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(54) **DETERGENT COMPOSITION**

(57) The need for a hand-dishwashing composition which provides good sudsing and a good suds profile even in the presence of greasy stains comprising higher chain-length saturated and/or unsaturated fatty acid chains, as well as improved removal of such stains, is met by formulating the composition with a non-heme fatty acid decarboxylase and a surfactant system.

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Description

REFERENCE TO A SEQUENCE LISTING

[0001] This application contains a Sequence Listing in computer readable form. The computer readable form is incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The present invention relates to a hand dishwashing detergent composition comprising a surfactant system and at least one non-heme fatty acid decarboxylase. The non-heme fatty acid decarboxylase improve sudsing and grease removal by catalyzing the conversion of at least one fatty acid selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, and mixtures thereof.

BACKGROUND OF THE INVENTION

[0003] Hand-dishwashing detergent compositions should have a good suds profile, in particular a long lasting suds profile. Users typically connate the presence of suds with good residual cleaning, a lack of suds can lead to over-use of the detergent composition, especially in the presence of greasy soils. The appearance of the suds, such as its density and whiteness is also often seen as an indicator of the cleaning efficacy of the wash solution. However, greasy soils inhibit suds generation and promote suds collapse, even when sufficient surfactancy is present to ensure good cleaning, including grease removal. It has now been found that greasy soils containing higher chain-length saturated and/or unsaturated fatty acid chains are particularly effective at inhibiting sudsing, especially inhibiting long lasting sudsing. In addition, such greasy soils containing higher chain-length saturated and/or unsaturated fatty acid chains are particularly hard to remove from dishes. Such greasy soils comprise long chain fatty acids, especially long chain unsaturated fatty acids, such as oleic acid, linoleic acid, and linolenic acid, and long chain saturated fatty acids, such as palmitic acid and stearic acid, which can act as a suds suppressors. Conversion of these long chain saturated and/or unsaturated fatty acids into suds neutral or potentially suds boosting compounds is as such desired.

[0004] The use of two different classes of fatty acid decarboxylases, OleT-like and UndA-like, to transform these long chain saturated and/or unsaturated fatty acids and as such enhance the sudsing profile of detergent compositions have been previous reported (EP 3,243,896B1). However, OleT-like decarboxylases require H_2O_2 as a co-substrate, which can be challenging to formulate in hand dish-washing compositions. Several efforts to substitute the use of H_2O_2 by coupling biological redox systems that utilize O_2 have been done (see for example CN 10,8467,861), but the reduced catalytic efficiency of the systems suggests that the use of peroxide may be necessary for practical applications. Furthermore, UndA-like decarboxylases (US 10,000,775 B2) utilize O_2, instead of H_2O_2, as a co-substrate, but all previously reported UndA-like variants convert exclusively medium chain fatty acids (C10-C14), with no detectable conversion of long chain fatty acids, which are particularly effective at suds inhibition and are particularly challenging to remove. Thus, there is still a need for fatty acid decarboxylases that transform such long chain fatty acids without the need of external co-substrates that are difficult to formulate in hand dish-washing compositions.

[0005] Hence, a need remains for a hand-dishwashing detergent which provides good sudsing and a good suds profile even in the presence of greasy stains comprising higher chain-length saturated and/or unsaturated fatty acid chains, as well as improved removal of such stains.

[0006] EP3243896A relates to detergent compositions, especially manual dishwashing detergent compositions and method of washing comprising a surfactant system and a fatty acid decarboxylase enzyme. US 2009/0142821 A1 relates to novel variants of cytochrome P450 oxygenases. These variants have an improved ability to use peroxide as an oxygen donor as compared to the corresponding wild-type enzyme. These variants also have an improved thermostability as compared to the cytochrome P450 BM-3 F87 A mutant. Preferred variants include cytochrome P450 BM-3 heme domain mutants having I58V, F87A, H100R, F107L, A135S, M145A/V, N239H, S274T, L3241, I366V, K434E, E442K, and/or V446I amino acid substitutions. S CHRISTOPHER DAVIS ET AL, "Oxidation of v-Oxo Fatty Acids by Cytochrome P450 BM-3 (CYP102)", ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (19960401), vol. 328, no. 1, pages 35 - 42 discusses the oxidation of aldehydes by cytochrome P450 enzymes either to the corresponding acid or, via a decarboxylation mechanism, to an olefin one carbon shorter than the parent substrate, and explores the factors that control partitioning between these two pathways. The authors have examined the cytochrome P450BM-3 (CYP102)-catalyzed oxidation of fatty acids with a terminal aldehyde group. P450BM-3 has been found to oxidize 18-oxooctadecanoic, 16-oxohexadecanoic, 14-oxotetradecanoic, and 12-oxododecanoic acids exclusively to the corresponding α,ω-diacids. The results demonstrated that aldehyde oxidation by cytochrome P450BM-3 is insensitive to changes in substrate structure expected to stabilize the transition state for decarboxylation. Decarboxylation, in contrast to the oxidation of aldehydes to acids, depends on specific substrate-protein interactions and is enzyme-specific. JAMES BELCHER ET AL., "Structure and Biochemical Properties of the Alkene Producing Cytochrome P450 OleTJE (CYP152L1) from the Jeotgalicoccus sp. 8456 Bacterium", JOURNAL OF BIOLOGICAL CHEMISTRY, (20140307), vol. 289, no. 10, doi:10.1074/jbc.M113.527325, ISSN 0021-9258, pages 6535 - 6550, presents the biochemical characterization and crystal structures of a cytochrome P450 fatty acid peroxygenase: the terminal alkene forming $OleT_{JE}$ (CYP152L1) from *Jeotgalicoccus* sp. 8456. GIRVAN HAZEL M ET AL., "Applications of microbial cytochrome P450 enzymes in biotechnology and synthetic biology", CURRENT OPINION IN CHEMICAL BIOLOGY, (20160322), vol. 31, doi:10.1016/J.CBPA.2016.02.018, ISSN 1367-5931, pages 136 - 145, XP029536984 [A] 1-15 is a review focusing on the enzymatic properties and reaction mechanisms of P450 enzymes, and on recent studies that highlight their broad applications in the production of oxychemicals.

SUMMARY OF THE INVENTION

[0007] The present invention relates to a hand-dishwashing composition comprising: a surfactant system comprising at least one anionic surfactant; and a non-heme fatty acid decarboxylase; wherein said decarboxylase comprises an amino acid selected from the group consisting of: a) leucine or isoleucine at position 41, b) alanine at position 57, c) glycine, alanine, isoleucine, leucine, valine, serine, or threonine at position 239, and d) combinations thereof; wherein said positions are numbered with reference to SEQ ID NO: 1; and wherein said decarboxylase catalyzes the conversion of at least one fatty acid selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, and mixtures thereof.

[0008] The present invention further relates to a method of manually washing dishware comprising the steps of delivering a detergent composition of the invention into a volume of water to form a wash solution and immersing the dishware in the solution.

DETAILED DESCRIPTION OF THE INVENTION

[0009] The need for compositions and methods which provide for good sudsing, including a good suds-profile, even in the presence of greasy stains comprising higher chain-length saturated and/or unsaturated fatty acid chains, can be met by formulating the hand-dishwashing composition with a non-heme fatty acid decarboxylase; wherein said decarboxylase comprises an amino acid selected from the group consisting of: a) leucine or isoleucine at position 41, b) alanine at position 57, c) glycine, alanine, isoleucine, leucine, valine, serine, or threonine at position 239, and d) combinations thereof; wherein said positions are numbered with reference to SEQ ID NO: 1. Such compositions are also particularly effective at removing grease stains comprising higher chain-length saturated and/or unsaturated fatty acid chains.

Definitions

[0010] As used herein, "dishware" includes cookware and tableware. (move this sentence to definitions section)

[0011] As used herein, the term "non-heme fatty acid decarboxylase" means an enzyme that catalyzes the decarboxylation of fatty acids to alkenes utilizing dioxygen as a co-substrate and non-heme iron or dinuclear iron as a cofactor.

[0012] As used herein, the articles "a" and "an" when used in a claim, are understood to mean one or more of what is claimed or described.

[0013] As used herein, the term "substantially free of' or "substantially free from" means that the indicated material is present in an amount of no more than about 5 wt%, preferably no more than about 2%, and more preferably no more than about 1 wt% by weight of the composition.

[0014] As used therein, the term "essentially free of' or "essentially free from" means that the indicated material is present in an amount of no more than about 0.1 wt% by weight of the composition, or preferably not present at an analytically detectible level in such composition. It may include compositions in which the indicated material is present only as an impurity of one or more of the materials deliberately added to such compositions.

[0015] All percentages and ratios used hereinafter are by weight of total composition, unless otherwise indicated. All percentages, ratios, and levels of ingredients referred to herein are based on the actual amount of the ingredient, and do not include solvents, fillers, or other materials with which the ingredient may be combined as a commercially available product, unless otherwise indicated.

[0016] As used herein the phrase "detergent composition" refers to compositions and formulations designed for cleaning soiled surfaces. Such compositions include dish-washing compositions.

[0017] As used herein the term "improved suds longevity" means an increase in the duration of visible suds in a washing process cleaning soiled articles using the composition comprising one or more enzymes of use in the compositions of the present invention, compared with the suds longevity provided by the same composition and process in the absence of the enzyme.

[0018] As used herein, the term "soiled surfaces" refers to soiled dishware.

[0019] As used herein, the term "water hardness" or "hardness" means uncomplexed cation ions (*i.e.*, Ca^{2+} or Mg^{2+}) present in water that have the potential to precipitate with anionic surfactants or any other anionically charged detergent actives under alkaline conditions, and thereby diminishing the surfactancy and cleaning capacity of surfactants. Further, the terms "high water hardness" and "elevated water hardness" can be used interchangeably and are relative terms for the purposes of the present invention, and are intended to include, but not limited to, a hardness level containing at least 12 grams of calcium ion per gallon water (gpg, "American grain hardness" units).

[0020] As used herein, the terms "protein," "polypeptide," and "peptide" are used interchangeably herein to denote a polymer of at least two amino acids covalently linked by an amide bond, regardless of length or post-translational modification (e.g., glycosylation, phosphorylation, lipidation, myristilation, ubiquitination, etc.). Included within this definition are D- and L-amino acids, and mixtures of D- and L-amino acids.

[0021] As used herein, "polynucleotide" and "nucleic acid" refer to two or more nucleosides that are covalently linked together. The polynucleotide may be wholly comprised ribonucleosides (i.e., an RNA), wholly comprised of 2' deoxyribonucleotides (i.e., a DNA) or mixtures of ribo- and 2' deoxyribonucleosides. While the nucleosides will typically be linked together via standard phosphodiester linkages, the polynucleotides may include one or more non-standard linkages. The polynucleotide may be single-stranded or double-stranded, or may include both single-stranded regions and double-stranded regions. Moreover, while a polynucleotide will typically be composed of the naturally occurring encoding nucleobases (i.e., adenine, guanine, uracil, thymine, and cytosine), it may include one or more modified and/or synthetic nucleobases (e.g., inosine, xanthine, hypoxanthine, etc.). Such modified or synthetic nucleobases can be encoding nucleobases.

[0022] As used herein, "coding sequence" refers to that portion of a nucleic acid (e.g., a gene) that encodes an amino acid sequence of a protein.

[0023] As used herein, "naturally occurring," "wild-type," and "WT" refer to the form found in nature. For example, a naturally occurring or wild-type polypeptide or polynucleotide sequence is a sequence present in an organism that can be isolated from a source in nature and which has not been intentionally modified by human manipulation.

[0024] As used herein, "non-naturally occurring" or "engineered" or "recombinant" when used in the present invention with reference to (e.g., a cell, nucleic acid, or polypeptide), refers to a material, or a material corresponding to the natural or native form of the material, that has been modified in a manner that would not otherwise exist in nature, or is identical thereto but produced or derived from synthetic materials and/or by manipulation using recombinant techniques. Non-limiting examples include, among others, recombinant cells expressing genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise expressed at a different level.

[0025] As used herein the term "identity" means the identity between two or more sequences and is expressed in terms of the identity or similarity between the sequences as calculated over the entire length of a sequence aligned against the entire length of the reference sequence. Sequence identity can be measured in terms of percentage identity; the higher the percentage, the more identical the sequences are. The percentage identity is calculated over the length of comparison. For example, the identity is typically calculated over the entire length of a sequence aligned against the entire length of the reference sequence. Methods of alignment of sequences for comparison are well known in the art and identity can be calculated by many known methods. Various programs and alignment algorithms are described in the art. It should be noted that the terms 'sequence identity' and 'sequence similarity' can be used interchangeably.

[0026] As used herein, "percentage of sequence identity," "percent identity," and "percent identical" refer to comparisons between polynucleotide sequences or polypeptide sequences, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which either the identical nucleic acid base or amino acid residue occurs in both sequences or a nucleic acid base or amino acid residue is aligned with a gap to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0027] As used herein, the term "variant" of non-heme fatty acid decarboxylase enzyme means a modified non-heme fatty acid decarboxylase enzyme amino acid sequence by or at one or more amino acids (for example 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more amino acid modifications) selected from substitutions, insertions, deletions and combinations thereof. The variant may have "conservative" substitutions, wherein a substituted amino acid has similar structural or chemical properties to the amino acid that replaces it, for example, replacement of leucine with isoleucine. A variant may have "non-conservative" changes, for example, replacement of a glycine with a tryptophan. Variants may also include sequences with amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing the activity of the protein may be found using computer programs well known in the art. Variants may also include truncated forms derived from a wild-type non-heme fatty acid decarboxylase enzyme, such as for example, a protein with a truncated N-terminus. Variants may also include forms derived by adding an extra amino acid sequence to a wild-type protein, such as for example, an N-terminal tag, a C-terminal tag or an insertion in the middle of the protein sequence.

[0028] As used herein, "reference sequence" refers to a defined sequence to which another sequence is compared. A reference sequence may be a subset of a larger sequence, for example, a segment of a full-length gene or polypeptide sequence. Generally, a reference sequence is at least 20 nucleotide or amino acid residues in length, at least 25 residues in length, at least 50 residues in length, or the full length of the nucleic acid or polypeptide. Since two polynucleotides or polypeptides may each (1) comprise a sequence (i.e., a portion of the complete sequence) that is similar between the two sequences, and (2) may further comprise a sequence that is divergent between the two sequences, sequence comparisons between two (or more) polynucleotides or polypeptide are typically performed by comparing sequences of the two polynucleotides over a comparison window to identify and compare local regions of sequence similarity. The term "reference sequence" is not intended to be limited to wild-type sequences, and can include engineered or altered sequences. For example, a "reference sequence" can be a previously engineered or altered amino acid sequence.

[0029] As used herein, "comparison window" refers to a conceptual segment of at least about 20 contiguous nucleotide positions or amino acids residues wherein a sequence may be compared to a reference sequence of at least 20 contiguous nucleotides or amino acids and wherein the portion of the sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The comparison window can be longer than 20 contiguous residues, and includes, optionally 30, 40, 50, 100, or longer windows.

[0030] As used herein, "corresponding to", "reference to" or "relative to" when used in the context of the numbering of a given amino acid or polynucleotide sequence refers to the numbering of the residues of a specified reference sequence when the given amino acid or polynucleotide sequence is compared to the reference sequence. In other words, the residue number or residue position of a given polymer is designated with respect to the reference sequence rather than by the actual numerical position of the residue within the given amino acid or polynucleotide sequence. For example, a given amino acid sequence, such as that of an engineered non-heme fatty acid decarboxylase, can be aligned to a reference sequence by introducing gaps to optimize residue matches between the two sequences. In these cases, although the gaps are present, the numbering of the residue in the given amino acid or polynucleotide sequence is made with respect to the reference sequence to which it has been aligned.

[0031] As used herein, "increased enzymatic activity" and "increased activity" refer to an improved property of a wild-type or an engineered enzyme, which can be represented by an increase in specific activity (e.g., product produced/time/weight protein) or an increase in percent conversion of the substrate to the product (e.g., percent conversion of starting amount of substrate to product in a specified time period using a specified amount of non-heme fatty acid decarboxylase) as compared to a reference enzyme. Any property relating to enzyme activity may be affected, including the classical enzyme properties of Km, Vmax or kcat, changes of which can lead to increased enzymatic activity. The non-heme fatty acid decarboxylase activity can be measured by any one of standard assays used for measuring non-heme fatty acid decarboxylases, such as change in substrate or product concentration. Comparisons of enzyme activities are made using a defined preparation of enzyme, a defined assay under a set condition, and one or more defined substrates, as further described in detail herein. Generally, when enzymes in cell lysates are compared, the numbers of cells and the amount of protein assayed are determined as well as use of identical expression systems and identical host cells to minimize variations in amount of enzyme produced by the host cells and present in the lysates.

[0032] As used herein, "conversion" refers to the enzymatic transformation of a substrate to the corresponding product.

[0033] As used herein "percent conversion" refers to the percent of the substrate that is converted to the product within a period of time under specified conditions. Thus, for example, the "enzymatic activity" or "activity" of a non-heme fatty acid decarboxylase polypeptide can be expressed as "percent conversion" of the substrate to the product.

[0034] As used herein, "amino acid difference" or "residue difference" refers to a difference in the amino acid residue at a position of a polypeptide sequence relative to the amino acid residue at a corresponding position in a reference sequence. The positions of amino acid differences generally are referred to herein as "Xn", where n refers to the corresponding position in the reference sequence upon which the residue difference is based. For example, a "residue difference at position X41 as compared to SEQ ID NO: 1" refers to a difference of the amino acid residue at the polypeptide position corresponding to position 41 of SEQ ID NO:1. Thus, if the reference polypeptide of SEQ ID NO:1 has a tyrosine at position 41, then a "residue difference at position X41 as compared to SEQ ID NO:1" refers to an amino acid substitution of any residue other than tyrosine at the position of the polypeptide corresponding to position 41 of SEQ ID NO:1. In most instances herein, the specific amino acid residue difference at a position is indicated as "XnY" where "Xn" specified the corresponding position as described above, and "Y" is the single letter identifier of the amino acid found in the engineered polypeptide (i.e., the different residue than in the reference polypeptide). In some instances, the present invention also provides specific amino acid differences denoted by the conventional notation "AnB", where A is the single letter identifier of the residue in the reference sequence, "n" is the number of the residue position in the reference sequence, and B is the single letter identifier of the residue substitution in the sequence of the engineered polypeptide. In some instances, a polypeptide of the present invention can include at least one amino acid residue difference relative to a reference sequence, which is indicated by a list of the specified positions where residue differences are present relative to the reference sequence. Where more than one amino acid can be used in a specific residue position of a polypeptide, the various amino acid residues that can be used are separated by a "/" (e.g., X41(A/G)). The present invention includes engineered polypeptide sequences comprising at least one amino acid differences that include either/or both conservative and non-conservative amino acid substitutions. The amino acid sequences of the specific recombinant non-heme fatty acid decarboxylase polypeptides included in the Sequence Listing of the present invention include an initiating methionine (M) residue (i.e., M represents residue position 1). The skilled artisan, however, understands that this initiating methionine residue can be removed by biological processing machinery, such as in a host cell or in vitro translation system, to generate a mature protein lacking the initiating methionine residue, but otherwise retaining the enzyme's properties. Consequently, the term "amino acid residue difference relative to SEQ ID NO:1 at position Xn" as used herein may refer to position "Xn" or to the corresponding position (e.g., position (X-1)n) in a reference sequence that has been processed so as to lack the starting methionine.

[0035] As used herein, the phrase "conservative amino acid substitutions" refers to the interchangeability of residues having similar side chains, and thus typically involves substitution of the amino acid in the polypeptide with amino acids within the same or similar defined class of amino acids. As such, an amino acid with an aliphatic side chain can be substituted with another aliphatic amino acid (e.g., alanine, valine, leucine, and isoleucine); an amino acid with a hydroxyl side chain can be substituted with another amino acid with a hydroxyl side chain (e.g., serine and threonine); an amino acids having aromatic side chains can be substituted with another amino acid having an aromatic side chain (e.g., phenylalanine, tyrosine, tryptophan, and histidine); an amino acid with a basic side chain can be substituted with another amino acid with a basic side chain (e.g., lysine and arginine); an amino acid with an acidic side chain can be substituted with another amino acid with an acidic side chain (e.g., aspartic acid or glutamic acid); and/or a hydrophobic or hydrophilic amino acid can be replaced with another hydrophobic or hydrophilic amino acid, respectively. The appropriate classification of any amino acid or residue will be apparent to those of skill in the art, especially in light of the detailed invention provided herein.

[0036] As used herein, the phrase "non-conservative substitution" refers to substitution of an amino acid in the polypeptide with an amino acid with significantly differing side chain properties. Non-conservative substitutions may use amino acids between, rather than within, the defined groups and affects (a) the structure of the peptide backbone in the area of the substitution (e.g., proline for glycine) (b) the charge or hydrophobicity, or (c) the bulk of the side chain. By way of example and not limitation, an exemplary non-conservative substitution can be an acidic amino acid substituted with a basic or aliphatic amino acid; an aromatic amino acid substituted with a small amino acid; and a hydrophilic amino acid substituted with a hydrophobic amino acid.

[0037] As used herein, "deletion" refers to modification of the polypeptide by removal of one or more amino acids from the reference polypeptide. Deletions can comprise removal of 1 or more amino acids, 2 or more amino acids, 5 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, or up to 20% of the total number of amino acids making up the polypeptide while retaining enzymatic activity and/or retaining the improved properties of an engineered enzyme. Deletions can be directed to the internal portions and/or terminal portions of the polypeptide. The deletion can comprise a continuous segment or can be discontinuous.

[0038] As used herein, "insertion" refers to modification of the polypeptide by addition of one or more amino acids to the reference polypeptide. The improved engineered non-heme fatty acid decarboxylase enzymes can comprise insertions of one or more amino acids to the naturally occurring non-heme fatty acid decarboxylase polypeptide as well as insertions of one or more amino acids to engineered non-heme fatty acid decarboxylase polypeptides. Insertions can be in the internal portions of the polypeptide, or to the carboxy or amino terminus. Insertions as used herein include fusion proteins as is known in the art. The insertion can be a contiguous segment of amino acids or separated by one or more of the amino acids in the naturally occurring polypeptide.

[0039] The term "amino acid substitution set" or "substitution set" refers to a group of amino acid substitutions in a polypeptide sequence, as compared to a reference sequence. A substitution set can have 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more amino acid substitutions. A substitution set can refer to the set of amino acid substitutions that is present in any of the variant non-heme fatty acid decarboxylases.

[0040] As used herein, "fragment" refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion, but where the remaining amino acid sequence is identical to the corresponding positions in the sequence. Fragments can typically have about 80%, about 90%, about 95%, about 98%, or about 99% of the full-length non-heme fatty acid decarboxylase polypeptide, for example, the polypeptide of SEQ ID NO: 1. The fragment can be "biologically active" (i.e., it exhibits the same enzymatic activity as the full-length sequence).

[0041] A "functional fragment", or a "biologically active fragment", used interchangeably, herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion(s) and/or internal deletions, but where the remaining amino acid sequence is identical to the corresponding positions in the sequence to which it is being compared and that retains substantially all of the activity of the full-length polypeptide.

[0042] As used herein, "isolated polypeptide" refers to a polypeptide which is substantially separated from other contaminants that naturally accompany it (e.g., protein, lipids, and polynucleotides). The term embraces polypeptides which have been removed or purified from their naturally-occurring environment or expression system (e.g., host cell or in vitro synthesis). The improved non-heme fatty acid decarboxylase enzymes may be present within a cell, present in the cellular medium, or prepared in various forms, such as lysates or isolated preparations. As such, the wild-type or engineered non-heme fatty acid decarboxylase polypeptides of the present invention can be an isolated polypeptide.

[0043] As used herein, "substantially pure polypeptide" refers to a composition in which the polypeptide species is the predominant species present (i.e., on a molar or weight basis it is more abundant than any other individual macromolecular species in the composition), and is generally a substantially purified composition when the object species comprises at least about 50 percent of the macromolecular species present by mole or % weight. Generally, a substantially pure wild-type or engineered non-heme fatty acid decarboxylase polypeptide composition will comprise about 60% or more, about 70% or more, about 80% or more, about 90% or more, about 91% or more, about 92% or more, about 93% or more, about 94% or more, about 95% or more, about 96% or more, about 97% or more, about 98% or more, or about 99% of all macromolecular species by mole or % weight present in the composition. Solvent species, small molecules (<500 Daltons), and elemental ion species are not considered macromolecular species. The isolated improved non-heme fatty acid decarboxylase polypeptide can be a substantially pure polypeptide composition.

[0044] As used herein, when used with reference to a nucleic acid or polypeptide, the term "heterologous" refers to a sequence that is not normally expressed and secreted by an organism (e.g., a wild-type organism). The term can encompass a sequence that comprises two or more subsequences which are not found in the same relationship to each other as normally found in nature, or is recombinantly engineered so that its level of expression, or physical relationship to other nucleic acids or other molecules in a cell, or structure, is not normally found in nature. For instance, a heterologous nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged in a manner not found in nature (e.g., a nucleic acid open reading frame (ORF) of the invention operatively linked to a promoter sequence inserted into an expression cassette, such as a vector). "Heterologous polynucleotide" can refer to any polynucleotide that is introduced into a host cell by laboratory techniques, and includes polynucleotides that are removed from a host cell, subjected to laboratory manipulation, and then reintroduced into a host cell.

[0045] As used herein, "codon optimized" refers to changes in the codons of the polynucleotide encoding a protein to those preferentially used in a particular organism such that the encoded protein is efficiently expressed in the organism of interest. The polynucleotides encoding the non-heme fatty acid decarboxylase enzymes may be codon optimized for optimal production from the host organism selected for expression.

[0046] As used herein, "suitable reaction conditions" refer to those conditions in the biocatalytic reaction solution (e.g., ranges of enzyme loading, substrate loading, temperature, pH, buffers, cosolvents, etc.) under which a non-heme fatty acid decarboxylase polypeptide of the present invention is capable of converting a substrate compound to a product compound (e.g., conversion of one compound to another compound).

[0047] As used herein, "substrate" in the context of a biocatalyst mediated process refers to the compound or molecule acted on by the biocatalyst.

[0048] As used herein "product" in the context of a biocatalyst mediated process refers to the compound or molecule resulting from the action of the biocatalyst.

Detergent Composition

[0049] The hand-dishwashing compositions of the present invention formulate a specific surfactant system with a specific non-heme fatty acid decarboxylase, in order to provide improved sudsing, especially long-lasting sudsing, in the presence of greasy stains comprising higher chain length saturated and/or unsaturated fatty acids, and improved removal of such stains.

[0050] The hand-dishwashing composition is preferably in liquid form, more preferably is an aqueous cleaning composition. As such, the composition can comprise from 50% to 90%, preferably from 60% to 75%, by weight of the total composition of water.

[0051] Preferably the pH of the detergent composition of the invention, measured as a 10% product concentration in demineralized water at 20°C, is adjusted to between 3 and 14, more preferably between 4 and 13, more preferably between 6 and 12 and most preferably between 8 and 10. The pH of the detergent composition can be adjusted using pH modifying ingredients known in the art.

[0052] The composition of the present invention can be Newtonian or non-Newtonian, preferably Newtonian. Preferably, the composition has a viscosity of from 10 mPa·s to 10,000 mPa·s, preferably from 100 mPa·s to 5,000 mPa·s, more preferably from 300 mPa·s to 2,000 mPa·s, or most preferably from 500 mPa·s to 1,500 mPa·s, alternatively combinations thereof. The viscosity is measured at 20°C with a Brookfield RT Viscometer using spindle 31 with the RPM of the viscometer adjusted to achieve a torque of between 40% and 60%.

Surfactant System

[0053] The cleaning composition comprises from 5% to 50%, preferably 8% to 45%, more preferably from 15% to 40%, by weight of the total composition of a surfactant system.

[0054] For improved sudsing, the surfactant system comprises anionic surfactant. The surfactant system preferably comprises from 60% to 90%, more preferably from 70% to 80% by weight of the surfactant system of the anionic surfactant. Alkyl sulphated anionic surfactants are preferred, particularly those selected from the group consisting of: alkyl sulphate, alkyl alkoxy sulphate, and mixtures thereof. More preferably, the anionic surfactant consists of alkyl sulphated anionic surfactant selected from the group consisting of: alkyl sulphate, alkyl alkoxy sulphate, and mixtures thereof.

[0055] For further improvements in sudsing, the surfactant system can comprise less than 30%, preferably less than 15%, more preferably less than 10% of further anionic surfactant, and most preferably the surfactant system comprises no further anionic surfactant. The alkyl sulphated anionic surfactant preferably has an average alkyl chain length of from 8 to 18, preferably from 10 to 14, more preferably from 12 to 14, most preferably from 12 to 13 carbon atoms. The alkyl sulphated anionic surfactant has an average degree of alkoxylation, of less than 5, preferably less than 3, more preferably from 0.5 to 2.0, most preferably from 0.5 to 0.9. Preferably, the alkyl sulphated anionic surfactant is ethoxylated. That is, the alkyl sulphated anionic surfactant has an average degree of ethoxylation, of less than 5, preferably less than 3, more preferably from 0.5 to 2.0, most preferably from 0.5 to 0.9.

[0056] The average degree of alkoxylation is the mol average degree of alkoxylation (*i.e.*, mol average alkoxylation degree) of all the alkyl sulphate anionic surfactant. Hence, when calculating the mol average alkoxylation degree, the mols of non-alkoxylated sulphate anionic surfactant are included:

$$\text{Mol average alkoxylation degree} = (x1 * \text{alkoxylation degree of surfactant } 1 + x2 * \text{alkoxylation degree of surfactant } 2 + \ldots) / (x1 + x2 + \ldots)$$

wherein x1, x2, ... are the number of moles of each alkyl (or alkoxy) sulphate anionic surfactant of the mixture and alkoxylation degree is the number of alkoxy groups in each alkyl sulphate anionic surfactant.

[0057] The alkyl sulphate anionic surfactant can have a weight average degree of branching of more than 10%, preferably more than 20%, more preferably more than 30%, even more preferably between 30% and 60%, most preferably between 30% and 50%. The alkyl sulphate anionic surfactant can comprise at least 5%, preferably at least 10%, most preferably at least 25%, by weight of the alkyl sulphate anionic surfactant, of branching on the C2 position (as measured counting carbon atoms from the sulphate group for non-alkoxylated alkyl sulphate anionic surfactants, and the counting from the alkoxy-group furthest from the sulphate group for alkoxylated alkyl sulphate anionic surfactants). More preferably, greater than 75%, even more preferably greater than 90%, by weight of the total branched alkyl content consists of C1-C5 alkyl moiety, preferably C1-C2 alkyl moiety. It has been found that formulating the inventive compositions using alkyl sulphate surfactants having the aforementioned degree of branching results in improved low temperature stability. Such compositions require less solvent in order to achieve good physical stability at low temperatures. As such, the compositions can comprise lower levels of organic solvent, of less than 5.0% by weight of the cleaning composition of organic solvent, while still having improved low temperature stability. Higher surfactant branching also provides faster initial suds generation, but typically less suds mileage. The weight average branching, described herein, has been found to provide improved low temperature stability, initial foam generation and suds longevity.

[0058] The weight average degree of branching for an anionic surfactant mixture can be calculated using the following formula:

$$\text{Weight average degree of branching (\%)} = [(x1 * \text{wt\% branched alcohol 1 in alcohol 1} + x2 * \text{wt\% branched alcohol 2 in alcohol 2} + \ldots) / (x1 + x2 + \ldots)] * 100$$

wherein x1, x2, ... are the weight in grams of each alcohol in the total alcohol mixture of the alcohols which were used as starting material before (alkoxylation and) sulphation to produce the alkyl (alkoxy) sulphate anionic surfactant. In the weight average degree of branching calculation, the weight of the alkyl alcohol used to form the alkyl sulphate anionic surfactant which is not branched is included.

[0059] The weight average degree of branching and the distribution of branching can typically be obtained from the technical data sheet for the surfactant or constituent alkyl alcohol. Alternatively, the branching can also be determined through analytical methods known in the art, including capillary gas chromatography with flame ionisation detection on medium polar capillary column, using hexane as the solvent. The weight average degree of branching and the distribution of branching is based on the starting alcohol used to produce the alkyl sulphate anionic surfactant.

[0060] The alkyl chain of the alkyl sulphated anionic surfactant preferably has a mol fraction of C12 and C13 chains of at least 50%, preferably at least 65%, more preferably at least 80%, most preferably at least 90%. Suds mileage is particularly improved, especially in the presence of greasy soils, when the C13/C12 mol ratio of the alkyl chain is at least 50/50, preferably at least 57/43, preferably from 60/40 to 90/10, more preferably from 60/40 to 80/20, most preferably from 60/40 to 70/30, while not compromising suds mileage in the presence of particulate soils.

[0061] Suitable counterions include alkali metal cation earth alkali metal cation, alkanolammonium or ammonium or substituted ammonium, but preferably sodium.

[0062] Suitable examples of commercially available alkyl sulphate anionic surfactants include, those derived from alcohols sold under the Neodol® brand-name by Shell, or the Lial®, Isalchem®, and Safol® brand-names by Sasol, or some of the natural alcohols produced by The Procter & Gamble Chemicals company. The alcohols can be blended in order to achieve the desired mol fraction of C12 and C13 chains and the desired C13/C12 ratio, based on the relative fractions of C13 and C12 within the starting alcohols, as obtained from the technical data sheets from the suppliers or from analysis using methods known in the art.

[0063] In order to improve surfactant packing after dilution and hence improve suds mileage, the surfactant system preferably comprises a co-surfactant. Preferred co-surfactants are selected from the group consisting of an amphoteric surfactant, a zwitterionic surfactant, and mixtures thereof. The co-surfactant is preferably an amphoteric surfactant, more preferably an amine oxide surfactant. The co-surfactant is included as part of the surfactant system.

[0064] The composition preferably comprises from 0.1% to 20%, more preferably from 0.5% to 15% and especially from 2% to 10% by weight of the cleaning composition of the co-surfactant. The surfactant system of the cleaning composition of the present invention preferably comprises from 10% to 40%, preferably from 15% to 35%, more preferably from 20% to 30%, by weight of the surfactant system of a co-surfactant. The anionic surfactant to the co-surfactant weight ratio can be from 1:1 to 8:1, preferably from 2:1 to 5:1, more preferably from 2.5:1 to 4:1.

[0065] As mentioned earlier, amine oxide surfactants are preferred for use as a co-surfactant. The amine oxide surfactant can be linear or branched, though linear are preferred. Suitable linear amine oxides are typically water-soluble, and characterized by the formula R1 - N(R2)(R3) O wherein R1 is a C8-18 alkyl, and the R2 and R3 moieties are selected from the group consisting of C1-3 alkyl groups, CI-3 hydroxyalkyl groups, and mixtures thereof. For instance, R2 and R3 can be selected from the group consisting of: methyl, ethyl, propyl, isopropyl, 2-hydroxethyl, 2-hydroxypropyl and 3-hydroxypropyl, and mixtures thereof, though methyl is preferred for one or both of R2 and R3. The linear amine oxide surfactants in particular may include linear C10-C18 alkyl dimethyl amine oxides and linear C8-C12 alkoxy ethyl dihydroxy ethyl amine oxides.

[0066] Preferably, the amine oxide surfactant is selected from the group consisting of: alkyl dimethyl amine oxide, alkyl amido propyl dimethyl amine oxide, and mixtures thereof. Alkyl dimethyl amine oxides are preferred, such as C8-18 alkyl dimethyl amine oxides, or C10-16 alkyl dimethyl amine oxides (such as coco dimethyl amine oxide). Suitable alkyl dimethyl amine oxides include C10 alkyl dimethyl amine oxide surfactant, C10-12 alkyl dimethyl amine oxide surfactant, C12-C14 alkyl dimethyl amine oxide surfactant, and mixtures thereof. C12-C14 alkyl dimethyl amine oxide are particularly preferred.

[0067] Alternative suitable amine oxide surfactants include mid-branched amine oxide surfactants. As used herein, "mid-branched" means that the amine oxide has one alkyl moiety having n1 carbon atoms with one alkyl branch on the alkyl moiety having n2 carbon atoms. The alkyl branch is located on the α carbon from the nitrogen on the alkyl moiety. This type of branching for the amine oxide is also known in the art as an internal amine oxide. The total sum of n1 and n2 can be from 10 to 24 carbon atoms, preferably from 12 to 20, and more preferably from 10 to 16. The number of carbon atoms for the one alkyl moiety (n1) is preferably the same or similar to the number of carbon atoms as the one alkyl branch (n2) such that the one alkyl moiety and the one alkyl branch are symmetric. As used herein "symmetric" means that | n1 - n2 | is less than or equal to 5, preferably 4, most preferably from 0 to 4 carbon atoms in at least 50 wt%, more preferably at least 75 wt% to 100 wt% of the mid-branched amine oxides for use herein. The amine oxide further comprises two moieties, independently selected from a CI-3 alkyl, a CI-3 hydroxyalkyl group, or a polyethylene oxide group containing an average of from about 1 to about 3 ethylene oxide groups. Preferably, the two moieties are selected from a CI-3 alkyl, more preferably both are selected as C1 alkyl.

[0068] Alternatively, the amine oxide surfactant can be a mixture of amine oxides comprising a mixture of low-cut amine oxide and mid-cut amine oxide. The amine oxide of the composition of the invention can then comprises:

a) from about 10% to about 45% by weight of the amine oxide of low-cut amine oxide of formula R1R2R3AO wherein R1 and R2 are independently selected from hydrogen, C1-C4 alkyls or mixtures thereof, and R3 is selected from C10 alkyls and mixtures thereof; and

b) from 55% to 90% by weight of the amine oxide of mid-cut amine oxide of formula R4R5R6AO wherein R4 and R5 are independently selected from hydrogen, C1-C4 alkyls or mixtures thereof, and R6 is selected from C12-C16 alkyls or mixtures thereof

[0069] In a preferred low-cut amine oxide for use herein R3 is n-decyl, with preferably both R1 and R2 being methyl. In the mid-cut amine oxide of formula R4R5R6AO, R4 and R5 are preferably both methyl.

[0070] Preferably, the amine oxide comprises less than about 5%, more preferably less than 3%, by weight of the amine oxide of an amine oxide of formula R7R8R9AO wherein R7 and R8 are selected from hydrogen, C1-C4 alkyls and mixtures thereof and wherein R9 is selected from C8 alkyls and mixtures thereof. Limiting the amount of amine oxides of formula R7R8R9AO improves both physical stability and suds mileage.

[0071] Suitable zwitterionic surfactants include betaine surfactants. Such betaine surfactants includes alkyl betaines, alkylamidobetaine, amidazoliniumbetaine, sulphobetaine (INCI Sultaines) as well as the Phosphobetaine, and preferably meets formula (II):

$$R^1\text{-}[CO\text{-}X(CH_2)_n]_x\text{-}N^+(R^2)(R_3)\text{-}(CH_2)_m\text{-}[CH(OH)\text{-}CH_2]_y\text{-}Y^-$$

wherein in formula (II),

R1 is selected from the group consisting of: a saturated or unsaturated C6-22 alkyl residue, preferably C8-18 alkyl residue, more preferably a saturated C10-16 alkyl residue, most preferably a saturated C12-14 alkyl residue;
X is selected from the group consisting of: NH, NR4 wherein R4 is a C1-4 alkyl residue, O, and S,
n is an integer from 1 to 10, preferably 2 to 5, more preferably 3,
x is 0 or 1, preferably 1,
R2 and R3 are independently selected from the group consisting of: a C1-4 alkyl residue, hydroxy substituted such as a hydroxyethyl, and mixtures thereof, preferably both R2 and R3 are methyl,
m is an integer from 1 to 4, preferably 1, 2 or 3,
y is 0 or 1, and
Y is selected from the group consisting of: COO, SO3, OPO(OR5)O or P(O)(OR5)O, wherein R5 is H or a C1-4 alkyl residue.

[0072] Preferred betaines are the alkyl betaines of formula (Ia), the alkyl amido propyl betaine of formula (Ib), the sulphobetaines of formula (Ic) and the amido sulphobetaine of formula (Id):

$$R^1\text{-}N(CH_3)_2\text{-}CH_2COO^- \qquad \text{(IIa)}$$

$$R^1\text{-}CO\text{-}NH\text{-}(CH_2)_3\text{-}N^+(CH_3)_2\text{-}CH_2COO^- \qquad \text{(IIb)}$$

$$R^1\text{-}N^+(CH_3)_2\text{-}CH_2CH(OH)CH_2SO_3^- \qquad \text{(IIc)}$$

$$R^1\text{-}CO\text{-}NH\text{-}(CH_2)_3\text{-}N^+(CH_3)_2\text{-}CH_2CH(OH)CH_2SO_3^- \qquad \text{(IId)}$$

in which R1 has the same meaning as in formula (II). Particularly preferred are the carbobetaines [i.e. wherein Y-=COO- in formula (II)] of formulae (Ia) and (Ib), more preferred are the alkylamidobetaine of formula (Ib).

[0073] Suitable betaines can be selected from the group consisting or [designated in accordance with INCI]: capryl/capramidopropyl betaine, cetyl betaine, cetyl amidopropyl betaine, cocamidoethyl betaine, cocamidopropyl betaine, cocobetaines, decyl betaine, decyl amidopropyl betaine, hydrogenated tallow betaine / amidopropyl betaine, isostearamidopropyl betaine, lauramidopropyl betaine, lauryl betaine, myristyl amidopropyl betaine, myristyl betaine, oleamidopropyl betaine, oleyl betaine, palmamidopropyl betaine, palmitamidopropyl betaine, palm-kernelamidopropyl betaine, stearamidopropyl betaine, stearyl betaine, tallowamidopropyl betaine, tallow betaine, undecylenamidopropyl betaine, undecyl betaine, and mixtures thereof. Preferred betaines are selected from the group consisting of: cocamidopropyl betaine, cocobetaines, lauramidopropyl betaine, lauryl betaine, myristyl amidopropyl betaine, myristyl betaine, and mixtures thereof. Cocamidopropyl betaine is particularly preferred.

[0074] Preferably, the surfactant system of the composition of the present invention further comprises from 1% to 25%, preferably from 1.25% to 20%, more preferably from 1.5% to 15%, most preferably from 1.5% to 5%, by weight of the surfactant system, of a non-ionic surfactant.

[0075] Suitable nonionic surfactants can be selected from the group consisting of: alkoxylated non-ionic surfactant, alkyl polyglucoside ("APG") surfactant, and mixtures thereof.

[0076] Suitable alkoxylated non-ionic surfactants can be linear or branched, primary or secondary alkyl alkoxylated non-ionic surfactants. Alkyl ethoxylated non-ionic surfactant are preferred. The ethoxylated non-ionic surfactant can comprise on average from 9 to 15, preferably from 10 to 14 carbon atoms in its alkyl chain and on average from 5 to 12, preferably from 6 to 10, most preferably from 7 to 8, units of ethylene oxide per mole of alcohol. Such alkyl ethoxylated nonionic surfactants can be derived from synthetic alcohols, such as OXO-alcohols and Fisher Tropsh alcohols, or from naturally derived alcohols, or from mixtures thereof. Suitable examples of commercially available alkyl ethoxylate nonionic surfactants include, those derived from synthetic alcohols sold under the Neodol® brand-name by Shell, or the Lial®, Isalchem®, and Safol® brand-names by Sasol, or some of the natural alcohols produced by The Procter & Gamble Chemicals company.

[0077] The compositions of the present invention can comprise alkyl polyglucoside ("APG") surfactant. The addition of alkyl polyglucoside surfactants have been found to improve sudsing beyond that of comparative nonionic surfactants such as alkyl ethoxylated surfactants. Preferably the alkyl polyglucoside surfactant is a C8-C16 alkyl polyglucoside surfactant, preferably a C8-C14 alkyl polyglucoside surfactant. The alkyl polyglucoside preferably has an average degree of polymerization of between 0.1 and 3, more preferably between 0.5 and 2.5, even more preferably between 1 and 2. Most preferably, the alkyl polyglucoside surfactant has an average alkyl carbon chain length between 10 and 16, preferably between 10 and 14, most preferably between 12 and 14, with an average degree of polymerization of between 0.5 and 2.5 preferably between 1 and 2, most preferably between 1.2 and 1.6. C8-C16 alkyl polyglucosides are commercially available from several suppliers (e.g., Simusol® surfactants from Seppic Corporation; and Glucopon® 600 CSUP, Glucopon® 650 EC, Glucopon® 600 CSUP/MB, and Glucopon® 650 EC/MB, from BASF Corporation).

Non-Heme fatty acid decarboxylases

[0078] Non-heme fatty acid decarboxylases catalyze the decarboxylation of fatty acids to alkenes utilizing dioxygen as a cosubstrate and dinuclear iron as a cofactor. The most well studied member of this family is UndA from Pseudomonas aeruginosa Pf-5 (SEQ ID NO: 1), an enzyme with high specificity for C10 to C14 fatty acids. Members from other genera, including Acinetobacer, Myxococcus, and Bukhoideria, have also been reported (see for example US 10,000,775 B2; Z. Rui et al., PNAS, (2014), 111, 18237-18242), with more than 1000 homologs identified from public databases.

[0079] UndA (SEQ ID NO: 1) is a small enzyme of 261 amino acids with no significant homology to other enzymes of known function. Crystal structures of this protein have been published (PDB ID: 4WWJ, 4WWX, 4WX0), revealing a hydrophobic pocket of limited size that is able to accommodate only medium chain fatty acids (e.g. C10 to C14), while excluding longer chain substrates (e.g. C16 or C18).

[0080] Without wishing to be bound by theory, sequence alignment of UndA (SEQ ID NO: 1) and related homologs suggests that several regions of conserved sequence motifs and amino acids may contribute to and/or define the active site of the enzyme. For instance, the residues E101, H104, E159, H194, and H201 are highly conserved and may be important for enzyme catalytic function since they bind the dinuclear iron cofactor. The sequence motif (A/P/Q/L)51-X-X-X-(R/A)55-X-(Y/F/V/A)57-(L/F/M)58-(I/V/A/S)59-(G/N/H/Q/T)60-(G/F/A/V/I/L)61-(W/F/Y)62-(P/L)63-(V/I/L)64-V65-(E/A)66-(Q/S/H)67-F68-(A/S/P)69-(L/V/K/S)70-Y71-M72-(A/S/G)73-X-(N/S/A/T)75-L76-(T/L)77-K78 forms an alpha-helix that contributes to the formation of the substrate binding pocket. The sequence motif G86-(E/V/D)-(D/T/E/A)-(M/E/K/S)-(A/T/I)-R91-(R/N/D)-(W/Y)-L94-(M/I/L)-(R/Q)-N97-(I/L)-(R/K/G)-V100-E101-(L/Q/E/A)-(N/R/K)-H104-(A/L/V)-X-(Y/W/H)-(W/Y/F)-X-(H/N/D)-W111 forms an alpha-helix that includes two amino acids, E101 and H104, that coordinate an iron in the catalytic center of the enzyme. The sequence motif L147-(I/A/P)-(V/I/E/A)-(A/C/S/G)-(I/M/L/I/V)-A152-A153-(T/S)-N155-(Y/L/W)-A157-(I/V)-E159-(G/W/S)-(A/V/I)-T162-G163-(E/D/V)-(W/L)165-(S/T)-(A/I/R) forms an alpha-helix that contributes to the formation of the substrate binding pocket, and contains the amino acid residue E159 that may be involved in iron or oxygen binding and/or serve as a proton donor for the regeneration of the enzyme. The sequence motif W190-L191-(K/R)-(M/L/A/V)-H194-(A/S)-(Q/H/S/R)-Y197-D198-D199-X-H201-P202-(W/Y/E/V)-E204-A205-(L/M)-(E/D)-(I/L)-(I/V) forms an alpha-helix that includes the amino acid residues H194 and H201 that coordinate to the irons in the catalytic center. The sequence motif (Y/C/M)235-(M/Y/F)-(Y/E/A/T/H)-(L/M/A)-(F/A/S/I/T/L/V/G)-(L/A/G/)240-(E/D/S/H)-(R/E/D/C/A)-(C/S/Y)243 forms an alpha-helix that contributes to the formation of the substrate binding pocket. Furthermore, without wishing to be bound by theory, residues 35, 36, 38, 40, 41, 44, 54, 57, 58, 60, 61, 108, 111, 130, 131, 133, 134, 165, 169, 235, 236, 238, 239, 240, and 243 in UndA (SEQ ID NO: 1) may be important for the substrate specificity of the enzyme. Indeed, the variant UndA F239A was recently demonstrated to decarboxylase C16 fatty acids (Knoot, C. J. and H. B. Pakrasi (2019). Sci. Rep. 9(1): 1-12.), but non-heme fatty acid decarboxylases that convert C18 fatty acids have not been reported.

[0081] The present invention provides hand dish-washing compositions comprising non-heme fatty acid decarboxylases having increased enzymatic activity for long-chain fatty acid substrates, such as palmitic acid, stearic acid, oleic acid, linoleic acid, and linolenic acid, as compared to the well-known naturally occurring wild-type fatty acid decarboxylases reported previously in the art (e.g. UndA SEQ ID NO: 1), and especially for long chain saturated fatty acids such as stearic acid and palmitic acid, and long chain unsaturated fatty acid substrates such as oleic acid, linoleic acid, and linolenic acid. Surprisingly, Applicant has found that non-heme fatty acid decarboxylases comprising small amino acid residues (e.g. glycine or alanine) at certain positions (e.g. 41, 57, 239) have an increased enzymatic activity towards long chain fatty acids, such as palmitic acid, stearic acid, oleic acid, linoleic acid, or linolenic acid, and especially for long chain saturated fatty acids such as stearic acid and palmitic acid, and unsaturated fatty acid substrates such as oleic acid, linoleic acid, and linolenic acid, in comparison to the well-known UndA (SEQ ID NO: 1) and that these decarboxylases can provide a benefit when formulated in hand dish-washing compositions.

[0082] The hand dish-washing composition can comprise a non-heme fatty acid decarboxylase; wherein said decarboxylase comprises an amino acid selected from the group consisting of: a) leucine or isoleucine at position 41, b) alanine at position 57, c) glycine, alanine, isoleucine, leucine, valine, serine, or threonine at position 239, and d) combinations thereof; wherein said positions are numbered with reference to SEQ ID NO: 1; and wherein said decarboxylase catalyzes the conversion of at least one fatty acid selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, and mixtures thereof, preferably stearic acid, oleic acid, and mixtures thereof. The hand dish-washing composition can comprise a non-heme fatty acid decarboxylase; wherein said decarboxylase comprises an amino acid selected from the group consisting of: a) alanine at position 57, b) glycine or alanine at position 239, and c) combinations thereof; wherein said positions are numbered with reference to SEQ ID NO: 1; and wherein said decarboxylase catalyzes the conversion of at least one fatty acid selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, and mixtures thereof, preferably stearic acid, oleic acid, and mixtures thereof, more preferably oleic acid. The hand dish-washing composition can comprise a non-heme fatty acid decarboxylase; wherein said decarboxylase comprises an alanine at position 57 and an alanine at position 239; wherein said positions are numbered with reference to SEQ ID NO: 1; and wherein said decarboxylase catalyzes the conversion of at least one fatty acid selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, and mixtures thereof, preferably stearic acid, oleic acid, and mixtures thereof.

[0083] A suitable non-heme fatty acid decarboxylase comprising an isoleucine at position 41 is SEQ ID NO: 2. A suitable non-heme fatty acid decarboxylase comprising a leucine at position 41 is SEQ ID NO: 3. Suitable non-heme fatty acid decarboxylases comprising an alanine at position 57 are SEQ ID NO: 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, and 57. Suitable non-heme fatty acid decarboxylases comprising a glycine at position 239 are SEQ ID NO: 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, and 70. Suitable non-heme fatty acid decarboxylases comprising an alanine at position 239 are SEQ ID NO: 21, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, and 83. Suitable non-heme fatty acid decarboxylases comprising a valine at position 239 are SEQ ID NO: 84, 85, 86, 87, 88, and 89. Suitable non-heme fatty acid decarboxylases comprising an isoleucine at position 239 are SEQ ID NO: 90 and 91. Suitable non-heme fatty acid decarboxylases comprising a leucine at position 239 are SEQ ID NO: 92, 93, 94, 95, and 96. Suitable non-heme fatty acid decarboxylases comprising a serine at position 239 are SEQ ID NO: 97, 98, 99, 100, and 101. Suitable non-heme fatty acid decarboxylases comprising a threonine at position 239 are SEQ ID NO: 102, 103, 104, 105, and 106. Suitable non-heme fatty acid decarboxylases comprising an alanine at position 57 and an alanine at position 239 are SEQ ID NO: 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, and 57.

[0084] The decarboxylases can have an increased enzymatic activity for a substrate selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, and linolenic acid, preferably stearic acid and oleic, of at least about 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 150-fold, 500-fold or more relative to the activity of wild-type decarboxylase (SEQ ID NO: 1) under suitable reaction conditions.

[0085] The hand dish-washing composition can comprise a non-heme fatty acid decarboxylase having at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, 100% identity to one or more sequences selected from the group consisting of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, and their functional fragments thereof. The hand dish-washing composition may comprise a decarboxylase selected from the group consisting of SEQ ID NO: 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, and 83, and their functional fragments. The hand dish-washing composition may comprise a decarboxylase selected from the group consisting of SEQ ID NO: 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and their functional fragments. The hand dish-washing composition may comprise a decarboxylase with SEQ ID NO: 4.

[0086] Identity, or homology, percentages as mentioned herein in respect of the present invention are those that can be calculated, for example, with AlignX obtainable from Thermo Fischer Scientific or with the alignment tool from Uniprot (https://www.uniprot.org/align/). Alternatively, a manual alignment can be performed. For enzyme sequence comparison the following settings can be used: Alignment algorithm: Needleman and Wunsch, J. Mol. Biol. 1970, 48: 443-453. As a comparison matrix for amino acid similarity the Blosum62 matrix can be used (Henikoff S. and Henikoff J.G., P.N.A.S.

USA 1992, 89: 10915-10919). The following gap scoring parameters can be used: Gap penalty: 12, gap length penalty: 2, no penalty for end gaps.

[0087] A given sequence is typically compared against the full-length sequence or fragments of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, and 106 to obtain a score. Polypeptides of the present disclosure include polypeptides containing an amino acid sequence having at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identity to the amino acid sequence of any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, and 106. Polypeptides of the disclosure also include polypeptides having at least 10, at least 12, at least 14, at least 16, at least 18, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, or at least 80 consecutive amino acids of the amino acid sequence of any one of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, and 106.

[0088] The present invention can also include variants of non-heme fatty acid decarboxylases, as discussed previously. Variants of non-heme fatty acid decarboxylases include polypeptide sequences resulting from modification of a wild-type non-heme fatty acid decarboxylase at one or more amino acids. A variant includes a "modified enzyme" or a "mutant enzyme" which encompasses proteins having at least one substitution, insertion, and/or deletion of an amino acid. A modified enzyme may have 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more amino acid modifications (selected from substitutions, insertions, deletions and combinations thereof).

[0089] The variants may have "conservative" substitutions. Suitable examples of conservative substitution includes one conservative substitution in the enzyme, such as a conservative substitution in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, and their functional fragments thereof. Other suitable examples include 10 or fewer conservative substitutions in the protein, such as five or fewer. An enzyme of the invention may therefore include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more conservative substitutions. An enzyme can be produced to contain one or more conservative substitutions by manipulating the nucleotide sequence that encodes that enzyme using, for example, standard procedures such as site-directed mutagenesis or PCR. Examples of amino acids which may be substituted for an original amino acid in an enzyme and which are regarded as conservative substitutions include: Ser for Ala; Lys for Arg; Gln or His for Asn; Glu for Asp; Asn for Gln; Asp for Glu; Pro for Gly; Asn or Gln for His; Leu or Val for Ile; Ile or Val for Leu; Arg or Gln for Lys; Leu or Ile for Met; Met, Leu or Tyr for Phe; Thr for Ser; Ser for Thr; Tyr for Trp; Trp or Phe for Tyr; and Ile or Leu for Val.

[0090] The variant of the non-heme fatty acid decarboxylase can comprise a polypeptide sequence comprising at least one amino acid substitution at positions selected from the group consisting of: 35, 36, 38, 40, 41, 44, 54, 57, 58, 60, 61, 108, 111, 130, 131, 133, 134, 165, 169, 235, 236, 238, 239, 240, 243, 247, 40/41, 40/44, 40/57, 40/165, 40/239, 40/240, 41/44, 41/57, 41/131, 41/165, 41/239, 41/240, 41/243, 44/57, 44/131, 44/165, 44/239, 44/240, 44/243, 57/131, 57/165, 57/239, 57/240, 57/243, 133/239, 239/240, 240/243, 40/41/57, 40/41/239, 40/41/240, 40/44/240, 40/57/240, 40/165/240, 40/57/239, 40/57/240, 40/239/240, 41/44/57, 41/44/239, 41/44/240, 41/57/165, 41/57/239, 41/57/240, 41/165/239, 41/165/240, 41/239/240, 44/57/239, 44/57/240, 44/165/240, 44/239/240, 57/165/239, 57/165/240, 57/239/240, 133/238/239, 60/133/239, 133/235/239, 165/239/240, 40/41/57/239, 40/41/57/240, 40/41/239/240, 40/57/239/240, 41/57/165/239, 41/57/165/240, 41/57/239/240, 57/61/239/240, 57/131/239/240, 57/134/239/240, 57/239/240/243, 131/134/240/243, 40/41/57/165, 40/41/57/239/240, 41/57/239/240/165, 57/130/134/239/240, 40/41/44/57/239/240, 40/41/57/165/239/240, and combinations thereof; wherein said positions are numbered with reference to SEQ ID NO: 1. The variant of the non-heme fatty acid decarboxylase can comprise a polypeptide sequence comprising at least one amino acid substitution selected from the group consisting of: alanine, asparagine, glutamine, glycine, histidine, isoleucine, leucine, methionine, phenylalanine, serine, threonine, tryptophan, and valine; more preferably alanine, glycine, isoleucine, leucine, methionine, phenylalanine, and valine.

[0091] The variant of the non-heme fatty acid decarboxylase can comprise a polypeptide sequence comprising at least one amino acid substitution selected from the group consisting of V35(A/T), V36(A/R/T), L40(A/F/H/M/T/V/W), Y41(A/F/G/I/L/M/N/V/W), M44(A/E/F/I/L/T/V/W), M54(A/G/I/N/Q), Y57(A/F/G/H/I/L/M/V), L58(A/F/G), G60A, G61A, W108(A/F/G/L/M), W111(A/F/G/LM/S/T/V), L131(A/D/F/G/H/I/M/N/T/V), A133G, L134(A/G/T/V), W165(A/F/G/I/L/V),

V169(A/I/L), Y235A, M236(A/G), L238(A/I/Q/Y), F239(A/G/I/S/T/V), L240(A/F/M/Q), C243(A/G/I/L/M/Q), and E247(A/G/I/L/V); wherein said positions are numbered with reference to SEQ ID NO: 1.

[0092] It is important that variants of enzymes retain and preferably improve the ability of the wild-type protein to catalyze the conversion of the fatty acids. Some performance drop in a given property of variants may of course be tolerated, but the variants should retain and preferably improve suitable properties for the relevant application for which they are intended. Screening of variants of one of the wild-types can be used to identify whether they retain and preferably improve appropriate properties.

[0093] The decarboxylase polypeptides described herein are not restricted to the genetically encoded amino acids. Thus, in addition to the genetically encoded amino acids, the polypeptides described herein may be comprised, either in whole or in part, of naturally-occurring and/or synthetic non-encoded amino acids. Certain commonly encountered non-encoded amino acids of which the polypeptides described herein may be comprised include, but are not limited to: the D-stereoisomers of the genetically-encoded amino acids; 2,3-diaminopropionic acid (Dpr); α-aminoisobutyric acid (Aib); ε-aminohexanoic acid (Aha); δ-aminovaleric acid (Ava); N-methylglycine or sarcosine (MeGly or Sar); ornithine (Orn); citrulline (Cit); t-butylalanine (Bua); t-butylglycine (Bug); N-methylisoleucine (Melle); phenylglycine (Phg); cyclohexylalanine (Cha); norleucine (Nle); naphthylalanine (Nal); 2-chlorophenylalanine (Oct); 3-chlorophenylalanine (Mcf); 4-chlorophenylalanine (Pcf); 2-fluorophenylalanine (Off); 3-fluorophenylalanine (Mff); 4-fluorophenylalanine (Pff); 2-bromophenylalanine (Obf); 3-bromophenylalanine (Mbf); 4-bromophenylalanine (Pbf); 2-methylphenylalanine (Omf); 3-methylphenylalanine (Mmf); 4-methylphenylalanine (Pmf); 2-nitrophenylalanine (Onf); 3-nitrophenylalanine (Mnf); 4-nitrophenylalanine (Pnf); 2-cyanophenylalanine (Ocf); 3-cyanophenylalanine (Mcf); 4-cyanophenylalanine (Pcf); 2-trifluoromethylphenylalanine (Otf); 3-trifluoromethylphenylalanine (Mtf); 4-trifluoromethylphenylalanine (Ptf); 4-aminophenylalanine (Paf); 4-iodophenylalanine (Pif); 4-aminomethylphenylalanine (Pamf); 2,4-dichlorophenylalanine (Opef); 3,4-dichlorophenylalanine (Mpcf); 2,4-difluorophenylalanine (Opff); 3,4-difluorophenylalanine (Mpff); pyrid-2-ylalanine (2pAla); pyrid-3-ylalanine (3pAla); pyrid-4-ylalanine (4pAla); naphth-1-ylalanine (InAla); naphth-2-ylalanine (2nAla); thiazolylalanine (taAla); benzothienylalanine (bAla); thienylalanine (tAla); furylalanine (fAla); homophenylalanine (hPhe); homotyrosine (hTyr); homotryptophan (hTrp); pentafluorophenylalanine (5ff); styrylkalanine (sAla); authrylalanine (aAla); 3,3-diphenylalanine (Dfa); 3-amino-5-phenypentanoic acid (Afp); penicillamine (Pen); 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid (Tic); β-2-thienylalanine (Thi); methionine sulfoxide (Mso); N(w)-nitroarginine (nArg); homolysine (hLys); phosphonomethylphenylalanine (pmPhe); phosphoserine (pSer); phosphothreonine (pThr); homoaspartic acid (hAsp); homoglutamic acid (hGlu); 1-aminocyclopent-(2 or 3)-ene-4 carboxylic acid; pipecolic acid (PA), azetidine-3-carboxylic acid (ACA); 1-aminocyclopentane-3-carboxylic acid; allylglycine (aOly); propargylglycine (pgGly); homoalanine (hAla); norvaline (nVal); homoleucine (hLeu), homovaline (hVal); homoisoleucine (hIle); homoarginine (hArg); N-acetyl lysine (AcLys); 2,4-diaminobutyric acid (Dbu); 2,3-diaminobutyric acid (Dab); N-methylvaline (MeVal); homocysteine (hCys); homoserine (hSer); hydroxyproline (Hyp) and homoproline (hPro). Additional non-encoded amino acids of which the polypeptides described herein may be comprised will be apparent to those of skill in the art. These amino acids may be in either the L- or D-configuration.

[0094] The invention also can include variants in the form of truncated forms or fragments derived from a wild-type enzyme, such as a protein with a truncated N-terminus or a truncated C-terminus. Variants of decarboxylase enzymes can comprise a fragment of any of the decarboxylase polypeptides described herein that retain functional decarboxylase activity and/or an improved property of an engineered decarboxylase polypeptide. Accordingly, the composition can comprise a polypeptide fragment having decarboxylase activity (e.g., capable of converting substrate to product under suitable reaction conditions), wherein the fragment comprises at least about 80%, 90%, 95%, 98%, or 99% of a full-length amino acid sequence of the engineered polypeptide.

[0095] The present invention can include a decarboxylase enzyme having an amino acid sequence comprising an insertion as compared to any one of the decarboxylase polypeptide sequences described herein. The insertions can comprise one or more amino acids, 2 or more amino acids, 3 or more amino acids, 4 or more amino acids, 5 or more amino acids, 6 or more amino acids, 8 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, where the associated functional activity and/or improved properties of the decarboxylase described herein is maintained. The insertions can be to amino or carboxy terminus, or internal portions of the decarboxylase polypeptide. The invention can also include variants derived by adding an extra amino acid sequence, such as an N-terminal tag or a C-terminal tag. Suitable tags are maltose binding protein (MBP) tag, glutathione S-transferase (GST) tag, thioredoxin (Trx) tag, His-tag, and any other tags known by those skilled in art. Tags can be used to improve solubility and expression levels during fermentation or as a handle for enzyme purification.

[0096] Enzymes can also be modified by a variety of chemical techniques to produce derivatives having essentially the same or preferably improved activity as the unmodified enzymes, and optionally having other desirable properties. For example, carboxylic acid groups of the protein, whether carboxyl-terminal or side chain, may be provided in the form of a salt of a pharmaceutically-acceptable cation or esterified, for example to form a C1-C6 alkyl ester, or converted to an amide, for example of formula CONR1R2 wherein R1 and R2 are each independently H or C1-C6 alkyl, or combined to form a heterocyclic ring, such as a 5- or 6-membered ring. Amino groups of the enzyme, whether amino-terminal or side chain, may be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or may be modified to C1-C20 alkyl or dialkyl amino or further converted to an amide. Hydroxyl groups of the protein side chains may be converted to alkoxy or ester groups, for example C1-C20 alkoxy or C1-C20 alkyl ester, using well-recognized techniques. Phenyl and phenolic rings of the protein side chains may be substituted with one or more halogen atoms, such as F, Cl, Br or I, or with C1-C20 alkyl, C1-C20 alkoxy, carboxylic acids and esters thereof, or amides of such carboxylic acids. Methylene groups of the protein side chains can be extended to homologous C2-C4 alkylenes. Thiols can be protected with any one of a number of well-recognized protecting groups, such as acetamide groups. Those skilled in the art will also recognize methods for introducing cyclic structures into the proteins of this disclosure to select and provide conformational constraints to the structure that result in enhanced stability.

[0097] The enzymes can be provided on a solid support, such as a membrane, resin, solid carrier, or other solid phase material. A solid support can be composed of organic polymers such as polystyrene, polyethylene, polypropylene, polyfluoroethylene, polyethyleneoxy, and polyacrylamide, as well as co-polymers and grafts thereof. A solid support can also be inorganic, such as glass, silica, controlled pore glass (CPG), reverse phase silica or metal, such as gold or platinum. The configuration of a solid support can be in the form of beads, spheres, particles, granules, a gel, a membrane or a surface. Surfaces can be planar, substantially planar, or nonplanar. Solid supports can be porous or non-porous, and can have swelling or non-swelling characteristics. A solid support can be configured in the form of a well, depression, or other container, vessel, feature, or location.

[0098] The polypeptides having decarboxylase activity can be bound or immobilized on the solid support such that they retain at least a portion of their improved properties relative to a reference polypeptide (e.g., SEQ ID NO: 1). Accordingly, it is further contemplated that any of the methods of using the decarboxylase polypeptides of the present invention can be carried out using the same decarboxylase polypeptides bound or immobilized on a solid support.

[0099] The decarboxylase polypeptide can be bound non-covalently or covalently. Various methods for conjugation and immobilization of enzymes to solid supports (e.g., resins, membranes, beads, glass, etc.) are well known in the art. Other methods for conjugation and immobilization of enzymes to solid supports (e.g., resins, membranes, beads, glass, etc.) are well known in the art (See, e.g., Yi et al., Proc. Biochem., 42: 895-898 [2007]; Martin et al., Appl. Microbiol. Biotechnol., 76: 843-851 [2007]; Koszelewski et al. J. Mol. Cat. B: Enz., 63: 39-44 [2010]; Truppo et al., Org. Proc. Res. Develop., published online: dx.doi.org/10.1021/op200157c; and Mateo et al., Biotechnol. Prog., 18:629-34 [2002], etc.). Solid supports useful for immobilizing the decarboxylase polypeptides of the present invention include, but are not limited to, beads or resins comprising polymethacrylate with epoxide functional groups, polymethacrylate with amino epoxide functional groups, styrene/DVB copolymer or polymethacrylate with octadecyl functional groups.

[0100] The enzymes may be incorporated into the hand dish-washing compositions *via* an additive particle, such as an enzyme granule or in the form of an encapsulate, or may be added in the form of a liquid formulation. Preferably the enzyme is incorporated into the cleaning composition *via* an encapsulate. Encapsulating the enzymes promote the stability of the enzymes in the composition and helps to counteract the effect of any hostile compounds present in the composition, such as bleach, protease, surfactant, chelant, etc. The non-heme fatty acid decarboxylase enzymes may be the only enzymes in the additive particle or may be present in the additive particle in combination with one or more additional co-enzymes.

[0101] The hand dish-washing composition can comprise a non-heme fatty acid decarboxylase, wherein said non-heme fatty acid decarboxylase is present in an amount of from 0.0001 wt% to 1 wt%, preferably from 0.001 wt% to 0.2 wt%, by weight of the hand dish-washing composition, based on active protein.

[0102] The hand dish-washing composition may further comprise one or more co-enzymes selected from the group consisting of: fatty-acid peroxidases (EC 1.11.1.3), unspecific peroxygenases (EC 1.11.2.1), plant seed peroxygenases (EC 1.11.2.3), fatty acid peroxygenases (EC1.11.2.4), linoleate diol synthases (EC 1.13.11.44), 5,8-linoleate diol synthases (EC 1.13.11.60 and EC 5.4.4.5), 7,8-linoleate diol synthases (EC 1.13.11.60 and EC 5.4.4.6), 9,14-linoleate diol synthases (EC 1.13.11.B1), 8,11-linoleate diol synthases, oleate diol synthases, other linoleate diol synthases, unspecific monooxygenase (EC 1.14.14.1), alkane 1-monooxygenase (EC 1.14.15.3), oleate 12-hydroxylases (EC 1.14.18.4), fatty acid amide hydrolase (EC 3.5.1.99), oleate hydratases (EC 4.2.1.53), linoleate isomerases (EC 5.2.1.5), linoleate (10E,12Z)-isomerases (EC 5.3.3.B2), fatty acid decarboxylases (OleT-like), alpha-dioxygenases, amylases, lipases, proteases, cellulases, and mixtures thereof; preferably fatty-acid peroxidases (EC 1.11.1.3), unspecific peroxygenases (EC 1.11.2.1), plant seed peroxygenases (EC 1.11.2.3), and fatty acid peroxygenases (EC 1.11.2.4), heme fatty acid decarboxylases (OleT-like), alpha-dioxygenases, and mixtures thereof.

[0103] Where necessary, the composition comprises, provides access to, or forms *in situ* any additional substrate necessary for the effective functioning of the enzyme. For example, molecular oxygen can be provided as an additional substrate for non-heme fatty acid decarboxylases. Molecular oxygen can be obtained from the atmosphere or from a precursor that can be transformed to produce oxygen in situ. In many applications, oxygen from the atmosphere can be present in sufficient amounts. The hand dish-washing composition may be supplemented with iron (Fe) or a source of iron, preferably a source of iron(II), to enhance or facilitate the conversion of the fatty acids. Non-limiting examples of sources of iron(II) are such as ammonium iron(II) sulfate, iron(II) sulfate, iron(II) chloride, iron(II) oxide, iron(II) acetate, iron(II) citrate, and iron(II) oxalate. The hand dish-washing composition may also be supplemented with a reducing agent. Non-limiting examples of reducing agents are ascorbic acid and cysteine. The hand dish-washing composition may be supplemented with combinations of various compounds and/or reagents, such as, for example, a source of iron, ascorbic acid, and/or cysteine.

Methods of Producing Decarboxylase Polypeptides

[0104] Standard methods of culturing organisms such as, for example, bacteria and yeast, for production of enzymes are well-known in the art and are described herein. For example, host cells may be cultured in a standard growth media under standard temperature and pressure conditions, and in an aerobic environment. Standard growth media for various host cells are commercially available and well-known in the art, as are standard conditions for growing various host cells.

[0105] Decarboxylase enzymes expressed in a host cell can be recovered from the cells and or the culture medium using any one or more of the well-known techniques for protein purification, including, among others, lysozyme treatment, sonication, filtration, salting-out, ultra-centrifugation, and chromatography. Suitable solutions for lysing and the high efficiency extraction of proteins from bacteria, such as E. coli, are commercially available under the trade name CelLytic B (Sigma-Aldrich). Chromatographic techniques for isolation of the decarboxylase polypeptide include, among others, reverse phase chromatography high performance liquid chromatography (HPLC), ion exchange chromatography, gel electrophoresis, and affinity chromatography. Conditions for purifying a particular enzyme will depend, in part, on factors such as net charge, hydrophobicity, hydrophilicity, molecular weight, molecular shape, etc., and will be apparent to those having skill in the art.

[0106] The decarboxylases may also be prepared and used in the form of cells expressing the enzymes, as crude extracts, or as isolated or purified preparations. The decarboxylases may be prepared as lyophilizates, in powder form (e.g., acetone powders), or prepared as enzyme solutions. The decarboxylases can be in the form of substantially pure preparations.

Adjunct Ingredients

[0107] The cleaning composition herein may optionally comprise a number of other adjunct ingredients such as additional enzymes, enzyme stabilisers, organic solvents, polymers, cleaning amines, chelants, builders (*e.g.*, preferably citrate), structurants, emollients, humectants, skin rejuvenating actives, scrubbing particles, bleach and bleach activators, perfumes, malodor control agents, pigments, dyes, opacifiers, beads, pearlescent particles, capsules, inorganic cations such as alkaline earth metals such as Ca/Mg-ions, antibacterial agents, preservatives, viscosity adjusters (*e.g.*, salt such as NaCl, and other mono-, di- and trivalent salts) and pH adjusters and buffering means (*e.g.*, carboxylic acids such as citric acid, HCl, NaOH, KOH, alkanolamines, phosphoric and sulfonic acids, carbonates such as sodium carbonates, bicarbonates, sesquicarbonates, borates, silicates, phosphates, imidazole and alike).

Additional Enzymes

[0108] Preferred compositions of the invention comprise one or more enzymes selected from lipases, proteases, cellulases, amylases and any combination thereof.

[0109] Each additional enzyme is typically present in an amount from 0.0001 wt% to 1 wt% (weight of active protein) more preferably from 0.0005 wt% to 0.5 wt%, most preferably 0.005-0.1%. It may be particularly preferred for the compositions of the present invention to additionally comprise a lipase enzyme. Lipases break down fatty ester soils into fatty acids which are then acted upon by the saturated and/or unsaturated fatty acid-transforming enzyme according to the invention into suds neutral or suds boosting agents.

[0110] It may be particularly preferred for the compositions of the present invention to additionally comprise a protease enzyme. Since oleic acid and other foam suppressing saturated and/or unsaturated fatty acids are present in body soils or even human skin, as protease enzyme acts as a skin care agent, or breaks down proteinaceous soils, fatty acids released are broken down, preventing suds suppression.

[0111] It may be particularly preferred for the compositions of the present invention to additionally comprise an amylase enzyme. Since oily soils are commonly entrapped in starchy soils, the amylase and saturated and/or unsaturated fatty acid transforming enzymes work synergistically together: fatty acid soils are released by breakdown of starchy soils with amylase, thus, the saturated and/or unsaturated fatty acid transforming enzyme of use in the invention is particularly effective in ensuring there is no negative impact on suds in the wash liquor.

Enzyme Stabiliser

[0112] Preferably the composition of the invention comprises an enzyme stabilizer. Suitable enzyme stabilizers may be selected from the group consisting of (a) univalent, bivalent and/or trivalent cations preferably selected from the group of inorganic or organic salts of alkaline earth metals, alkali metals, aluminum, iron, copper and zinc, preferably alkali metals and alkaline earth metals, preferably alkali metal and alkaline earth metal salts with halides, sulfates, sulfites, carbonates, hydrogencarbonates, nitrates, nitrites, phosphates, formates, acetates, propionates, citrates, maleates, tartrates, succinates, oxalates, lactates, and mixtures thereof. The salt can be selected from the group consisting of sodium chloride, calcium chloride, potassium chloride, sodium sulfate, potassium sulfate, sodium acetate, potassium acetate, sodium formate, potassium formate, calcium lactate, calcium nitrate and mixtures thereof. Most preferred are salts selected from the group consisting of calcium chloride, potassium chloride, potassium sulfate, sodium acetate, potassium acetate, sodium formate, potassium formate, calcium lactate, calcium nitrate, and mixtures thereof, and in particular potassium salts selected from the group of potassium chloride, potassium sulfate, potassium acetate, potassium formate, potassium propionate, potassium lactate and mixtures thereof. Most preferred are potassium acetate and potassium chloride. Preferred calcium salts are calcium formate, calcium lactate and calcium nitrate including calcium nitrate tetrahydrate. Calcium and sodium formate salts may be preferred. These cations are present at at least 0.01 wt%, preferably at least 0.03 wt%, more preferably at least 0.05 wt%, most preferably at least 0.25 wt% up to 2 wt% or even up to 1 wt% by weight of the total composition. These salts are formulated from 0.1 wt% to 5 wt%, preferably from 0.2 wt% to 4 wt%, more preferably from 0.3 wt% to 3 wt%, most preferably from 0.5 wt% to 2 wt% relative to the total weight of the composition. Further enzyme stabilizers can be selected from the group (b) carbohydrates selected from the group consisting of oligosaccharides, polysaccharides and mixtures thereof, such as a monosaccharide glycerate as described in WO201219844; (c) mass efficient reversible protease inhibitors selected from the group consisting of phenyl boronic acid and derivatives thereof, preferably 4-formyl phenylboronic acid; (d) alcohols such as 1,2-propane diol, propylene glycol; (e) peptide aldehyde stabilizers such as tripeptide aldehydes such as Cbz-Gly-Ala-Tyr-H, or disubstituted alaninamide; (f) carboxylic acids such as phenyl alkyl dicarboxylic acid as described in WO2012/19849 or multiply substituted benzyl carboxylic acid comprising a carboxyl group on at least two carbon atoms of the benzyl radical such as described in WO2012/19848, phthaloyl glutamine acid, phthaloyl asparagine acid, aminophthalic acid and/or an oligoamino-biphenyl-oligocarboxylic acid; and (g) mixtures thereof.

[0113] The composition of the present invention may optionally comprise from 0.01% to 3%, preferably from 0.05% to 2%, more preferably from 0.2% to 1.5%, or most preferably 0.5% to 1%, by weight of the total composition of a salt, preferably a monovalent, divalent inorganic salt or a mixture thereof, preferably sodium chloride. Most preferably the composition alternatively or further comprises a multivalent metal cation in the amount of from 0.01 wt% to 3 wt%, preferably from 0.05% to 2%, more preferably from 0.2% to 1.5%, or most preferably 0.5% to 1% by weight of said composition, preferably said multivalent metal cation is magnesium, aluminium, copper, calcium or iron, more preferably magnesium, most preferably said multivalent salt is magnesium chloride. Without wishing to be bound by theory, it is believed that use of a multivalent cation helps with the formation of protein/ protein, surfactant/ surfactant or hybrid protein/ surfactant network at the oil water and air water interface that is strengthening the suds.

[0114] Preferably the composition of the present invention comprises one or more carbohydrates selected from the group comprising O-glycan, N-glycan, and mixtures thereof. Preferably the cleaning composition further comprises one or more carbohydrates selected from the group comprising derivatives of glucose, mannose, lactose, galactose, allose, altrose, gulose, idose, talose, fucose, fructose, sorbose, tagatose, psicose, arabinose, ribose, xylose, lyxose, ribulose, and xylulose. More preferably the cleaning composition comprises one or more carbohydrates selected from the group of α-glucans and β-glucans. Glucans are polysaccharides of D-glucose monomers, linked by glycosidic bonds. Suitable α-glucans are dextran, starch, floridean starch, glycogen, pullulan, and their derivatives. Suitable β-glucans are cellulose, chrysolaminarin, curdlan, laminarin, lentinan, lichenin, oat beta-glucan, pleuran, zymosan, and their derivatives.

Hydrotrope

[0115] The composition of the present invention may optionally comprise from 1% to 10%, or preferably from 0.5% to 10%, more preferably from 1% to 6%, or most preferably from 0.1% to 3%, or combinations thereof, by weight of the total composition of a hydrotrope, preferably sodium cumene sulfonate. Other suitable hydrotropes for use herein include anionic-type hydrotropes, particularly sodium, potassium, and ammonium xylene sulfonate, sodium, potassium and ammonium toluene sulfonate, sodium potassium and ammonium cumene sulfonate, and mixtures thereof, as disclosed in U.S. Patent 3,915,903. Preferably the composition of the present invention is isotropic. An isotropic composition is distinguished from oil-in-water emulsions and lamellar phase compositions. Polarized light microscopy can assess whether the composition is isotropic. See e.g., The Aqueous Phase Behaviour of Surfactants, Robert Laughlin, Academic Press, 1994, pp. 538-542. Preferably an isotropic composition is provided. Preferably the composition comprises 0.1% to 3% by weight of the total composition of a hydrotrope, preferably wherein the hydrotrope is selected from sodium, potassium, and ammonium xylene sulfonate, sodium, potassium and ammonium toluene sulfonate, sodium potassium and ammonium cumene sulfonate, and mixtures thereof.

Organic solvent

[0116] The composition of the present invention may optionally comprise an organic solvent. Suitable organic solvents include C4-14 ethers and diethers, polyols, glycols, alkoxylated glycols, C6-C16 glycol ethers, alkoxylated aromatic alcohols, aromatic alcohols, aliphatic linear or branched alcohols, alkoxylated aliphatic linear or branched alcohols, alkoxylated C1-C5 alcohols, C8-C14 alkyl and cycloalkyl hydrocarbons and halo hydrocarbons, and mixtures thereof. Preferably the organic solvents include alcohols, glycols, and glycol ethers, alternatively alcohols and glycols. The composition comprises from 0% to less than 50%, preferably from 0.01% to 25%, more preferably from 0.1% to 10%, or most preferably from 0.5% to 5%, by weight of the total composition of an organic solvent, preferably an alcohol, more preferably an ethanol, a polyalkyleneglycol, more preferably polypropyleneglycol, and mixtures thereof.

Polymer:

[0117] The composition can comprise a polymer, preferably at a level of from 0.1% to 5%, more preferably from 0.2% to 3%, even more preferably from 0.3% to 2% by weight of the liquid composition. Suitable polymers can be selected from triblock copolymers, amphiphilic alkoxylated polyalkyleneimine, ethoxylated polyalkyleneimine, polyester soil release polymers, and mixtures thereof, preferably triblock copolymers, amphiphilic alkoxylated polyalkyleneimine, and mixtures thereof.

[0118] Suitable triblock copolymers comprise alkylene oxide moieties according to Formula (I): (EO)x(PO)y(EO)x, wherein EO represents ethylene oxide, and each x represents the number of EO units within the EO block. Each x is independently a number average between 3 and 50, preferably between 5 and 25, more preferably between 10 and 15. Preferably x is the same for both EO blocks, wherein the "same" means that the x between the two EO blocks varies within a maximum 2 units, preferably within a maximum of 1 unit, more preferably both x's are the same number of units. PO represents propylene oxide, and y represents the number of PO units in the PO block. Each y is a number average between 5 and 60, preferably between 10 and 40, more preferably between 25 and 35.

[0119] The triblock co-polymer can have a ratio of y to each x of from 0.8:1 to 5:1, preferably from 1:1 to 3:1, more preferably from 1.5:1 to 2.5:1. The triblock co-polymer can have an average weight percentage of total EO of between 30% and 50% by weight of the triblock co-polymer. As such, the triblock co-polymer can have an average weight percentage of total PO of between 50% and 70% by weight of the triblock copolymer. It is understood that the average total weight % of EO and PO for the triblock co-polymer adds up to 100%, excluding the end-caps. The end-caps are preferably hydrogen, hydroxyl, methyl, and mixtures thereof, more preferably hydrogen, methyl, and mixtures thereof, and most preferably hydrogen. The triblock co-polymer has a number average molecular weight of between 550 and 8000, preferably between 1000 and 4500, more preferably between 2000 and 3100. Number average molecular weight and compositional analysis of the co-polymer is determined using a 1H NMR spectroscopy (*see* Thermo scientific application note No. AN52907). It is an established tool for polymer characterization, including number-average molecular weight determination and co-polymer composition analysis.

[0120] EO-PO-EO triblock co-polymers are commercially available from BASF such as the Pluronic® PE series, and from the Dow Chemical Company such as Tergitol™ L series. Particularly preferred triblock co-polymer from BASF are sold under the tradenames Pluronic® L44 (MW ca 2200, ca 40wt% EO), Pluronic® PE6400 (MW ca 2900, ca 40wt% EO), Pluronic® PE4300 (MW ca 1600, ca 30wt% EO), and Pluronic® PE 9400 (MW ca 4600, 40 wt% EO). Particularly preferred triblock co-polymer from the Dow Chemical Company is sold under the tradename of Tergitol™ L64 (MW ca 2900, ca 40 wt% EO). The preparation method for such triblock co-polymers is well known to polymer manufacturers.

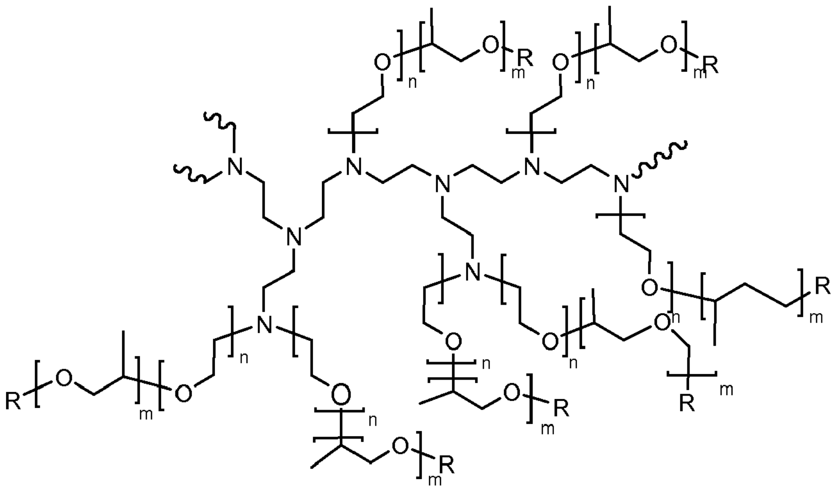
[0121] Suitable amphiphilic polymers can be selected from the group consisting of: amphiphilic alkoxylated polyalkyleneimine and mixtures thereof. Preferably, the amphiphilic alkoxylated polyalkyleneimine is an alkoxylated polyethyleneimine polymer comprising a polyethyleneimine backbone having a weight average molecular weight range of from 100 to 5,000, preferably from 400 to 2,000, more preferably from 400 to 1,000 Daltons. The polyethyleneimine backbone comprises the following modifications:

(i) one or two alkoxylation modifications per nitrogen atom, dependent on whether the modification occurs at an internal nitrogen atom or at an terminal nitrogen atom, in the polyethyleneimine backbone, the alkoxylation modification consisting of the replacement of a hydrogen atom on by a polyalkoxylene chain having an average of about 1 to about 50 alkoxy moieties per modification, wherein the terminal alkoxy moiety of the alkoxylation modification is capped with hydrogen, a C1-C4 alkyl or mixtures thereof;

(ii) a substitution of one C1-C4 alkyl moiety and one or two alkoxylation modifications per nitrogen atom, dependent on whether the substitution occurs at a internal nitrogen atom or at an terminal nitrogen atom, in the polyethyleneimine

backbone, the alkoxylation modification consisting of the replacement of a hydrogen atom by a polyalkoxylene chain having an average of about 1 to about 50 alkoxy moieties per modification wherein the terminal alkoxy moiety is capped with hydrogen, a C1-C4 alkyl or mixtures thereof; or
(iii) a combination thereof.

[0122] A preferred amphiphilic alkoxylated polyethyleneimine polymer has the general structure of formula (II):



(II)

wherein the polyethyleneimine backbone has a weight average molecular weight of about 600, n of formula (II) has an average of about 10, m of formula (II) has an average of about 7 and R of formula (II) is selected from hydrogen, a C_1-C_4 alkyl and mixtures thereof, preferably hydrogen. The degree of permanent quaternization of formula (II) may be from 0% to about 22% of the polyethyleneimine backbone nitrogen atoms. The molecular weight of this amphiphilic alkoxylated polyethyleneimine polymer preferably is between 10,000 and 15,000 Da.

[0123] More preferably, the amphiphilic alkoxylated polyethyleneimine polymer has the general structure of formula (II) but wherein the polyethyleneimine backbone has a weight average molecular weight of about 600 Da, n of Formula (II) has an average of about 24, m of Formula (II) has an average of about 16 and R of Formula (II) is selected from hydrogen, a C_1-C_4 alkyl and mixtures thereof, preferably hydrogen. The degree of permanent quaternization of Formula (II) may be from 0% to about 22% of the polyethyleneimine backbone nitrogen atoms, and is preferably 0%. The molecular weight of this amphiphilic alkoxylated polyethyleneimine polymer preferably is between 25,000 and 30,000, most preferably 28,000 Da.

[0124] The amphiphilic alkoxylated polyethyleneimine polymers can be made by the methods described in more detail in PCT Publication No. WO 2007/135645.

[0125] Alternatively, the alkoxylated polyalkyleneimine polymer can be an ethoxylated polyalkyleneimine which comprises no further alkoxylation, and as such, is hydrophilic rather than amphiphilic. That is, the ethoxylated polyalkyleneimine comprises no further alkoxylation such as propoxylation or butoxylation. Preferred ethoxylated polyalkyleneimines consist of alkyleneimine monomer units and ethoxylation (-EO-) monomer units, with the exception of any end-caps, which are typically hydrogen. Ethyleneimine monomer units are highly preferred alkyleneimine monomer units. More preferably, the hydrophilic ethoxylated polyethyleneimine polymer has the general structure of formula (II) but wherein the polyethyleneimine backbone has a weight average molecular weight of about 600 Da, n of Formula (II) has an average of about 20, m of Formula (II) is zero and R of Formula (II) is selected from hydrogen, a C_1-C_4 alkyl and mixtures thereof, preferably hydrogen. The degree of permanent quaternization of Formula (II) may be from 0% to about 22% of the polyethyleneimine backbone nitrogen atoms, and is preferably 0%. The molecular weight of this ethoxylated polyethyleneimine polymer preferably is between 10,000 and 15,000, most preferably 12,600 Da.

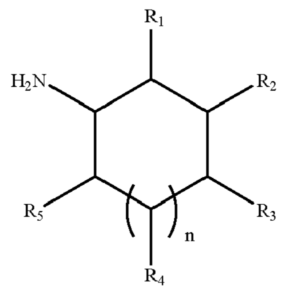
[0126] Polyester soil release agents are also suitable polymers. Soil release agents are polymers having soil release properties, i.e. having the property to enhance the cleaning efficacy of the detergent composition by improving release of greasy and oil during the laundry process. See soil release agents' definition, p.278-279, "Liquid Detergents" by Kuo-Yann Lai.

[0127] Suitable polyester soil release agents can encompass simple copolymeric blocks of ethylene terephthalate or propylene terephthalate with polyethylene oxide or polypropylene oxide terephthalate (see US 3,959,230 and US 3,893,929). Other suitable polyester soil release agents can be polyesters with repeat units containing 10-15% by weight of ethylene terephthalate together with 90-80% by weight of polyoxyethylene terephthalate, derived from a polyoxyethylene glycol of average molecular weight 300-5,000. Commercial examples include ZELCON® 5126 from Dupont and MILEASE®T from ICI. Suitable polymeric soil release agents can be prepared by art-recognized methods. US 4, 702, 857 and US 4,711,730 describe the preferred method of synthesis for the block polyesters of use.

Cyclic Polyamine

[0128] The composition can comprise a cyclic polyamine having amine functionalities that helps cleaning. The composition of the invention preferably comprises from about 0.1% to about 3%, more preferably from about 0.2% to about 2%, and especially from about 0.5% to about 1%, by weight of the composition, of the cyclic polyamine.

[0129] The amine can be subjected to protonation depending on the pH of the cleaning medium in which it is used. Preferred cyclic polyamines have the following Formula (IV):



(IV)

wherein R_1, R_2, R_3, R_4 and R_5 are independently selected from the group consisting of NH2, -H, linear or branched alkyl having from about 1 to about 10 carbon atoms, and linear or branched alkenyl having from about 1 to about 10 carbon atoms, n is from about 1 to about 3, preferably n is 1, and wherein at least one of the Rs is NH2 and the remaining "Rs" are independently selected from the group consisting of NH2, -H, linear or branched alkyl having about 1 to about 10 carbon atoms, and linear or branched alkenyl having from about 1 to about 10 carbon atoms. Preferably, the cyclic polyamine is a diamine, wherein n is 1, R_2 is NH2, and at least one of R_1, R_3, R_4 and R_5 is CH3 and the remaining Rs are H.

[0130] The cyclic polyamine has at least two primary amine functionalities. The primary amines can be in any position in the cyclic amine but it has been found that in terms of grease cleaning, better performance is obtained when the primary amines are in positions 1,3. It has also been found that cyclic amines in which one of the substituents is -CH3 and the rest are H provided for improved grease cleaning performance.

[0131] Accordingly, the most preferred cyclic polyamine for use with the detergent composition of the present invention are cyclic polyamine selected from the group consisting of: 2-methylcyclohexane-1,3-diamine, 4-methylcyclohexane-1,3-diamine and mixtures thereof. These specific cyclic polyamines work to improve suds and grease cleaning profile through-out the dishwashing process when formulated together with the surfactant system of the composition of the present invention.

Chelant

[0132] The detergent composition herein can comprise a chelant at a level of from 0.1% to 20%, preferably from 0.2% to 5%, more preferably from 0.2% to 3% by weight of total composition.

[0133] As commonly understood in the detergent field, chelation herein means the binding or complexation of a bi- or multidentate ligand. These ligands, which are often organic compounds, are called chelants, chelators, chelating agents, and/or sequestering agent. Chelating agents form multiple bonds with a single metal ion. Chelants, are chemicals that form soluble, complex molecules with certain metal ions, inactivating the ions so that they cannot normally react with other elements or ions to produce precipitates or scale, or forming encrustations on soils turning them harder to be removed. The ligand forms a chelate complex with the substrate. The term is reserved for complexes in which the metal ion is bound to two or more atoms of the chelant.

[0134] Preferably, the composition of the present invention comprises one or more chelant, preferably selected from the group comprising carboxylate chelants, amino carboxylate chelants, amino phosphonate chelants such as MGDA (methylglycine-N,N-diacetic acid), GLDA (glutamic-N,N- diacetic acid), and mixtures thereof.

[0135] Suitable chelating agents can be selected from the group consisting of amino carboxylates, amino phosphonates, polycarboxylate chelating agents and mixtures thereof.

[0136] Other chelants include homopolymers and copolymers of polycarboxylic acids and their partially or completely neutralized salts, monomeric polycarboxylic acids and hydroxycarboxylic acids and their salts. Suitable polycarboxylic acids are acyclic, alicyclic, heterocyclic and aromatic carboxylic acids, in which case they contain at least two carboxyl groups which are in each case separated from one another by, preferably, no more than two carbon atoms. A suitable hydroxycarboxylic acid is, for example, citric acid. Another suitable polycarboxylic acid is the homopolymer of acrylic acid. Preferred are the polycarboxylates end capped with sulfonates.

Method of washing

[0137] Other aspects of the invention are directed to methods of washing ware especially dishware with a composition of the present invention. Accordingly, there is provided a method of manually washing dishware comprising the steps of delivering a hand-dishwashing composition of the invention into a volume of water to form a wash solution and immersing the dishware in the solution. Preferably the non-heme fatty acid decarboxylase is present at a concentration from 0.005 ppm to 15 ppm, preferably from 0.02 ppm to 0.5 ppm, in an aqueous wash liquor during the washing process. As such, the composition herein will be applied in its diluted form to the dishware. Soiled surfaces *e.g.* dishes are contacted with an effective amount, typically from 0.5 mL to 20 mL (per 25 dishes being treated), preferably from 3mL to 10 mL, of the detergent composition of the present invention, preferably in liquid form, diluted in water. The actual amount of detergent composition used will be based on the judgment of user, and will typically depend upon factors such as the particular product formulation of the composition, including the concentration of active ingredients in the composition, the number of soiled dishes to be cleaned, the degree of soiling on the dishes, and the like. Generally, from 0.01 mL to 150 mL, preferably from 3 mL to 40 mL of a liquid detergent composition of the invention is combined with from 2,000 mL to 20,000 mL, more typically from 5,000 mL to 15,000 mL of water in a sink having a volumetric capacity in the range of from 1,000 mL to 20,000 mL, more typically from 5,000 mL to 15,000 mL. The soiled dishes are immersed in the sink containing the diluted compositions then obtained, where contacting the soiled surface of the dish with a cloth, sponge, or similar article cleans them. The cloth, sponge, or similar article may be immersed in the detergent composition and water mixture prior to being contacted with the dish surface, and is typically contacted with the dish surface for a period of time ranged from 1 to 10 seconds, although the actual time will vary with each application and user. The contacting of cloth, sponge, or similar article to the surface is preferably accompanied by a concurrent scrubbing of the surface.

[0138] Alternatively, the dishwashing composition can be applied directly onto a cleaning implement or the dishes to be cleaned without any pre-dilution step, or with slight dissolutions as is the case when applied using a damp sponge or other implement.

TEST METHODS

[0139] The following assays set forth must be used in order that the invention described and claimed herein may be more fully understood.

Test Method 1 - Enzyme activity assay for non-heme fatty acid decarboxylases

[0140] Enzymatic reactions with non-heme fatty acid decarboxylases can be performed as follows. Aliquots of sodium salts of fatty acids (e.g. sodium palmitate, sodium stearate, sodium oleate, sodium linoleate, or sodium linolenate; final concentration 100 μM), ammonium iron(II) sulfate (final concentration 100 μM), and ascorbic acid (final concentration 1 mM) are resuspended in a suitable reaction buffer (pH 6 to pH 8). The reaction is started by addition of the enzyme (final concentration 10 μM) and the solutions are incubated for up to 240 minutes at a suitable temperature. Aliquots of 100 μL of the reaction solutions are collected at different time points and mixed with 900 μL of isopropyl alcohol to stop the reaction. Analysis of the samples is performed by reversed-phase LC/MS/MS or GC/MS using standard procedures known in the art to determine the concentrations of salts of fatty acid remaining in the solutions and the percent conversion is calculated. As used herein, a non-heme fatty acid decarboxylase catalyzes the conversion of a fatty acid when the percent conversion of said fatty acid is at least 5% under optimal reaction conditions in 240 minutes or less time.

EXAMPLES

[0141] Hereinafter, the present invention is described in more detail based on examples. All percentages are by weight unless otherwise specified.

Example 1 - Production of non-heme fatty acid decarboxylases

[0142] A codon optimized gene encoding for a non-heme fatty acid decarboxylase (SEQ ID NO: 4), including an N-terminal amino acid sequence containing a His-tag, is designed and synthesized. After gene synthesis, the complete synthetic gene sequence is subcloned into a pET30a vector for heterologous expression. Then, *Escherichia coli* BL21

(DE3) cells are transformed with the recombinant plasmid and a single colony is inoculated into TB medium containing kanamycin. Pre-starter cultures are then inoculated into a bioreactor containing the same media and cultivation is performed at 25 °C. At an OD_{600nm} = 4, isopropyl β-D-1-thiogalactopyranoside (IPTG; final concentration 0.5 mM) and iron(III) chloride ($FeCl_3$; final concentration 50 μM) are added to induce protein expression. Cells are harvested by centrifugation and the pellets are lysed by sonication. After centrifugation, the supernatant is collected and the protein is purified by one-step purification using a nickel affinity column and standard protocols known in the art. The protein is stored in a buffer containing 50 mM Tris-HCl, 150 mM NaCl, and 10% Glycerol at pH 8.0.

Example 2. Exemplary Manual Dish-Washing Detergent Composition

[0143]

Level (as 100% active)	
Sodium alkyl ethoxy sulfate (C1213EO0.6S)	22.91%
n-C12-14 Di Methyl Amine Oxide	7.64%
Lutensol XP80 (non-ionic surfactant supplied by BASF)	0.45%
Sodium Chloride	1.2%
Poly Propylene Glycol (weight average molecular wt. 2000)	1%
Ethanol	2%
Sodium Hydroxide	0.24%
Non-heme fatty acid decarboxylase (SEQ ID NO: 4)	0.1%
Minors (perfume, preservative, dye) + water	To 100 %
pH (@ 10% solution)	9

[0144] All percentages and ratios given for enzymes are based on active protein. All percentages and ratios herein are calculated by weight unless otherwise indicated. All percentages and ratios are calculated based on the total composition unless otherwise indicated.

[0145] It should be understood that every maximum numerical limitation given throughout this specification includes every lower numerical limitation, as if such lower numerical limitations were expressly written herein. Every minimum numerical limitation given throughout this specification will include every higher numerical limitation, as if such higher numerical limitations were expressly written herein. Every numerical range given throughout this specification will include every narrower numerical range that falls within such broader numerical range, as if such narrower numerical ranges were all expressly written herein.

[0146] 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."

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

Leu Gly Glu Cys Ile Glu Arg Ser Tyr Arg Cys Met Ala Leu Phe Gly
225 230 235 240

Asp Arg Cys Val Arg Arg Gln His Val Thr Arg Asp Val Gln Arg Gly
245 250 255

Ala Ser Leu Ala Thr Leu Ala
260

<210> 4
<211> 255
<212> PRT
<213> Acinetobacter baylyi

<400> 4

Met Phe Glu Ser Asn Ser Tyr Arg Ile Ile Ala Met Ser Ala Leu Leu
1 5 10 15

Glu Gly Thr Asp Leu Lys Ile Thr Pro His Ser Pro Trp Ala Gln Gln
20 25 30

Phe Trp Asp Glu Leu Ile Pro Ala Lys Asp Arg Val Gly Gln His Pro
35 40 45

Leu Phe Gln Asp Met Ala Asn Gly Arg Leu Asn Leu Lys Cys Phe Arg

50 55 60

Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala His Phe Pro Ser Tyr
65 70 75 80

Met Ala Leu Ala Leu Ser Lys Ala Thr Asp Phe Thr Glu Ala Gly Val
85 90 95

Thr Glu Thr Arg Asn Trp Leu Ile Gln Asn Ile Lys Val Glu Glu Arg
100 105 110

His Leu Asn Trp Tyr Arg Asp Trp Ala Gly Gly Phe Gly Leu Thr Val
115 120 125

Glu Glu Leu Asp Arg Val Arg Pro Pro Val Ala Met Asp Ala Val Asn
130 135 140

His Phe Leu Trp Asn Ile Asn Thr Lys Gly Ser Leu Ala Glu Cys Leu
145 150 155 160

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

Gln Val Tyr Lys Gly Ile Asn Ala Tyr Ile Asp His Pro Glu Val Ser
180 185 190

Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala His Ala His Tyr Asp
195 200 205

Asp Ile His Pro Tyr Glu Ala Met Glu Leu Ile Lys Arg Leu Gly Glu
210 215 220

Gly Lys Pro Glu Ile Gln Glu Lys Ala Phe Gln Ala Ala Gln Asp Gly
225 230 235 240

Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu Cys Tyr Lys His Gln
245 250 255

<210> 5
<211> 244
<212> PRT
<213> Alcanivorax sp.

<400> 5

Met Arg Ala Ala Asn Tyr Lys Lys Gly Leu Glu Leu Thr Asp His Ser
1 5 10 15

Pro Trp Ala Gln Thr Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Gln

```
            20                  25                  30

Val Val Glu His Pro Val Phe Val Glu Met Gly Ala Gly Thr Leu Ser
        35                  40                  45

Leu Pro Arg Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
    50                  55                  60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Gln Pro Gly
65                  70                  75                  80

Arg Tyr Pro Gly His Glu Glu Ser Lys Asn Trp Leu Ile Ser Asn Ile
                85                  90                  95

Lys Val Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
            100                 105                 110

Phe Gly Ile Thr Leu Glu Glu Leu Glu Phe Val Thr Pro Pro Pro Ala
        115                 120                 125

Met Asp Ala Val Asn His Tyr Leu Trp His Met Gly Arg Gln Ala Ser
    130                 135                 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Gln Ala Tyr Gln Glu
                165                 170                 175

Asn Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
            180                 185                 190

His Ala Ser Tyr Asp Asp Ala His Pro His Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Leu Thr Cys Val Asp Gln Gln Ser Arg Glu Arg Ala Phe Ala Ala
    210                 215                 220

Ala Val Lys Gly Leu Glu Tyr Tyr Val Leu Ala Leu Asp His Cys Tyr
225                 230                 235                 240

Ala Gln Ser Asp


&lt;210&gt;  6
&lt;211&gt;  244
&lt;212&gt;  PRT
&lt;213&gt;  Alcanivorax sp.
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<220>
<221> misc_feature
<222> (222)..(222)
<223> Xaa can be any naturally occurring amino acid

<400> 6

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Met Arg Ala Ala Asn Tyr Lys Lys Gly Leu Glu Leu Thr Asp His Ser
1               5                   10                  15

Pro Trp Ala Gln Thr Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Gln
            20                  25                  30

Val Val Glu His Pro Val Phe Val Glu Met Gly Ala Gly Thr Leu Ser
        35                  40                  45

Leu Pro Arg Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
    50                  55                  60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Gln Pro Gly
65                  70                  75                  80

Arg Tyr Pro Gly His Glu Glu Ser Lys Asn Trp Leu Ile Ser Asn Ile
                85                  90                  95

Lys Val Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
            100                 105                 110

Phe Gly Ile Thr Leu Glu Glu Leu Glu Phe Val Thr Pro Pro Pro Ala
        115                 120                 125

Met Asp Ala Val Asn His Tyr Leu Trp His Met Gly Arg Gln Ala Ser
    130                 135                 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Gln Ala Tyr Gln Glu
                165                 170                 175

Asn Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
            180                 185                 190

His Ala Ser Tyr Asp Asp Ala His Pro His Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Leu Thr Cys Val Asp Gln Gln Ser Arg Glu Arg Ala Xaa Ala Ala
    210                 215                 220
```

Ala Val Lys Gly Leu Glu Tyr Tyr Val Leu Ala Leu Asp His Cys Tyr
225 230 235 240

Ala Gln Ser Asp

<210> 7
<211> 244
<212> PRT
<213> Alcanivorax sp.

<400> 7

Met Arg Ala Ala Asn Tyr Lys Lys Ala Leu Glu Leu Thr Ala His Ser
1 5 10 15

Pro Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asp Arg
20 25 30

Val Val Arg His Pro Leu Phe Asp Glu Met Ala Ala Gly Ser Leu Ser
35 40 45

Leu Pro Arg Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Arg Pro Gly
65 70 75 80

Arg His Ala Gly His Glu Glu Ala Lys Asn Trp Leu Ile Gly Asn Ile
85 90 95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
100 105 110

Phe Gly Ile Thr Leu Arg Asp Leu Glu Phe Val Glu Pro Pro Ala Ala
115 120 125

Met Asp Ala Val Asn His Phe Leu Trp Asn Met Gly His Gln Gly Thr
130 135 140

Leu Glu Glu Gly Ile Ala Ser Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Gln Glu
165 170 175

Asn Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
180 185 190

His Ala Ser Tyr Asp Asp Asp His Pro His Glu Ala Met Glu Leu Ile
195 200 205

Lys Leu Val Cys Val Asp Glu Ala Gln Lys Glu Arg Ala Phe Ala Ala
210 215 220

Ala Ser Lys Gly Leu Glu Tyr Tyr Ile Gln Ala Leu Asp Tyr Cys Tyr
225 230 235 240

Asp Gln Ala Gly

<210> 8
<211> 244
<212> PRT
<213> Alcanivorax jadensis

<400> 8

Met Arg Ala Ala Asn Tyr Lys Lys Gly Leu Glu Leu Thr Asp His Gly
1 5 10 15

Pro Trp Ala Gln Ala Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Arg
20 25 30

Val Val Glu His Pro Val Phe Val Glu Met Gly Ala Gly Thr Leu Ser
35 40 45

Leu Pro Arg Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Gln Pro Gly
65 70 75 80

Arg Tyr Pro Gly His Glu Glu Ser Lys Asn Trp Leu Ile Ser Asn Ile
85 90 95

Lys Val Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
100 105 110

Phe Gly Ile Ser Leu Glu Glu Leu Glu Phe Val Thr Pro Pro Ala Ala
115 120 125

Met Asp Ala Val Asn His Tyr Leu Trp His Met Gly Arg Gln Ala Ser
130 135 140

Leu Glu Glu Gly Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Gln Ala Tyr Gln Glu
165 170 175

Asn Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
180 185 190

His Ala Ser Tyr Asp Asp Ala His Pro His Glu Ala Met Glu Leu Ile
195 200 205

Lys Leu Thr Cys Ala Asp Glu Ala Ser Arg Glu Arg Ala Phe Ala Ala
210 215 220

Ala Ala Lys Gly Leu Glu Tyr Tyr Ile Leu Ala Leu Asp His Cys Tyr
225 230 235 240

Thr Glu Ser Asp

<210> 9
<211> 244
<212> PRT
<213> Alcanivorax sp.

<400> 9

Met Arg Ala Ala Asn Tyr Lys Lys Ala Leu Glu Leu Thr Ala His Ser
1 5 10 15

Pro Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asp Arg
20 25 30

Val Val Arg His Pro Leu Phe Glu Glu Met Ala Ala Gly Ser Leu Ser
35 40 45

Leu Pro Arg Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Arg Pro Gly
65 70 75 80

Arg His Ala Gly His Glu Glu Ala Lys Asn Trp Leu Ile Gly Asn Ile
85 90 95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
100 105 110

Phe Gly Ile Thr Leu Arg Asp Leu Glu Phe Val Glu Pro Pro Ala Ala
115 120 125

```
Met Asp Ala Val Asn His Phe Leu Trp Asn Met Gly His Gln Gly Thr
    130                 135                 140

Leu Glu Glu Gly Ile Ala Ser Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Gln Glu
                165                 170                 175

Asn Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
            180                 185                 190

His Ala Ser Tyr Asp Asp Asp His Pro His Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Leu Val Cys Val Asp Glu Ala Gln Lys Glu Arg Ala Phe Ala Ala
    210                 215                 220

Ala Ser Arg Gly Leu Glu Tyr Tyr Ile Gln Ala Leu Asp Tyr Cys Tyr
225                 230                 235                 240

Asp Gln Thr Asn
```

<210> 10
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 10

```
Met Gly Ala Leu Thr Gln Gly Leu Val Leu Glu Ile Thr Pro His Ser
1               5                   10                  15

Gly Trp Ala Gln Ala Phe Trp Asp Asp Leu Val Pro Val Lys Glu Arg
            20                  25                  30

Val Ser His His Pro Leu Phe Ile Asp Met Ala Asn Gly Lys Leu Ser
        35                  40                  45

Leu Ala Cys Phe Arg Leu Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50                  55                  60

His Phe Pro Ser Tyr Met Ala Leu Ala Leu Ser Lys Ala Thr Asp Phe
65                  70                  75                  80

Thr Gln Pro Gly Val Thr Glu Ser Arg Asp Trp Leu Ile Gln Asn Ile
                85                  90                  95
```

Lys Ile Glu Glu Arg His Leu Asn Trp Tyr Arg Glu Trp Ala Val Gly
100 105 110

Phe Gly Leu Thr Val Asp Glu Leu Asp Arg Val Thr Pro Pro Val Glu
115 120 125

Met Asn Ala Val Asn His Phe Leu Trp Asn Met Asn Tyr Arg Ser Ser
130 135 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile Asn Ala Tyr Ile Asp
165 170 175

His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
180 185 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
195 200 205

Lys Arg Leu Cys Asp His Gln Pro Glu Leu Gln Thr Lys Ala Phe Lys
210 215 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Tyr Cys
225 230 235 240

Tyr Lys Gln His Ala
245

<210> 11
<211> 245
<212> PRT
<213> Acinetobacter ursingii

<400> 11

Met Gly Ala Leu Thr Gln Gly Leu Val Leu Glu Ile Thr Pro His Ser
1 5 10 15

Gly Trp Ala Gln Ala Phe Trp Asp Asp Leu Val Pro Val Lys Glu Arg
20 25 30

Val Ser His His Pro Leu Phe Ile Asp Met Ala Asn Gly Lys Leu Ser
35 40 45

Leu Ala Cys Phe Arg Leu Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
50 55 60

His Phe Pro Ser Tyr Met Ala Leu Ala Leu Ser Lys Ala Thr Asp Phe
65 70 75 80

Thr Gln Pro Gly Val Thr Glu Ser Arg Asp Trp Leu Ile Gln Asn Ile
85 90 95

Lys Ile Glu Glu Arg His Leu Asn Trp Tyr Arg Asp Trp Ala Val Gly
100 105 110

Phe Gly Leu Thr Val Asn Glu Leu Asp Arg Val Thr Pro Pro Val Glu
115 120 125

Met Asn Ala Val Asn His Phe Leu Trp Asn Met Asn Tyr Arg Ser Ser
130 135 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile Asn Ala Tyr Ile Asp
165 170 175

His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
180 185 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
195 200 205

Lys Arg Leu Cys Asp His Gln Pro Glu Leu Gln Thr Lys Ala Phe Lys
210 215 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Tyr Cys
225 230 235 240

Tyr Lys Gln His Ala
245

<210> 12
<211> 245
<212> PRT
<213> Acinetobacter ursingii

<400> 12

Met Gly Ala Leu Thr Gln Gly Leu Val Leu Glu Ile Thr Pro His Ser
1 5 10 15

Gly Trp Ala Gln Ala Phe Trp Asp Asp Leu Val Pro Val Lys Glu Arg
20 25 30

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

Leu Ala Cys Phe Arg Leu Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50                  55                  60

His Phe Pro Ser Tyr Met Ala Leu Ala Leu Ser Lys Ala Thr Asp Phe
65                  70                  75                  80

Thr Gln Pro Gly Val Thr Glu Ser Arg Asp Trp Leu Ile Gln Asn Ile
                85                  90                  95

Lys Ile Glu Glu Arg His Leu Asn Trp Tyr Arg Asp Trp Ala Val Gly
            100                 105                 110

Phe Gly Leu Thr Ile Asp Glu Leu Asp Arg Val Thr Pro Pro Val Glu
        115                 120                 125

Met Asn Ala Val Asn His Phe Leu Trp Asn Met Asn Tyr Arg Ser Ser
    130                 135                 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile Asn Ala Tyr Ile Asp
                165                 170                 175

His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
            180                 185                 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Cys Asp His Gln Pro Glu Leu Gln Lys Lys Ala Phe Lys
    210                 215                 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Tyr Cys
225                 230                 235                 240

Tyr Lys Gln Gln Ala
                245
```

<210> 13
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 13

Met Gly Ala Leu Thr Gln Gly Leu Val Leu Glu Ile Thr Pro His Ser
1 5 10 15

Gly Trp Ala Gln Ala Phe Trp Asp Asp Leu Val Pro Val Lys Glu Arg
20 25 30

Val Ser His His Pro Leu Phe Ile Asp Met Ala Asn Gly Lys Leu Ser
35 40 45

Leu Ala Cys Phe Arg Leu Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
50 55 60

His Phe Pro Ser Tyr Met Ala Leu Ala Leu Ser Lys Ala Thr Asp Phe
65 70 75 80

Thr Gln Pro Gly Val Thr Glu Ser Arg Asp Trp Leu Ile Gln Asn Ile
85 90 95

Lys Ile Glu Glu Arg His Leu Asn Trp Tyr Arg Asp Trp Ala Val Gly
100 105 110

Phe Gly Leu Thr Val Asp Glu Leu Asp Arg Val Thr Pro Pro Val Glu
115 120 125

Met Asn Ala Val Asn His Phe Leu Trp Asn Met Asn Tyr Arg Ser Ser
130 135 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile Asn Ala Tyr Ile Asp
165 170 175

His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
180 185 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
195 200 205

Lys Arg Leu Cys Asp His Gln Pro Glu Leu Gln Thr Lys Ala Phe Lys
210 215 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Tyr Cys
225 230 235 240

Tyr Lys Gln His Ala

245

<210> 14
<211> 245
<212> PRT
<213> Alcanivorax sp.

<400> 14

```
Met Arg Ala Ala Asn Tyr Lys Lys Ala Leu Glu Leu Thr Glu His Thr
1               5                   10                  15

Pro Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Lys
            20                  25                  30

Val Val Asn His Pro Val Phe Ala Glu Met Ala Ser Gly Gln Leu Ser
        35                  40                  45

Leu Pro Arg Phe Arg Cys Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
    50                  55                  60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Arg Pro Gly
65                  70                  75                  80

Arg Phe Pro Gly His Glu Gln Ala Lys Asn Trp Leu Ile Gly Asn Ile
                85                  90                  95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
            100                 105                 110

Phe Gly Leu Thr Leu Glu Asp Leu Glu Phe Val Glu Pro Pro Ala Ala
        115                 120                 125

Met Asp Ala Val Asn Asn Phe Leu Trp Thr Met Gly Arg Gln Gly Ser
    130                 135                 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Gln Glu
                165                 170                 175

Asp Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
            180                 185                 190

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

Lys Leu Leu Cys Val Glu Gln Glu Ser Arg Asp Arg Ala Phe Lys Ala
```

210 215 220

Ala Gln Arg Gly Leu Glu Tyr Tyr Ile Gln Ala Leu Asp Tyr Cys Tyr
225 230 235 240

Gln Thr Pro Glu Ala
245

<210> 15
<211> 245
<212> PRT
<213> Alcanivorax nanhaiticus

<400> 15

Met Arg Ala Ala Asn Tyr Lys Lys Ala Leu Glu Ile Thr Glu His Ser
1 5 10 15

Pro Trp Ala Gln Gln Phe Trp Asp Glu Leu Val Pro Leu Lys Asp Lys
20 25 30

Val Val His His Pro Leu Phe Val Glu Met Ala Ser Gly Gly Leu Ser
35 40 45

Leu Pro Arg Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Arg Pro Gly
65 70 75 80

Arg His Pro Gly His Glu Glu Ala Lys Asn Trp Leu Ile Ser Asn Ile
85 90 95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
100 105 110

Phe Gly Leu Thr Met His Asp Leu Glu Phe Val Asp Pro Pro Ala Ala
115 120 125

Met Asp Ala Val Asn His Phe Leu Trp Ser Ile Gly Arg Gln Ser Ser
130 135 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Glu Asp
165 170 175

Gln Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala

180 185 190

His Ala Ser Tyr Asp Asp Asp His Pro His Glu Ala Met Glu Leu Ile
195 200 205

Lys Leu Ile Cys Val Asp Glu Glu Ser Arg Glu Arg Ala Tyr Lys Ala
210 215 220

Ala Phe Lys Gly Leu Glu Tyr Tyr Val His Ala Leu Asp Phe Cys Tyr
225 230 235 240

Ala Asn Ala Asp Glu
245

<210> 16
<211> 245
<212> PRT
<213> Alcanivorax hongdengensis

<400> 16

Met Arg Ala Ala Gln Tyr Lys Lys Ala Leu Glu Leu Thr Glu His Ser
1 5 10 15

Pro Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Gln
20 25 30

Val Val Glu His Pro Val Phe Val Glu Met Ala Glu Gly Ser Leu Ser
35 40 45

Gln Pro Arg Phe Arg Cys Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Ala Leu Asn Leu Ala Lys Thr Arg Pro Gly
65 70 75 80

Arg Gln Pro Gly His Glu Glu Ala Lys Asn Trp Leu Ile Glu Asn Ile
85 90 95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
100 105 110

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

Met Asp Ala Val Asn Asn Tyr Leu Trp Ser Met Gly His Gln Ala Ser
130 135 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr

145 150 155 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Glu Ser Tyr Gln Glu
165 170 175

Arg Gly Ile Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
180 185 190

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

Lys Arg Leu Ala Val Asp Asp Glu Arg Arg Asp Lys Ala Phe Lys Ala
210 215 220

Ala Lys Arg Gly Leu Glu Tyr Tyr Ile Val Ala Leu Asp His Cys Tyr
225 230 235 240

Gln Asn Tyr Pro Gly
245

<210> 17
<211> 245
<212> PRT
<213> gamma proteobacterium

<400> 17

Met Pro Ala Lys Lys Tyr Lys Glu Ala Leu Glu Leu Thr Pro His Pro
1 5 10 15

Glu Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Lys
20 25 30

Val Ala Gln His Arg Leu Phe Arg Glu Met Ala Asp Gly Ser Leu Ser
35 40 45

Leu Glu Arg Phe Arg Arg Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Gln His Leu Ala Lys Thr Arg Pro Gly
65 70 75 80

Ile Met Pro Gly His Glu Glu Ala Lys Ile Trp Leu Ile Asp Asn Ile
85 90 95

Arg Val Glu Gln Arg His Ala Phe Trp Tyr Gln Asp Trp Ala Glu Gly
100 105 110

Phe Gly Ile Glu Ile Glu Ala Leu Glu Arg Cys Glu Pro Pro Ala Ala

115 120 125

Met Asp Ala Ile Asn His Phe Leu Trp Asn Met Gly Ala His Gly Ser
130 135 140

Leu Glu Glu Gly Leu Ala Ala Thr Asn Leu Ala Val Glu Trp Ala Thr
145 150 155 160

Gly Glu Trp Ser Gln Gln Val Ala Lys Gly Ile Arg Arg Tyr Thr Glu
165 170 175

His Asp Thr Ile Thr Ile Asn Arg Arg Thr Glu Ala Trp Leu Arg Ala
180 185 190

His Ala Ala Tyr Asp Asp Glu His Pro Tyr Glu Ala Met Glu Leu Ile
195 200 205

Lys Arg Thr Ala Thr Thr Asp Asp Ala Arg Thr Arg Ala Phe Lys Ala
210 215 220

Ala Gln Arg Gly Leu Glu Tyr Tyr Ile Leu Ala Leu Asp Asp Cys Tyr
225 230 235 240

Asp Pro Leu Leu Gly
245

<210> 18
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 18

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Ser Glu Trp Ala Gln Gln Phe Trp Asp Asp Leu Leu Pro Ser Lys Glu
20 25 30

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

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Glu Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn

85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Gln Val Lys Pro Pro Val
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Ala Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Gln Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 19
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 19

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Ser Glu Trp Ala Gln Gln Phe Trp Asp Asp Leu Leu Pro Ser Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Met Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val

50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Glu Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Asn Val Lys Pro Pro Val
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Val Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Gln Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 20
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 20

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Ala His
1 5 10 15

Ser Glu Trp Ser Gln Lys Phe Trp Asp Glu Leu Phe Pro Ala Lys Glu

```
            20                  25                  30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
        35                  40                  45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50                  55                  60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Thr Lys Ala Thr Ser
65                  70                  75                  80

Phe Ser Leu Glu Gly Val Ile Asp Thr Arg Asn Trp Leu Ile Gln Asn
                85                  90                  95

Ile Lys Val Glu Glu Ser His Leu Arg Trp Tyr Gln Asp Trp Ala Arg
            100                 105                 110

Gly Phe Gly Leu Thr Ala Glu Met Leu Asn Glu Val Arg Pro Pro Ala
        115                 120                 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
    130                 135                 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145                 150                 155                 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Ala Tyr Thr
                165                 170                 175

Glu His Pro Lys Val Ser Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
            180                 185                 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
    210                 215                 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Ala
225                 230                 235                 240

Cys Tyr Lys Leu Arg
                245
```

<210> 21
<211> 245
<212> PRT
<213> Acinetobacter bohemicus

<400> 21

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Ala His
1   5   10   15

Ser Glu Trp Ser Gln Asn Phe Trp Asp Glu Leu Phe Pro Ala Lys Glu
            20   25   30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
        35   40   45

Ser Leu Glu Cys Phe Arg Ser Thr Leu Leu Asn Phe Tyr Pro Leu Val
    50   55   60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ser
65   70   75   80

Phe Ser Leu Glu Gly Val Thr Asp Thr Arg Asn Trp Leu Ile Gln Asn
                85   90   95

Ile Lys Val Glu Glu Arg His Leu Tyr Trp Tyr Gln Asp Trp Ala Arg
            100   105   110

Gly Phe Gly Val Thr Ala Glu Met Leu Asn Glu Val Arg Pro Pro Ala
        115   120   125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Ile Asn Phe Arg Gly
    130   135   140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145   150   155   160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
                165   170   175

Glu His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
            180   185   190

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

Ile Lys Arg Leu Cys Asp Lys Asn Pro Val Leu Gln Lys Lys Ala Phe
    210   215   220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Ala
225   230   235   240

Cys Tyr Lys Leu Arg
245

<210> 22
<211> 253
<212> PRT
<213> Acinetobacter sp.

<400> 22

Met Thr Gln Leu Lys Asn Arg Tyr Glu Lys Val Leu Glu Ile Thr Ala
1 5 10 15

His Glu Ala Trp Ser Gln Lys Phe Trp Asp Asp Leu Thr Pro Ser Lys
20 25 30

Asp Arg Ile Ser Gln His Pro Phe Phe Lys Ala Met Ala Asp Gly Ser
35 40 45

Leu Ser Val Glu Ser Phe Arg Tyr Ala Leu Thr Asn Phe Tyr Pro Leu
50 55 60

Val Ala His Phe Pro Ser Tyr Met Gly Leu Ala Leu Ser Lys Ala Thr
65 70 75 80

Ala Phe His Leu Pro Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln
85 90 95

Asn Ile Lys Val Glu Glu Arg His Leu Asp Trp Tyr Arg Asp Trp Ala
100 105 110

Ala Gly Phe Gly Val Asp Val Gln Ser Leu Asp Glu Ile Glu Pro Pro
115 120 125

Pro Ala Met Asn Ala Val Asn His Phe Leu Trp Asn Ile Asn Thr Arg
130 135 140

Gly Ser Leu Val Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp
145 150 155 160

Ala Thr Gly Asp Trp Ser Cys Gln Val Tyr Ala Gly Ile Glu Lys Tyr
165 170 175

Lys Leu His Pro Glu Val Asn Val Asp Lys Arg Thr Leu Ala Trp Leu
180 185 190

Arg Ala His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu
195 200 205

Leu Ile Lys Arg Leu Cys Gly Asp Asn Thr Glu Leu Gln Lys Lys Ala
    210   215   220

Phe His Ala Ala Lys Thr Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp
225   230   235   240

Glu Cys Leu Lys Met Gln Ser Asn Tyr Lys Lys Ala Ile
                245   250

<210> 23
<211> 248
<212> PRT
<213> Acinetobacter soli

<400> 23

Met Ser Ala Tyr Thr Lys Gly Thr Ala Leu Glu Ile Thr Ser His Ser
1   5   10   15

Pro Trp Ala Gln Gln Phe Trp Asp Glu Leu Ile Pro Tyr Lys Asp Arg
            20   25   30

Val Ser Gln His Pro Leu Phe Gln Asn Met Ala Ser Gly Gln Leu Ser
        35   40   45

Leu Asp Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50   55   60

His Phe Pro Ser Tyr Met Ala Leu Gly Leu Ser Lys Ala Ile Asp Phe
65   70   75   80

Ser Ala Gln Gly Val Thr Glu Thr Arg Asn Trp Leu Ile Gln Asn Ile
                85   90   95

Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly Gly
            100   105   110

Phe Gly Leu Ser Ile Asp Gln Leu Asn Gln Val Arg Pro Pro Val Ala
        115   120   125

Met Asn Ala Val Asn His Phe Leu Trp His Thr Asn Thr Thr Gly Ser
    130   135   140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145   150   155   160

Gly Asp Trp Ser Val Gln Val Tyr Lys Gly Ile His Ala Tyr Ile Asp
                165   170   175

```
His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
            180                 185                 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Cys Ala Asp Gln Pro Glu Leu Gln Gln Lys Ala Phe Leu
    210                 215                 220

Ala Ala Lys Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225                 230                 235                 240

Tyr Lys Leu Gln Ser Arg Thr Ala
                245


<210>  24
<211>  248
<212>  PRT
<213>  Acinetobacter soli

<400>  24

Met Ser Ala Tyr Thr Lys Gly Thr Ala Leu Glu Ile Thr Ser His Ser
1               5                   10                  15

Pro Trp Ala Gln Gln Phe Trp Asp Glu Leu Ile Pro Tyr Lys Asp Arg
            20                  25                  30

Val Ser Gln His Pro Leu Phe Gln Asn Met Ala Ser Gly Gln Leu Ser
        35                  40                  45

Leu Asp Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50                  55                  60

His Phe Pro Ser Tyr Met Ala Leu Gly Leu Ser Lys Ala Ile Asp Phe
65                  70                  75                  80

Ser Ala Gln Gly Val Thr Glu Thr Arg Asn Trp Leu Ile Gln Asn Ile
                85                  90                  95

Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly Gly
            100                 105                 110

Phe Gly Leu Ser Ile Asp Gln Leu Asn Gln Val Arg Pro Pro Val Ala
        115                 120                 125

Met Asn Ala Val Asn His Phe Leu Trp His Thr Asn Thr Thr Gly Ser
    130                 135                 140
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```
Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Asp Trp Ser Val Gln Val Tyr Lys Gly Ile His Ala Tyr Leu Asp
                165                 170                 175

Gln Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
            180                 185                 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Cys Ala Asp Gln Pro Glu Leu Gln Gln Lys Ala Phe Leu
    210                 215                 220

Ala Ala Lys Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225                 230                 235                 240

Tyr Lys Leu Gln Ser Lys Thr Ala
                245


<210>  25
<211>  248
<212>  PRT
<213>  Acinetobacter soli

<400>  25

Met Ser Ala Tyr Thr Lys Gly Thr Ala Leu Glu Ile Thr Ser His Ser
1               5                   10                  15

Pro Trp Ala Gln Gln Phe Trp Asp Glu Leu Ile Pro Tyr Lys Asp Arg
            20                  25                  30

Val Ser Gln His Pro Leu Phe Gln Asn Met Ala Ser Gly Gln Leu Ser
        35                  40                  45

Leu Asp Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50                  55                  60

His Phe Pro Ser Tyr Met Ala Leu Gly Leu Ser Lys Ala Ile Asp Phe
65                  70                  75                  80

Ser Ala Gln Gly Val Thr Glu Thr Arg Asn Trp Leu Ile Gln Asn Ile
                85                  90                  95

Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly Gly
            100                 105                 110
```

Phe Gly Leu Ser Ile Asp Gln Leu Asn Gln Val Arg Pro Pro Val Ala
115 120 125

Met Asn Ala Val Asn His Phe Leu Trp His Thr Asn Thr Thr Gly Ser
130 135 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Asp Trp Ser Val Gln Val Tyr Lys Gly Ile His Ala Tyr Ile Asp
165 170 175

His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
180 185 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
195 200 205

Lys Arg Leu Cys Ala Asp Gln Pro Glu Leu Gln Gln Lys Ala Phe Leu
210 215 220

Ala Ala Lys Asp Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225 230 235 240

Tyr Lys Leu Gln Ser Lys Thr Ala
245

<210> 26
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 26

Met Ser Ala Tyr Thr Lys Gly Thr Ala Leu Glu Ile Thr Ser His Ser
1 5 10 15

Pro Trp Ala Gln Gln Phe Trp Asp Glu Leu Ile Pro Tyr Lys Asp Arg
20 25 30

Val Ser Gln His Pro Leu Phe Gln Asn Met Ala Ser Gly Gln Leu Ser
35 40 45

Leu Asp Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
50 55 60

His Phe Pro Ser Tyr Met Ala Leu Gly Leu Ser Lys Ala Ile Asp Phe
65 70 75 80

```
Ser Ala Gln Gly Val Thr Glu Thr Arg Asn Trp Leu Ile Gln Asn Ile
                85                  90                  95

Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly Gly
            100                 105                 110

Phe Gly Leu Ser Ile Asp Gln Leu Asn Gln Val Arg Pro Pro Val Ala
        115                 120                 125

Met Asn Ala Val Asn His Phe Leu Trp His Thr Asn Thr Thr Gly Ser
    130                 135                 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Asp Trp Ser Val Gln Val Tyr Lys Gly Ile His Ala Tyr Ile Asp
                165                 170                 175

His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
            180                 185                 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Cys Ala Asp Gln Pro Glu Leu Gln Gln Lys Ala Phe Leu
    210                 215                 220

Ala Ala Lys Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225                 230                 235                 240

Tyr Lys Leu Gln Ser Lys Thr Ala
                245


<210>  27
<211>  256
<212>  PRT
<213>  Alcanivorax sp.

<400>  27

Met Ala Ile Ala Arg Tyr Lys Gln Ala Leu Glu Leu Thr Pro His Ala
1               5                   10                  15

Pro Trp Ala Gln Arg Phe Trp Asp Ala Leu Val Pro Leu Lys Asp Arg
            20                  25                  30

Val Ala Gly His Pro Leu Phe Gln Glu Met Gly Glu Gly Ala Leu Ser
        35                  40                  45
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Leu Pro Arg Phe Arg Asp Ala Leu Leu His Phe Tyr Pro Leu Val Glu
    50                  55                  60

His Phe Pro Lys Tyr Met Gly Leu Ala Leu Ala Lys Thr Arg Pro Gly
65                  70                  75                  80

Leu Tyr Pro Gly His Glu Glu Thr Arg Asn Trp Leu Ile Gly Asn Ile
                85                  90                  95

Lys Val Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Ala Gly
            100                 105                 110

Phe Gly Leu Ala Leu Ala Glu Leu Glu Gln Val Arg Pro Pro Ala Ala
        115                 120                 125

Met Asn Ala Ile Asn His Tyr Leu Trp Asp Val Gly His Gln Gly Ser
    130                 135                 140

Leu Asp Glu Ser Ile Ala Ala Thr Asn Leu Ala Val Glu Trp Ala Thr
145                 150                 155                 160

Gly Glu Trp Ser Gln His Val Val Ser Gly Met Gln His Tyr Ala Glu
                165                 170                 175

Gln Gly Gln Ala Ser Ile Thr Arg His Thr Leu Ala Trp Leu Arg Ala
            180                 185                 190

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

Lys Arg Leu Ala Thr Asp Glu Pro Ala Arg Gln Arg Ala Phe Ala Ala
    210                 215                 220

Ala Gln Arg Gly Leu Glu Tyr Tyr Leu Leu Ala Leu Asp Asp Cys Tyr
225                 230                 235                 240

Gln Gln Gly Glu Gln Arg Thr Ala Gln Thr Ala Pro Asp Leu Gly Glu
                245                 250                 255


<210>  28
<211>  245
<212>  PRT
<213>  Alcanivorax sp.

<400>  28

Met Arg Ala Ala Asn Tyr Lys Lys Ala Leu Glu Leu Thr Glu His Thr
1               5                   10                  15
```

Pro Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Lys
20 25 30

Val Val Asn His Pro Val Phe Ala Glu Met Ala Ser Gly Arg Leu Ser
35 40 45

Leu Pro Arg Phe Arg Cys Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Leu Pro Gly
65 70 75 80

Arg Phe Pro Gly His Glu Gln Ala Lys Asn Trp Leu Ile Ser Asn Ile
85 90 95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
100 105 110

Phe Gly Leu Thr Leu Glu Asp Leu Glu Phe Val Glu Pro Pro Ala Ala
115 120 125

Met Asp Ala Val Asn Asn Phe Leu Trp Thr Met Gly Arg Gln Gly Ser
130 135 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Gln Glu
165 170 175

Asp Gly Val Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
180 185 190

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

Lys Leu Leu Cys Val Glu Gln Glu Ser Arg Asp Arg Ala Phe Lys Ala
210 215 220

Ala Gln Arg Gly Leu Glu Tyr Tyr Ile Gln Ala Leu Asp Tyr Cys Tyr
225 230 235 240

Gln Thr Pro Glu Ala
245

<210> 29
<211> 245
<212> PRT

<213> Alcanivorax sp.

<400> 29

```
Met Arg Ala Ala Asn Tyr Lys Lys Ala Leu Glu Leu Thr Glu His Thr
1               5                   10                  15

Pro Trp Ala Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Lys
            20                  25                  30

Val Val Asn His Pro Val Phe Ala Glu Met Ala Ser Gly Gln Leu Ser
        35                  40                  45

Leu Pro Arg Phe Arg Cys Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu
    50                  55                  60

Asn Phe Pro Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Leu Pro Gly
65                  70                  75                  80

Arg Phe Pro Gly His Glu Gln Ala Lys Asn Trp Leu Ile Gly Asn Ile
                85                  90                  95

Lys Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly
            100                 105                 110

Phe Gly Leu Thr Leu Glu Asp Leu Glu Phe Val Glu Pro Pro Ala Ala
        115                 120                 125

Met Asp Ala Val Asn Asn Phe Leu Trp Thr Met Gly Arg Gln Gly Ser
    130                 135                 140

Leu Glu Glu Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Glu Trp Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Gln Glu
                165                 170                 175

Asp Gly Ile Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala
            180                 185                 190

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

Lys Leu Ile Cys Val Asp Gln Ala Ser Arg Glu Arg Ala Phe Lys Ala
    210                 215                 220

Ala Gln Arg Gly Leu Glu Tyr Tyr Ile Gln Ala Leu Asp Tyr Cys Tyr
225                 230                 235                 240
```

```
Gln Thr Pro Glu Ala
                245


<210>  30
<211>  226
<212>  PRT
<213>  Alcanivorax sp.

<400>  30

Gln Gln Phe Trp Asp Asp Leu Val Pro Leu Lys Asn Lys Val Val Asn
1               5                   10                  15


His Pro Val Phe Ala Glu Met Ala Ser Gly Gln Leu Ser Leu Pro Arg
            20                  25                  30


Phe Arg Cys Ala Leu Leu Asn Phe Tyr Pro Leu Val Glu Asn Phe Pro
        35                  40                  45


Lys Tyr Met Gly Leu Asn Leu Ala Lys Thr Arg Pro Gly Arg Phe Pro
    50                  55                  60


Gly His Glu Gln Ala Lys Asn Trp Leu Ile Gly Asn Ile Lys Ile Glu
65                  70                  75                  80


Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Met Gly Phe Gly Leu
                85                  90                  95


Thr Leu Glu Asp Leu Glu Phe Val Glu Pro Pro Ala Ala Met Asp Ala
            100                 105                 110


Val Asn Asn Phe Leu Trp Thr Met Gly Arg Gln Gly Ser Leu Glu Glu
        115                 120                 125


Gly Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr Gly Glu Trp
    130                 135                 140


Ser Gln Ser Val Val Lys Gly Met Lys Ala Tyr Gln Glu Asp Gly Val
145                 150                 155                 160


Ala Thr Ile Asn Arg His Ser Met Ala Trp Leu Arg Ala His Ala Ser
                165                 170                 175


Tyr Asp Asp Asp His Pro His Glu Ala Met Glu Leu Val Lys Leu Leu
            180                 185                 190


Cys Val Glu Gln Glu Ser Arg Asp Arg Ala Phe Lys Ala Ala Gln Arg
        195                 200                 205
```

Gly Leu Glu Tyr Tyr Ile Gln Ala Leu Asp Tyr Cys Tyr Gln Thr Pro
210 215 220

Glu Ala
225

<210> 31
<211> 258
<212> PRT
<213> Alcanivorax gelatiniphagus

<400> 31

Met Gly Val Ala Arg Tyr Lys Asp Ala Leu Thr Leu Thr Glu His Pro
1 5 10 15

Ser Trp Ala Gln Arg Phe Trp Asp Ala Leu Val Pro Leu Lys Asp Arg
20 25 30

Val Val Asp His Pro Leu Phe Val Glu Met Gly Glu Gly His Leu Ser
35 40 45

Leu Glu Arg Phe Gln Asp Ala Leu Leu His Phe Tyr Pro Leu Val Glu
50 55 60

Asn Phe Pro Lys Tyr Met Gly Leu Ala Leu Ala Lys Thr Arg Ala Gly
65 70 75 80

Arg Ala Pro Gly His Glu Asp Thr Lys Asn Trp Leu Ile Gly Asn Ile
85 90 95

Arg Ile Glu Gln Arg His Ala Tyr Trp Tyr Gln Asp Trp Ala Ala Gly
100 105 110

Phe Gly Leu Ser Arg Glu Arg Leu Glu Thr Thr Thr Pro Pro Pro Ala
115 120 125

Met Asp Ala Val Asn Gln Phe Leu Trp Thr Thr Gly His Gln Gly Thr
130 135 140

Leu Glu Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Glu Trp Ser Gln Arg Val Val Ala Gly Val Lys His Tyr Ala Glu
165 170 175

Gln Gly Arg Ala Glu Ile Asn Arg His Thr Met Ala Trp Leu Arg Ala
180 185 190

His Ala Ser Tyr Asp Asp Ala His Pro His Glu Ala Met Glu Leu Ile
        195   200   205

Lys Leu Leu Ala Val Asp Glu Pro Ser Arg Arg Arg Ala Phe Thr Ala
    210   215   220

Ala Arg Arg Gly Leu Glu Tyr Tyr Leu Leu Ala Leu Asp Asp Cys Tyr
225   230   235   240

Arg His Ser Gly Glu Arg Ala Pro Thr Glu Leu Pro Gly Leu Leu Asp
                245   250   255

Ser Val

<210> 32
<211> 248
<212> PRT
<213> Acinetobacter venetianus

<400> 32

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Thr His
1   5   10   15

Ser Glu Trp Ser Gln Arg Phe Trp Asp Asp Leu Val Pro Ala Lys Glu
            20   25   30

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

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50   55   60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ala
65   70   75   80

Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
                85   90   95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
            100   105   110

Gly Phe Gly Leu Thr Leu Glu Met Leu Asn Glu Val Arg Pro Pro Ala
        115   120   125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
    130   135   140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
165 170 175

Glu His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
210 215 220

Arg Ala Ala Gln Asp Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 33
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 33

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Ser Gly Trp Ala Gln Gln Phe Trp Asp Glu Leu Leu Pro Ser Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Thr Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Glu Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Asn Ala Arg Pro Pro Val
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Ile Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Ala Tyr Thr
165 170 175

Gln His Pro Glu Val His Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Gly Leu Gln Arg Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 34
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 34

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Ser Glu Trp Ala Gln Gln Phe Trp Asp Asp Leu Leu Pro Ala Lys Glu
20 25 30

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

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Glu Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Gln Val Lys Pro Pro Val
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Val Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Gln Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 35
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 35

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Ser Gly Trp Ala Gln Arg Phe Trp Asp Glu Leu Leu Pro Ser Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50   55   60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Ala
65   70   75   80

Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
                85   90   95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
            100   105   110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Asn Val Lys Pro Pro Val
        115   120   125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
    130   135   140

Ser Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145   150   155   160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Asn Tyr Thr
                165   170   175

Gln His Pro Asp Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
            180   185   190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Ile Leu Gln Arg Lys Ala Phe
    210   215   220

Leu Ala Ala Gln Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Ala
225   230   235   240

Cys Tyr Lys Leu Gln His Lys Ser
                245

<210> 36
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 36

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1   5   10   15

Ser Glu Trp Ala Gln Gln Phe Trp Asp Asp Leu Leu Pro Ala Lys Glu
20 25 30

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

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Glu Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Gln Val Lys Pro Pro Val
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Ala Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Ser Val Leu Gln Gln Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 37
<211> 248

<212> PRT
<213> Acinetobacter sp.

<400> 37

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Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1               5                   10                  15

Ser Gly Trp Ala Gln Arg Phe Trp Asp Glu Leu Leu Pro Ser Lys Glu
            20                  25                  30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Cys Leu
        35                  40                  45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50                  55                  60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Ala
65                  70                  75                  80

Phe Ser Leu Glu Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
                85                  90                  95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
            100                 105                 110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Asn Val Lys Pro Pro Val
        115                 120                 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
    130                 135                 140

Ser Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145                 150                 155                 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
                165                 170                 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
            180                 185                 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
    210                 215                 220

Leu Ala Ala Lys Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Glu
225                 230                 235                 240
```

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 38
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 38

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Ser Gly Trp Ala Gln Arg Phe Trp Asp Glu Leu Leu Pro Ser Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Cys Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ser Leu Ala Lys Ala Thr Asp
65 70 75 80

Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Asp Met Leu Asn Asn Val Lys Pro Pro Val
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Ser Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Ala Leu Gln Lys Lys Ala Phe
210 215 220

Leu Ala Ala Lys Glu Gly Leu Glu Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 39
<211> 248
<212> PRT
<213> Acinetobacter sp.

<400> 39

Met Thr Ala Met Asn Gln Tyr Ala Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Thr Glu Trp Ala Gln Arg Phe Trp Asp Gly Leu Leu Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Ser Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Met
100 105 110

Gly Phe Gly Leu Thr Leu Glu Met Leu Asn Glu Val Thr Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Thr Thr Asn Tyr Arg Gly
130 135 140

Ser Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Arg Lys Ala Phe
210 215 220

Leu Ala Ala Lys Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 40
<211> 248
<212> PRT
<213> Acinetobacter parvus

<400> 40

Met Thr Ala Met Asn Gln Tyr Ala Thr Lys Leu Glu Ile Thr Pro His
1 5 10 15

Asn Glu Trp Ala Gln Arg Phe Trp Asp Gly Leu Leu Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Ser Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Met
100 105 110

Gly Phe Gly Leu Thr Leu Glu Met Leu Asn Glu Val Thr Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Thr Thr Asn Tyr Arg Gly
130 135 140

Ser Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
165 170 175

Gln His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Arg Lys Ala Phe
210 215 220

Leu Ala Ala Lys Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 41
<211> 249
<212> PRT
<213> Acinetobacter sp.

<400> 41

Met Thr Ile Ile Lys Gln Gln Tyr Gly Thr Lys Leu Glu Ile Thr Thr
1 5 10 15

His Ser Glu Trp Ser Gln Gln Phe Trp Asp Gln Leu Val Pro Ala Lys
20 25 30

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

Leu Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu
50 55 60

Val Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr
65 70 75 80

Ala Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln
85 90 95

Asn Ile Lys Val Glu Glu Arg His Leu His Trp Tyr Gln Asp Trp Ala
100 105 110

Lys Gly Phe Gly Leu Thr Thr Glu Met Leu Asn Asp Val Arg Pro Pro
115 120 125

Ala Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg
130 135 140

Gly Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp
145 150 155 160

Ala Thr Gly Asp Trp Ser Ile His Val Tyr Lys Gly Ile Gln Ser Tyr
165 170 175

Thr Gln His Pro Glu Val Thr Ile Asn Lys Arg Ser Leu Ala Trp Leu
180 185 190

Arg Ala His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu
195 200 205

Leu Ile Lys Arg Leu Cys Asp Lys Asp Pro Ile Leu Gln Arg Lys Ala
210 215 220

Phe Leu Ala Ala Lys Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp
225 230 235 240

Glu Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 42
<211> 245
<212> PRT
<213> Acinetobacter kyonggiensis

<400> 42

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Ala His
1 5 10 15

Ser Glu Trp Ser Gln Lys Phe Trp Asp Glu Leu Phe Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Ser Leu Glu Gly Val Ile Asp Thr Arg Asn Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Ser His Leu Arg Trp Tyr Gln Asp Trp Ala Arg
100 105 110

Gly Phe Gly Leu Thr Ala Glu Met Leu Asn Glu Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Ala Tyr Thr
165 170 175

Glu His Pro Lys Val Ser Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Ala
225 230 235 240

Cys Tyr Lys Leu Arg
245

<210> 43
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 43

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Leu Thr Ala His
1 5 10 15

Ser Glu Trp Ser Gln Lys Phe Trp Asp Glu Leu Phe Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50   55   60

Ala His Phe Pro Ser Tyr Met Ala Gly Thr Leu Ala Lys Ala Thr Ser
65   70   75   80

Leu Ser Leu Glu Gly Val Ile Asp Thr Arg Asn Trp Leu Ile Gln Asn
                85   90   95

Ile Lys Val Glu Glu Arg His Leu His Trp Tyr Gln Asp Trp Ala Arg
            100   105   110

Gly Phe Gly Leu Thr Val Glu Met Leu Asn Glu Val Arg Pro Pro Val
        115   120   125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Ile Asn Phe Arg Gly
    130   135   140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145   150   155   160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Ile
                165   170   175

Glu His Pro Glu Val Ser Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
            180   185   190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
    210   215   220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Thr
225   230   235   240

Cys Tyr Lys Leu Arg
                245

<210> 44
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 44

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Ala His
1   5   10   15

Ser Glu Trp Ser Gln Lys Phe Trp Asp Glu Leu Phe Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ala Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Ser Leu Glu Gly Val Ile Asp Thr Arg Asn Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Ser His Leu Arg Trp Tyr Gln Asp Trp Ala Arg
100 105 110

Gly Phe Gly Leu Thr Ala Glu Met Leu Asn Glu Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Ala Tyr Thr
165 170 175

Glu His Pro Lys Val Ser Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Ala
225 230 235 240

Cys Tyr Lys Leu Arg
245

<210> 45

<211> 244
<212> PRT
<213> Acinetobacter baylyi

<400> 45

```
Met Ser Ala Leu Leu Glu Gly Thr Asp Leu Lys Ile Thr Pro His Ser
1               5                   10                  15

Pro Trp Ala Gln Gln Phe Trp Asp Glu Leu Ile Pro Ala Lys Asp Arg
            20                  25                  30

Val Gly Gln His Pro Leu Phe Gln Asp Met Ala Asn Gly Arg Leu Asn
        35                  40                  45

Leu Lys Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50                  55                  60

His Phe Pro Ser Tyr Met Ala Leu Ala Leu Ser Lys Ala Thr Asp Phe
65                  70                  75                  80

Thr Glu Ala Gly Val Thr Glu Thr Arg Asn Trp Leu Ile Gln Asn Ile
                85                  90                  95

Lys Val Glu Glu Arg His Leu Asn Trp Tyr Arg Asp Trp Ala Gly Gly
            100                 105                 110

Phe Gly Leu Thr Val Glu Glu Leu Asp Arg Val Arg Pro Pro Val Ala
        115                 120                 125

Met Asp Ala Val Asn His Phe Leu Trp Asn Ile Asn Thr Lys Gly Ser
    130                 135                 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile Asn Ala Tyr Ile Asp
                165                 170                 175

His Pro Glu Val Ser Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
            180                 185                 190

His Ala His Tyr Asp Asp Ile His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Gly Glu Gly Lys Pro Glu Ile Gln Glu Lys Ala Phe Gln
    210                 215                 220

Ala Ala Gln Asp Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu Cys
```

225 230 235 240

Tyr Lys His Gln

<210> 46
<211> 250
<212> PRT
<213> Acinetobacter pittii

<400> 46

Met Thr Ala Leu Asn Gln Tyr Gly Met Asn Leu Glu Ile Thr Pro His
1 5 10 15

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

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

Ser Leu Asp Ser Phe Arg Tyr Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Gly Lys Ala Thr Gly
65 70 75 80

Phe Ser Glu Pro Gly Val Thr Glu Ala Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Lys Trp Tyr Arg Asp Trp Ala Arg
100 105 110

Gly Phe Gly Leu Thr Val Glu Glu Leu Asp His Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asn Met Ser His Arg Gly
130 135 140

Asn Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile His Thr Tyr Thr
165 170 175

Asn His Pro Glu Val Thr Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

Ala His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu

195 200 205

Ile Lys Arg Leu Cys Asn Asp Arg Pro Asp Trp Gln Gln Lys Ala Phe
210 215 220

His Ala Ala Glu Glu Gly Leu Arg Tyr Tyr Glu Leu Ala Leu Asp Asp
225 230 235 240

Cys Tyr Arg Val Gln Leu Gln Ala Ser Ala
245 250

<210> 47
<211> 250
<212> PRT
<213> Acinetobacter sp.

<400> 47

Met Thr Ala Leu Asn Gln Tyr Gly Met His Leu Glu Ile Thr Pro His
1 5 10 15

Asn Gly Trp Ser Gln Gln Phe Trp Asp Asp Leu Leu Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Phe Phe Ser Glu Met Ala Asn Gly Gly Leu
35 40 45

Ser Leu Asn Ser Phe Arg Tyr Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Gly Lys Ala Thr Gly
65 70 75 80

Phe Ser Glu Pro Gly Val Thr Glu Ala Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Lys Trp Tyr Arg Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Glu Lys Leu Asp Ser Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asn Met Ser His Arg Gly
130 135 140

Asn Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile His Ala Tyr Thr

165 170 175

Asp His Pro Glu Val Thr Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asn Asp Arg Pro Asp Trp Gln Gln Lys Ala Phe
210 215 220

His Ala Ala Glu Glu Gly Leu Arg Tyr Tyr Glu Leu Ala Leu Asp Asp
225 230 235 240

Cys Tyr Arg Val Gln Leu Gln Ala Ser Ala
245 250

<210> 48
<211> 250
<212> PRT
<213> Acinetobacter sp.

<400> 48

Met Thr Ala Leu Asn Gln Tyr Gly Met His Leu Glu Ile Thr Pro His
1 5 10 15

Asn Glu Trp Ser Gln Gln Phe Trp Asp Asp Leu Leu Pro Val Lys Glu
20 25 30

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

Ser Leu Asp Ser Phe Arg Tyr Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Gly
65 70 75 80

Phe Ser Glu Pro Gly Val Thr Glu Ala Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Gln Trp Tyr Arg Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Leu Asp Glu Leu Asp His Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asn Met Ser His Arg Gly

130 135 140

Asn Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile His Thr Tyr Thr
165 170 175

Asp His Pro Gln Val Ser Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asn Asp Arg Ser Asp Trp Gln Lys Lys Ala Phe
210 215 220

His Ala Ala Glu Glu Gly Leu Arg Tyr Tyr Glu Leu Ala Leu Asp Asp
225 230 235 240

Cys Tyr Lys Val Gln Leu Gln Ala Ser Ala
245 250

<210> 49
<211> 250
<212> PRT
<213> Acinetobacter

<400> 49

Met Thr Ala Leu Asn Gln Tyr Gly Met His Leu Glu Ile Thr Pro His
1 5 10 15

Asn Gly Trp Ser Gln Gln Phe Trp Asp Asp Leu Leu Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Phe Phe Ser Glu Met Ala Asn Gly Gly Leu
35 40 45

Ser Leu Asn Ser Phe Arg Tyr Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Gly Lys Ala Thr Gly
65 70 75 80

Phe Ser Glu Pro Gly Val Thr Glu Ala Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Lys Trp Tyr Arg Asp Trp Ala Gly

100 105 110

Gly Phe Gly Leu Thr Val Glu Lys Leu Asp Ser Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asn Met Ser His Arg Gly
130 135 140

Asn Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile His Ala Tyr Thr
165 170 175

Asp His Pro Asp Val Thr Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asn Asp Arg Pro Asp Trp Gln Gln Lys Ala Phe
210 215 220

His Ala Ala Glu Glu Gly Leu Arg Tyr Tyr Glu Leu Ala Leu Asp Asp
225 230 235 240

Cys Tyr Arg Val Gln Leu Gln Ala Ser Ala
245 250

<210> 50
<211> 248
<212> PRT
<213> Acinetobacter venetianus

<400> 50

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Thr His
1 5 10 15

Ser Glu Trp Ser Gln Arg Phe Trp Asp Asp Leu Val Pro Ala Lys Glu
20 25 30

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

Ser Leu Glu Cys Phe Arg Ser Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ala

65 70 75 80

Phe Ser Leu Asp Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Asn Trp Tyr Gln Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Ile Glu Met Leu Asn Glu Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Val Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
165 170 175

Glu His Pro Glu Val Asn Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Val Leu Gln Lys Lys Ala Phe
210 215 220

Arg Ala Val Gln Asp Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln His Lys Asn
245

<210> 51
<211> 244
<212> PRT
<213> Acinetobacter baumannii

<400> 51

Met Thr Ala Leu Asn Gln Tyr Gly Met Ser Leu Glu Ile Thr Pro His
1 5 10 15

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

Arg Val Ser Lys His Pro Phe Phe Thr Glu Met Ala Asn Gly Gly Leu

```
        35                  40                  45

Ser Leu Glu Ser Phe Arg Tyr Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50                  55                  60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ala
65                  70                  75                  80

Phe Ala Glu Pro Gly Val Thr Glu Thr Arg Asp Trp Leu Ile Gln Asn
                85                  90                  95

Ile Lys Val Glu Glu Arg His Leu Gln Trp Tyr Arg Asp Trp Ala Arg
            100                 105                 110

Gly Phe Gly Leu Thr Val Glu Gln Leu Asp Ser Val Arg Pro Pro Ala
        115                 120                 125

Ser Met Asn Ala Val Asn His Phe Leu Trp Asn Met Ser His Arg Gly
    130                 135                 140

Asn Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145                 150                 155                 160

Thr Gly Asp Trp Ser Ile Gln Val Tyr Lys Gly Ile His Ala Tyr Thr
                165                 170                 175

Asp His Pro Glu Val Thr Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
            180                 185                 190

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

Ile Lys Arg Leu Cys Asn Glu Arg Pro Asp Trp Gln Gln Lys Ala Phe
    210                 215                 220

His Ala Ala Glu Glu Gly Leu Arg Tyr Tyr Glu Leu Ala Leu Asp Asp
225                 230                 235                 240

Gln Ala Ser Ala


<210>  52
<211>  245
<212>  PRT
<213>  Acinetobacter sp.

<400>  52

Met Thr Val Leu Lys Asn Glu Phe Thr Leu Glu Ile Thr Pro His Ser
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1               5                   10                  15

Val Trp Ala Gln Lys Phe Trp Asp Glu Leu Ile Pro Ala Lys Glu Arg
            20                  25                  30

Val Ser Gln His Pro Val Phe Ile Gly Met Ser Asn Gly Thr Leu Ser
        35                  40                  45

Leu Glu Cys Phe Arg Ala Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
    50                  55                  60

Gln Phe Pro Ser Tyr Met Ala Leu Ala Leu Ala Lys Ala Thr Gln Phe
65                  70                  75                  80

Asn Glu Ala Gly Val Val Gln Thr Arg Asp Trp Leu Ile Gln Asn Ile
                85                  90                  95

Lys Val Glu Glu Arg His Leu Thr Trp Tyr Arg Asp Trp Ala Gly Gly
            100                 105                 110

Phe Gly Leu Thr Val Asp Gln Leu Asp His Val Thr Pro Pro Pro Ala
        115                 120                 125

Met Asn Ala Val Asn His Tyr Leu Trp Ser Ile Asn Tyr Arg Gly Ser
    130                 135                 140

Leu Ala Glu Gly Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145                 150                 155                 160

Gly Asp Trp Ser Ser His Val Tyr Lys Gly Ile His Asn Tyr His Asn
                165                 170                 175

His Pro Asp Val Lys Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg Ala
            180                 185                 190

His Ala His Tyr Asp Asp Ile His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Cys Glu Gly Lys Pro Glu Leu Gln Gln Lys Ala Phe His
    210                 215                 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225                 230                 235                 240

Tyr Lys Leu Gln Gly
                245
```

<210> 53
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 53

Met Thr Ile Leu Lys Asn Glu Phe Ser Leu Glu Ile Thr Pro His Ser
1 5 10 15

Glu Trp Ala Gln Lys Phe Trp Asp Asp Leu Ile Pro Ala Lys Glu Arg
20 25 30

Val Ser Gln His Pro Leu Phe Leu Gly Met Ala Asn Gly Thr Leu Lys
35 40 45

Leu Glu Cys Phe Arg Ala Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
50 55 60

Gln Phe Pro Ser Tyr Met Ala Leu Ala Leu Ser Lys Ala Ile His Phe
65 70 75 80

Gln Glu Gln Gly Val Val Glu Ser Arg Asp Trp Leu Ile Gln Asn Ile
85 90 95

Lys Val Glu Glu Arg His Leu Ala Trp Tyr Arg Asp Trp Ala Gly Gly
100 105 110

Phe Gly Leu Ser Ile Asp Gln Leu Asp Thr Val Thr Pro Pro Pro Ala
115 120 125

Met Asn Ala Val Asn His Phe Leu Trp Ser Val Asn Tyr Arg Ser Ser
130 135 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Asp Trp Ser Leu His Val Tyr Lys Gly Ile Arg Gly Tyr Glu Asn
165 170 175

His Pro Glu Val Gln Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg Ala
180 185 190

His Ala His Tyr Asp Asp Leu His Pro Tyr Glu Ala Met Glu Leu Ile
195 200 205

Lys Arg Leu Cys Asp Gly Lys Pro Glu Leu Gln Leu Lys Ala Phe Asn
210 215 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225 230 235 240

Tyr Lys Leu Gln Ala
245

<210> 54
<211> 245
<212> PRT
<213> Acinetobacter sp.

<400> 54

Met Thr Val Leu Lys Asn Glu Phe Thr Leu Glu Ile Thr Pro His Asn
1 5 10 15

Met Trp Ala Gln Lys Phe Trp Asp Glu Leu Ile Pro Ala Lys Glu Arg
20 25 30

Val Ser Gln His Pro Val Phe Ile Gly Met Ala Asn Gly Thr Leu Ser
35 40 45

Leu Glu Cys Phe Arg Ala Ala Leu Leu Asn Phe Tyr Pro Leu Val Ala
50 55 60

Gln Phe Pro Ser Tyr Met Ala Leu Ala Leu Ala Lys Ala Thr Gln Phe
65 70 75 80

Asn Glu Ala Gly Val Val Pro Thr Arg Asp Trp Leu Ile Gln Asn Ile
85 90 95

Lys Val Glu Glu Arg His Leu Thr Trp Tyr Arg Asp Trp Ala Ser Gly
100 105 110

Phe Gly Leu Thr Val Asp Gln Leu Asp His Val Thr Pro Pro Pro Ala
115 120 125

Met Asn Ala Val Asn His Tyr Leu Trp Ser Ile Asn Tyr Arg Gly Ser
130 135 140

Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala Thr
145 150 155 160

Gly Asp Trp Ser Ser His Val Tyr Lys Gly Ile His Asn Tyr Gln Asn
165 170 175

His Pro Asp Val Lys Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg Ala
180 185 190

```
His Ala His Tyr Asp Asp Ile His Pro Tyr Glu Ala Met Glu Leu Ile
        195                 200                 205

Lys Arg Leu Cys Glu Gly Lys Pro Glu Leu Gln Gln Lys Ala Phe His
    210                 215                 220

Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu Cys
225                 230                 235                 240

Tyr Lys Leu Gln Gly
                245
```

<210> 55
<211> 246
<212> PRT
<213> Acinetobacter sp.

<400> 55

```
Met Met Thr Val Leu Lys Asn Glu Leu Thr Leu Glu Ile Thr Pro His
1               5                   10                  15

Ser Met Trp Ala Gln Lys Phe Trp Asp Glu Leu Ile Pro Ala Lys Glu
            20                  25                  30

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

Ser Leu Glu Cys Phe Arg Ala Ala Leu Leu Asn Phe Tyr Pro Leu Val
    50                  55                  60

Ala Gln Phe Pro Ser Tyr Met Ala Leu Ala Leu Ala Lys Ala Thr Gln
65                  70                  75                  80

Phe Asn Glu Ala Gly Val Val Pro Thr Arg Asp Trp Leu Ile Gln Asn
                85                  90                  95

Ile Lys Val Glu Glu Arg His Leu Thr Trp Tyr Arg Asp Trp Ala Gly
            100                 105                 110

Gly Phe Gly Leu Thr Val Asp Gln Leu Asp Tyr Val Thr Pro Pro Pro
        115                 120                 125

Ala Met Asn Ala Val Asn His Tyr Leu Trp Ser Ile Asn Tyr Arg Gly
    130                 135                 140

Ser Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145                 150                 155                 160
```

Thr Gly Asp Trp Ser Ser His Val Tyr Lys Gly Ile His Asn Tyr Gln
165 170 175

Asn His Pro Asp Val Lys Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

Ala His Ala His Tyr Asp Asp Ile His Pro Tyr Glu Ala Met Glu Leu
195 200 205

Ile Lys Arg Leu Cys Glu Gly Lys Pro Glu Leu Gln Gln Lys Ala Phe
210 215 220

His Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln Gly
245

<210> 56
<211> 246
<212> PRT
<213> Serratia sp.

<400> 56

Met Met Thr Val Leu Lys Asn Glu Leu Thr Leu Glu Ile Thr Pro His
1 5 10 15

Ser Met Trp Ala Gln Lys Phe Trp Asp Glu Leu Ile Pro Ala Lys Glu
20 25 30

Arg Val Ser Gln His Pro Val Phe Thr Gly Met Ala Asn Gly Thr Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ala Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala Gln Phe Pro Ser Tyr Met Ala Leu Ala Leu Ala Lys Ala Thr Gln
65 70 75 80

Phe Asn Glu Ala Gly Val Val Pro Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Ser Trp Tyr Arg Asp Trp Ala Gly
100 105 110

Gly Phe Gly Leu Thr Val Asp Gln Leu Asp His Val Thr Pro Pro Pro
115 120 125

Ala Met Asn Ala Val Asn His Tyr Leu Trp Ser Ile Asn Tyr Arg Gly
130 135 140

Ser Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Ser Ser His Val Tyr Lys Gly Ile His Asn Tyr Gln
165 170 175

Asn His Pro Asp Val Lys Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

Ala His Ala His Tyr Asp Asp Ile His Pro Tyr Glu Ala Met Glu Leu
195 200 205

Ile Lys Arg Leu Cys Glu Gly Lys Pro Glu Leu Gln Gln Lys Ala Phe
210 215 220

His Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu
225 230 235 240

Cys Tyr Lys Leu Gln Gly
245

<210> 57
<211> 246
<212> PRT
<213> Acinetobacter sp.

<400> 57

Met Met Thr Val Leu Lys Asn Glu Phe Thr Leu Glu Ile Thr Pro His
1 5 10 15

Asn Met Trp Ala Gln Lys Phe Trp Asp Glu Leu Ile Pro Ala Lys Glu
20 25 30

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

Ser Leu Glu Cys Phe Arg Ala Ala Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala Gln Phe Pro Ser Tyr Met Ala Leu Ala Leu Ala Lys Ala Thr Gln
65 70 75 80

Phe Asn Glu Ala Gly Val Val Pro Thr Arg Asp Trp Leu Ile Gln Asn
85 90 95

```
Ile Lys Val Glu Glu Arg His Leu Thr Trp Tyr Arg Asp Trp Ala Ser
            100                 105                 110

Gly Phe Gly Leu Thr Val Asp Gln Leu Asp His Val Thr Pro Pro Pro
        115                 120                 125

Ala Met Asn Ala Val Asn His Tyr Leu Trp Ser Ile Asn Tyr Arg Gly
    130                 135                 140

Ser Leu Ala Glu Cys Leu Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145                 150                 155                 160

Thr Gly Asp Trp Ser Ser His Val Tyr Lys Gly Ile His Asn Tyr Gln
                165                 170                 175

Asn His Pro Asp Val Lys Ile Asp Lys Arg Ser Leu Ala Trp Leu Arg
            180                 185                 190

Ala His Ala His Tyr Asp Asp Ile His Pro Tyr Glu Ala Met Glu Leu
        195                 200                 205

Ile Lys Arg Leu Cys Glu Gly Lys Pro Glu Leu Gln Gln Lys Ala Phe
    210                 215                 220

His Ala Ala Arg Glu Gly Leu Glu Tyr Tyr Ala Leu Ala Leu Asp Glu
225                 230                 235                 240

Cys Tyr Lys Leu Gln Gly
                245


<210>  58
<211>  257
<212>  PRT
<213>  Dyella sp.

<400>  58

Met Asn Asn His Phe Glu Arg Thr Gly Pro Leu Thr Glu Leu Thr Ser
1               5                   10                  15

Tyr Pro Gln Trp Ala Gln Asp Leu Val Ala Ala Cys Glu Pro Ala Arg
            20                  25                  30

Arg Arg Val Arg Asp His Leu Met Trp Asp Leu Met Gly Thr Gly Arg
        35                  40                  45

Ile Asp His Ala Thr Met Arg Asn Phe Met Val Gly Thr Trp Ser Leu
    50                  55                  60
```

Ile Glu Arg Phe Pro Ser Phe Met Ala Gln Asn Leu Leu Lys Thr Gln
65   70   75   80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
            100   105   110

Glu Gly Ala Gly Val Ala Arg Glu Glu Val Leu Lys Gly Arg Pro Pro
        115   120   125

Arg Gly Thr Gln Ala Ala Ala Glu Trp Cys His Glu Val Cys Gly Arg
    130   135   140

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

Val Thr Gly Asp Trp Ser Gln Lys Val Tyr Asp Ser Val Ala Tyr Ala
                165   170   175

Gln Gly Leu Pro Gln Ala Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
            180   185   190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
        195   200   205

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

Leu Gln Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225   230   235   240

Glu Arg Cys Leu Val Gln Glu Val Ala Glu Gln Val Glu Glu Gln Ala
                245   250   255

Ala

<210> 59
<211> 257
<212> PRT
<213> Dyella soli

<400> 59

Met Asn Ala Gln Phe Glu Arg Thr Gly Ser Leu Thr Glu Leu Thr Ser
1   5   10   15

```
Tyr Pro Gln Trp Ala Gln Asp Met Val Ala Ala Cys Glu Pro Ala Arg
            20                  25                  30

Arg Ser Val Arg Asp His Val Met Trp Asp Gln Met Arg Glu Gly Arg
        35                  40                  45

Ile Asp Pro Ala Thr Met Arg His Phe Met Val Gly Thr Trp Ser Leu
    50                  55                  60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Gln
65                  70                  75                  80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
            100                 105                 110

Glu Gly Ala Gly Val Ser Arg Glu Ser Val Leu Asp Gly Leu Pro Pro
        115                 120                 125

Arg Gly Thr Gln Ala Ala Ala Asp Trp Cys His Glu Val Cys Gly Gly
    130                 135                 140

Asp Ser Leu Ala Ala Gly Ile Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145                 150                 155                 160

Val Thr Gly Glu Trp Ser Gln Lys Val Phe Asp Ser Leu Ala Tyr Ala
                165                 170                 175

Glu Ser Leu Pro Ala Thr Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
            180                 185                 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
        195                 200                 205

Val Cys Thr Leu Met Gly Thr Arg Pro Pro Ala Glu Ala Val Glu His
    210                 215                 220

Leu Arg Glu Cys Ile Val Arg Ser Tyr Thr Ser Leu His Tyr Gly Leu
225                 230                 235                 240

Glu Arg Cys Leu Ala Arg Pro Leu Val Glu Glu Val Glu Glu Gln Ala
                245                 250                 255

Ala
```

<210> 60
<211> 257
<212> PRT
<213> Dyella sp.

<400> 60

```
Met Asn Thr Asn Phe Glu Arg Thr Gly Pro Leu Gly Glu Leu Ser Ser
1               5                   10                  15

Tyr Pro Gln Trp Ala Gln Asp Met Ile Ala Ala Cys Glu Pro Ala Arg
            20                  25                  30

Arg Arg Val Arg Asp His Leu Met Trp Asp Leu Met Gly Glu Gly Arg
        35                  40                  45

Ile Asp Pro Val Thr Met Ala Asn Phe Met Ile Gly Thr Trp Ser Leu
    50                  55                  60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Met Lys Thr Gln
65                  70                  75                  80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
            100                 105                 110

Asp Gly Ala Gly Val Pro Arg Gln Gln Val Phe Asp Gly Leu Pro Pro
        115                 120                 125

Arg Gly Thr Gln Ala Ala Thr Glu Trp Cys Leu Glu Val Ser Gly Gln
    130                 135                 140

Asp Thr Leu Ala Ala Gly Met Leu Ala Thr Asn Tyr Ala Ile Glu Gly
145                 150                 155                 160

Val Thr Gly Glu Trp Ser Gln Lys Val Tyr Asp Ser Val Ala Tyr Ala
                165                 170                 175

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

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
        195                 200                 205

Val Cys Thr Leu Met Gly Asn Asn Pro Ala Pro Glu Glu Val Asp His
    210                 215                 220
```

Leu Arg Glu Cys Ile Glu Arg Ser Tyr Ala Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Val Gln Pro His Val Glu Glu Val Glu Glu Gln Ala
245 250 255

Ala

<210> 61
<211> 258
<212> PRT
<213> Dyella sp.

<400> 61

Met Ala Asp Lys Phe Lys Leu Asn Gly Ser Leu Thr Lys Leu Ser Ser
1 5 10 15

Tyr Pro Gln Trp Ala Gln Thr Met Val Glu Ser Cys Glu Pro Ser Arg
20 25 30

Lys Arg Val Arg Asp His Ala Val Trp Asp Met Met Cys Asp Ala Thr
35 40 45

Ile Asp Asn His Thr Met Arg Asn Phe Met Leu Gly Thr Trp Pro Leu
50 55 60

Ile Glu Arg Phe Pro Ser Tyr Met Ala Asn Ser Leu Met Lys Thr Arg
65 70 75 80

Tyr Gly Arg Ser Pro Gly Asp Asp Leu Ala Arg Arg Trp Leu Val Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Asp Gly Ala Gly Val Asp Arg Gln Asp Val Leu Thr Ser Thr Pro Pro
115 120 125

Gln Gly Thr Gln Leu Ala Ala Asp Trp Cys Glu Glu Val Cys Glu Ser
130 135 140

Asp Ser Leu Val Ala Gly Met Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Gln Lys Val Tyr Glu Ser Ala Ala Tyr Ala
165 170 175

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

Met His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Ile Cys Ala Leu Met Gly Asn Ala Pro Asp Pro Gly Glu Ile Glu His
210 215 220

Val Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu Tyr Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Val His Ser Arg Glu His Glu Pro Arg Asp Ala Ala
245 250 255

Cys Met

<210> 62
<211> 257
<212> PRT
<213> Dyella jiangningensis

<400> 62

Met Asn Thr His Phe Glu Arg Thr Gly Pro Leu Gly Asp Leu Ser Ser
1 5 10 15

Tyr Pro Gln Trp Ala Gln Asp Leu Val Ala Ala Cys Glu Pro Ala Arg
20 25 30

Arg Arg Val Arg Asp His Ala Met Trp Asp Leu Met Gly Glu Gly Arg
35 40 45

Ile Asp Ala Val Thr Met Arg Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Gln
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Asp Gly Ser Gly Val Pro Arg Ala Glu Val Leu Asp Gly Arg Pro Pro
115 120 125

Arg Gly Thr Gln Ala Ala Thr Glu Trp Cys Leu Glu Val Cys Gly Gln
130 135 140

Asp Ser Leu Ala Ala Gly Met Leu Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Gln Lys Val Tyr Asp Ser Val Ala Tyr Ala
165 170 175

Glu Ser Leu Pro Ser Ala Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Ser Arg Pro Ala Pro Glu Ala Val Glu His
210 215 220

Leu Arg Glu Cys Val Glu Arg Ser Tyr Leu Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Leu Gln Pro Gln Met Lys Glu Val Glu Glu Gln Ala
245 250 255

Ala

<210> 63
<211> 257
<212> PRT
<213> Dyella sp.

<400> 63

Met Asn Thr Asn Thr Val Arg Thr Gly Ser Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Lys Trp Ala Arg Asp Met Ile Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Ala Asp Gly Ser
35 40 45

Ile Asp Leu Ser Thr Met Arg Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Gln Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Glu Gly Ala Gly Val Ser Arg Glu Glu Ile Ile Asp Gly Met Pro Pro
115 120 125

Arg Gly Thr Gln Thr Ala Ala Glu Trp Cys His Asp Val Cys Gly Arg
130 135 140

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

Val Thr Gly Glu Trp Ser Gln Lys Val Phe Asp Ser Val Ala Tyr Ala
165 170 175

Asn Ser Leu Pro Ala Thr Gly Arg Lys Ser Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Ser Gln Pro Ala Pro Glu Glu Val Glu His
210 215 220

Val Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Met Arg His Pro Val Gly Glu Met Glu Glu Gln Ala
245 250 255

Ala

<210> 64
<211> 257
<212> PRT
<213> Dyella jiangningensis

<400> 64

Met Asn Thr Gln Phe Glu Arg Thr Gly Pro Leu Gly Asp Leu Ser Ser
1 5 10 15

Tyr Pro Gln Trp Ala Gln Asp Leu Val Ala Ala Cys Glu Pro Ala Arg
20 25 30

Arg Arg Val Arg Asp His Val Met Trp Asp Leu Met Gly Asp Gly Arg
35 40 45

Ile Asp Pro Leu Thr Met Arg Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Gln
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Asp Gly Ser Gly Val Pro Arg Glu Glu Val Ile Asp Gly Arg Pro Pro
115 120 125

Arg Gly Thr Gln Ala Ala Thr Glu Trp Cys Leu Glu Val Cys Gly Gln
130 135 140

Asp Asn Leu Ala Ala Gly Met Leu Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Gln Lys Val Tyr Asp Ser Val Ala Tyr Ala
165 170 175

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

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Asn Arg Pro Ala Pro Glu Ala Val Glu His
210 215 220

Leu Arg Glu Cys Val Glu Arg Ser Tyr Leu Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Leu Gln Pro Gln Val Lys Glu Val Glu Glu Gln Ala
245 250 255

Ala

<210> 65
<211> 257

<212> PRT
<213> Dyella sp.

<400> 65

Met Asn Thr Asn Thr Val Arg Thr Gly Ser Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Lys Trp Ala Arg Asp Met Ile Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Ser Ala Gly Ser
35 40 45

Ile Asp Pro Gln Thr Met Arg Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Ser Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Glu Gly Ala Gly Val Pro Arg Glu Asp Val Leu Asp Gly Met Pro Pro
115 120 125

Arg Gly Thr Gln Thr Ala Ala Asp Trp Cys Tyr Asp Val Cys Gly Arg
130 135 140

Asp Ser Leu Ala Ala Gly Ile Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Gln Lys Val Tyr Asp Ser Val Ala Tyr Ala
165 170 175

Asn Ser Leu Pro Glu Thr Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Ser Gln Pro Ala Pro Glu Glu Val Glu His
210 215 220

Val Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Met Arg His Ala Val Gly Glu Val Glu Glu Gln Ala
245 250 255

Ala

<210> 66
<211> 257
<212> PRT
<213> Dyella sp.

<400> 66

Met Asn Thr Asn Thr Val Arg Thr Gly Ser Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Lys Trp Ala Arg Glu Met Val Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Arg Asp Gly Ser
35 40 45

Ile Asp Pro Gln Thr Met His Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Ser Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Glu Gly Ala Gly Val Pro Arg Glu Asp Val Leu Asp Gly Thr Pro Pro
115 120 125

Arg Gly Thr Gln Thr Ala Ala Asp Trp Cys His Asp Val Cys Gly Arg
130 135 140

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

Val Thr Gly Glu Trp Ser Ala Lys Val Tyr Asp Ser Val Ala Tyr Ala
165 170 175

Asn Ser Leu Pro Glu Ala Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Ser Gln Pro Ala Pro Glu Glu Val Glu His
210 215 220

Val Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Val Gln His Ala Val Gly Glu Val Glu Glu Gln Ala
245 250 255

Ala

<210> 67
<211> 257
<212> PRT
<213> Dyella sp.

<400> 67

Met Asn Thr His Phe Glu Arg Thr Gly Thr Leu Thr Glu Leu Thr Ser
1 5 10 15

Tyr Pro Arg Trp Val Gln Glu Leu Val Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Ser Glu Gly His
35 40 45

Ile Asp Gln Ala Thr Met Arg Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Gln Asn Leu Leu Lys Thr Gln
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Glu Gly Ala Gly Ile Ala Arg Asp Val Val Leu Asn Gly Arg Pro Pro
115 120 125

Arg Gly Thr Gln Ala Ala Ala Glu Trp Cys His Glu Val Cys Gly Asn
130 135 140

Asp Thr Leu Ala Ala Gly Met Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Gln Lys Val Phe Asp Ser Leu Ala Tyr Ala
165 170 175

Gln Ser Leu Pro Ala Ala Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Asn His Pro Ala Pro Glu Glu Val Asp His
210 215 220

Leu Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Val Lys Pro Tyr Ala Glu Glu Val Glu Glu Gln Ala
245 250 255

Ala

<210> 68
<211> 257
<212> PRT
<213> Dyella japonica

<400> 68

Met Asn Thr Asn Thr Val Arg Thr Gly Ser Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Lys Trp Ala Arg Asp Met Val Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Ser Asp Gly Ser
35 40 45

Ile Asp Leu Gln Thr Met His Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Ser Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Glu Gly Ala Gly Val Pro Arg Glu Asp Val Leu Asp Gly Met Pro Pro
115 120 125

Arg Gly Thr Gln Thr Ala Ala Asp Trp Cys His Asp Val Cys Gly Arg
130 135 140

Asp Ser Leu Ala Ala Gly Ile Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Gln Lys Val Tyr Asp Ser Val Ala Tyr Ala
165 170 175

Asn Ser Leu Pro Glu Ala Gly Arg Lys Ala Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Ser Gln Pro Ala Pro Glu Glu Val Glu His
210 215 220

Val Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Met Gln His Thr Val Gly Ala Val Glu Glu Gln Ala
245 250 255

Ala

<210> 69
<211> 257
<212> PRT
<213> Dyella sp.

<400> 69

Met Asn Thr Asn Thr Val Arg Thr Gly Ser Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Lys Trp Ala Arg Glu Met Ile Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Ser Glu Gly Ser
35 40 45

```
Ile Asp Leu Ala Thr Val Arg Asn Phe Met Val Gly Thr Trp Ser Leu
    50                  55                  60

Ile Glu Arg Phe Pro Gly Phe Met Ala Leu Ser Leu Leu Lys Thr Arg
65                  70                  75                  80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
            100                 105                 110

Glu Gly Ser Gly Val Ser Arg Glu Glu Val Leu Asp Gly Met Pro Pro
        115                 120                 125

Arg Gly Thr Gln Thr Ala Ala Glu Trp Cys His Asp Val Cys Ala Arg
    130                 135                 140

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

Val Thr Gly Glu Trp Ser Gln Lys Val Phe Asp Ser Val Ala Tyr Ala
                165                 170                 175

Asn Ser Leu Pro Ala Ala Gly Arg Lys Ser Thr Leu Arg Trp Leu Gln
            180                 185                 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
        195                 200                 205

Val Cys Thr Leu Met Gly Ser Gln Pro Ala Ala Glu Glu Val Glu His
    210                 215                 220

Leu Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225                 230                 235                 240

Glu Arg Cys Leu Val Gln His Thr Val Asn Glu Val Ala Glu Gln Ala
                245                 250                 255

Ala
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<210> 70
<211> 257
<212> PRT
<213> Dyella japonica

<400> 70

Met Asn Thr Asn Asn Val Arg Thr Gly Ser Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Lys Trp Ala Arg Asp Met Ile Glu Ala Cys Glu Pro Ala Arg
20 25 30

Arg Ser Val Arg Asp His Val Met Trp Asp Met Met Ser Glu Gly Ser
35 40 45

Ile Asp Leu Ala Thr Val Arg Asn Phe Met Val Gly Thr Trp Ser Leu
50 55 60

Ile Glu Arg Phe Pro Gly Phe Met Ala Leu Ser Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
100 105 110

Glu Gly Ser Gly Val Ser Arg Glu Glu Val Leu Asp Gly Leu Pro Pro
115 120 125

Arg Gly Thr Gln Thr Ala Ala Glu Trp Cys His Asp Val Cys Ala Arg
130 135 140

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

Val Thr Gly Glu Trp Ser Gln Lys Val Phe Asp Ser Val Ala Tyr Ala
165 170 175

Asn Ser Leu Pro Ala Ala Gly Arg Lys Ser Thr Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Met Gly Ser Gln Pro Ala Glu Glu Glu Val Glu His
210 215 220

Leu Arg Glu Cys Ile Glu Arg Ser Tyr Val Ser Leu His Tyr Gly Leu
225 230 235 240

Glu Arg Cys Leu Val Gln His Ala Val Asn Glu Val Ala Glu Gln Ala

245 250 255

Ala

<210> 71
<211> 252
<212> PRT
<213> Vogesella sp.

<400> 71

Met Asn Arg Glu Phe Val Arg Ser Gly Ala Leu Arg Ser Pro His Ser
1 5 10 15

Tyr Pro Glu Trp Ala Gln Gln Leu Leu Ala Asp Cys Ala Ala Ala Arg
20 25 30

Gln Arg Val Val Arg His Glu Phe Tyr Gln Arg Leu Arg Asp Ala Glu
35 40 45

Leu Gly Asp Asp Ala Leu Arg Leu Phe Leu Ile Gly Val Trp Pro Val
50 55 60

Val Glu Gln Phe Pro Leu Tyr Met Ala Gln Asn Leu Leu Lys Thr Arg
65 70 75 80

Tyr Gly Arg His Arg Gly Glu Asp Met Ala Arg Arg Phe Leu Val Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Ala Asp Tyr Trp Leu Ala Trp Ala
100 105 110

Ala Ala Cys Gly Ile Ala Ala Thr Glu Leu Gln Ala Gln Arg Val Pro
115 120 125

Glu Pro Leu Gln Gln Leu Gly His Trp Cys Arg His Asn Ser Arg His
130 135 140

His Ser Leu Leu Leu Ala Leu Ala Ala Thr Asn Tyr Ala Ile Asp Gly
145 150 155 160

Ala Thr Gly Glu Trp Thr Gln Leu Val Cys Ala Pro Gly Ile Tyr Glu
165 170 175

Ala Ser Leu Pro Ala Met Gln Arg Lys Ser Ala Met Arg Trp Leu Lys
180 185 190

Leu His Ala Arg Tyr Asp Asp Asp His Pro Trp Glu Ala Leu Asp Ile

195 200 205

Val Cys Thr Leu Ala Gly Arg Asp Ala Asp Ala Gly Thr Arg Arg Ala
210 215 220

Leu Gln Ala Ala Ile Gly Asn Ser Tyr His Tyr Met Gln Leu Ala Leu
225 230 235 240

Asp Cys Cys Leu Gln Gln Glu Gln Ala Val Pro Gly
245 250

<210> 72
<211> 266
<212> PRT
<213> Steroidobacter cummioxidans

<400> 72

Met Asp Ser Pro Phe Val Arg Thr Gly Pro Leu Met Ala Leu Ala Ser
1 5 10 15

Tyr Pro His Trp Leu Gln Glu Leu Ile Ala Asp Cys Asp Val Ala Arg
20 25 30

His Ala Val Val Thr His Glu Ile Phe Gln Gln Met His Ala Gly Met
35 40 45

Leu Pro Ala Thr Ala Met Arg Arg Phe Leu Gly Ser Phe Trp Pro Val
50 55 60

Ile Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys Val Gln
65 70 75 80

Tyr Gly Leu Gly Ala Gly His Ala Met Ala Arg Lys Tyr Leu Ile Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Val Glu Tyr Trp Ile Asp Trp Ser
100 105 110

Gln Ala His Gly Leu Thr Arg Asp Glu Leu Leu Ser Gly Trp Arg Ser
115 120 125

Asn Ser Ala Asp Ala Leu Ser His Trp Cys Trp His Thr Cys Glu Arg
130 135 140

Asp Pro Leu Ala Ile Ala Met Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Thr Thr Gly Glu Trp Ala Ala Phe Val Cys Ser Ser Ser Ala Tyr Glu

165 170 175

Asn Gly Phe Ser Asn Glu Ala Arg Lys Gln Ala Met Lys Trp Leu Arg
180 185 190

Val His Ala His Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Ile Ala Thr Leu Leu Gly Gln Lys Pro Glu Ala Arg Asp Ile Ala Asn
210 215 220

Val Arg Ser Ala Ile Val Lys Ser Tyr His Tyr Met Ser Ala Ala Phe
225 230 235 240

Asp Asp Cys Phe Ala Ala Glu Gln Arg Asn Ala Pro Arg Arg Gln Cys
245 250 255

Arg Pro Gly Val Pro Thr Leu Leu Ala Ser
260 265

<210> 73
<211> 267
<212> PRT
<213> Rivibacter sp.

<400> 73

Met Lys Glu Phe Gln Arg Thr Gly Glu Leu Lys Asp Ile Gly Ser Tyr
1 5 10 15

Pro Leu Trp Leu Gln Gln Val Val Arg Asp Thr Gln Arg Asp Lys Leu
20 25 30

Arg Val Val Asp His Glu Leu Phe Ala Leu Met Arg Asp Ala Lys Leu
35 40 45

Pro Leu Ala Ala Met Gln Arg Phe Leu Val Gly Val Trp Pro Thr Ile
50 55 60

Glu Arg Phe Pro Arg Phe Met Ser Met Thr Leu Lys Lys Val Ser Tyr
65 70 75 80

Gly Arg Ser Pro Gly Glu Asp Met Ala Arg Arg Tyr Leu Met His Asn
85 90 95

Ile Arg Val Glu Gln Lys His Ala Glu Tyr Trp Val Glu Trp Ala Arg
100 105 110

Ser Ala Gly Leu Thr Ala Arg Asp Leu Ala Glu Ser Glu Glu Thr Glu

```
        115                 120                 125

Gly Leu Lys Ala Leu Ala His Trp Cys Trp Phe Val Cys Asp Gln Gly
    130                 135                 140

Ser Leu Ser Val Ala Ile Ala Ala Thr Asn Tyr Ala Val Glu Gly Ala
145                 150                 155                 160

Thr Gly Glu Trp Ser Cys Val Val Cys Ser Lys Ala Asp Tyr Ala Glu
                165                 170                 175

Ser Leu Pro Ala Glu Val Arg Gly Pro Ala Met Arg Trp Leu Arg Val
            180                 185                 190

His Ala Glu Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Asp Ile Val
        195                 200                 205

Ala Thr Leu Leu Gly His Ala Pro Ser Gln Arg Glu Ile Asp Asp Val
    210                 215                 220

Arg Arg Ala Ile Arg Ala Ser Tyr Ala Tyr Met Ala Met Ala Leu Asp
225                 230                 235                 240

His Ala Met Ala Ala Ala Ile His Gly Ser Phe Asp Glu Thr Ala Ser
                245                 250                 255

Asn Ala Ser Thr Leu Gly Met Leu Asp Ala Ala
            260                 265


<210>  74
<211>  259
<212>  PRT
<213>  Metallibacterium scheffleri

<400>  74

Met Asn Asn Glu Phe Val Arg Thr Gly Ala Leu Lys Asp Leu Arg Ser
1               5                   10                  15

Tyr Pro Leu Trp Ala Gln Glu Val Met Glu Ser Cys Glu Pro Ala Lys
            20                  25                  30

Arg Ala Val Leu Glu His Pro Ile Trp Ala Met Met Arg Glu Gly Ser
        35                  40                  45

Leu Ser Asp Ala Ala Met Gln Arg Phe Ile Leu Ser Ala Trp Pro Val
    50                  55                  60

Ile Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys Ala Arg
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65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Asp Tyr Trp Leu Asp Trp Ser
100 105 110

Asp Ala Val Gly Ala Pro Arg Glu Val Val Leu Gly Asp Asn Ala Ala
115 120 125

Ala Pro Glu Ala Gly Ile Leu Ser His Trp Cys Trp Gln Val Ser Ala
130 135 140

Ser Asp Thr Leu Ala Ala Gly Met Leu Ala Thr Asn Tyr Ala Val Glu
145 150 155 160

Gly Ile Thr Gly Glu Trp Ala Gln Leu Val Thr Gln Asp Asp Ile Tyr
165 170 175

Ala Tyr Gly Phe Glu Ala Arg Ile Arg Ala Lys Ala Met Arg Trp Leu
180 185 190

Lys Leu His Ala Glu Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu
195 200 205

Ile Val Ser Thr Leu Val Gly Pro His Pro Ser Pro Glu Thr Thr Asn
210 215 220

His Leu Arg Arg Cys Val Leu Asn Thr Tyr Val Tyr Lys Arg Ile Ala
225 230 235 240

Leu Glu His Cys Met Gln Ala Gln Gln Arg Asn Thr Ser Val Gln Ala
245 250 255

Val Ala Ala

<210> 75
<211> 267
<212> PRT
<213> Ideonella azotifigens

<400> 75

Met Asn Asn Glu Phe Ala Leu Gln Gly Ala Leu Thr Asp Ile Arg Ser
1 5 10 15

Tyr Pro Asp Trp Val Gln Asp Leu Val Ser Glu Cys Glu Pro Thr Arg

```
            20                  25                  30

Leu Gly Val Thr Gln His Glu Leu Phe Arg Leu Met Arg Asp Ala Arg
        35                  40                  45

Leu Ala Pro Gly Gln Thr Arg Asn Phe Leu Ala Gly Ile Trp Pro Val
    50                  55                  60

Ile Glu Gln Phe Pro Gln Tyr Met Ala Leu Asn Leu Leu Lys Val Ala
65                  70                  75                  80

Leu Gly Arg Val Arg Gly His Asp Gln Ala Arg Arg Tyr Leu Ile Arg
                85                  90                  95

Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Gln Ala Trp Ala
            100                 105                 110

Leu Ala Ala Gly Leu Ser Leu Asp Asp Leu Val His Gly Ala Val Pro
        115                 120                 125

Pro Ala Thr Glu Ala Leu Ser His Trp Cys Trp His Ser Cys Glu Arg
    130                 135                 140

Asp Ser Leu Ala Ala Gly Met Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145                 150                 155                 160

Ala Thr Gly Glu Trp Ala Asp Leu Val Cys Ala Ser Asp Ala Tyr Glu
                165                 170                 175

Asn Ser Leu Pro Glu Leu His Arg Thr Lys Ala Met Lys Trp Leu Lys
            180                 185                 190

Leu His Ala Lys Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
        195                 200                 205

Ile Ser Thr Leu Val Gly Met Thr Pro Asn Arg Gly Tyr Val Asp Leu
    210                 215                 220

Ile Arg Ser Arg Val Leu Thr Ser Tyr Asn Tyr Met Lys Met Ala Leu
225                 230                 235                 240

Asp Lys Cys Leu Asp Ala Pro Phe Pro Val Gln Val Pro Arg Trp Asp
                245                 250                 255

Pro Ser Arg Tyr Glu Ala Val Arg Glu Arg Val
            260                 265
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<210> 76
<211> 270
<212> PRT
<213> Steroidobacter agariperforans

<400> 76

Met Glu Ser Leu Phe Val Arg Thr Gly Pro Leu Leu Ala Leu Thr Ser
1   5   10   15

Tyr Pro Gln Trp Leu Gln Glu Ile Val Ser Glu Cys Asp Asp Ala Arg
            20   25   30

His Thr Val Ile Ala His Glu Ile Phe Gln Gln Met His Ala Gly Val
        35   40   45

Leu Pro Ala Thr Ala Met Arg Cys Phe Leu Ala Ser Phe Trp Pro Val
    50   55   60

Ile Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys Val Gln
65   70   75   80

Tyr Gly Leu Gly Ala Gly His Ala Met Ala Arg Lys Tyr Leu Ile Arg
                85   90   95

Asn Ile Arg Val Glu Gln Asn His Val Glu Tyr Trp Ile Asp Trp Ser
            100   105   110

Gln Gly His Gly Leu Thr Arg Asp Asn Leu Leu Ser Gly Trp Arg Ser
        115   120   125

Asp Ser Ala Asp Ala Leu Ser His Trp Cys Trp His Thr Cys Glu Arg
    130   135   140

Asp Pro Leu Ala Ile Ala Met Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145   150   155   160

Ala Thr Gly Glu Trp Ala Ala Phe Val Cys Gly Ser Ser Ala Tyr Glu
                165   170   175

Asn Gly Phe Pro Asp Asp Val Arg Lys Gln Ala Met Lys Trp Leu Arg
            180   185   190

Val His Ala His Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
        195   200   205

Ile Ala Thr Leu Leu Gly His Gln Pro Gln Ala Arg Asp Ile Ala Asn
    210   215   220

Val Arg Ser Ala Ile Val Lys Ser Tyr His Tyr Met Ser Ala Ala Phe
225 230 235 240

Asp Asp Cys Leu Thr Glu Asp Lys Arg Arg Ala Pro Arg Arg Gln His
245 250 255

Arg Pro Gly Val Pro Ala Leu Gln Leu Ala Glu Asp Leu Ser
260 265 270

<210> 77
<211> 266
<212> PRT
<213> Steroidobacter sp.

<400> 77

Met Glu Ser Gln Phe Val Arg Thr Gly Ala Leu Met Ala Leu Glu Ser
1 5 10 15

Tyr Pro Glu Trp Leu Gln Asp Ile Val Ala Glu Cys Asp Asp Ala Arg
20 25 30

His Thr Val Val Ala His Glu Ile Phe Gln Gln Met His Ala Gly Val
35 40 45

Leu Ser Pro Ala Ala Met Arg Cys Phe Leu Ala Ser Phe Trp Pro Val
50 55 60

Ile Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys Val Gln
65 70 75 80

Tyr Gly Leu Gly Ala Gly His Thr Met Ala Arg Lys Tyr Leu Ile Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Val Glu Tyr Trp Ile Asp Trp Ser
100 105 110

Gln Gly His Gly Leu Ser Arg Asp Ala Leu Leu Ser Gly Trp Arg Ser
115 120 125

Asn Ser Ala Asp Ala Leu Ser His Trp Cys Trp His Thr Cys Glu Arg
130 135 140

Asp Pro Leu Ala Val Ala Met Ala Ala Thr Asn Phe Ala Ile Glu Gly
145 150 155 160

Thr Thr Gly Glu Trp Ala Ala Phe Val Cys Ser Ser Ser Thr Tyr Glu
165 170 175

Asn Gly Phe Ala Asn Asp Val Arg Lys Gln Ala Met Lys Trp Leu Arg
180 185 190

Val His Ala His Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Ile Ala Thr Leu Leu Gly His Gln Pro Gln Ala Arg Glu Ile Ala Asn
210 215 220

Val Arg Ser Ala Ile Val Lys Ser Tyr Gln Tyr Met Ser Ser Ala Phe
225 230 235 240

Asp Asp Cys Leu Ala Glu Glu Lys Arg Gln Ala Pro Arg Arg Gln His
245 250 255

Arg Pro Gly Val Pro Ala Leu Leu Ala Ser
260 265

<210> 78
<211> 270
<212> PRT
<213> Methylibium sp.

<400> 78

Met Ser His Asp Phe Arg Arg Thr Gly Asp Leu Lys Ser Ile Gly Ser
1 5 10 15

Tyr Pro Val Trp Val Gln Arg Val Val Arg Glu Thr Ala Pro Tyr Lys
20 25 30

Gln Arg Val Val Glu His Glu Leu Phe Ala Leu Met Arg Glu Gly Lys
35 40 45

Leu Pro Met Ser Ala Met Arg Arg Phe Leu Val Gly Val Trp Pro Thr
50 55 60

Ile Glu Gln Phe Pro Arg Phe Met Ser Met Asn Leu Lys Lys Ile Gly
65 70 75 80

Tyr Gly Asp Ser Val Gly Glu Asp Met Ala Arg Arg Tyr Leu Ile Gln
85 90 95

Asn Ile Arg Val Glu Gln Lys His Ser Glu His Trp Ala Thr Trp Ala
100 105 110

Ser Ser Ala Gly Leu Thr Leu His Asp Leu Arg Thr Gly Gln Asp Val
115 120 125

Glu Glu Met Ala Ala Leu Ala His Trp Cys Trp Phe Ile Ser Asp Gln
    130   135   140

Ala Lys Leu Ala Val Ala Ile Ala Ala Thr Asn Tyr Ala Val Glu Gly
145   150   155   160

Ala Thr Gly Glu Trp Ser Cys Val Val Cys Ser Lys Asn Thr Tyr Ala
                165   170   175

Gln Ser Leu Pro Glu Asp Ile Arg Val Pro Ala Met Arg Trp Leu Lys
            180   185   190

Val His Ala Glu Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Asp Ile
        195   200   205

Val Ala Thr Leu Leu Gly His Ala Pro Ser Gln Gln Asp Ile Thr Glu
    210   215   220

Val Arg Arg Ala Ile Gln Ser Ser Tyr Thr Tyr Met Lys Met Ala Leu
225   230   235   240

Asp Ser Ala Leu Met Ala Ser Ile His Gly Ser Phe Asp Glu Thr Ala
                245   250   255

Ser Asn Ser Ala Thr Leu Gly Leu Glu Gly Leu His Ala Ala
            260   265   270

<210> 79
<211> 220
<212> PRT
<213> Cytophagaceae bacterium

<400> 79

Pro Thr Met Gln Arg Phe Met Val Gly Ile Trp Pro Thr Ile Glu Gln
1   5   10   15

Phe Pro Arg Phe Met Ala Met Asn Leu Lys Lys Val Gly Tyr Ala Asp
            20   25   30

Ser Leu Gly Glu Asp Met Ala Arg Arg Tyr Leu Ile Gln Asn Ile Arg
        35   40   45

Val Glu Gln Lys His Ala Glu His Trp Ala Ala Trp Ala Arg Ser Ala
    50   55   60

Asp Val Asn Leu Ser Asp Leu Arg Ser Gly Glu Ile Ser Gly Glu Ser
65   70   75   80

Thr Glu Glu Leu His Ser Leu Ala His Trp Cys Trp Tyr Ile Cys Asp
85 90 95

Gln Pro Ser Leu Ala Val Ala Val Ala Ala Thr Asn Tyr Ala Ile Glu
100 105 110

Gly Ala Thr Gly Glu Trp Ala Cys Leu Val Cys Ser Thr Asp Lys Tyr
115 120 125

Ser Gln Ser Ile Pro Asp Asp Ile Arg Ser Ser Ser Met Arg Trp Leu
130 135 140

Lys Val His Ala Glu Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Asp
145 150 155 160

Ile Ile Ser Thr Leu Leu Gly His Ala Pro Ser Thr Ala Glu Val Ala
165 170 175

Lys Ile Arg Lys Ser Ile Lys Thr Ser Tyr Arg Tyr Met Glu Leu Ala
180 185 190

Leu Asp Ala Ala Val Ala Ala Ala His Val Ser Phe Asp Glu Thr Ala
195 200 205

Ser Asn Ser Ser Thr Leu Gly Asp Leu Tyr Ala Ala
210 215 220

<210> 80
<211> 245
<212> PRT
<213> Acinetobacter bohemicus

<400> 80

Met Thr Ala Met Asn Gln Tyr Gly Thr Lys Leu Glu Ile Thr Ala His
1 5 10 15

Ser Glu Trp Ser Gln Lys Phe Trp Asp Glu Leu Phe Pro Ala Lys Glu
20 25 30

Arg Val Ser Lys His Pro Leu Phe Leu Asp Met Ala Asn Gly Ser Leu
35 40 45

Ser Leu Glu Cys Phe Arg Ser Thr Leu Leu Asn Phe Tyr Pro Leu Val
50 55 60

Ala His Phe Pro Ser Tyr Met Ala Gly Ala Leu Ala Lys Ala Thr Ser
65 70 75 80

Phe Ser Ser Asp Gly Val Ile Asp Thr Arg Asn Trp Leu Ile Gln Asn
85 90 95

Ile Lys Val Glu Glu Arg His Leu Tyr Trp Tyr Gln Asp Trp Ala Arg
100 105 110

Gly Phe Gly Val Thr Ala Glu Met Leu Asn Glu Val Arg Pro Pro Ala
115 120 125

Ala Met Asn Ala Val Asn His Phe Leu Trp Asp Ile Asn Phe Arg Gly
130 135 140

Thr Leu Ala Glu Ser Ile Ala Ala Thr Asn Leu Ala Ile Glu Trp Ala
145 150 155 160

Thr Gly Asp Trp Thr Ile Gln Val Tyr Lys Gly Ile Gln Thr Tyr Thr
165 170 175

Glu His Pro Glu Val Thr Ile Asn Lys Arg Ser Leu Ala Trp Leu Arg
180 185 190

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

Ile Lys Arg Leu Cys Asp Lys Asp Pro Ala Leu Gln Lys Lys Ala Phe
210 215 220

Leu Ala Ala Gln Glu Gly Leu Ala Tyr Tyr Glu Leu Ala Leu Asp Ala
225 230 235 240

Cys Tyr Lys Leu Arg
245

<210> 81
<211> 247
<212> PRT
<213> Myxococcus xanthus

<400> 81

Met Ser Ser Ala Ala Pro His Arg Tyr Ser Pro Pro Val Leu Thr Leu
1 5 10 15

Thr Ala His Pro Arg Trp Leu Glu Ser Met Leu Glu Ser Val Arg Asp
20 25 30

Glu Trp Asn Ala Ala Cys Trp Pro Pro Leu Phe Arg Ala Thr Ala Asp
35 40 45

Gly Gln Arg Pro Pro Leu Arg His Trp Arg Arg Val Leu Ser His Phe
    50   55   60

Phe Leu Ile Val Glu Ser Phe Pro Lys Tyr Met Gly Leu Ser Leu Ala
65   70   75   80

Lys Thr Thr Tyr Gly Gln Arg Pro Gly Asp Ala Ser Ala Arg Arg Trp
                85   90   95

Leu Leu Gln Asn Leu Gly Val Glu Ala Lys His Ala Glu Trp Phe Ile
            100   105   110

Asp Trp Met Arg Gly Ile Gly Leu Ala Pro Glu Asp Val Phe Thr Gln
        115   120   125

Arg Pro Leu Pro Glu Val Arg Ala Leu His Glu Phe Leu Leu Asp Thr
    130   135   140

Cys Ala His Gly Thr Leu Ala Glu Gly Val Ala Ala Ser Asn Trp Ala
145   150   155   160

Val Glu Gly Ile Thr Gly Val Trp Thr Arg Glu Val Val Glu Pro Phe
                165   170   175

Arg Ala Tyr Ala Glu Asp Gly Ala Arg Ile Asp Ala Tyr Ser Met Met
            180   185   190

Trp Leu Lys Val His Ala Arg Tyr Asp Asp Gln His Pro Glu Glu Ala
        195   200   205

Leu Glu Ile Ile Lys Leu Ser Thr Asp Ala Gly Thr Gly Glu Pro Phe
    210   215   220

Arg Val Gln Ala Ala Ala Arg Lys Ser Leu Gln Met Tyr Ala Ala Ala
225   230   235   240

Leu His Ala Cys Cys Asn Asp
                245

<210> 82
<211> 258
<212> PRT
<213> Myxococcus stipitatus

<400> 82

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

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Ala His Arg Tyr Ala Pro Pro Pro Leu Thr Pro Thr Pro His Pro Arg
            20                  25                  30

Trp Val Glu Ser Phe Leu Asp Ala Thr Arg Arg Asp Trp Asp Ala Ala
        35                  40                  45

Cys Trp Pro Pro Leu Phe Arg Asp Thr Ala Asp Gly Leu His Pro Pro
    50                  55                  60

Leu Ser Ser Trp Arg Arg Val Leu Ser Gln Phe Phe Leu Ile Val Glu
65                  70                  75                  80

Ser Phe Pro Lys Tyr Met Gly Leu Ser Leu Ala Lys Thr Thr Tyr Gly
                85                  90                  95

Gln Ser Pro Gly Asp Ala Ser Ile Arg Arg Trp Leu Leu Gln Asn Leu
            100                 105                 110

Gly Val Glu Ala Lys His Ala Glu Trp Tyr Ile Asp Trp Val Arg Ala
        115                 120                 125

Ile Gly Val Ser Pro Glu Ser Leu Phe Arg Leu Arg Pro Leu Pro Ala
    130                 135                 140

Val Gln Ala Leu His Thr His Leu Leu Asp Thr Cys Thr Arg Gly Ser
145                 150                 155                 160

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

Gly Val Trp Thr Arg Glu Val Met Glu Pro Phe Arg Asp Tyr Ala Ala
            180                 185                 190

Glu Gly Val Arg Val Asp Ala Ala Ser Met Met Trp Leu Lys Ala His
        195                 200                 205

Ala Arg Tyr Asp Asp Leu His Pro Val Glu Ala Leu Glu Ile Ile Lys
    210                 215                 220

Leu Ser Thr Asp Pro Arg Gly Asp Glu Pro Val Arg Val Leu Ala Ala
225                 230                 235                 240

Thr Arg Lys Ser Leu Arg Leu Tyr Thr Ala Ala Leu Arg Ala Cys Cys
                245                 250                 255

Ser Asp
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<210> 83
<211> 222
<212> PRT
<213> Myxococcus fulvus

<400> 83

Met Leu Glu Ser Leu Arg Glu Asp Trp Asn Thr Ala Cys Trp Pro Pro
1 5 10 15

Leu Phe Arg Ala Thr Ala Asp Gly Gln Arg Pro Pro Leu Arg His Trp
20 25 30

Arg Arg Val Leu Ala His Phe Phe Pro Ile Val Glu Ala Phe Pro Lys
35 40 45

Tyr Met Gly Leu Ser Leu Ala Lys Thr Thr Tyr Gly Gln Arg Pro Gly
50 55 60

Asp Ala Ser Ala Arg Arg Trp Leu Leu Gln Asn Leu Gly Val Glu Ala
65 70 75 80

Lys His Ala Glu Trp Phe Ile Asp Trp Met Arg Gly Ile Gly Leu Ala
85 90 95

Pro Glu Asp Val Phe Arg Gln Arg Pro Leu Pro Glu Val Arg Ala Leu
100 105 110

His Glu His Leu Leu Asp Thr Cys Ala Arg Gly Thr Leu Ala Glu Gly
115 120 125

Val Ala Ala Ser Asn Trp Ala Val Glu Gly Ile Thr Gly Val Trp Thr
130 135 140

Arg Glu Val Val Glu Pro Phe Arg Ala Tyr Ala Glu Glu Gly Ala Arg
145 150 155 160

Ile Asp Ala Tyr Ser Met Met Trp Leu Lys Val His Ala Arg Tyr Asp
165 170 175

Asp Gln His Pro Glu Glu Ala Leu Glu Ile Ile Lys Leu Ser Thr Asp
180 185 190

Ala Ser Ser Gly Glu Pro Phe Arg Val Gln Ala Ala Ala Arg Lys Ser
195 200 205

Leu Arg Met Tyr Ala Ala Ala Leu His Ala Cys Cys Arg Asp
210 215 220

<210> 84
<211> 252
<212> PRT
<213> Vogesella indigofera

<400> 84

Met Asn Arg Glu Phe Val Arg Ser Gly Ala Leu Arg Ser Pro His Ser
1 5 10 15

Tyr Pro Glu Trp Ala Gln Gln Leu Leu Ala Asp Cys Ala Ala Ala Arg
20 25 30

Gln Arg Val Val Arg His Glu Phe Tyr Gln Arg Leu Arg Asp Ala Glu
35 40 45

Leu Gly Asp Asp Ala Leu Arg Leu Phe Leu Ile Gly Val Trp Pro Val
50 55 60

Val Glu Gln Phe Pro Leu Tyr Met Ala Gln Asn Leu Leu Lys Thr Arg
65 70 75 80

Tyr Gly Arg His Arg Gly Glu Asp Met Ala Arg Arg Leu Leu Val Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Ala Asp Tyr Trp Leu Ala Trp Ala
100 105 110

Ala Ala Cys Gly Ile Ala Ala Thr Glu Leu Gln Ala Gln Arg Val Pro
115 120 125

Glu Pro Leu Gln Gln Leu Gly His Trp Cys Arg His Asn Ser Arg His
130 135 140

His Ser Leu Leu Leu Ala Leu Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Ala Thr Gly Glu Trp Thr Gln Leu Val Cys Ala Pro Gly Ile Tyr Glu
165 170 175

Ala Ser Leu Pro Ala Thr Gln Arg Gln Ser Ala Met Arg Trp Leu Lys
180 185 190

Val His Ala Arg Tyr Asp Asp Asp His Pro Trp Glu Ala Leu Asp Ile
195 200 205

Val Cys Thr Leu Ala Gly Arg Asp Ala Asp Ala Ser Thr Arg Arg Ala
210 215 220

Leu Gln Thr Ala Ile Gly Asn Ser Tyr His Tyr Met Gln Leu Val Leu
225   230   235   240

Asp Cys Cys Leu Gln Leu Glu Gln Ala Val Pro Gly
                245   250

<210> 85
<211> 256
<212> PRT
<213> Rudaea cellulosilytica

<400> 85

Met Asn Ser Arg Phe Glu Arg Thr Gly Pro Ile Asp Glu Leu Ser Ser
1   5   10   15

Tyr Pro Ala Trp Ala Gln Asp Met Val Asp Ser Cys Ala Asp Ala Lys
            20   25   30

Arg Glu Val Val Glu His Glu Leu Phe Ala Leu Met Arg Glu Ala Gln
        35   40   45

Leu Ser Thr Glu Ser Thr Ala Ser Phe Met Thr Gly Val Trp Pro Val
    50   55   60

Ile Glu Arg Phe Pro Ala Tyr Met Ser Ala Ser Leu Met Lys Thr Arg
65   70   75   80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Asp Trp Ala
            100   105   110

Glu Gly Ala Gly Val Ser Arg Asp Lys Val Leu Asn Gly Trp Val Pro
        115   120   125

Thr Asp Ala Met Val Leu Ala Asn Trp Cys Glu Glu Val Ser Thr Gly
    130   135   140

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

Ala Thr Gly Glu Trp Ser Gln Arg Val Tyr Glu Gly Ala Ala Tyr Arg
                165   170   175

Glu Ser Met Pro Thr Pro Gln Ala Leu Arg Trp Leu Lys Leu His Ala
            180   185   190

Ala Tyr Asp Asp Glu His Pro Trp Glu Ala Leu Glu Ile Val Cys Ala
195 200 205

Leu Val Gly Asn Asn Pro Val Pro Gln Gln Val Ala His Leu Arg Glu
210 215 220

Cys Val Arg Arg Ser Tyr Thr Ser Met Arg Ile Val Ile Asp Arg Cys
225 230 235 240

Leu Ala Ala Ser Arg Tyr Gly Met Asp Ile Leu Arg Glu Val Ala Ala
245 250 255

<210> 86
<211> 258
<212> PRT
<213> Rhodanobacter sp.

<400> 86

Met His Thr Pro Phe Glu Arg Thr Gly Pro Leu Thr Glu Leu Gly Ser
1 5 10 15

Tyr Pro Gln Trp Ala Gln Asp Met Val Ala Asp Cys Glu Ser Thr Lys
20 25 30

Gln Ser Val Leu Asp His Glu Leu Trp Ala Met Met Arg Glu Val Arg
35 40 45

Leu Gly Gln Thr Ser Thr Ala Ser Phe Met Val Gly Val Trp Pro Phe
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Arg
65 70 75 80

Tyr Gly Arg Ser Leu Gly Asp Asp Met Ala Arg Arg Trp Leu Val Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Ala Trp Ala
100 105 110

Glu Gly Ser Gly Val Pro Arg Glu Glu Val Leu Ser Ala Arg Pro Pro
115 120 125

His Gly Thr Gln Thr Leu Ala Asn Trp Cys Glu Glu Ile Ser Thr Ile
130 135 140

Gly Thr Leu Ala Ala Gly Met Ile Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Arg Pro Ile Tyr Glu Ser Thr Ala Tyr Ala
165 170 175

Glu Ser Phe Pro Pro Arg Thr Arg Thr Gly Ser Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Ile His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Leu Gly Arg Thr Pro Lys Ile Asp Glu Val Thr His
210 215 220

Leu Gly Glu Cys Val Arg Arg Ser Tyr Thr Ser Met Arg Ile Val Gly
225 230 235 240

Asp Leu Cys Met Gln Ala Arg Ser Pro Ser Thr Leu Met Lys Glu Val
245 250 255

Ala Ala

<210> 87
<211> 258
<212> PRT
<213> Rhodanobacter sp.

<400> 87

Met His Thr Arg Phe Glu Arg Thr Gly Pro Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Gln Trp Ala Gln Asp Met Val Val Asp Cys Glu Ser Thr Lys
20 25 30

Gln Ser Val Leu Asp His Glu Leu Trp Ala Met Met Arg Glu Val Arg
35 40 45

Leu Asp His Ala Ser Thr Ala Asn Phe Met Val Gly Val Trp Pro Phe
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Ala Trp Ala
100 105 110

Glu Gly Ser Gly Val Pro Arg Asp Asp Val Leu Asn Ala Arg Pro Pro
115 120 125

His Gly Thr Gln Thr Leu Ala Asn Trp Cys Glu Glu Ile Ser Ala Asn
130 135 140

Gly Thr Leu Ala Ala Gly Met Ile Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Arg Pro Ile Tyr Glu Ser Thr Ala Tyr Ala
165 170 175

Glu Ser Phe Pro Pro Gly Ile Arg Thr Gly Ser Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Ile His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Leu Gly Met Thr Pro Lys Ala Asp Glu Val Ala His
210 215 220

Leu Gly Glu Cys Val Arg Arg Ser Tyr Thr Ser Met Arg Ile Val Gly
225 230 235 240

Asp Leu Cys Met Gln Thr His Arg Pro Ser Thr Trp Met Lys Glu Ala
245 250 255

Ala Ala

<210> 88
<211> 258
<212> PRT
<213> Rhodanobacter sp.

<400> 88

Met His Thr Arg Phe Glu Arg Thr Gly Pro Leu Thr Glu Leu Ser Ser
1 5 10 15

Tyr Pro Gln Trp Ala Gln Asp Met Val Val Asp Cys Glu Ser Thr Lys
20 25 30

Gln Ser Val Leu Asp His Glu Leu Trp Ala Met Met Arg Glu Val Arg
35 40 45

Leu Asp His Ala Ser Thr Ala Asn Phe Met Val Gly Val Trp Pro Phe
50 55 60

Ile Glu Arg Phe Pro Ser Phe Met Ala Leu Asn Leu Leu Lys Thr Arg
65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Ala Trp Ala
100 105 110

Glu Gly Ser Gly Val Pro Arg Asp Asp Val Leu Asn Ala Arg Pro Pro
115 120 125

His Gly Thr Gln Thr Leu Ala Asn Trp Cys Glu Glu Ile Ser Ala Asn
130 135 140

Gly Thr Leu Ala Ala Gly Met Ile Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ser Arg Pro Ile Tyr Glu Ser Thr Ala Tyr Ala
165 170 175

Glu Ser Phe Pro Pro Arg Ile Arg Thr Gly Ser Leu Arg Trp Leu Gln
180 185 190

Leu His Ala Ala Tyr Asp Asp Ile His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Cys Thr Leu Leu Gly Met Thr Pro Lys Ala Asp Glu Val Ala His
210 215 220

Leu Gly Glu Cys Val Arg Arg Ser Tyr Thr Ser Met Arg Ile Val Gly
225 230 235 240

Asp Leu Cys Met Gln Thr His Arg Pro Ser Thr Trp Met Lys Glu Ala
245 250 255

Ala Ala

<210> 89
<211> 257
<212> PRT
<213> Rhodanobacter sp.

<400> 89

Met Asn Thr Arg Phe Glu Arg Thr Gly Pro Leu Thr Glu Leu Ser Ser
1 5 10 15

```
Tyr Pro Gln Trp Ala Gln Asp Met Val Ala Asp Cys Ala Ser Thr Lys
            20                  25                  30

Gln Lys Val Leu Asp His Glu Leu Trp Ala Arg Met Ala Asp Thr Thr
        35                  40                  45

Leu Asp Pro Val Ala Thr Ser Asn Phe Met Val Ala Val Trp Pro Phe
    50                  55                  60

Ile Glu Arg Phe Pro Ser Tyr Met Ala Leu Asn Leu Leu Lys Thr Arg
65                  70                  75                  80

Tyr Gly Arg Ser Pro Gly Asp Asp Leu Ala Arg Arg Trp Leu Val Arg
                85                  90                  95

Asn Ile Arg Val Glu Gln Asn His Ala Glu Tyr Trp Leu Ser Trp Ala
            100                 105                 110

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

Phe Gly Ser Gln Val Leu Ala Asp Trp Cys Glu Asp Ile Ser Ala His
    130                 135                 140

Gly Thr Leu Ala Ala Gly Met Leu Ala Thr Asn Tyr Ala Ile Glu Gly
145                 150                 155                 160

Val Thr Gly Glu Trp Ser Gln Pro Ile Tyr Glu Ser Gln Ile Tyr Ala
                165                 170                 175

Glu Ser Phe Pro Pro Asn Val Arg Thr Gly Ser Leu Arg Trp Leu Gln
            180                 185                 190

Leu His Ala Ala Tyr Asp Asp Ile His Pro Trp Glu Ala Leu Glu Ile
        195                 200                 205

Val Cys Thr Ile Val Gly Ala Ala Pro Lys Ala Val Glu Val Ala His
    210                 215                 220

Leu Gly Glu Cys Val Arg Arg Ser Tyr Thr Ser Met His Met Val Gly
225                 230                 235                 240

Asp Leu Cys Met Gln Ala His Arg Tyr Phe Asn Thr Thr Lys Ala Val
                245                 250                 255

Ala
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<210> 90
<211> 262
<212> PRT
<213> Crenobacter luteus

<400> 90

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Met Ser Pro Pro Phe Val Arg Thr Gly Pro Leu Thr Glu Ala Ala Ser
1               5                   10                  15

Tyr Pro Asp Trp Ala Gln Gln Leu Leu Leu Asp Cys His Ala Ala Lys
            20                  25                  30

Arg Arg Val Thr Gly His Glu Leu Tyr Leu Arg Met Arg Asp Ala Glu
        35                  40                  45

Leu Gly Pro Met Ala Met Gln Leu Phe Leu Val Gly Ala Trp Pro Val
    50                  55                  60

Val Glu Gln Phe Pro Gln Tyr Met Ala Gln Asn Leu Leu Lys Val Arg
65                  70                  75                  80

Tyr Gly Arg Gln Arg Gly Glu Asp Met Ala Arg Arg Phe Leu Ile His
                85                  90                  95

Asn Ile Arg Val Ala Gln Ser His Ala Glu His Trp Ile Ala Trp Ala
            100                 105                 110

Glu Ala Cys Gly Ile Gly Arg Ala Glu Leu His Ala Gln Arg Val Pro
        115                 120                 125

Ser Glu Met His Ala Leu Ser His Trp Cys Trp His Ile Cys Ala His
    130                 135                 140

Asp Pro Leu Trp Leu Ala Met Ala Ala Thr Asn Tyr Ala Ile Glu Asp
145                 150                 155                 160

Ala Thr Gly Asp Trp Ala Ala Leu Val Cys Ser Ser Gly Ala Tyr Glu
                165                 170                 175

Ala Ser Phe Ala Pro Gly Ala Arg Arg Arg Ala Thr Arg Trp Leu Thr
            180                 185                 190

Leu His Ala His Asp Asp Ala Pro Pro Trp Glu Ala Leu Glu Ile Val
        195                 200                 205

Cys Thr Leu Ile Gly Thr His Ala Asp Pro Ser Thr Val Ala Ala Leu
    210                 215                 220
```

Arg Asp Ala Ile Cys Lys Ser Tyr Asp Tyr Met Arg Leu Ile Leu Asp
225   230   235   240

Arg Cys Leu Gln Ala Glu Val Ser Arg Pro Pro Ala Ser Pro Arg Lys
                245   250   255

Ala Phe Val Gln Leu Gly
            260

<210> 91
<211> 262
<212> PRT
<213> Crenobacter luteus

<400> 91

Met Ser Pro Pro Phe Val Arg Thr Gly Pro Leu Thr Glu Ala Ala Ser
1   5   10   15

Tyr Pro Asp Trp Ala Gln Gln Leu Leu Leu Asp Cys His Ala Ala Lys
            20   25   30

Arg Arg Val Thr Gly His Glu Leu Tyr Leu Arg Met Arg Asp Ala Glu
        35   40   45

Leu Gly Pro Met Ala Met Gln Leu Phe Leu Val Gly Ala Trp Pro Val
    50   55   60

Val Glu Gln Phe Pro Gln Tyr Met Ala Gln Asn Leu Leu Lys Val Arg
65   70   75   80

Tyr Gly Arg Gln Arg Gly Glu Asp Met Ala Arg Arg Phe Leu Ile His
                85   90   95

Asn Ile Arg Val Ala Gln Ser His Ala Glu His Trp Ile Ala Trp Ala
            100   105   110

Glu Ala Cys Gly Ile Gly Arg Ala Glu Leu His Ala Gln Arg Val Pro
        115   120   125

Ser Glu Met His Ala Leu Ser His Trp Cys Trp His Ile Cys Ala His
    130   135   140

Asp Pro Leu Trp Leu Ala Met Ala Ala Thr Asn Tyr Ala Ile Glu Asp
145   150   155   160

Ala Thr Gly Asp Trp Ala Ala Leu Val Cys Ser Ser Gly Ala Tyr Glu
                165   170   175

Ala Ser Phe Ala Pro Gly Ala Arg Arg Arg Ala Thr Arg Trp Leu Thr
180 185 190

Leu His Ala His Asp Asp Ala Pro Pro Trp Glu Ala Leu Glu Ile Val
195 200 205

Cys Thr Leu Val Gly Thr His Ala Asp Pro Ser Thr Val Ala Ala Leu
210 215 220

Arg Asp Ala Ile Cys Lys Ser Tyr Asp Tyr Met Arg Leu Ile Leu Asp
225 230 235 240

Arg Cys Leu Gln Ala Glu Val Ser Arg Pro Pro Ala Ser Pro Arg Lys
245 250 255

Ala Phe Val Gln Leu Gly
260

<210> 92
<211> 264
<212> PRT
<213> Chromobacterium sp.

<400> 92

Met Ser Lys Glu Ile Gly Phe Val Arg Ser Gly Pro Leu Met Asp Leu
1 5 10 15

His Ser Tyr Pro Glu Trp Thr Arg Glu Leu Val Arg His Cys Asp Ala
20 25 30

Phe Lys Arg Gln Val Val Glu His Glu Leu Phe Arg Gln Met Arg Asp
35 40 45

Gly Val Leu Pro Ala Ala Ile His Gln Ala Phe Leu Arg Gly Gly Trp
50 55 60

Pro Val Ile Glu Gln Phe Pro Gln Tyr Met Ala Lys Asn Leu Leu Lys
65 70 75 80

Val Arg Tyr Gly Gln His Arg Gly His Asp Met Ala Arg Arg Tyr Leu
85 90 95

Ile Arg Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Val Gln
100 105 110

Trp Ala Ala Ala Ser Gly Val Asp Thr Asp Ser Leu Leu Arg Asn Pro
115 120 125

Gln Ala Leu Glu Thr Leu Ser Leu Ser His Trp Cys His Gln Val Cys
130 135 140

Glu Arg Glu Ser Leu Glu Val Ala Met Ala Ala Thr Asn Tyr Ala Ile
145 150 155 160

Glu Gly Ala Thr Gly Glu Trp Cys Ala Ala Val Cys Ser Lys Glu Asp
165 170 175

Tyr Ala Arg Gln Phe Pro Lys Glu Lys Arg Ala Lys Ala Met Lys Trp
180 185 190

Leu Ala Leu His Ala His Tyr Asp Asp Glu His Pro Trp Glu Ala Leu
195 200 205

Glu Ile Ile Val Thr Leu Val Gly Glu Asn Pro Asn Ala Gln Gln Val
210 215 220

Ala Glu Leu Arg His Ala Ile Cys Gln Ser His Arg Tyr Met Arg Leu
225 230 235 240

Leu Leu Asp His Tyr Met Ser Gln Pro Ala Pro Glu Thr Cys Ala Arg
245 250 255

Val Cys Ala Glu Pro Ala Leu Ala
260

<210> 93
<211> 261
<212> PRT
<213> Aquitalea sp.

<400> 93

Met Lys Asp Gln His Gln Phe Val Arg Thr Gly Pro Leu Met Glu Val
1 5 10 15

Ala Ser Tyr Pro Glu Trp Thr Gln Glu Met Val His Tyr Cys Asp Arg
20 25 30

Phe Lys Ser Glu Val Val Glu His Asp Leu Phe Thr Gln Met Lys Glu
35 40 45

Ala Arg Leu Glu His Ser Ile His Lys Ala Phe Leu Ser Gly Gly Trp
50 55 60

Pro Val Ile Asp Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys
65 70 75 80

```
Ile Arg Tyr Gly Gln Gly Glu Gly His Asp Met Ala Arg Arg Tyr Leu
                85                  90                  95

Ile Arg Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Val Asn
            100                 105                 110

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

His Ala Leu Glu Thr Leu Ser Leu Ser Gln Trp Cys Trp Gln Val Cys
    130                 135                 140

Asp Arg Glu Ser Leu Ala Val Ala Met Ala Ala Thr Asn Tyr Ala Ile
145                 150                 155                 160

Glu Gly Ala Thr Gly Glu Trp Ser Ala Arg Val Cys Ser Glu Asp Arg
                165                 170                 175

Tyr Ala Asn Leu Phe Asp Glu Glu Val Arg Gly Lys Ala Met Lys Trp
            180                 185                 190

Leu Lys Leu His Ala Lys Tyr Asp Asp Ala His Pro Trp Glu Ala Leu
        195                 200                 205

Glu Ile Ile Val Thr Leu Val Gly Leu His Pro Ser Gln Glu Thr Ile
    210                 215                 220

Thr Lys Leu Arg Asn Ala Ile Cys Lys Ser His Gln Phe Met Arg Leu
225                 230                 235                 240

Leu Leu Asp His Tyr Met Arg Pro Ala Thr Gln Leu Gly Gly Arg Gln
                245                 250                 255

Gln Leu Ala Leu Ala
            260


<210>  94
<211>  261
<212>  PRT
<213>  Aquitalea magnusonii

<400>  94

Met Ser Asp Gln Gln Pro Phe Val Arg Thr Gly Pro Leu Met Asp Val
1               5                   10                  15

Ser Ser Tyr Pro Ala Trp Thr Gln Asp Leu Val Tyr His Cys Asp Arg
            20                  25                  30
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Tyr Lys Ser Glu Val Val Glu His Glu Leu Phe Gly Arg Met Gln Gln
        35                  40                  45

Ala Cys Leu Asp His Ala Thr His Lys Ala Phe Leu Ser Gly Gly Trp
    50                  55                  60

Pro Val Ile Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys
65                  70                  75                  80

Ile Arg Tyr Gly Gln Gly Pro Gly Gln Asp Met Ala Arg Arg Tyr Leu
                85                  90                  95

Ile Arg Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Val Asn
            100                 105                 110

Trp Ala Ala Ala Ser Gly Val Asp Val Pro Ala Met Leu His Gly Thr
        115                 120                 125

His Ala Leu Glu Thr Leu Cys Leu Ser Gln Trp Cys Trp Gln Val Cys
    130                 135                 140

Asp Arg Asp Ser Leu Ala Val Ala Ile Ala Ala Thr Asn Tyr Ala Ile
145                 150                 155                 160

Glu Gly Ala Thr Gly Glu Trp Ser Ala Arg Val Cys Ala Glu Pro His
                165                 170                 175

Tyr Ala Gln Leu Phe Asp Glu Thr Val Arg Ala Lys Ala Met Lys Trp
            180                 185                 190

Leu Lys Leu His Ala Lys Tyr Asp Asp Ala His Pro Trp Glu Ala Leu
        195                 200                 205

Glu Ile Ile Val Thr Leu Val Gly Leu Asn Pro Ser Ala Glu Thr Ile
    210                 215                 220

Ser Arg Leu Arg His Ala Ile Cys Arg Ser His Gln Phe Met Arg Met
225                 230                 235                 240

Leu Leu Asp Tyr Tyr Met Arg Ser Ala Thr Pro Pro Val Ala Ala Gly
                245                 250                 255

Leu Met Arg Pro Ala
            260
```

<210> 95

<211> 264
<212> PRT
<213> Chromobacterium haemolyticum

<400> 95

Met Ser Lys Glu Ile Gly Phe Val Arg Ser Gly Pro Leu Met Asp Leu
1 5 10 15

His Ser Tyr Pro Glu Trp Thr Arg Glu Leu Val Arg His Cys Asp Ala
20 25 30

Phe Lys Arg Gln Val Val Glu His Glu Leu Phe Arg Gln Met Arg Asp
35 40 45

Gly Val Leu Pro Asn Ala Val His Gln Ala Phe Leu Arg Gly Gly Trp
50 55 60

Pro Val Ile Glu Gln Phe Pro Gln Tyr Met Ala Lys Asn Leu Leu Lys
65 70 75 80

Val Arg Tyr Gly Gln His Arg Gly His Asp Met Ala Arg Arg Tyr Leu
85 90 95

Ile Arg Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Val Gln
100 105 110

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

Gln Ala Leu Glu Thr Leu Ser Leu Ser His Trp Cys His Gln Ile Cys
130 135 140

Glu Arg Glu Ser Leu Glu Val Ala Met Ala Ala Thr Asn Tyr Ala Ile
145 150 155 160

Glu Gly Ala Thr Gly Glu Trp Cys Ala Ala Val Cys Ser Lys Glu Asp
165 170 175

Tyr Ala Arg Gln Phe Pro Lys Glu Lys Arg Ala Lys Ala Met Lys Trp
180 185 190

Leu Ala Leu His Ala His Tyr Asp Asp Glu His Pro Trp Glu Ala Leu
195 200 205

Glu Ile Ile Val Thr Leu Val Gly Glu Asp Pro Ser Ser Arg Gln Val
210 215 220

Ala Glu Leu Arg His Ala Ile Cys Gln Ser His Arg Tyr Met Arg Leu

225 230 235 240

Leu Leu Asp His Tyr Met Ser Gln Pro Ala Pro Glu Ile Cys Ala Arg
245 250 255

Pro Cys Ala Glu Pro Ala Leu Ala
260

<210> 96
<211> 264
<212> PRT
<213> Chromobacterium sp.

<400> 96

Met Ser Lys Glu Ile Gly Phe Val Arg Ser Gly Pro Leu Met Asp Leu
1 5 10 15

His Ser Tyr Pro Glu Trp Thr Arg Glu Leu Val Arg His Cys Asp Ala
20 25 30

Phe Lys Arg Gln Val Val Glu His Glu Leu Phe Arg Gln Met Arg Asp
35 40 45

Gly Val Leu Pro Ala Ala Ile His Gln Ala Phe Leu Arg Gly Gly Trp
50 55 60

Pro Val Ile Glu Gln Phe Pro Gln Tyr Met Ala Lys Asn Leu Leu Lys
65 70 75 80

Val Arg Tyr Gly Gln His Arg Gly His Asp Met Ala Arg Arg Tyr Leu
85 90 95

Ile Arg Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Val Gln
100 105 110

Trp Ala Ala Ala Ser Gly Val Asp Ala Asp Ser Leu Leu Arg Asn Pro
115 120 125

Gln Ala Leu Glu Thr Leu Ser Leu Ser His Trp Cys His Gln Val Cys
130 135 140

Glu Arg Glu Ser Leu Glu Val Ala Met Ala Ala Thr Asn Tyr Ala Ile
145 150 155 160

Glu Gly Ala Thr Gly Glu Trp Cys Ala Ala Val Cys Ser Lys Glu Asp
165 170 175

Tyr Ala Arg Gln Phe Pro Lys Glu Lys Arg Ala Lys Ala Met Lys Trp

180 185 190

Leu Ala Leu His Ala His Tyr Asp Asp Glu His Pro Trp Glu Ala Leu
195 200 205

Glu Ile Ile Val Thr Leu Val Gly Glu Asp Pro Ser Ala Arg Gln Val
210 215 220

Ala Glu Leu Arg His Ala Ile Cys Gln Ser His Arg Tyr Met Arg Leu
225 230 235 240

Leu Leu Asp His Tyr Met Ser Gln Pro Thr Pro Glu Ala Cys Ala Arg
245 250 255

Val Ser Ala Glu Pro Ala Leu Ala
260

<210> 97
<211> 252
<212> PRT
<213> Massilia glaciei

<400> 97

Met Val Glu Glu Phe Thr Arg Thr Gly Pro Tyr Met Glu Leu Gly Ser
1 5 10 15

Tyr Pro Val Trp Ala Gln Glu Met Met His Ser Thr Val Lys Ala Lys
20 25 30

His Lys Val Val Asp His Glu Leu Phe Ala Met Met Lys Glu Ala Ala
35 40 45

Leu Pro Glu Pro Glu Thr Asn Lys Phe Leu Val Gly Gly Trp Pro Val
50 55 60

Ile Glu Gln Phe Pro Gln Phe Met Ala Val Asn Leu Cys Lys Val Gln
65 70 75 80

Tyr Gly Arg Ser Arg Gly Glu Asp Met Ala Arg Lys Tyr Leu Met Arg
85 90 95

Asn Ile Arg Val Glu Gln His His Ala Asp Leu Trp Thr Gln Trp Ala
100 105 110

Ala Ala Cys Gly Val Asp Lys Lys Asp Leu Leu Asp Ser Ala Val Pro
115 120 125

Val Glu Thr Gln Ala Leu Asn His Trp Cys Trp His Ser Cys Glu Arg

130 135 140

Ser Ser Leu Ala Thr Ser Met Ala Ala Thr Asn Leu Ala Ile Glu Gly
145 150 155 160

Ala Thr Gly Glu Trp Ser Thr Leu Ile Cys Ser Ser Asp Thr Tyr Glu
165 170 175

Asn Ser Phe Pro Pro Glu Leu Arg Lys Gln Ala Thr Arg Trp Leu Arg
180 185 190

Leu His Ala Gln Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Ile Cys Ser Leu Ile Gly Asn Arg Ala Glu Pro Lys Tyr Val Ala Tyr
210 215 220

Leu Ala Gln Cys Ile Ser Asn Ser Tyr Glu Tyr Met Ala Leu Ser Leu
225 230 235 240

Asp Arg Cys Met Ser His Glu Pro Val Ala Ala His
245 250

<210> 98
<211> 244
<212> PRT
<213> Burkholderia sp.

<400> 98

Met Asp Pro Thr Phe Gln Arg Val Gly Asp Leu Lys Asp Ile Ala Ser
1 5 10 15

Tyr Pro Ala Trp Leu Gly Asp Val Leu Asn Asp Thr Ser Glu Ala Lys
20 25 30

Gln Ala Ile Val Lys His Pro Ile Phe Ala Ala Met Arg Glu Ala Lys
35 40 45

Leu Glu Ala Arg Gln Ala Glu Ala Phe Leu Val Asn Gly Trp Pro Val
50 55 60

Val Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Gln Lys Val Arg
65 70 75 80

Tyr Gly His Ser Arg Gly Glu Asp Leu Ala Arg Arg Tyr Leu Thr Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Ala Asp Tyr Trp Val Asp Trp Ala

100 105 110

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

Thr Leu Ala Tyr Ala Leu Ser His Trp Cys Trp Lys Ser Ser Ser Thr
130 135 140

Asp Pro Leu Ala Ala Ser Ile Ala Ala Thr Asn Phe Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Glu Trp Ala Thr Leu Val Cys Ser Ser Glu Thr Tyr Ala
165 170 175

Asn Ser Phe Pro Val Ser Ile Arg Arg Lys Ala Met Arg Trp Leu Ser
180 185 190

Leu His Ala His Tyr Asp Asp Ala His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Val Ala Thr Leu Leu Gly Asn Ala Pro Gly Val Asp Glu Val His Glu
210 215 220

Val Arg Arg Ser Ile Ala Met Ser Tyr Glu Tyr Phe Lys Met Ser Leu
225 230 235 240

Asp Cys Cys Leu

<210> 99
<211> 248
<212> PRT
<213> Janthinobacterium sp.

<400> 99

Met Tyr Glu Gln Phe Gln Arg Ser Gly Pro Leu Met Asp Leu Asn Ser
1 5 10 15

Tyr Pro Ala Trp Ala Gln Asp Met Val Leu Ala Thr Ala Pro Ala Lys
20 25 30

Asn Lys Val Val Ala His Glu Leu Phe Ala Arg Met Arg Glu Ala Ser
35 40 45

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

Ile Glu Gln Phe Pro Gln Tyr Met Ala Val Asn Leu Cys Lys Ile Gln

65 70 75 80

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

Asn Ile Arg Val Glu Gln Asn His Ala Asp His Trp Val Glu Trp Ala
100 105 110

Lys Ala Cys Gly Ile Ser Met Arg Asp Leu Phe Asp Ser Gln Ala Pro
115 120 125

Val Glu Ser Gln Ala Leu Asn His Trp Cys Trp His Ser Cys Glu Arg
130 135 140

Ala Ser Leu Ala Thr Ser Met Ala Val Thr Asn Leu Ala Ile Glu Gly
145 150 155 160

Ala Thr Gly Glu Trp Ala Asn Leu Ile Cys Ser Ser Asp Ala Tyr Glu
165 170 175

Asn Ser Phe Ala Pro Glu Leu Arg Arg Pro Ala Thr Arg Trp Leu Arg
180 185 190

Leu His Ala Gln Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Glu Ile
195 200 205

Ile Cys Ser Leu Ile Gly Arg Arg Ala Glu Pro Lys Tyr Val Asp Ile
210 215 220

Leu Val Gln Gly Leu Ser Asn Ser Tyr Gln Tyr Met Ala Leu Ser Leu
225 230 235 240

Asp Arg Ser Met Ala Pro Ser Gly
245

<210> 100
<211> 244
<212> PRT
<213> Janthinobacterium agaricidamnosum

<400> 100

Met Ser Asn Glu Phe Lys Arg Arg Gly Pro Leu Lys Glu Ala Glu Ser
1 5 10 15

Tyr Pro Pro Trp Leu Gln Gln Val Leu Arg Asp Thr Ser Gln Ala Arg
20 25 30

Gln Leu Val Ala Gly His Gly Val Phe Ala Gly Met Arg Asp Ala Arg

35 40 45

Leu Gly Ala Arg Glu Phe Tyr Ala Phe Phe Val Asn Gly Trp Pro Val
50 55 60

Val Glu Gln Phe Pro Gln Tyr Met Ala Met Asn Leu Leu Lys Ala Arg
65 70 75 80

Phe Gly Arg Ser Glu Gly Glu Asp Met Ala Arg Arg Tyr Leu Thr Arg
85 90 95

Asn Ile Arg Val Glu Gln Asn His Ala Asp Tyr Trp Val Asp Trp Ala
100 105 110

Gly Met His Asp Val Ser Lys Ser Thr Leu Leu Arg Ala Glu Gly Pro
115 120 125

Pro Ala Ala Phe Ala Leu Ser His Trp Cys Trp Ser Ser Ser Ser Ala
130 135 140

Asp Leu Leu Ala Gln Ser Met Ala Ala Thr Asn Tyr Ala Ile Glu Gly
145 150 155 160

Val Thr Gly Asp Trp Ala Thr Leu Val Cys Ser Ala Ser His Tyr Glu
165 170 175

Asp Ser Phe Pro Ala Ala Ser Arg Lys Lys Ala Met Arg Trp Leu Gln
180 185 190

Leu His Ala His Tyr Asp Asp Ala His Pro Trp Glu Ala Leu Asp Ile
195 200 205

Val Ala Thr Leu Leu Gly Ser Glu Pro Ser Gln Glu Ser Ile Asp Gly
210 215 220

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

Asp Cys Cys Val

<210> 101
<211> 249
<212> PRT
<213> Janthinobacterium sp.

<400> 101

Met Asn Glu Lys Phe Val Arg Asn Gly Pro Leu Met Glu Leu Asp Ser

```
1               5                   10                  15

Tyr Pro Arg Trp Ala Gln Asp Met Met Leu Ser Thr Leu Glu Ala Lys
            20                  25                  30

Glu Lys Val Val Lys His Asp Leu Phe Ala Met Met Arg Asp Ala Val
        35                  40                  45

Leu Thr Pro Lys Ala Met Arg Asn Phe Leu Ile Gly Gly Trp Pro Val
    50                  55                  60

Val Val Gln Phe Pro Gln Phe Met Ala Val Asn Leu Cys Lys Ile Gln
65                  70                  75                  80

Tyr Gly Arg Ser Leu Gly Glu Asn Met Ala Arg Lys Tyr Leu Met Lys
                85                  90                  95

Asn Ile Arg Val Glu Gln Asn His Ala Glu His Trp Val Glu Trp Ala
            100                 105                 110

Lys Ala Cys Ala Val Ser Glu Arg Asp Leu Leu Asp Ser Tyr Leu Pro
        115                 120                 125

Val Glu Ser Gln Ala Leu Ser His Trp Cys Trp His Ser Ser Glu His
    130                 135                 140

Thr Ser Leu Ala Thr Ser Met Ala Ala Thr Asn Leu Ala Ile Glu Gly
145                 150                 155                 160

Ala Thr Gly Glu Trp Ala Ser Leu Val Cys Ser Ala Pro Asp Tyr Glu
                165                 170                 175

Asn Ser Phe Ala Pro Glu Glu Arg Lys Lys Ala Met Arg Trp Leu Lys
            180                 185                 190

Leu His Ala His Tyr Asp Asp Thr His Pro Trp Glu Ala Leu Asp Ile
        195                 200                 205

Ile Ala Ser Leu Ile Gly Trp Glu Ile Glu Pro Lys Tyr Ala Glu Leu
    210                 215                 220

Leu Gly Gln Cys Val Met Asn Ser Tyr Lys Cys Met Thr Leu Ser Leu
225                 230                 235                 240

Asn Cys Tyr Leu Ser Glu Ile Cys Gly
                245
```

<210> 102
<211> 252
<212> PRT
<213> Rivicola pingtungensis

<400> 102

Met Asn Ala Pro Phe Ser Arg Thr Gly Pro Leu Met Glu Leu Ser Ser
1 5 10 15

Tyr Pro Asp Trp Ala Arg Gln Leu Val Glu Asp Cys Ala Ala Asp Arg
20 25 30

Ala Arg Val Thr Gln His Val Leu Phe Gln Arg Met Arg Asp Ala Thr
35 40 45

Leu Pro Tyr Pro Ile Met Arg Tyr Phe Leu Ile Gly Val Trp Pro Val
50 55 60

Ile Glu Gln Phe Pro Gln Tyr Met Ala Phe Asn Leu Leu Lys Val Arg
65 70 75 80

Tyr Gly Arg His Pro Gly Glu Asp Leu Ala Arg Thr Trp Leu Ile Arg
85 90 95

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Gln Ser Phe Ala Pro Ala Glu Arg Val Arg Ala Met Arg Trp Leu Lys
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Leu Ala Ser Gly Val Lys Arg Glu Asp Leu Met Phe Ser Pro Val Pro
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Val Pro Met Leu Ala Leu Cys His Trp Cys Trp His Thr Cys Asp Arg
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Ala Thr Gly Glu Trp Ala Leu Lys Val Cys Ser Arg Asp Leu Tyr Glu
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Gln Ser Phe Thr Pro Ala His Arg Ala Lys Ala Met Arg Trp Leu Lys
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Ile Cys Thr Leu Leu Gly Asn Asn Pro Thr Ala Arg Asp Phe Ala His
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Asp Tyr Ser Leu Asn Ala Glu Gln Val Ala Thr Ile Pro Gly Gln Leu
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Leu Ser Leu Val Tyr Pro Glu Glu Arg Lys Arg Ala Ala
            260                 265
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Claims

1. A hand-dishwashing composition comprising:

   a) a surfactant system comprising at least one anionic surfactant; and
   b) a non-heme fatty acid decarboxylase; wherein said decarboxylase comprises an amino acid selected from the group consisting of: a) leucine or isoleucine at position 41, b) alanine at position 57, c) glycine, alanine, isoleucine, leucine, valine, serine, or threonine at position 239, and d) combinations thereof; wherein said positions are numbered with reference to SEQ ID NO: 1; and wherein said decarboxylase catalyzes the conversion of at least one fatty acid selected from the group consisting of: palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, and mixtures thereof.

2. The composition according to claim 1, wherein said decarboxylase comprises a polypeptide sequence having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 100% identity to one or more sequences selected from the group consisting of: SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, and their functional fragments thereof.

3. The composition according to claim 2, wherein said decarboxylase comprises a polypeptide sequence having at least 80%, 90%, 95%, 98%, 100% identity to one or more sequences selected from the group consisting of: SEQ ID NO: 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and their functional fragments; preferably comprising a polypeptide sequence having at least 80%, 90%, 95%, 98%, 100% identity to SEQ ID NO: 4.

4. The composition according to any preceding claim, wherein the composition further comprises one or more co-enzymes selected from the group consisting of: fatty-acid peroxidases (EC 1.11.1.3), unspecific peroxygenases (EC 1.11.2.1), plant seed peroxygenases (EC 1.11.2.3), fatty acid peroxygenases (EC1.11.2.4), linoleate diol synthases (EC 1.13.11.44), 5,8-linoleate diol synthases (EC 1.13.11.60 and EC 5.4.4.5), 7,8-linoleate diol synthases (EC 1.13.11.60 and EC 5.4.4.6), 9,14-linoleate diol synthases (EC 1.13.11.B1), 8,11-linoleate diol synthases, oleate diol synthases, other linoleate diol synthases, unspecific monooxygenase (EC 1.14.14.1), alkane 1-monooxygenase (EC 1.14.15.3), oleate 12-hydroxylases (EC 1.14.18.4), fatty acid amide hydrolase (EC 3.5.1.99), oleate hydratases (EC 4.2.1.53), linoleate isomerases (EC 5.2.1.5), linoleate (10E,12Z)-isomerases (EC 5.3.3.B2), fatty acid decarboxylases (OleT-like), alpha-dioxygenases, amylases, lipases, proteases, cellulases, and mixtures thereof; preferably fatty-acid peroxidases (EC 1.11.1.3), unspecific peroxygenases (EC 1.11.2.1), plant seed peroxygenases (EC 1.11.2.3), and fatty acid peroxygenases (EC1.11.2.4), heme fatty acid decarboxylases (OleT-like), alpha-dioxygenases, and mixtures thereof.

5. The composition according to any preceding claim, wherein said one or more non-heme fatty acid decarboxylases are present in an amount of from 0.0001 wt% to 1 wt%, preferably from 0.001 wt% to 0.2 wt%, by weight of the hand dish-washing composition, based on active protein.

6. The composition according to any preceding claims, wherein the composition comprises from 5% to 50%, preferably 8% to 45%, more preferably from 15% to 40%, by weight of the total composition of a surfactant system.

7. The composition according to any preceding claims, wherein the anionic surfactant comprises alkyl sulphated anionic surfactant selected from the group consisting of: alkyl sulphate, alkyl alkoxy sulphate, and mixtures thereof.

8. The composition according to claim 7, wherein the alkyl sulphated anionic surfactant has an average alkyl chain length of from 8 to 18, preferably from 10 to 14, more preferably from 12 to 14, most preferably from 12 to 13 carbon atoms.

9. The composition according to any of claims 7 or 8, wherein the alkyl sulphated anionic surfactant has an average degree of alkoxylation, of less than 5, preferably less than 3, more preferably from 0.5 to 2.0, most preferably from 0.5 to 0.9.

10. The composition according to any of claims 7 to 9, wherein the alkyl sulphated anionic surfactant has a weight average degree of branching of more than 10%, preferably more than 20%, more preferably more than 30%, even

more preferably between 30% and 60%, most preferably between 30% and 50%.

11. The composition according to any preceding claims, wherein the surfactant system further comprises a co-surfactant, wherein the co-surfactant is selected from the group consisting of: an amphoteric surfactant, a zwitterionic surfactant, and mixtures thereof.

12. The composition according to claim 11, wherein the co-surfactant is an amphoteric surfactant, preferably an amphoteric surfactant selected from amine oxide surfactant, more preferably wherein the amine oxide surfactant is selected from the group consisting of: alkyl dimethyl amine oxide, alkyl amido propyl dimethyl amine oxide, and mixtures thereof.

13. The composition according to any of claims 11 or 12, wherein the weight ratio of the anionic surfactant to the co-surfactant is from 1:1 to 8:1, preferably from 2:1 to 5:1, more preferably from 2.5:1 to 4:1.

14. A method of manually washing dishware comprising the steps of delivering a detergent composition according to any preceding claims into a volume of water to form a wash solution and immersing the dishware in the solution.

15. The method according to claim 14, wherein the non-heme fatty acid decarboxylase is present at a concentration of from 0.005 ppm to 15 ppm, preferably from 0.02 ppm to 0.5 ppm, in an aqueous wash liquor during the washing process.

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EUROPEAN SEARCH REPORT

Application Number
EP 19 19 9988

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X	EP 3 511 403 A1 (PROCTER & GAMBLE [US]) 17 July 2019 (2019-07-17) * paragraph [0036]; claims 1-15; example 2 *	1-15	INV. C11D3/386
X	WO 2017/196786 A1 (PROCTER & GAMBLE [US]) 16 November 2017 (2017-11-16) * page 6, line 3 - line 8; sequence 2 *	1-15	
A	CN 104 643 884 A (HE YE) 27 May 2015 (2015-05-27) * claim 1; examples 1-3 *	1-15	
A,D	US 10 000 775 B2 (UNIV CALIFORNIA [US]) 19 June 2018 (2018-06-19) * claims 1-20 *	1-15	
A	ZHU ZHIWEI ET AL: "Enabling the synthesis of medium chain alkanes and 1-alkenes in yeast", METABOLIC ENGINEERING, vol. 44, 20 September 2017 (2017-09-20), pages 81-88, XP085285777, ISSN: 1096-7176, DOI: 10.1016/J.YMBEN.2017.09.007 * page 86 *	1-15	

TECHNICAL FIELDS SEARCHED (IPC)
C11D

The present search report has been drawn up for all claims

1

Place of search	Date of completion of the search	Examiner
The Hague	12 March 2020	van Klompenburg, Wim

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

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12-03-2020

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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

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