5wt% ethylenediamine disuccinic acid (EDDS).

17. Use according to any preceding claim, wherein the composition comprises 4,4'-bis-(triazinylamino)-stilbene-2,2'-disulfonic acid brightener and/or 4,4'-distyryl biphenyl brightener.

18. Use according to any preceding claim, wherein the composition comprises from 0.5wt% to 4wt% disodium 4,5-dihydroxy-1,3-benzenedisulfonate.

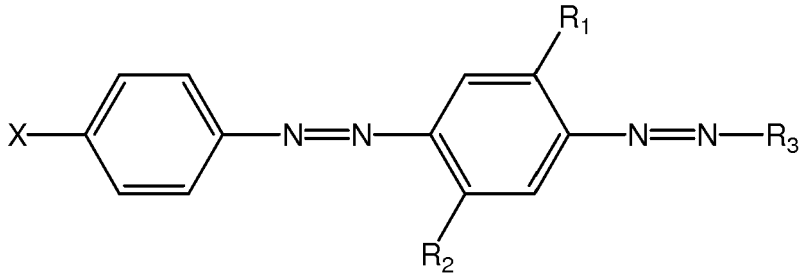
19. Use according to any preceding claim, wherein the composition comprises acyl hydrazone bleach catalyst, wherein the acyl hydrazone bleach catalyst has the formula I:



wherein, R^1 is selected from the groups comprising CF_3, C_{1-28} alkyl, C_{2-28} alkenyl, C_{2-22} alkynyl, C_{3-12} cycloalkyl, C_{3-12} cycloalkenyl, phenyl, naphthyl, C_{7-9} aralkyl, C_{3-20} heteroalkyl, C_{3-12} cycloheteroalkyl or a mixture thereof;
R^2 and R^3 are independently selected from the group comprising hydrogen, substituted C_{1-28} alkyl, C_{2-28} alkenyl, C_{2-22} alkynyl, C_{3-12} cycloalkyl, C_{3-12} cycloalkenyl, C_{7-9} aralkyl, C_{3-28} heteroalkyl, C_{3-12} cycloheteroalkyl, C_{5-16} heteroaralkyl, phenyl, naphthyl, heteroaryl or a mixture thereof;
or R^2 and R^3 are linked to form a substituted 5-, 6-, 7-, 8- or 9-membered ring that optionally comprises heteroatoms;
and R^4 is selected from the groups comprising hydrogen, C_{1-28} alkyl, C_{2-28} alkenyl, C_{2-22} alkynyl, C_{3-12} cycloalkyl, C_{3-12} cycloalkenyl, C_{7-9} aralkyl, C_{3-20} heteroalkyl, C_{3-12} cycloheteroalkyl, C_{5-16} heteroaralkyl, substituted phenyl, naphthyl, heteroaryl or a mixture thereof.

20. Use according to any preceding claim, wherein the composition comprises:

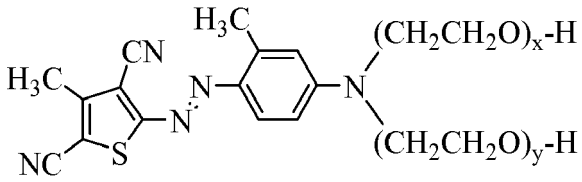
(a) hueing agent having the following structure:



wherein:

R1 and R2 are independently selected from the group consisting of: H; alkyl; alkoxy; alkyleneoxy; alkyl capped alkyleneoxy; urea; and amido;
R3 is a substituted aryl group;
X is a substituted group comprising sulfonamide moiety and optionally an alkyl and/or aryl moiety, and wherein the substituent group comprises at least one alkyleneoxy chain that comprises an average molar distribution of at least four alkyleneoxy moieties; and/or

(b) hueing agent having the following structure:



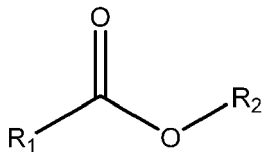
wherein the index values x and y are independently selected from 1 to 10; and/or
(c) hueing agent selected from Acid Violet 50, Direct Violet 9, 66 and 99, Solvent Violet 13 and any combination thereof.

21. Use according to any preceding claim, wherein the composition comprises an enzyme selected from:

(a) protease having at least 90% identity to the amino acid sequence of *Bacillus amyloliquefaciens* as shown in SEQ ID NO:9;
(b) protease having at least 90% identity to the amino acid sequence of *Bacillus amyloliquefaciens BPN'* as shown in SEQ ID NO:10, and which comprises one or more mutations selected from group consisting of V4I, S9R, A15T, S24G, S33T, S53G, V68A, N76D, S78N, S101M/N, Y167F, and Y217Q;
(c) protease having at least 90% identity to the amino acid sequence of *Bacillus thermoproteolyticus* as shown in SEQ ID NO:11;
(d) protease having at least 90% identity to the amino acid sequence of *Bacillus lentus* as shown in SEQ IS NO:12, and which comprises one or mutations selected from the group consisting of S3T, V4I, A194P, V199M, V205I, and L217D;
(e) protease having at least 90% identity to the amino acid sequence of *Bacillus sp. TY145* as shown in SEQ ID NO:13;
(f) protease having at least 90% identity to the amino acid sequence of *Bacillus sp. KSM-KP43* as shown in SEQ ID NO:14;
(g) variant of the wild-type amylase from *Bacillus sp.* which has at least 90% identity for amino acid sequence SEQ ID NO:5, and which comprises one or more mutations at positions N195, G477, G304, W140, W189, D134, V206, Y243, E260, F262, W284, W347, W439, W469 and/or G476, and optionally which comprises the deletions of D183* and/or G184*;
(h) variant of the wild-type amylase from *Bacillus sp.* which has at least 90% identity for amino acid sequence SEQ ID NO:6, and which comprises one or more mutations at positions 9, 26, 30, 33, 82, 37, 106, 118, 128, 133, 149, 150, 160, 178, 182, 186, 193, 195, 202, 214, 231, 256, 257, 258, 269, 270, 272, 283, 295, 296, 298, 299, 303, 304, 305, 311, 314, 315, 318, 319, 320, 323, 339, 345, 361, 378, 383, 419, 421, 437, 441, 444, 445,

446, 447, 450, 458, 461, 471, 482 and/or 484, preferably that also contain the deletions of D183* and G184*;
(i) variant of the wild-type amylase from *Bacillus sp. KSM-K38* which has at least 90% identity for amino acid sequence SEQ ID NO:7;
(j) variant of the wild-type amylase from *Cytophaga sp.* which has at least 60% identity for amino acid sequence SEQ ID NO:8;
(k) a variant of the wild-type lipase from *Thermomyces lanuginosus* which has at least 90% identity for amino acid sequence SEQ ID NO:1;
(l) variant of the wild-type lipase from *Thermomyces lanuginosus* which has at least 90% identity for amino acid sequence SEQ ID NO:1, and which comprises T231R and/or N233R mutations;
(m) variant of the wild-type lipase from *Thermomyces lanuginosus* which has at least 90% identity for amino acid sequence SEQ ID NO:1, and which comprises G91A, D96G, G225R, T231R and/or N233R mutations;
(n) cellulase that is a wild-type or variant of a microbially-derived endoglucanase endogenous to *Bacillus* sp. exhibiting endo-beta-1,4-glucanase activity (E.C. 3.2.1.4) which has at least 90% identity to the amino acid sequence SEQ ID NO:2;
(o) cellulase that is a wild-type or variant of a microbially-derived endoglucanase endogenous to *Paenibacillus polymyxa* exhibiting endo-beta-1,4-glucanase activity (E.C. 3.2.1.4) which has at least 90% identity to amino acid sequence SEQ ID NO:3;
(p) cellulase that is a hybrid fusion endoglucanase comprising a Glycosyl Hydrolase Family 45 catalytic domain that is a wild-type or variant of a microbially-derived endoglucanase endogenous to *Melanocarpus albomyces,* and a carbohydrate binding module that is a wild-type or variant of a carbohydrate binding module endogenous to *Trichoderma reesei,* and which has at least 90% identity to amino acid sequence SEQ ID NO:4;
(q) an enzyme selected from mannanase, pectate lyase, laccase, polyesterase, galactanase, acyltransferase, and any combination thereof; and
(r) any combination thereof.

22. Use according to any preceding claim, wherein the composition comprises a perfume, wherein the perfume comprises from 60wt% to 85wt% ester perfume raw materials having the structure:



wherein R1 and R2 are independently selected from C1 to C30 linear or branched, cyclic or non-cyclic, aromatic or non-aromatic, saturated or un-saturated, substituted or unsubstituted alkyl,
and optionally wherein the composition comprises alkyl ethoxylated sulphate having an average degree of ethoxylation of from 0.5 to 2.0.

23. Use according to any preceding claim, wherein the composition comprises polyvinyl N oxide polymer.

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Application Number
EP 16 19 2078

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The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
The Hague	16 March 2017	Kanbier, Titia

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