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(54) Title: DETERGENT COMPOSITION COMPRISING PROTEASE VARIANTS

(57) Abstract: The present invention relates to protease variants and methods for obtaining protease variants. The present invention also relates to polynucleotides encoding the variants; nucleic acid constructs, vectors, and host cells comprising the polynucleotides; and methods of using the variants.

## DETERGENT COMPOSITION COMPRISING PROTEASE VARIANTS

### Reference to a Sequence Listing

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

### Background of the Invention

#### Field of the Invention

The present invention relates to novel protease variants exhibiting alterations relative to the parent protease in one or more properties including: wash performance, detergent stability and/or storage stability. The variants of the invention are suitable for use in e.g. cleaning or detergent compositions, such as laundry detergent compositions and dish wash compositions, including automatic dish wash compositions. The present invention also relates to isolated DNA sequences encoding the variants, expression vectors, host cells, and methods for producing and using the variants of the invention.

#### Description of the Related Art

Enzymes have been used within the detergent industry as part of washing formulations for many decades. Proteases are from a commercial perspective the most relevant enzyme in such formulations, but other enzymes including lipases, amylases, cellulases, hemicellulases or mixtures of enzymes are also often used. To improve the cost and/or the performance of proteases there is an ongoing search for proteases with altered properties, such as increased activity at low temperatures, increased stability, increased specific activity at a given pH, altered Ca<sup>2+</sup> dependency, increased stability in the presence of other detergent ingredients (e.g. bleach, surfactants etc.) etc. One family of proteases, which are often used in detergents, are the subtilases. This family has previously been further grouped into 6 different sub-groups by Siezen RJ and Leunissen JAM, 1997, Protein Science, 6, 501-523. One of these sub-groups is the Subtilisin family which includes subtilases such as BPN', subtilisin 309 (SAVINASE<sup>®</sup>, Novozymes A/S), subtilisin Carlsberg (ALCALASE<sup>®</sup>, Novozymes A/S), subtilisin S41 (a subtilase from the psychrophilic Antarctic *Bacillus* TA41, Davail S et al. 1994, The Journal of Biological Chemistry, 269(26), 99. 17448-17453) and subtilisin S39 (a subtilase from the psychrophilic Antarctic *Bacillus* TA39, Narinx E et al. 1997, Protein Engineering, 10 (11), pp. 1271-1279). TY145 is a subtilase from *Bacillus* sp. TY145, NCIMB 40339, which was first described in WO 92/17577 (Novozymes A/S) and in the later application WO2004/067737 (Novozymes A/S) disclosing the three-dimensional structure and the use of protein engineering to alter functionality of a TY-145 subtilase.

### Summary of the Invention

The present invention relates to protease variants, comprising an alteration at one or more (e.g., several) positions corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant have protease activity and wherein the variants has an amino acid sequence which is at least 75 % identical to the mature polypeptide of SEQ ID NO 2 or to SEQ ID NO: 3.

The present invention relates to a method for obtaining a protease variant, comprising introducing into a parent protease a substitution at one or more positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has an amino acid sequence which is at least 75 %, at least 80%, at least 85%, at least 90% or at least 95% identical to SEQ ID NO 3; and recovering the variant. The present invention also relates to isolated polynucleotides encoding the variants; nucleic acid constructs, vectors, and host cells comprising the polynucleotides; and methods of producing the variants.

### Overview of sequences listing

SEQ ID NO 1 = is the DNA sequence of TY-145 protease isolated from *Bacillus sp.*

SEQ ID NO 2 = is the amino acid sequence as deduced from SEQ ID NO: 1.

SEQ ID NO 3 = is the amino acid sequence of the mature TY145.

### Definitions

The term "protease" is defined herein as an enzyme that hydrolyses peptide bonds. It includes any enzyme belonging to the EC 3.4 enzyme group (including each of the thirteen subclasses thereof). The EC number refers to Enzyme Nomenclature 1992 from NC-IUBMB, Academic Press, San Diego, California, including supplements 1-5 published in Eur. J. Biochem. 1994, 223, 1-5; Eur. J. Biochem. 1995, 232, 1-6; Eur. J. Biochem. 1996, 237, 1-5; Eur. J. Biochem. 1997, 250, 1-6; and Eur. J. Biochem. 1999, 264, 610-650; respectively. The term "subtilases" refer to a sub-group of serine protease according to Siezen *et al.*, *Protein Engng.* 4 (1991) 719-737 and Siezen *et al.* *Protein Science* 6 (1997) 501-523. Serine proteases or serine peptidases is a subgroup of proteases characterised by having a serine in the active site, which forms a covalent adduct with the substrate. Further the subtilases (and the serine proteases) are characterised by having two active site amino acid residues apart from the serine, namely a histidine and an aspartic acid residue. The subtilases may be divided into 6 sub-divisions, i.e. the Subtilisin family, the Thermitase family, the Proteinase K family, the Lantibiotic peptidase family, the Kexin family and the Pyrolysins family. The term "protease activity" means a proteolytic activity (EC 3.4). Proteases of the invention are endopeptidases (EC 3.4.21). There are several protease activity types: The three main activity types are: trypsin-like where there is cleavage of amide substrates following Arg or Lys at P1, chymotrypsin-like where cleavage occurs following one of the hydrophobic amino acids at P1, and elastase-like with cleavage following an Ala at P1. For purposes of the present invention, protease

activity is determined according to the procedure described in "Materials and Methods" below. The protease variants of the present invention have at least 20%, *e.g.*, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the protease activity of the mature polypeptide with SEQ ID NO: 3.

The term "parent" or protease parent means a protease to which an alteration is made to produce the enzyme variants of the present invention. Thus the parent is a protease having the identical amino acid sequence of said variant but not having the alterations at one or more of said specified positions. It will be understood, that in the present context the expression "having identical amino acid sequence" relates to 100 % sequence identity. The parent may be a naturally occurring (wild-type) polypeptide or a variant thereof. In a particular embodiment the parent is a protease with at least 70%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, *e.g.* at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6 or 100% identity to a polypeptide with SEQ ID NO: 3.

The term "protease variant" means a protease having protease activity comprising an alteration, *i.e.*, a substitution, insertion, and/or deletion, preferably substitution, at one or more (or one or several) positions compared to its parent which is a protease having the identical amino acid sequence of said variant but not having the alterations at one or more of said specified positions. A substitution means a replacement of an amino acid occupying a position with a different amino acid; a deletion means removal of an amino acid occupying a position; and an insertion means adding amino acids *e.g.* 1 to 10 amino acids, preferably 1-3 amino acids adjacent to an amino acid occupying a position.

The term "isolated variant" means a variant that is modified by the hand of man. In one aspect, the variant is at least 1% pure, *e.g.*, at least 5% pure, at least 10% pure, at least 20% pure, at least 40% pure, at least 60% pure, at least 80% pure, and at least 90% pure, as determined by SDS-PAGE.

The term "isolated polynucleotide" means a polynucleotide that is modified by the hand of man. In one aspect, the isolated polynucleotide is at least 1% pure, *e.g.*, at least 5% pure, at least 10% pure, at least 20% pure, at least 40% pure, at least 60% pure, at least 80% pure, at least 90% pure, and at least 95% pure, as determined by agarose electrophoresis. The polynucleotides may be of genomic, cDNA, RNA, semisynthetic, synthetic origin, or any combinations thereof.

The term "allelic variant" means any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

The term "substantially pure variant" means a preparation that contains at most 10%, at most 8%, at most 6%, at most 5%, at most 4%, at most 3%, at most 2%, at most 1%, and at most 0.5% by weight of other polypeptide material with which it is natively or recombinantly associated. Preferably, the variant is at least 92% pure, *e.g.*, at least 94% pure, at least 95% pure, at least 96% pure, at least 97% pure, at least 98% pure, at least 99%, at least 99.5% pure, and 100% pure by weight of the total polypeptide material present in the preparation. The variants of the present invention are preferably in a substantially pure form. This can be accomplished, for example, by preparing the variant by well known recombinant methods or by classical purification methods.

The term "wild-type protease" means a protease expressed by a naturally occurring organism, such as a bacterium, archaea, yeast, fungus, plant or animal found in nature. An example of a wild-type protease is TY-145 *i.e.* the mature polypeptide of SEQ ID NO 2 *i.e.* amino acids 1 to 311 or the mature polypeptide with SEQ ID NO 3.

The term "mature polypeptide" means a polypeptide in its final form following translation and any post-translational modifications, such as N-terminal processing, C-terminal truncation, glycosylation, phosphorylation, etc. In one aspect, the mature polypeptide corresponds to the amino acid sequence with SEQ ID NO: 3.

The term "mature polypeptide coding sequence" means a polynucleotide that encodes a mature polypeptide having protease activity. In one aspect, the mature polypeptide coding sequence is nucleotides 331 to 1263 of SEQ ID NO: 1 based on the SignalP (Nielsen et al., 1997, Protein Engineering 10: 1-6)] that predicts nucleotides 1 to 81 of SEQ ID NO: 1 is the signal peptide.

The term "cDNA" means a DNA molecule that can be prepared by reverse transcription from a mature, spliced, mRNA molecule obtained from a prokaryotic or eukaryotic cell. cDNA lacks intron sequences that may be present in the corresponding genomic DNA. The initial, primary RNA transcript is a precursor to mRNA that is processed through a series of steps, including splicing, before appearing as mature spliced mRNA.

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

The term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or is modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature or which is synthetic. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

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

The term “control sequences” means all components necessary for the expression of a polynucleotide encoding a variant of the present invention. Each control sequence may be native or foreign to the polynucleotide encoding the variant or native or foreign to each other. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the polynucleotide encoding a variant.

The term “expression” includes any step involved in the production of the variant including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

The term “expression vector” means a linear or circular DNA molecule that comprises a polynucleotide encoding a variant and is operably linked to additional nucleotides that provide for its expression.

The term “transcription promoter” is used for a promoter which is a region of DNA that facilitates the transcription of a particular gene. Transcription promoters are typically located near the genes they regulate, on the same strand and upstream (towards the 5' region of the sense strand).

The term “transcription terminator” is used for a section of the genetic sequence that marks the end of gene or operon on genomic DNA for transcription.

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

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

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

The term “high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 50% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 65°C.

The term “very high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 50% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 70°C.

The term “medium stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 35% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 55°C.

The term “medium-high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and either 35% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 60°C.

The term “low stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 25% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 50°C.

The term “very low stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 25% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 45°C.

The term “improved property” means a characteristic associated with a variant that is improved compared to the parent or compared to a protease with SEQ ID NO: 3, or compared to a protease having the identical amino acid sequence of said variant but not having the alterations at one or more of said specified positions. Such improved properties include, but are not limited to, wash performance, protease activity, thermal activity profile, thermostability, pH activity profile, pH stability, substrate/cofactor specificity, improved surface properties, substrate specificity, product specificity, increased stability, improved stability under storage conditions, and chemical stability.

The term “improved protease activity” is defined herein as an altered protease activity (as

defined above) e.g. by increased protein conversion of a protease variant displaying an alteration of the activity relative (or compared) to the activity of the parent protease, or compared to a protease with SEQ ID NO: 3, or relative to a protease having the identical amino acid sequence of said variant but not having the alterations at one or more of said specified positions,.

The term "stability" includes storage stability and stability during use, e.g. during a wash process and reflects the stability of the protease variant according to the invention as a function of time e.g. how much activity is retained when the protease variant is kept in solution in particular in a detergent solution. The stability is influenced by many factors e.g. pH, temperature, detergent composition e.g. amount of builder, surfactants etc. The protease stability may be measured using the assay described in example 2. The term "improved stability" or "increased stability" is defined herein as a variant protease displaying an increased stability in solutions, relative to the stability of the parent protease, relative to a protease having the identical amino acid sequence of said variant but not having the alterations at one or more of said specified positions or relative to SEQ ID NO: 3. The terms "improved stability" and "increased stability" includes "improved chemical stability", "detergent stability" or "improved detergent stability".

The term "improved chemical stability" is defined herein as a variant enzyme displaying retention of enzymatic activity after a period of incubation in the presence of a chemical or chemicals, either naturally occurring or synthetic, which reduces the enzymatic activity of the parent enzyme. Improved chemical stability may also result in variants being more able to catalyze a reaction in the presence of such chemicals. In a particular aspect of the invention the improved chemical stability is an improved stability in a detergent, in particular in a liquid detergent. The term "detergent stability" or "improved detergent stability" is in particular an improved stability of the protease activity when a protease variant of the present invention is mixed into a liquid detergent formulation, especially into a liquid detergent formulation according to table 1 and then stored at temperatures between 15 and 50 °C, e. g. 20°C, 30°C or 40°C.

The term "improved thermal activity" means a variant displaying an altered temperature-dependent activity profile at a specific temperature relative to the temperature-dependent activity profile of the parent or relative to a protease with SEQ ID NO: 3. The thermal activity value provides a measure of the variant's efficiency in enhancing catalysis of a hydrolysis reaction over a range of temperatures. A more thermo active variant will lead to an increase in enhancing the rate of hydrolysis of a substrate by an enzyme composition thereby decreasing the time required and/or decreasing the enzyme concentration required for activity. Alternatively, a variant with a reduced thermal activity will enhance an enzymatic reaction at a temperature lower than the temperature optimum of the parent defined by the temperature-dependent activity profile of the parent.

The term "improved wash performance" is defined herein as a protease variant according to the invention displaying an improved wash performance relative to the wash performance of the parent protease, relative to a protease with SEQ ID NO: 3 or relative to a protease having the identical amino acid sequence of said variant but not having the alterations at one or more of said specified



positions e.g. by increased stain removal. The term "wash performance" includes wash performance in laundry but also e.g. in dish wash. The wash performance may be quantified as described under the definition of "wash performance" herein.

The term "detergent composition", includes unless otherwise indicated, granular or powder-form all-purpose or heavy-duty washing agents, especially cleaning detergents; liquid, gel or paste-form all-purpose washing agents, especially the so-called heavy-duty liquid (HDL) types; liquid fine-fabric detergents; hand dishwashing agents or light duty dishwashing agents, especially those of the high-foaming type; machine dishwashing agents, including the various tablet, granular, liquid and rinse-aid types for household and institutional use; liquid cleaning and disinfecting agents, including antibacterial hand-wash types, cleaning bars, soap bars, mouthwashes, denture cleaners, car or carpet shampoos, bathroom cleaners; hair shampoos and hair-rinses; shower gels, foam baths; metal cleaners; as well as cleaning auxiliaries such as bleach additives and "stain-stick" or pre-treat types. The terms "detergent composition" and "detergent formulation" are used in reference to mixtures which are intended for use in a wash medium for the cleaning of soiled objects. In some embodiments, the term is used in reference to laundering fabrics and/or garments (e.g., "laundry detergents"). In alternative embodiments, the term refers to other detergents, such as those used to clean dishes, cutlery, etc. (e.g., "dishwashing detergents"). It is not intended that the present invention be limited to any particular detergent formulation or composition. The term "detergent composition" is not intended to be limited to compositions that contain surfactants. It is intended that in addition to the variants according to the invention, the term encompasses detergents that may contain, e.g., surfactants, builders, chelators or chelating agents, bleach system or bleach components, polymers, fabric conditioners, foam boosters, suds suppressors, dyes, perfume, tannish inhibitors, optical brighteners, bactericides, fungicides, soil suspending agents, anti corrosion agents, enzyme inhibitors or stabilizers, enzyme activators, transferase(s), hydrolytic enzymes, oxido reductases, bluing agents and fluorescent dyes, antioxidants, and solubilizers.

The term "fabric" encompasses any textile material. Thus, it is intended that the term encompass garments, as well as fabrics, yarns, fibers, non-woven materials, natural materials, synthetic materials, and any other textile material.

The term "textile" refers to woven fabrics, as well as staple fibers and filaments suitable for conversion to or use as yarns, woven, knit, and non-woven fabrics. The term encompasses yarns made from natural, as well as synthetic (e.g., manufactured) fibers. The term, "textile materials" is a general term for fibers, yarn intermediates, yarn, fabrics, and products made from fabrics (e.g., garments and other articles).

The term "non-fabric detergent compositions" include non-textile surface detergent compositions, including but not limited to compositions for hard surface cleaning, such as dishwashing detergent compositions, oral detergent compositions, denture detergent compositions, and personal cleansing compositions.

The term "effective amount of enzyme" refers to the quantity of enzyme necessary to achieve

the enzymatic activity required in the specific application, e.g., in a defined detergent composition. Such effective amounts are readily ascertained by one of ordinary skill in the art and are based on many factors, such as the particular enzyme used, the cleaning application, the specific composition of the detergent composition, and whether a liquid or dry (e.g., granular, bar) composition is required, and the like. The term "effective amount" of a protease variant refers to the quantity of protease variant described hereinbefore that achieves a desired level of enzymatic activity, e.g., in a defined detergent composition.

The term "water hardness" or "degree of hardness" or "dH" or "°dH" as used herein refers to German degrees of hardness. One degree is defined as 10 milligrams of calcium oxide per litre of water.

The term "relevant washing conditions" is used herein to indicate the conditions, particularly washing temperature, time, washing mechanics, detergent concentration, type of detergent and water hardness, actually used in households in a detergent market segment.

The term "adjunct materials" means any liquid, solid or gaseous material selected for the particular type of detergent composition desired and the form of the product (e.g., liquid, granule, powder, bar, paste, spray, tablet, gel, or foam composition), which materials are also preferably compatible with the protease variant enzyme used in the composition. In some embodiments, granular compositions are in "compact" form, while in other embodiments, the liquid compositions are in a "concentrated" form.

The term "stain removing enzyme" as used herein, describes an enzyme that aids the removal of a stain or soil from a fabric or a hard surface. Stain removing enzymes act on specific substrates, e.g., protease on protein, amylase on starch, lipase and cutinase on lipids (fats and oils), pectinase on pectin and hemicellulases on hemicellulose. Stains are often depositions of complex mixtures of different components which either results in a local discolouration of the material by itself or which leaves a sticky surface on the object which may attract soils dissolved in the washing liquor thereby resulting in discolouration of the stained area. When an enzyme acts on its specific substrate present in a stain the enzyme degrades or partially degrades its substrate thereby aiding the removal of soils and stain components associated with the substrate during the washing process. For example, when a protease acts on a grass stain it degrades the protein components in the grass and allows the green/brown colour to be released during washing.

The term "reduced amount" means in this context that the amount of the component is smaller than the amount which would be used in a reference process under otherwise the same conditions. In a preferred embodiment the amount is reduced by, e.g., at least 5%, such as at least 10%, at least 15%, at least 20% or as otherwise herein described.

The term "low detergent concentration" system includes detergents where less than about 800 ppm of detergent components is present in the wash water. Asian, e.g., Japanese detergents are typically considered low detergent concentration systems.

The term "medium detergent concentration" system includes detergents wherein between

about 800 ppm and about 2000 ppm of detergent components is present in the wash water. North American detergents are generally considered to be medium detergent concentration systems.

The term "high detergent concentration" system includes detergents wherein greater than about 2000 ppm of detergent components is present in the wash water. European detergents are generally considered to be high detergent concentration systems.

### **Conventions for Designation of Variants**

For purposes of the present invention, the mature polypeptide disclosed in SEQ ID NO: 3 is used to determine the corresponding amino acid residue in another protease. The amino acid sequence of another protease is aligned with the mature polypeptide disclosed in SEQ ID NO: 3, and based on the alignment, the amino acid position number corresponding to any amino acid residue in the mature polypeptide disclosed in SEQ ID NO: 3 is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *J. Mol. Biol.* 48: 443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice *et al.*, 2000, *Trends Genet.* 16: 276-277), preferably version 5.0.0 or later. The parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix.

Identification of the corresponding amino acid residue in another protease can be determined by an alignment of multiple polypeptide sequences using several computer programs including, but not limited to, MUSCLE (multiple sequence comparison by log-expectation; version 3.5 or later; Edgar, 2004, *Nucleic Acids Research* 32: 1792-1797), MAFFT (version 6.857 or later; Katoh and Kuma, 2002, *Nucleic Acids Research* 30: 3059-3066; Katoh *et al.*, 2005, *Nucleic Acids Research* 33: 511-518; Katoh and Toh, 2007, *Bioinformatics* 23: 372-374; Katoh *et al.*, 2009, *Methods in Molecular Biology* 537: 39-64; Katoh and Toh, 2010, *Bioinformatics* 26: 1899-1900), and EMBOSS EMMA employing ClustalW (1.83 or later; Thompson *et al.*, 1994, *Nucleic Acids Research* 22: 4673-4680), using their respective default parameters.

When the other enzyme has diverged from the mature polypeptide of SEQ ID NO: 3 such that traditional sequence-based comparison fails to detect their relationship (Lindahl and Elofsson, 2000, *J. Mol. Biol.* 295: 613-615), other pairwise sequence comparison algorithms can be used. Greater sensitivity in sequence-based searching can be attained using search programs that utilize probabilistic representations of polypeptide families (profiles) to search databases. For example, the PSI-BLAST program generates profiles through an iterative database search process and is capable of detecting remote homologs (Atschul *et al.*, 1997, *Nucleic Acids Res.* 25: 3389-3402). Even greater sensitivity can be achieved if the family or superfamily for the polypeptide has one or more representatives in the protein structure databases. Programs such as GenTHREADER (Jones, 1999, *J. Mol. Biol.* 287: 797-815; McGuffin and Jones, 2003, *Bioinformatics* 19: 874-881) utilize information from a variety of sources (PSI-BLAST, secondary structure prediction, structural alignment profiles, and solvation potentials) as input to a neural network that predicts the structural fold for a query

sequence. Similarly, the method of Gough *et al.*, 2000, *J. Mol. Biol.* 313: 903-919, can be used to align a sequence of unknown structure with the superfamily models present in the SCOP database. These alignments can in turn be used to generate homology models for the polypeptide, and such models can be assessed for accuracy using a variety of tools developed for that purpose.

For proteins of known structure, several tools and resources are available for retrieving and generating structural alignments. For example the SCOP super families of proteins have been structurally aligned, and those alignments are accessible and downloadable. Two or more protein structures can be aligned using a variety of algorithms such as the distance alignment matrix (Holm and Sander, 1998, *Proteins* 33: 88-96) or combinatorial extension (Shindyalov and Bourne, 1998, *Protein Engineering* 11: 739-747), and implementation of these algorithms can additionally be utilized to query structure databases with a structure of interest in order to discover possible structural homologs (e.g., Holm and Park, 2000, *Bioinformatics* 16: 566-567).

In describing the variants of the present invention, the nomenclature described below is adapted for ease of reference. The accepted IUPAC single letter or three letters amino acid abbreviations are employed. Amino acid positions are indicated with #<sub>1</sub>, #<sub>2</sub>, etc.

Substitutions: For an amino acid substitution, the following nomenclature is used: Original amino acid, position, substituted amino acid. Accordingly, the substitution of serine at position #<sub>1</sub> with tryptophan is designated as "Ser#<sub>1</sub>Trp" or "S#<sub>1</sub>W". Multiple mutations are separated by addition marks ("+") or by commas (,), e.g., "Ser#<sub>1</sub>Trp + Ser#<sub>2</sub>Pro" or S#<sub>1</sub>W, S#<sub>2</sub>P, representing substitutions at positions #<sub>1</sub> and #<sub>2</sub> of serine (S) with tryptophan (W) and proline (P), respectively. If more than one amino acid may be substituted in a given position these are listed in brackets, such as [X] or {X}. Thus if both Trp and Lys according to the invention may be substituted instead of the amino acid occupying at position #<sub>1</sub> this is indicated as X#<sub>1</sub> {W, K} or X#<sub>2</sub> [W, K] where the X indicate that different proteases may be parent e.g. such as a protease with SEQ ID NO 3 or a protease having at least 70% identity hereto. Thus in some cases the variants are represented as #<sub>1</sub> {W, K} or X#<sub>2</sub>P indicating that the amino acids to be substituted vary depending on the parent.

Deletions: For an amino acid deletion, the following nomenclature is used: Original amino acid, position, \*. Accordingly, the deletion of serine at position #<sub>1</sub> is designated as "Ser#<sub>1</sub>\*" or "S#<sub>1</sub>\*". Multiple deletions are separated by addition marks ("+") or commas, e.g., "Ser#<sub>1</sub>\* + Ser#<sub>2</sub>\*" or "S#<sub>1</sub>\*, S#<sub>2</sub>\*".

Insertions: The insertion of an additional amino acid residue such as e.g. a lysine after G#<sub>1</sub> may be indicated by: Gly#<sub>1</sub>GlyLys or G#<sub>1</sub>GK. Alternatively insertion of an additional amino acid residue such as lysine after G#<sub>1</sub> may be indicated by: \*#<sub>1</sub>aL. When more than one amino acid residue is inserted, such as e.g. a Lys, and Ala after #<sub>1</sub> this may be indicated as: Gly#<sub>1</sub>GlyLysAla or G#<sub>1</sub>GKA. In such cases, the inserted amino acid residue(s) may also be numbered by the addition of lower case letters to the position number of the amino acid residue preceding the inserted amino acid residue(s), in this example: \*#<sub>1</sub>aK \*#<sub>1</sub>bA.

Multiple alterations. Variants comprising multiple alterations are separated by addition marks (“+”) or by commas (,), e.g., “Ser#<sub>1</sub>Trp+Ser#<sub>2</sub>Pro” or “S#<sub>1</sub>W, S#<sub>2</sub>P” representing a substitution of serine at positions #<sub>1</sub> and #<sub>2</sub> with tryptophan and proline, respectively as described above.

Different alterations. Where different alterations can be introduced at a position, the different alterations are separated by a comma, e.g., “Ser#<sub>1</sub>Trp, Lys” or S#<sub>1</sub>W, K represents a substitution of serine at position #<sub>1</sub> with tryptophan or lysine. Thus, “Ser#<sub>1</sub>Trp, Lys + Ser#<sub>2</sub>Asp” designates the following variants: “Ser#<sub>1</sub>Trp+Ser#<sub>2</sub>Pro”, “Ser#<sub>1</sub>Lys+Ser#<sub>2</sub>Pro” or S#<sub>1</sub>W, K + S#<sub>2</sub>D.

### Detailed Description of the Invention

The present invention concerns protease variants, comprising a substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has a sequence identity to SEQ ID NO: 3 of at least 75% and less than 100%, and wherein the variant has protease activity. Previously unanticipated, the inventors have found that protease variants containing one or more substitutions corresponding to the positions 171, 173, 175 or 179 of SEQ ID NO 3 have improved stability in detergent compared to a protease having the identical amino acid sequence of said variant but not having the substitution(s) at one or more of said specified positions or compared to a protease with SEQ ID NO: 3. The amino acids corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3 form part of an active site loop corresponding to positions 170 to 180 of SEQ ID NO 3, which defines parts of the S1 substrate binding pocket, see Figure 1. Thus the present invention provides protease variants, comprising a substitution at one or more (e.g., several) positions corresponding to positions 171, 173, 175 or 179, wherein the variant has protease activity. New protease variants containing one or more substitution(s) in the loop region 170-180 (SEQ ID NO 3 numbering), were generated and tested for stability in detergent as described in “Material and Methods” and the inventors demonstrate that one or more substitutions of one or more amino acid at a position corresponding to positions 171, 173, 175 or 179 of the mature polypeptide SEQ ID NO: 3 significantly improved the detergent stability compared to a protease having the identical amino acid sequence of said variant but not having a substitution at one or more of said specified positions or compared to a protease with SEQ ID NO: 3.

Surprisingly the variants according to the invention may in addition to improved stability also have improved wash performance. Thus in a preferred embodiment the variants according to the invention have improved the detergent stability and/or improved wash performance compared to a protease having the identical amino acid sequence of said variant but not having a substitution at one or more of said specified positions or compared to a protease with SEQ ID NO:3. In a preferred embodiment the protease variant comprises a substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has at least 70% identity to the protease with SEQ ID NO: 3 (*Bacillus* sp. TY145). Thus one aspect of the invention relates to a protease variant, comprising a substitution at one or more positions

corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has an amino acid sequence which is at least 75% identical to SEQ ID NO 3; and recovering the variant. Thus the invention relates to such variant comprising substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has at least 70%, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to SEQ ID NO: 3. In one embodiment the variant is a polypeptide encoded by a polynucleotide having at least 70% identity to the mature polypeptide coding sequence of SEQ ID NO: 1 or a sequence encoding the mature polypeptide of SEQ ID NO: 2. In one embodiment the variant according to the invention is a polypeptide encoded by a polynucleotide having at least 70% identity e.g., such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99% e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6,, but less than 100%, sequence identity to the mature polynucleotide of SEQ ID NO: 1.

A particular embodiment, concerns a protease variant, comprising a substitution at one or more positions corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant is a variant of a parent protease which has at least 70%, such as at least 71%, at least 72%, at least 73%, at least 74%, such as at least 75%, e.g., such as at least 76% at least 77% at least 78% at least 79% at least 80%, at least 81% at least 82% at least 83% at least 84% at least 85%, at least 86% at least 87% at least 88% at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, or 100% sequence identity to SEQ ID NO: 3. In one particular embodiment the protease variant is a TY-145 (SEQ ID NO 3) variant comprising a substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3. In another embodiment the invention relates to a variant comprising a substitution at two, three, four or five positions corresponding to positions 171, 173, 175, 179 or 180 of SEQ ID NO: 3. A preferred embodiment concerns a protease variant, comprising substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has at least 70%, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%,

at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to SEQ ID NO: 3. A particularly preferred embodiment concerns a protease variant comprising a substitution of one or more amino acid selected from the group consisting of Cys, Val, Gln, Thr, Glu, His, Lys, Met, Asn, Tyr, Ala, Pro and Trp in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3. A particular embodiment concerns a protease variant comprising a substitution of one or more amino acid selected from the group consisting of Cys, Val, Gln, Thr, Glu, His, Lys, Met, Asn, Tyr, Ala, Pro and Trp in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has at least 70% identity to SEQ ID NO: 3 such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to SEQ ID NO: 3. Another particular preferred embodiment concerns a protease variant comprising one or more of the substitutions selected from the group consisting of S171{W, K, E, N}; S173P; S175 {A, V, P} or G179{C, V, Q, S, T, E, H, K, M, N, A, Y} of SEQ ID NO: 3, wherein the variant has at least 70% identity to SEQ ID NO: 3 such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to the SEQ ID NO: 3. An even more preferred embodiment concerns a protease variant comprising one or both of the substitutions 173P and/or S175P of SEQ ID NO: 3, wherein the variant has at least 70% identity to SEQ ID NO: 3 such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to the SEQ ID NO: 3.

In one aspect, the protease variant comprises a substitution at position 171, in a preferred aspect the variant comprises a substitution at position 171 with W, K, E or N, in another preferred

aspect, the variant comprises an W at position 171, in yet another preferred aspect, the variant comprises the substitution S171W, wherein the parent is the mature polypeptide with SEQ ID NO: 3. In another preferred aspect, the variant comprises an K at position 171, in yet another preferred aspect, the variant comprises the substitution S171K, wherein the parent is the mature polypeptide with SEQ ID NO: 3. In another preferred aspect, the variant comprises an E at position 171, in yet another preferred aspect, the variant comprises the substitution S171E, wherein the parent is the mature polypeptide with SEQ ID NO: 3. In another preferred aspect, the variant comprises an N at position 171, in yet another preferred aspect, the variant comprises the substitution S171N, wherein the parent is the mature polypeptide with SEQ ID NO: 3

In a further aspect, the variant comprises a substitution at position 171 with W, K, E or N wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an W at position 171, in yet another preferred aspect, the variant comprises the substitution S171W, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an K at position 171, in yet another preferred aspect, the variant comprises the substitution S171K, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an E at position 171, in yet another preferred aspect, the variant comprises the substitution S171E, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an N at position 171, in yet another preferred aspect, the variant comprises the substitution S171N, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In an even further aspect, the variant comprises a substitution at position



171 with W, K, E or N wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in Example 2 as described under "Material and Methods". In another preferred aspect, the variant comprises a W at position 171, in yet another preferred aspect, the variant comprises the substitution S171W, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods". In another preferred aspect, the variant comprises an K at position 171, in yet another preferred aspect, the variant comprises the substitution S171K, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods". In another preferred aspect, the variant comprises an E at position 171, in yet another preferred aspect, the variant comprises the substitution S171E, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods"

In another preferred aspect, the variant comprises a N at position 171, in yet another preferred aspect, the variant comprises the substitution S171N, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at

least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods"

In one aspect, the protease variant comprises a substitution at position 173, in a preferred aspect the variant comprises a substitution at position 173 with P in another preferred aspect, the variant comprises the substitution S173P, wherein the parent is polypeptide with SEQ ID NO: 3 In another preferred aspect, the variant comprises an P at position 173, in yet another preferred aspect, the variant comprises the substitution S173P, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In an even further aspect, the variant comprises a substitution at position 173 with P, in yet another preferred aspect, the variant comprises the substitution S173P, wherein the variant has at least 70% sequence identity to SEQ ID NO: 2, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in Example 2 as described under "Material and Methods".

In one aspect, the protease variant comprises a substitution at position 175, in a preferred aspect the variant comprises a substitution at position 175 with A, V or P, in another preferred aspect, the variant comprises an A at position 175, in yet another preferred aspect, the variant comprises the substitution S175A, wherein the parent is a polypeptide with SEQ ID NO: 3. In another preferred aspect, the variant comprises an V at position 175, in yet another preferred aspect, the variant comprises the substitution S175V, wherein the parent is the mature polypeptide with SEQ ID NO: 3. In another preferred aspect, the variant comprises an P at position 175, in yet another preferred aspect, the variant comprises the substitution S175P, wherein the parent is a polypeptide with SEQ ID NO: 3.

In a further aspect, the variant comprises a substitution at position 175 with A, V or P wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred

aspect, the variant comprises an A at position 175, in yet another preferred aspect, the variant comprises the substitution S175A, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an V at position 175, in yet another preferred aspect, the variant comprises the substitution S175V, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an P at position 175, in yet another preferred aspect, the variant comprises the substitution S175P, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In an even further aspect, the variant comprises a substitution at position 175 with A, V or P wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in Example 2 as described under "Material and Methods". In another preferred aspect, the variant comprises an A at position 175, in yet another preferred aspect, the variant comprises the substitution S175A, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods". In another preferred aspect, the variant comprises an V at position 175, in yet another preferred aspect, the variant comprises the substitution S175V, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e.

g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods". In another preferred aspect, the variant comprises an P at position 175, in yet another preferred aspect, the variant comprises the substitution S175P, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods"

In another preferred aspect, the variant comprises a C at position 179, in yet another preferred aspect, the variant comprises the substitution G179C, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with C, in yet another preferred aspect, the variant comprises the substitution G179C, wherein the variant has at least 70% sequence identity to SEQ ID NO: 2, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another aspect, the variant comprises a substitution at position 179 with C, in yet another preferred aspect, the variant comprises the substitution G179C, wherein the variant has at least 70% sequence identity to SEQ ID NO: 2, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods"

In another preferred aspect, the variant comprises a V at position 179, in yet another preferred aspect, the variant comprises the substitution G179V, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with V, in yet another preferred aspect, the variant comprises the substitution G179V, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at

least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises a substitution at position 179 with V, in yet another preferred aspect, the variant comprises the substitution G179V, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises a Q at position 179, in yet another preferred aspect, the variant comprises the substitution G179Q, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with Q, in yet another preferred aspect, the variant comprises the substitution G179Q, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with Q, in yet another preferred aspect, the variant comprises the substitution G179Q, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an S at position 179, in yet another preferred aspect, the variant comprises the substitution G179S, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with S, in yet another preferred aspect, the variant comprises the substitution G179, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with S, in yet another preferred aspect, the variant comprises

the substitution G179, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an T at position 179, in yet another preferred aspect, the variant comprises the substitution G179T, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with T, in yet another preferred aspect, the variant comprises the substitution G179T, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another aspect, the variant comprises a substitution at position 179 with T, in yet another preferred aspect, the variant comprises the substitution G179T, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an E at position 179, in yet another preferred aspect, the variant comprises the substitution G179E, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with E, in yet another preferred aspect, the variant comprises the substitution G179E, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with E, in yet another preferred aspect, the variant comprises the substitution G179E, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than

100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an H at position 179, in yet another preferred aspect, the variant comprises the substitution G179H, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with H, in yet another preferred aspect, the variant comprises the substitution G179H, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with H, in yet another preferred aspect, the variant comprises the substitution G179H, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods" In another preferred aspect, the variant comprises a K at position 179, in yet another preferred aspect, the variant comprises the substitution G179K, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with K, in yet another preferred aspect, the variant comprises the substitution G179K, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with K, in yet another preferred aspect, the variant comprises the substitution G179K, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an M at position 179, in yet another

preferred aspect, the variant comprises the substitution G179M, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with M, in yet another preferred aspect, the variant comprises the substitution G179M, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%. In another aspect, the variant comprises a substitution at position 179 with M, in yet another preferred aspect, the variant comprises the substitution G179M, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an N at position 179, in yet another preferred aspect, the variant comprises the substitution G179N, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with N, in yet another preferred aspect, the variant comprises the substitution G179N, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a further aspect, the variant comprises a substitution at position 179 with N, in yet another preferred aspect, the variant comprises the substitution G179N, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods".

In another preferred aspect, the variant comprises an A at position 179, in yet another preferred aspect, the variant comprises the substitution G179A, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with A, in yet another preferred aspect, the variant comprises the substitution G179H, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at



least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with A, in yet another preferred aspect, the variant comprises the substitution G179A, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods"

In another preferred aspect, the variant comprises an Y at position 179, in yet another preferred aspect, the variant comprises the substitution G179Y, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 179 with Y, in yet another preferred aspect, the variant comprises the substitution G179Y, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In a another aspect, the variant comprises a substitution at position 179 with Y, in yet another preferred aspect, the variant comprises the substitution G179Y, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in the Example 2 as described under "Material and Methods"

In one aspect, the protease variant further comprises a substitution at position 180, in a preferred aspect the variant further comprises a substitution at position 180 with Y in another preferred aspect, the variant further comprises the substitution F180Y, wherein the parent is a polypeptide with SEQ ID NO: 3. In a further aspect, the variant comprises a substitution at position 180 with Y, in yet another preferred aspect, the variant further comprises the substitution F180Y, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%. In another preferred aspect, the variant comprises an Y at position 180, in yet another preferred aspect, the variant further

comprises the substitution F180Y, wherein the variant has at least 70% sequence identity to SEQ ID NO: 3, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, and having an increased stability relative to a protease with SEQ ID NO: 3 or a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions, when tested in Example 2 as described under "Material and Methods".

In another aspect, the variant comprises substitutions at positions corresponding to positions 171 and 173, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171 and 175, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171 and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171 and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 173 and 175, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 173 and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 173 and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 175 and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 175 and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 173, and 175, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 173, and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 173, and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 175, and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 175, and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 179, and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 173, 175, and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 173, 175, and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 175, 179, and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 173, 175, and 179, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 173, 175, and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 173, 175, 179 and 180, such as those described above.

In another aspect, the variant comprises substitutions at positions corresponding to positions 171, 173, 175, 179 and 180, such as those described above.

In another aspect, the variant comprises one or more (several) substitutions selected from the group consisting of S171 {W, K, E, N}, S173 {P}, S175 {A, V, P} or G179 {C, V, Q, S, T, E, H, K, M, N, A, Y}. In another aspect the variant mentioned above further comprise the substitution F180Y.

In another aspect, the variant comprises the substitutions S171W + S173P of the polypeptide with SEQ ID NO: 3

In another aspect, the variant comprises the substitutions S171K + S173P of the polypeptide with SEQ ID NO: 3

In another aspect, the variant comprises the substitutions S171E + S173P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S175A of the polypeptide with SEQ ID NO: 3

In another aspect, the variant comprises the substitutions S171W + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S175V of the polypeptide with SEQ ID NO: 3

In another aspect, the variant comprises the substitutions S171N + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S175P of the polypeptide with SEQ ID NO: 3

In another aspect, the variant comprises the substitutions S171W + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + F180Y of the polypeptide with SEQ ID NO: 3

In another aspect, the variant comprises the substitutions S173P + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175A + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175V + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175A of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175V of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175P of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175A + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175V + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S173P + S175P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175V + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175V + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175V + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175V + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175P + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175A + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175V + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171W + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171K + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171E + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

In another aspect, the variant comprises the substitutions S171N + S173P + S175P + G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} + F180Y of the polypeptide with SEQ ID NO: 3.

The variant may further comprise a substitution at one or more (several) other positions. For example, the variants may comprise an alteration at a position corresponding to positions selected from the group consisting of 39, 40, 70, 74, 81, 102, 121, 132, 137, 144, 155, 159, 162, 174, 176; 177, 241, 247, 256, 274, 286, 297 of SEQ ID NO 3. In one embodiment the variant of the invention comprises one of the following substitutions: Y39D; T40{D,P}; Q70N; T74M; L81{F,H,V}; A102T; I121{V,T}; G132 {I,E}; I137{M,E}; S144{Q,R}; D155N; G159S; V162R; G174{S,T}; N176G; T177S; T241P; I247M; H256F;S274I; V286Q; T297P wherein each position correspond to the positions of SEQ ID NO 3.

In another aspect, a variant according to the invention comprises a substitution at one or more (e.g., several) positions corresponding to positions 171, 173, 175 or 179. In another aspect, a variant according to the invention comprises a substitution at two positions corresponding to any of positions 171, 173, 175, 179 and 180. In another aspect, a variant according to the invention comprises a substitution at three positions corresponding to any of positions 171, 173, 175, 179 and 180. In another aspect, a variant according to the invention comprises a substitution at four positions



corresponding to any of positions 171, 173, 175, 179 and 180. In another aspect, a variant according to the invention comprises a substitution at each position corresponding to positions 171, 173, 175, 179 and 180.

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

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

Alternatively, the amino acid changes are of such a nature that the physico-chemical properties of the polypeptides are altered. For example, amino acid changes may improve the thermal stability of the polypeptide, alter the substrate specificity, change the pH optimum, and the like.

For example, the variants may comprise a substitution at a position corresponding to any of the positions 171, 173, 175 or 179 and further comprises an alteration at any of the positions selected from the group consisting of positions 39, 40, 70, 74, 81, 102, 121, 132, 137, 144, 155, 159, 162, 174, 176; 177, 180, 241, 247, 256, 274, 286, 297. In a preferred embodiment the alteration at any of the positions selected from the group consisting of 39, 40, 70, 74, 81, 102, 121, 132, 137, 144, 155, 159, 162, 174, 176; 177, 180, 241, 247, 256, 274, 286, 297 is a substitution. In a particular preferred embodiment the variants according to the invention comprises any of the following substitutions S171 {W, K, E, N}, S173P, S175 {A, V, P} or G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of SEQ ID NO: 3, wherein the variant further comprises one or more substitution selected from the group consisting of: Y39D; T40{D,P}; Q70N; T74M; L81{F,H,V}; A102T; I121{V,T}; G132 {I,E}; I137{M,E}; S144{Q,R}; D155N; G159S; V162R; G174{S,T}; N176G; T177S; F180Y; T241P; I247M; H256F;S274I; V286Q; T297P.

In one embodiment of the invention, the variants according to the invention comprise any of the following substitutions compared to SEQ ID NO 3:

S171N S175P
I121V S175P
L81V S175P
A102T S175P
I137E S175P
S175A G179S
I121V S175A
L81F S175A
L81H S175A
L81V S175A
A102T S175A
I137E S175A
S144Q S175P
S144Q S175A
S144R G179Q
I121T S175P
S144R S171N
S173P S274I
I137M S173P
S171N S173P
L81F S173P
L81H S173P
A102T S173P
S144Q S173P
S144R F180Y
I137E S173P
S173P S175P F180Y
S173Y G174S S175A F180Y
S173P G174T S175V T177S F180Y
S173P G174K S175P N176G T177S F180Y
S173P T241P
G179S F180Y G183A A187V
S173Y G174S S175A F180Y T241P
D155N G159S S173Y G174S S175A F180Y
S173Y G174S S175A F180Y S274I

S173Y G174S S175A F180Y V286Q
T40D S173Y G174S S175A F180Y
V162R S173P G174T S175V T177S F180Y
I121V S173P G174T S175V T177S F180Y
L81V S173P G174T S175V T177S F180Y
A102T S173P G174T S175V T177S F180Y
S173P G174T S175V T177S F180Y T241P
I137E S173P G174T S175V T177S F180Y
S144Q S173P G174T S175V T177S F180Y
Q70N S173P G174T S175V T177S F180Y
D155N G159S S173P G174T S175V T177S F180Y
S173P G174T S175V T177S F180Y S274I
S173P G174T S175V T177S F180Y V286Q
T40D S173P G174T S175V T177S F180Y
S171N S173P G174T S175V T177S F180Y
V162R S173P G174K S175P N176G T177S F180Y
I121V S173P G174K S175P N176G T177S F180Y
L81V S173P G174K S175P N176G T177S F180Y
A102T S173P G174K S175P N176G T177S F180Y
S173P G174K S175P N176G T177S F180Y T241P
I137E S173P G174K S175P N176G T177S F180Y
S144Q S173P G174K S175P N176G T177S F180Y
Q70N S173P G174K S175P N176G T177S F180Y
D155N G159S S173P G174K S175P N176G T177S F180Y
S173P G174K S175P N176G T177S F180Y S274I
S173P G174K S175P N176G T177S F180Y V286Q
T40D S173P G174K S175P N176G T177S F180Y
S171N S173P G174K S175P N176G T177S F180Y
I121V I137E S173Y G174S S175A F180Y
L81V I137E S173Y G174S S175A F180Y
I137E S173Y G174S S175A F180Y T241P
Q70N I137E S173Y G174S S175A F180Y
I137E S173Y G174S S175A F180Y S274I
I137E S173Y G174S S175A F180Y T297P
I121V I137E S173P G174T S175V T177S F180Y

L81V I137E S173P G174T S175V T177S F180Y
I137E S173P G174T S175V T177S F180Y T241P
Q70N I137E S173P G174T S175V T177S F180Y
I137E S173P G174T S175V T177S F180Y V286Q
I137E S173P G174T S175V T177S F180Y T297P
I137E S171N S173P G174T S175V T177S F180Y
I137E S173P G174T S175A T177S F180Y
I121V I137E S173P G174K S175P N176G T177S F180Y
Q70N I137E S173P G174K S175P N176G T177S F180Y
I137E S173P G174K S175P N176G T177S F180Y S274I
I137E S173P G174K S175P N176G T177S F180Y V286Q
I137E S173P G174K S175P N176G T177S F180Y T297P
I137E S171N S173P G174K S175P N176G T177S F180Y
I137E S173P G174K S175A N176G T177S F180Y
V162R S173Y G174S S175A F180Y
A102T S173Y G174S S175A F180Y
G132I S173P G174T S175V T177S F180Y
S173P G174T S175V T177S F180Y T297P
S173P G174T S175A T177S F180Y
S173P S175A
I137E S144Q S173Y G174S S175A F180Y
T40L I137E S173Y G174S S175A F180Y
I137E S173Y S175A F180Y
I137E S173P S175V T177S F180Y
I137E S173P S175P N176G T177S F180Y
S171N S173Y G174S S175A F180Y
S173P G174K S175A N176G T177S F180Y
I137E S173Y G174S S175A F180Y V286Q
I137E S173P G174T S175V T177S F180Y S274I
T74M I137E S173P
T79I I137E S173P
L81G S173P
L34I I137E S173P
Y39D I137E S173P
T40P I137E S173P

I137E S173P I247M
I137E S173P H256F
I137E S144Q S173P G174T S175V T177S F180Y
I137E S144Q S173P G174K S175P N176G T177S F180Y
S173Y G174S S175P F180Y
I137E S173Y G174S S175P F180Y
S173P G174T S175P T177S F180Y
I137E S173P G174T S175P T177S F180Y
I137E S173P G174T S175P T177S F180Y T297P
V162R S171N S173P G174K S175P N176G T177S F180Y
I137E S171N S173P G174K S175P N176G T177S F180Y T241P
I137E S171N S173P G174K S175P N176G T177S F180Y T297P
I137E S173P S175P F180Y
V162R S173P S175P F180Y
S173P S175P F180Y S274I
S173P S175P F180Y T241P
S173P S175P F180Y T297P
S173P S175P F180Y V286Q
I137E S173Y G174S S175A F180Y
S144Q S173Y G174S S175A F180Y
Q70N S173Y G174S S175A F180Y
I121V S173Y G174S S175A F180Y
L81V S173Y G174S S175A F180Y
G132I S173P G174K S175P N176G T177S F180Y
S173P G174K S175P N176G T177S F180Y T297P

Essential amino acids in a polypeptide can be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, 1989, *Science* 244: 1081-1085). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant mutant molecules are tested for protease activity to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton *et al.*, 1996, *J. Biol. Chem.* 271: 4699-4708. The active site of the enzyme or other biological interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction, or photoaffinity labeling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos *et al.*, 1992, *Science* 255: 306-312; Smith *et al.*, 1992, *J. Mol. Biol.* 224: 899-904; Wlodaver *et al.*, 1992, *FEBS Lett.* 309: 59-64. The identity of essential amino acids can also be inferred from an alignment with a

related polypeptide. For TY-145 (SEQ ID NO: 3) the catalytic triad comprising the amino acids D35, H72 and S251 is essential for protease activity of the enzyme.

In an embodiment, the variant has improved catalytic activity compared to the parent enzyme.

In an embodiment, the variant has improved stability compared to the parent enzyme or compared to a protease having the identical amino acid sequence of said variant but not having a substitution at one or more of said specified positions or compared to a protease with SEQ ID NO: 3, wherein stability is measured in Example 2 as described in "Material and Methods" herein.

In an embodiment, a variant according to the invention has improved stability compared to the parent enzyme or compared to a protease having the identical amino acid sequence of said variant but not having a substitution at one or more of said specified positions or compared to a protease with SEQ ID NO: 3.

## **Parent proteases**

### Protease variant

The term "variant" and the term "protease variant" are defined above.

### Homologous protease sequences

The homology between two amino acid sequences is in this context described by the parameter "identity" for purposes of the present invention, the degree of identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm as described above. The output from the routine is besides the amino acid alignment the calculation of the "Percent Identity" between the two sequences.

Based on this description it is routine for a person skilled in the art to identify suitable homologous proteases, which can be modified according to the invention.

Substantially homologous parent protease variants may have one or more (several) amino acid substitutions, deletions and/or insertions, in the present context the term "one or more" is used interchangeably with the term "several". These changes are preferably of a minor nature, that is conservative amino acid substitutions as described above and other substitutions that do not significantly affect the three-dimensional folding or activity of the protein or polypeptide; small deletions, typically of one to about 30 amino acids; and small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue, a small linker peptide of up to about 20-25 residues, or a small extension that facilitates purification (an affinity tag), such as a poly-histidine tract, or protein A (Nilsson *et al.*, 1985, *EMBO J.* 4: 1075; Nilsson *et al.*, 1991, *Methods Enzymol.* 198: 3. See, also, in general, Ford *et al.*, 1991, *Protein Expression and Purification* 2: 95-107.

Although the changes described above preferably are of a minor nature, such changes may also be of a substantive nature such as fusion of larger polypeptides of up to 300 amino acids or more both as amino- or carboxyl-terminal extensions.

The parent protease may comprise or consist of the amino acid sequence of SEQ ID NO: 3 or an allelic variant thereof; or a fragment thereof having protease activity. In one aspect, the parent protease comprises or consists of the amino acid sequence of SEQ ID NO: 3.

The parent protease may be (a) a polypeptide having at least 70% sequence identity to the mature polypeptide of SEQ ID NO: 3; (b) a polypeptide encoded by a polynucleotide that hybridizes under medium or high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 1, (ii) a sequence encoding the mature polypeptide of SEQ ID NO: 2, or (iii) the full-length complement of (i) or (ii); or (c) a polypeptide encoded by a polynucleotide having at least 70% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 1.

In an aspect, the parent protease has a sequence identity to the polypeptide with SEQ ID NO: 3 of at least 70%, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76% at least 77% at least 78% at least 79% at least 80%, at least 81% at least 82% at least 83% at least 84% at least 85%, at least 86% at least 87% at least 88% at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, or 100%, which have protease activity.

In one aspect, the amino acid sequence of the parent protease differs by no more than 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9, from the mature polypeptide with SEQ ID NO: 3.

In another aspect, the parent comprises or consists of the amino acid sequence of SEQ ID NO: 3. In another aspect, the parent comprises or consists of amino acids 1 to 311 of SEQ ID NO: 2.

In another aspect, the parent protease is encoded by a polynucleotide that hybridizes under very low stringency conditions, low stringency conditions, medium stringency conditions, or high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 1, (ii) a sequence encoding the mature polypeptide of SEQ ID NO: 2, or (iii) the full-length complement of (i) or (ii), (Sambrook *et al.*, 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York).

The polynucleotide of SEQ ID NO: 1 or a subsequence thereof, as well as the polypeptide of SEQ ID NO: 3 or a fragment thereof may be used to design nucleic acid probes to identify and clone DNA encoding a parent from strains of different genera or species according to methods well known in the art. In particular, such probes can be used for hybridization with the genomic DNA or cDNA of a cell of interest, following standard Southern blotting procedures, in order to identify and isolate the corresponding gene therein. Such probes can be considerably shorter than the entire sequence, but should be at least 15, e.g., at least 25, at least 35, or at least 70 nucleotides in length. Preferably, the nucleic acid probe is at least 100 nucleotides in length, e.g., at least 200 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides, at least 600 nucleotides, at least 700 nucleotides, at least 800 nucleotides, or at least 900 nucleotides in length. Both DNA and RNA probes can be used. The probes are typically labeled for detecting the corresponding gene

(for example, with  $^{32}\text{P}$ ,  $^3\text{H}$ ,  $^{35}\text{S}$ , biotin, or avidin). Such probes are encompassed by the present invention.

A genomic DNA or cDNA library prepared from such other strains may be screened for DNA that hybridizes with the probes described above and encodes a parent. Genomic or other DNA from such other strains may be separated by agarose or polyacrylamide gel electrophoresis, or other separation techniques. DNA from the libraries or the separated DNA may be transferred to and immobilized on nitrocellulose or other suitable carrier material. In order to identify a clone or DNA that hybridizes with SEQ ID NO: 1 or a subsequence thereof, the carrier material is used in a Southern blot.

For purposes of the present invention, hybridization indicates that the polynucleotide hybridizes to a labeled nucleic acid probe corresponding to (i) SEQ ID NO: 1; (ii) the mature polypeptide coding sequence of SEQ ID NO: 1; (iii) a sequence encoding the mature polypeptide of SEQ ID NO: 2; (iv) the full-length complement thereof; or (v) a subsequence thereof; under very low to very high stringency conditions. Molecules to which the nucleic acid probe hybridizes under these conditions can be detected using, for example, X-ray film or any other detection means known in the art.

In one aspect, the nucleic acid probe is the mature polypeptide coding sequence of SEQ ID NO: 1. In another aspect, the nucleotide acid probe is a 80 to 1140 nucleotides long fragment of SEQ ID NO: 1, e.g. 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or 1100 nucleotides long. In another aspect, the nucleic acid probe is a polynucleotide that encodes the polypeptide of SEQ ID NO: 2; the mature polypeptide thereof; or a fragment thereof. In another aspect, the nucleic acid probe is SEQ ID NO: 1 or a sequence encoding the mature polypeptide of SEQ ID NO: 2.

In another embodiment, the parent is encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 1 or a sequence encoding the mature polypeptide of SEQ ID NO: 2 of at least 71%, at least 72%, at least 73%, at least 74%, at least 70%, e.g., at least 75%, at least 76%, at least 77% at least 78% at least 79% at least 80%, at least 81% at least 82% at least 83% at least 84% at least 85%, at least 86% at least 87% at least 88% at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6 or 100%.

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

The parent may be a fusion polypeptide or cleavable fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide of the present invention. A fusion polypeptide is produced by fusing a polynucleotide encoding another polypeptide to a polynucleotide of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fusion polypeptide is under control of the same promoter(s) and terminator.



Fusion polypeptides may also be constructed using intein technology in which fusion polypeptides are created post-translationally (Cooper *et al.*, 1993, *EMBO J.* 12: 2575-2583; Dawson *et al.*, 1994, *Science* 266: 776-779).

A fusion polypeptide can further comprise a cleavage site between the two polypeptides. Upon secretion of the fusion protein, the site is cleaved releasing the two polypeptides. Examples of cleavage sites include, but are not limited to, the sites disclosed in Martin *et al.*, 2003, *J. Ind. Microbiol. Biotechnol.* 3: 568-576; Svetina *et al.*, 2000, *J. Biotechnol.* 76: 245-251; Rasmussen-Wilson *et al.*, 1997, *Appl. Environ. Microbiol.* 63: 3488-3493; Ward *et al.*, 1995, *Biotechnology* 13: 498-503; and Contreras *et al.*, 1991, *Biotechnology* 9: 378-381; Eaton *et al.*, 1986, *Biochemistry* 25: 505-512; Collins-Racie *et al.*, 1995, *Biotechnology* 13: 982-987; Carter *et al.*, 1989, *Proteins: Structure, Function, and Genetics* 6: 240-248; and Stevens, 2003, *Drug Discovery World* 4: 35-48.

The parent may be obtained from organisms of any genus. For purposes of the present invention, the term "obtained from" as used herein in connection with a given source shall mean that the parent encoded by a polynucleotide is produced by the source or by a strain in which the polynucleotide from the source has been inserted. In one aspect, the parent is secreted extracellularly.

The parent may be a bacterial protease. For example, the parent may be a Gram-positive bacterial polypeptide such as a *Bacillus*, *Clostridium*, *Enterococcus*, *Geobacillus*, *Lactobacillus*, *Lactococcus*, *Oceanobacillus*, *Staphylococcus*, *Streptococcus*, or *Streptomyces* protease, or a Gram-negative bacterial polypeptide such as a *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neisseria*, *Pseudomonas*, *Salmonella*, or *Ureaplasma* protease.

In one aspect, the parent is a *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis* protease

In one aspect, the parent is a *Bacillus sp.* protease, *e.g.*, the protease with SEQ ID NO: 3 or the mature polypeptide of SEQ ID NO 2.

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

The parent may be identified and obtained from other sources including microorganisms isolated from nature (*e.g.*, soil, composts, water, etc.) or DNA samples obtained directly from natural materials (*e.g.*, soil, composts, water, etc.) using the above-mentioned probes. Techniques for isolating microorganisms and DNA directly from natural habitats are well known in the art. A polynucleotide encoding a parent may then be obtained by similarly screening a genomic DNA or cDNA library of another microorganism or mixed DNA sample. Once a polynucleotide encoding a

parent has been detected with the probe(s), the polynucleotide can be isolated or cloned by utilizing techniques that are known to those of ordinary skill in the art (see, e.g., Sambrook *et al.*, 1989, *supra*).

### Preparation of Variants

The present invention also relates to methods for obtaining a variant having protease activity, comprising: (a) introducing into a parent protease a substitution at one or more (e.g., several) positions corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has protease activity; and (b) recovering the variant.

The variants can be prepared using any mutagenesis procedure known in the art, such as site-directed mutagenesis, synthetic gene construction, semi-synthetic gene construction, random mutagenesis, shuffling, etc.

Site-directed mutagenesis is a technique in which one or more (e.g., several) mutations are introduced at one or more defined sites in a polynucleotide encoding the parent.

Site-directed mutagenesis can be accomplished *in vitro* by PCR involving the use of oligonucleotide primers containing the desired mutation. Site-directed mutagenesis can also be performed *in vitro* by cassette mutagenesis involving the cleavage by a restriction enzyme at a site in the plasmid comprising a polynucleotide encoding the parent and subsequent ligation of an oligonucleotide containing the mutation in the polynucleotide. Usually the restriction enzyme that digests the plasmid and the oligonucleotide is the same, permitting sticky ends of the plasmid and the insert to ligate to one another. See, e.g., Scherer and Davis, 1979, *Proc. Natl. Acad. Sci. USA* 76: 4949-4955; and Barton *et al.*, 1990, *Nucleic Acids Res.* 18: 7349-4966.

Site-directed mutagenesis can also be accomplished *in vivo* by methods known in the art. See, e.g., U.S. Patent Application Publication No. 2004/0171154; Storici *et al.*, 2001, *Nature Biotechnol.* 19: 773-776; Kren *et al.*, 1998, *Nat. Med.* 4: 285-290; and Calissano and Macino, 1996, *Fungal Genet. Newslett.* 43: 15-16.

Any site-directed mutagenesis procedure can be used in the present invention. There are many commercial kits available that can be used to prepare variants.

Synthetic gene construction entails *in vitro* synthesis of a designed polynucleotide molecule to encode a polypeptide of interest. Gene synthesis can be performed utilizing a number of techniques, such as the multiplex microchip-based technology described by Tian *et al.* (2004, *Nature* 432: 1050-1054) and similar technologies wherein oligonucleotides are synthesized and assembled upon photo-programmable microfluidic chips.

Single or multiple amino acid substitutions, deletions, and/or insertions can be made and tested using known methods of mutagenesis, recombination, and/or shuffling, followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer, 1988, *Science* 241: 53-57; Bowie and Sauer, 1989, *Proc. Natl. Acad. Sci. USA* 86: 2152-2156; WO 95/17413; or WO 95/22625. Other methods that can be used include error-prone PCR, phage display (e.g.,

Lowman *et al.*, 1991, *Biochemistry* 30: 10832-10837; US5,223,409; WO 92/06204) and region-directed mutagenesis (Derbyshire *et al.*, 1986, *Gene* 46: 145; Ner *et al.*, 1988, *DNA* 7: 127).

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

Semi-synthetic gene construction is accomplished by combining aspects of synthetic gene construction, and/or site-directed mutagenesis, and/or random mutagenesis, and/or shuffling. Semi-synthetic construction is typified by a process utilizing polynucleotide fragments that are synthesized, in combination with PCR techniques. Defined regions of genes may thus be synthesized *de novo*, while other regions may be amplified using site-specific mutagenic primers, while yet other regions may be subjected to error-prone PCR or non-error prone PCR amplification. Polynucleotide subsequences may then be shuffled.

Thus, the invention also relates to a method for obtaining a protease variant, comprising introducing into a parent protease a substitution at one or more positions corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3; and recovering the variant.

Another embodiment concerns a method for obtaining a protease variant, comprising substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, especially a method as described above, wherein the parent protease is selected from the group consisting of: a polypeptide having at least 70%, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76% at least 77% at least 78% at least 79% at least 80%, at least 81% at least 82% at least 83% at least 84% at least 85%, at least 86% at least 87% at least 88% at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5% or at least 99.6% sequence identity to SEQ ID NO: 3;

a polypeptide encoded by a polynucleotide that hybridizes under medium or high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 1, (ii) a sequence encoding the mature polypeptide of SEQ ID NO: 2, or (iii) the full-length complement of (i) or (ii);

a polypeptide encoded by a polynucleotide having at least 70% identity to the mature polypeptide coding sequence of SEQ ID NO: 1 or a sequence encoding the mature polypeptide of SEQ ID NO: 2; and

a fragment of the mature polypeptide of SEQ ID NO: 2, which has protease activity.

Thus, a particular aspect concerns a method for obtaining a protease variant, comprising introducing into a parent protease a substitution of one or more amino acids in the loop corresponding

to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the substitution(s) is/are performed in SEQ ID NO: 3, and wherein the substitutions are selected from the group consisting of S171 {W, K, E, N}, S173 {P}, S175 {A, V, P} or G179 {C, V, Q, S, T, E, H, K, M, N, A, Y}. Additionally a further substitution can be introduced at position corresponding to 180 of SEQ ID NO: 3, especially the substitution is F180Y.

One aspect of the invention relates to methods of producing the variants according to the invention, wherein the method comprises substitution of at least one amino acid in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein (a) the variant has a sequence identity to SEQ ID NO: 3 of at least 70% and less than 100% and (b) the variant has protease activity.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 171 of SEQ ID NO: 3 and further comprises a substitution at one or more positions corresponding to positions 173, 175, 179 and 180 of SEQ ID NO: 3.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 173 of SEQ ID NO: 3 and further comprises a substitution at one or more positions corresponding to positions 171, 175, 179 and 180 of SEQ ID NO: 3.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 175 of SEQ ID NO: 3 and further comprises a substitution at one or more positions corresponding to positions 171, 173, 179 and 180 of SEQ ID NO: 3.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 179 of SEQ ID NO: 3 and further comprises a substitution at one or more positions corresponding to positions 171, 173, 175 and 180 of SEQ ID NO: 3.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 180 of SEQ ID NO: 3 and further comprises a substitution at one or more positions corresponding to positions 171, 173, 175 and 179 of SEQ ID NO: 3.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 171 of SEQ ID NO: 3 with an amino acid selected from {W, K, E, N}.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 173 of SEQ ID NO: 3 with P.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 175 of SEQ ID NO: 3 with an amino acid selected from {A, V, P}.

In one embodiment, the variant produced according to said method comprises a substitution at a position corresponding to position 179 of SEQ ID NO: 3 with an amino acid selected from {C, V, Q, S, T, E, H, K, M, N, A, Y}.

In one embodiment, the variant produced according to said method may further comprise a substitution at a position corresponding to position 180 of SEQ ID NO: 3 with Y.

### Polynucleotides

The present invention also relates to isolated polynucleotides encoding a variant of the present invention.

### Nucleic Acid Constructs

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

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

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

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

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

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

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

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

The control sequence may also be a signal peptide coding region that encodes a signal peptide linked to the N-terminus of a variant and directs the variant into the cell's secretory pathway. The 5'-end of the coding sequence of the polynucleotide may inherently contain a signal peptide coding sequence naturally linked in translation reading frame with the segment of the coding sequence that encodes the variant. Alternatively, the 5'-end of the coding sequence may contain a signal peptide coding sequence that is foreign to the coding sequence. A foreign signal peptide coding sequence may be required where the coding sequence does not naturally contain a signal peptide coding sequence. Alternatively, a foreign signal peptide coding sequence may simply replace the natural signal peptide coding sequence in order to enhance secretion of the variant. However, any signal peptide coding sequence that directs the expressed variant into the secretory pathway of a host cell may be used.

Effective signal peptide coding sequences for bacterial host cells are the signal peptide coding sequences obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus stearothermophilus* neutral proteases (*nprT*, *nprS*, *nprM*), and *Bacillus subtilis* *prsA*. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

The control sequence may also be a propeptide coding sequence that encodes a propeptide positioned at the N-terminus of a variant. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to an active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding sequence may be obtained from the genes for *Bacillus subtilis* alkaline protease (*aprE*), *Bacillus subtilis* neutral protease (*nprT*), *Myceliophthora thermophila* laccase (WO 95/33836), *Rhizomucor miehei* aspartic proteinase, and *Saccharomyces cerevisiae* alpha-factor.

Where both signal peptide and propeptide sequences are present, the propeptide sequence is positioned next to the N-terminus of the variant and the signal peptide sequence is positioned next to the N-terminus of the propeptide sequence.

It may also be desirable to add regulatory sequences that regulate expression of the variant relative to the growth of the host cell. Examples of regulatory systems are those that cause expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the *lac*, *tac*, and *trp* operator systems.

### Expression Vectors

The present invention also relates to recombinant expression vectors comprising a polynucleotide encoding a variant of the present invention, a promoter, and transcriptional and translational stop signals. The various nucleotide and control sequences may be joined together to produce a recombinant expression vector that may include one or more convenient restriction sites to allow for insertion or substitution of the polynucleotide encoding the variant at such sites. Alternatively, the polynucleotide may be expressed by inserting the polynucleotide or a nucleic acid construct comprising the polynucleotide into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) that can be conveniently subjected to recombinant DNA procedures and can bring about expression of the polynucleotide. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector may be a linear or closed circular plasmid.

The vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one that, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids that together contain the total DNA to be introduced into the genome of the host cell, or a transposon, may be used.

The vector preferably contains one or more selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

Examples of bacterial selectable markers are *Bacillus licheniformis* or *Bacillus subtilis* *dal* genes, or markers that confer antibiotic resistance such as ampicillin, chloramphenicol, kanamycin, neomycin, spectinomycin or tetracycline resistance.

The vector preferably contains an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the polynucleotide's sequence encoding the variant or any other element of the vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a

precise location, the integrational elements should contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, 400 to 10,000 base pairs, and 800 to 10,000 base pairs, which have a high degree of sequence identity to the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding polynucleotides. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term "origin of replication" or "plasmid replicator" means a polynucleotide that enables a plasmid or vector to replicate *in vivo*.

Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAM $\beta$ 1 permitting replication in *Bacillus*.

More than one copy of a polynucleotide of the present invention may be inserted into a host cell to increase production of a variant. An increase in the copy number of the polynucleotide can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the polynucleotide where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the polynucleotide, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, *e.g.*, Sambrook *et al.*, 1989, *supra*).

## Host Cells

The present invention also relates to recombinant host cells, comprising a polynucleotide encoding a variant of the present invention operably linked to one or more control sequences that direct the production of a variant of the present invention. A construct or vector comprising a polynucleotide is introduced into a host cell so that the construct or vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier. The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The choice of a host cell will to a large extent depend upon the gene encoding the variant and its source.

The host cell may be any cell useful in the recombinant production of a variant, *e.g.*, a prokaryote or a eukaryote.

The prokaryotic host cell may be any Gram-positive or Gram-negative bacterium. Gram-positive bacteria include, but are not limited to, *Bacillus*, *Clostridium*, *Enterococcus*, *Geobacillus*,



*Lactobacillus*, *Lactococcus*, *Oceanobacillus*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*. Gram-negative bacteria include, but are not limited to, *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neisseria*, *Pseudomonas*, *Salmonella*, and *Ureaplasma*.

The bacterial host cell may be any *Bacillus* cell including, but not limited to, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* cells.

The bacterial host cell may also be any *Streptococcus* cell including, but not limited to, *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, and *Streptococcus equi* subsp. *Zooepidemicus* cells.

The bacterial host cell may also be any *Streptomyces* cell, including, but not limited to, *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, and *Streptomyces lividans* cells.

The introduction of DNA into a *Bacillus* cell may be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Mol. Gen. Genet.* 168: 111-115), competent cell transformation (see, e.g., Young and Spizizen, 1961, *J. Bacteriol.* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *J. Mol. Biol.* 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, *J. Bacteriol.* 169: 5271-5278). The introduction of DNA into an *E. coli* cell may be effected by protoplast transformation (see, e.g., Hanahan, 1983, *J. Mol. Biol.* 166: 557-580) or electroporation (see, e.g., Dower *et al.*, 1988, *Nucleic Acids Res.* 16: 6127-6145). The introduction of DNA into a *Streptomyces* cell may be effected by protoplast transformation, electroporation (see, e.g., Gong *et al.*, 2004, *Folia Microbiol. (Praha)* 49: 399-405), conjugation (see, e.g., Mazodier *et al.*, 1989, *J. Bacteriol.* 171: 3583-3585), or transduction (see, e.g., Burke *et al.*, 2001, *Proc. Natl. Acad. Sci. USA* 98: 6289-6294). The introduction of DNA into a *Pseudomonas* cell may be effected by electroporation (see, e.g., Choi *et al.*, 2006, *J. Microbiol. Methods* 64: 391-397), or conjugation (see, e.g., Pinedo and Smets, 2005, *Appl. Environ. Microbiol.* 71: 51-57). The introduction of DNA into a *Streptococcus* cell may be effected by natural competence (see, e.g., Perry and Kuramitsu, 1981, *Infect. Immun.* 32: 1295-1297), protoplast transformation (see, e.g., Catt and Jollick, 1991, *Microbios* 68: 189-207), electroporation (see, e.g., Buckley *et al.*, 1999, *Appl. Environ. Microbiol.* 65: 3800-3804) or conjugation (see, e.g., Clewell, 1981, *Microbiol. Rev.* 45: 409-436). However, any method known in the art for introducing DNA into a host cell can be used.

### **Methods of Production**

The present invention also relates to methods of producing a variant, comprising: (a) cultivating a host cell of the present invention under conditions suitable for expression of the variant; and (b) recovering the variant.

The host cells are cultivated in a nutrient medium suitable for production of the variant using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, or small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the variant to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the variant is secreted into the nutrient medium, the variant can be recovered directly from the medium. If the variant is not secreted, it can be recovered from cell lysates.

The variant may be detected using methods known in the art that are specific for the variants with protease activity. These detection methods include, but are not limited to, use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the variant.

The variant may be recovered using methods known in the art. For example, the variant may be recovered from the nutrient medium by conventional procedures including, but not limited to, collection, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

The variant may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation), SDS-PAGE, or extraction (see, e.g., *Protein Purification*, Janson and Ryden, editors, VCH Publishers, New York, 1989) to obtain substantially pure variants.

In an alternative aspect, the variant is not recovered, but rather a host cell of the present invention expressing the variant is used as a source of the variant.

## **Compositions**

In one certain aspect, the variants according to the invention has improved stability in detergents compared to the parent enzyme or compared to a protease having the identical amino acid sequence of said variant but not having the substitutions at one or more of said specified positions or compared to a protease with SEQ ID NO 3, wherein stability is measured in Example 2 as described in "Material and Methods" herein.

Besides enzymes the detergent compositions may comprise additional components. The choice of additional components is within the skill of the artisan and includes conventional ingredients, including the exemplary non-limiting components set forth below. The choice of components may include, for fabric care, the consideration of the type of fabric to be cleaned, the type and/or degree of soiling, the temperature at which cleaning is to take place, and the formulation of the detergent product. Although components mentioned below are categorized by general header according to a particular

functionality, this is not to be construed as a limitation, as a component may comprise additional functionalities as will be appreciated by the skilled artisan.

### Detergent compositions of the present invention

The variants of the present invention may be added to a detergent composition in an amount corresponding to 0.001-100 mg of protein, such as 0.01-100 mg of protein, preferably 0.005-50 mg of protein, more preferably 0.01-25 mg of protein, even more preferably 0.05-10 mg of protein, most preferably 0.05-5 mg of protein, and even most preferably 0.01-1 mg of protein per liter of wash liquor.

The variants of the present invention may be stabilized using stabilizing agents, which may be selected from the group containing propylene glycol, glycerol, a sugar, a sugar alcohol, lactic acid, boric acid, borate and phenyl boronic acid derivatives, such as those where the residue R in the phenyl boronic acid derivative is a C<sub>1</sub>-C<sub>6</sub> alkyl group and among these, more preferably, CH<sub>3</sub>, CH<sub>3</sub>CH<sub>2</sub> or CH<sub>3</sub>CH<sub>2</sub>CH<sub>2</sub>. The residue R in the phenyl boronic acid derivative may also be hydrogen. One example of a phenyl boronic acid derivative is 4-formylphenylboronic acid (4-FPBA) with the following formula:



Phenyl boronic acid derivatives can furthermore have other chemical modifications on the phenyl ring, and in particular they can contain one or more methyl, amino, nitro, chloro, fluoro, bromo, hydroxyl, formyl, ethyl, acetyl, t-butyl, anisyl, benzyl, trifluoroacetyl, N-hydroxysuccinimide, t-butylloxycarbonyl, benzoyl, 4-methylbenzyl, thioanisyl, thiocresyl, benzyloxymethyl, 4-nitrophenyl, benzyloxycarbonyl, 2-nitrobenzoyl, 2-nitrophenylsulfenyl, 4-toluenesulfonyl, pentafluorophenyl, diphenylmethyl, 2-chlorobenzyloxycarbonyl, 2,4,5-trichlorophenyl, 2-bromobenzyloxycarbonyl, 9-fluorenylmethyloxycarbonyl, triphenylmethyl, 2,2,5,7,8-pentamethylchroman-6-sulfonyl residues or groups or combinations thereof. All stabilizing agents can be present in the detergent composition in all protonated or deprotonated forms. Furthermore, all such compounds, in particular their deprotonated forms, can be associated with cations. Preferred cations in this respect are monovalent or polyvalent, in particular divalent, cations, in particular Na ions (Na<sup>+</sup>), K ions (K<sup>+</sup>), Li ions (Li<sup>+</sup>), Ca ions (Ca<sup>2+</sup>), Mg ions (Mg<sup>2+</sup>), Mn ions (Mn<sup>2+</sup>) and Zn ions (Zn<sup>2+</sup>). The detergent compositions may comprise two or more stabilizing agents e.g. such as those selected from the group consisting of propylene glycol, glycerol, 4-formylphenyl boronic acid and borate. One example is a detergent composition comprising 4-formylphenyl boronic acid and/or borate. The phenyl boronic acid derivative may be contained in the detergent composition in a quantity of from 0.00001 to 5.0 wt%, preferably from 0.0001 to 3.0 wt%, from 0.001 to 2.0 wt%, from 0.005 to 1.0 wt%, from 0.01 to 0.5 wt%, from 0.02 to 0.3 wt%. Preferably, the boric acid / borate is contained in a quantity of from 0.001 to 5.5 wt.% and increasingly preferably of from 0.01 to 4.5 wt.%, from 0.05 to 3.5 and from 0.1 to 3, 0.4 bis 2.49, 0.5

bis 1.5 wt.% in the detergent composition. Addition of a combination of borate and 4-formylphenyl boronic acid has been found to be particularly effective, leading to a high increase in enzyme stability in detergent compositions. Preferably, the boric acid / borate is contained in a quantity of from 0.001 to 5.5 wt.% and increasingly preferably from 0.075 to 4.5 wt.%, from 0.09 to 3.5 and from 0.1 to 2.49 wt.%, and the phenyl boronic acid derivative is contained in a quantity of from 0.001 to 0.08 wt.% and increasingly preferably from 0.003 to 0.06 wt.%, from 0.005 to 0.05 wt.%, from 0.007 to 0.03 wt.% and from 0.009 to 0.01 wt.% in a detergent composition. Particularly preferred is the addition of 4-formylphenyl boronic acid in an amount of 1.0 to 2.0 wt% in combination with 1.0 wt% borate.

The variants according to the invention may also be stabilized using peptide aldehydes or ketones such as described in WO2005/105826 and WO2009/118375. A variant of the present invention may also be incorporated in the detergent formulations disclosed in WO97/07202, which is hereby incorporated by reference.

### Surfactants

The detergent composition may comprise one or more surfactants, which may be anionic and/or cationic and/or non-ionic and/or semi-polar and/or zwitterionic, or a mixture thereof. In a particular embodiment, the detergent composition includes a mixture of one or more nonionic surfactants and one or more anionic surfactants. The surfactant(s) is typically present at a level of from about 0.1% to 60% by weight, such as about 1% to about 40%, or about 3% to about 20%, or about 3% to about 10%. The surfactant(s) is chosen based on the desired cleaning application, and includes any conventional surfactant(s) known in the art. Any surfactant known in the art for use in detergents may be utilized.

When included therein the detergent will usually contain from about 1% to about 40% by weight, such as from about 5% to about 30%, including from about 5% to about 15%, or from about 20% to about 25% of an anionic surfactant. Non-limiting examples of anionic surfactants include sulfates and sulfonates, in particular, linear alkylbenzenesulfonates (LAS), isomers of LAS, branched alkylbenzenesulfonates (BABS), phenylalkanesulfonates, alpha-olefinsulfonates (AOS), olefin sulfonates, alkene sulfonates, alkane-2,3-diylbis(sulfates), hydroxyalkanesulfonates and disulfonates, alkyl sulfates (AS) such as sodium dodecyl sulfate (SDS), fatty alcohol sulfates (FAS), primary alcohol sulfates (PAS), alcohol ethersulfates (AES or AEOS or FES, also known as alcohol ethoxysulfates or fatty alcohol ether sulfates), secondary alkanesulfonates (SAS), paraffin sulfonates (PS), ester sulfonates, sulfonated fatty acid glycerol esters, alpha-sulfo fatty acid methyl esters (alpha-SFMe or SES) including methyl ester sulfonate (MES), alkyl- or alkenylsuccinic acid, dodeceny/tetradeceny succinic acid (DTSA), fatty acid derivatives of amino acids, diesters and monoesters of sulfo-succinic acid or soap, and combinations thereof.

When included therein the detergent will usually contain from about 1% to about 40% by weight of a cationic surfactant. Non-limiting examples of cationic surfactants include alklydimethylehanolamine quat (ADMEAQ), cetyltrimethylammonium bromide (CTAB), dimethyldistearylammonium chloride

(DSDMAC), and alkylbenzyltrimethylammonium, and combinations thereof, Alkyl quaternary ammonium compounds, Alkoxyated quaternary ammonium (AQA),

When included therein the detergent will usually contain from about 0.2% to about 40% by weight of a non-ionic surfactant, for example from about 0.5% to about 30%, in particular from about 1% to about 20%, from about 3% to about 10%, such as from about 3% to about 5%, or from about 8% to about 12%. Non-limiting examples of non-ionic surfactants include alcohol ethoxylates (AE or AEO), alcohol propoxylates, propoxylated fatty alcohols (PFA), alkoxyated fatty acid alkyl esters, such as ethoxylated and/or propoxylated fatty acid alkyl esters, alkylphenol ethoxylates (APE), nonylphenol ethoxylates (NPE), alkylpolyglycosides (APG), alkoxyated amines, fatty acid monoethanolamides (FAM), fatty acid diethanolamides (FADA), ethoxylated fatty acid monoethanolamides (EFAM), propoxylated fatty acid monoethanolamide (PFAM), polyhydroxy alkyl fatty acid amides, or N-acyl N-alkyl derivatives of glucosamine (glucamides, GA, or fatty acid glucamide, FAGA), as well as products available under the trade names SPAN and TWEEN, and combinations thereof.

When included therein the detergent will usually contain from about 1% to about 40% by weight of a semipolar surfactant. Non-limiting examples of semipolar surfactants include amine oxides (AO) such as alkyldimethylamineoxide, *N*-(coco alkyl)-*N,N*-dimethylamine oxide and *N*-(tallow-alkyl)-*N,N*-bis(2-hydroxyethyl)amine oxide, fatty acid alkanolamides and ethoxylated fatty acid alkanolamides, and combinations thereof.

When included therein the detergent will usually contain from about 1% to about 40% by weight of a zwitterionic surfactant. Non-limiting examples of zwitterionic surfactants include betaine, alkyldimethylbetaine, and sulfobetaine, and combinations thereof.

### **Hydrotropes**

A hydrotrope is a compound that solubilises hydrophobic compounds in aqueous solutions (or oppositely, polar substances in a non-polar environment). Typically, hydrotropes have both hydrophilic and a hydrophobic character (so-called amphiphilic properties as known from surfactants); however the molecular structure of hydrotropes generally do not favor spontaneous self-aggregation, see e.g. review by Hodgdon and Kaler (2007), *Current Opinion in Colloid & Interface Science* 12: 121-128. Hydrotropes do not display a critical concentration above which self-aggregation occurs as found for surfactants and lipids forming micellar, lamellar or other well defined meso-phases. Instead, many hydrotropes show a continuous-type aggregation process where the sizes of aggregates grow as concentration increases. However, many hydrotropes alter the phase behavior, stability, and colloidal properties of systems containing substances of polar and non-polar character, including mixtures of water, oil, surfactants, and polymers. Hydrotropes are classically used across industries from pharma, personal care, food, to technical applications. Use of hydrotropes in detergent compositions allow for example more concentrated formulations of surfactants (as in the process of compacting liquid detergents by removing water) without inducing undesired phenomena such as phase separation or high viscosity.

The detergent may contain 0-5% by weight, such as about 0.5 to about 5%, or about 3% to about 5%, of a hydrotrope. Any hydrotrope known in the art for use in detergents may be utilized. Non-limiting examples of hydrotropes include sodium benzene sulfonate, sodium p-toluene sulfonates (STS), sodium xylene sulfonates (SXS), sodium cumene sulfonates (SCS), sodium cymene sulfonate, amine oxides, alcohols and polyglycoethers, sodium hydroxynaphthoate, sodium hydroxynaphthalene sulfonate, sodium ethylhexyl sulfate, and combinations thereof.

### **Builders and Co-Builders**

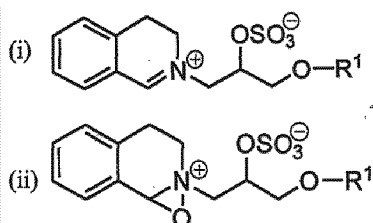
The detergent composition may contain about 0-65% by weight, such as about 5% to about 50% of a detergent builder or co-builder, or a mixture thereof. In a dish wash detergent, the level of builder is typically 40-65%, particularly 50-65%. The builder and/or co-builder may particularly be a chelating agent that forms water-soluble complexes with Ca and Mg. Any builder and/or co-builder known in the art for use in laundry, ADW and hard surfaces cleaning detergents may be utilized. Non-limiting examples of builders include zeolites, diphosphates (pyrophosphates), triphosphates such as sodium triphosphate (STP or STPP), carbonates such as sodium carbonate, soluble silicates such as sodium metasilicate, layered silicates (e.g., SKS-6 from Hoechst), ethanolamines such as 2-aminoethan-1-ol (MEA), iminodiethanol (DEA) and 2,2',2''-nitrilotriethanol (TEA), and carboxymethylinulin (CMI), and combinations thereof.

The detergent composition may also contain 0-65% by weight, such as about 5% to about 40%, of a detergent co-builder, or a mixture thereof. The detergent composition may include a co-builder alone, or in combination with a builder, for example a zeolite builder. Non-limiting examples of co-builders include homopolymers of polyacrylates or copolymers thereof, such as poly(acrylic acid) (PAA) or copoly(acrylic acid/maleic acid) (PAA/PMA). Further non-limiting examples include citrate, chelators such as aminocarboxylates, aminopolycarboxylates and phosphonates, and alkyl- or alkenylsuccinic acid. Additional specific examples include 2,2',2''-nitrilotriacetic acid (NTA), ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTPA), iminodisuccinic acid (IDS), ethylenediamine-N,N'-disuccinic acid (EDDS), methylglycinediacetic acid (MGDA), glutamic acid-N,N'-diacetic acid (GLDA), 1-hydroxyethane-1,1-diylbis(phosphonic acid) (HEDP), ethylenediaminetetrakis(methylene)tetrakis(phosphonic acid) (EDTMPA), diethylenetriaminepentakis(methylene)pentakis(phosphonic acid) (DTPMPA), N-(2-hydroxyethyl)iminodiacetic acid (EDG), aspartic acid-N-monoacetic acid (ASMA), aspartic acid-N,N'-diacetic acid (ASDA), aspartic acid-N- monopropionic acid (ASMP), iminodisuccinic acid (IDA), N-(2-sulfomethyl) aspartic acid (SMAS), N-(2-sulfoethyl) aspartic acid (SEAS), N-(2-sulfomethyl) glutamic acid (SMGL), N-(2-sulfoethyl) glutamic acid (SEGL), N-methyliminodiacetic acid (MIDA),  $\alpha$ -alanine-N,N'-diacetic acid ( $\alpha$ -ALDA), serine-N,N'-diacetic acid (SEDA), isoserine-N,N'-diacetic acid (ISDA), phenylalanine-N,N'-diacetic acid (PHDA), anthranilic acid-N,N'-diacetic acid (ANDA), sulfanilic acid-N,N'-diacetic acid (SLDA), taurine-N,N'-diacetic acid (TUDA) and sulfomethyl-N,N'-diacetic acid (SMDA), N-(hydroxyethyl)-ethylenediaminetriacetate (HEDTA), diethanolglycine (DEG), Diethylenetriamine

Penta (Methylene Phosphonic acid) (DTPMP), aminotris(methylenephosphonic acid) (ATMP), and combinations and salts thereof. Further exemplary builders and/or co-builders are described in, e.g., WO 09/102854, US 5977053.

### Bleaching Systems

The detergent may contain 0-10% by weight, such as about 1% to about 5%, of a bleaching system. Any bleaching system known in the art for use in laundry, ADW and hard surfaces cleaning detergents may be utilized. Suitable bleaching system components include bleaching catalysts, photobleaches, bleach activators, sources of hydrogen peroxide such as sodium percarbonate and sodium perborates, preformed peracids and mixtures thereof. Suitable preformed peracids include, but are not limited to, peroxydicarboxylic acids and salts, percarbonic acids and salts, perimidic acids and salts, peroxymonosulfuric acids and salts, for example, Oxone (R), and mixtures thereof. Non-limiting examples of bleaching systems include peroxide-based bleaching systems, which may comprise, for example, an inorganic salt, including alkali metal salts such as sodium salts of perborate (usually mono- or tetra-hydrate), percarbonate, persulfate, perphosphate, persilicate salts, in combination with a peracid-forming bleach activator. By bleach activator is meant herein a compound which reacts with peroxygen bleach like hydrogen peroxide to form a peracid. The peracid thus formed constitutes the activated bleach. Suitable bleach activators to be used herein include those belonging to the class of esters amides, imides or anhydrides. Suitable examples are tetraacetyl ethylene diamine (TAED), sodium 3,5,5 trimethyl hexanoyloxybenzene sulphonat, diperoxy dodecanoic acid, 4-(dodecanoyloxy)benzenesulfonate (LOBS), 4-(decanoyloxy)benzenesulfonate, 4-(decanoyloxy)benzoate (DOBS), 4-(3,5,5-trimethylhexanoyloxy)benzenesulfonate (ISONOBS), tetraacetylenediamine (TAED) and 4-(nonanoyloxy)benzenesulfonate (NOBS), and/or those disclosed in WO98/17767. A particular family of bleach activators of interest was disclosed in EP624154 and particularly preferred in that family is acetyl triethyl citrate (ATC). ATC or a short chain triglyceride like Triacin has the advantage that it is environmental friendly as it eventually degrades into citric acid and alcohol. Furthermore acethyl triethyl citrate and triacetin has a good hydrolytical stability in the product upon storage and it is an efficient bleach activator. Finally ATC provides a good building capacity to the laundry additive. Alternatively, the bleaching system may comprise peroxyacids of, for example, the amide, imide, or sulfone type. The bleaching system may also comprise peracids such as 6-(phthaloylamino)percapronic acid (PAP). The bleaching system may also include a bleach catalyst. In some embodiments the bleach component may be an organic catalyst selected from the group consisting of organic catalysts having the following formulae:



(iii) and mixtures thereof; wherein each R<sup>1</sup> is independently a branched alkyl group containing from 9 to 24 carbons or linear alkyl group containing from 11 to 24 carbons, preferably each R<sup>1</sup> is independently a branched alkyl group containing from 9 to 18 carbons or linear alkyl group containing from 11 to 18 carbons, more preferably each R<sup>1</sup> is independently selected from the group consisting of 2-propylheptyl, 2-butyloctyl, 2-pentylnonyl, 2-hexyldecyl, n-dodecyl, n-tetradecyl, n-hexadecyl, n-octadecyl, iso-nonyl, iso-decyl, iso-tridecyl and iso-pentadecyl. Other exemplary bleaching systems are described, e.g., in WO2007/087258, WO2007/087244, WO2007/087259, WO2007/087242. Suitable photobleaches may for example be sulfonated zinc phthalocyanine

### **Polymers**

The detergent may contain 0-10% by weight, such as 0.5-5%, 2-5%, 0.5-2% or 0.2-1% of a polymer. Any polymer known in the art for use in detergents may be utilized. The polymer may function as a co-builder as mentioned above, or may provide antiredeposition, fiber protection, soil release, dye transfer inhibition, grease cleaning and/or anti-foaming properties. Some polymers may have more than one of the above-mentioned properties and/or more than one of the below-mentioned motifs. Exemplary polymers include (carboxymethyl)cellulose (CMC), poly(vinyl alcohol) (PVA), poly(vinylpyrrolidone) (PVP), poly(ethyleneglycol) or poly(ethylene oxide) (PEG), ethoxylated poly(ethyleneimine), carboxymethyl inulin (CMI), and polycarboxylates such as PAA, PAA/PMA, poly-aspartic acid, and lauryl methacrylate/acrylic acid copolymers, hydrophobically modified CMC (HM-CMC) and silicones, copolymers of terephthalic acid and oligomeric glycols, copolymers of polyethylene terephthalate and polyoxyethylene terephthalate (PET-POET), PVP, poly(vinylimidazole) (PVI), poly(vinylpyridin-N-oxide) (PVPO or PVPNO) and polyvinylpyrrolidone-vinylimidazole (PVPVI). Further exemplary polymers include sulfonated polycarboxylates, polyethylene oxide and polypropylene oxide (PEO-PPO) and diquaternium ethoxy sulfate. Other exemplary polymers are disclosed in, e.g., WO 2006/130575. Salts of the above-mentioned polymers are also contemplated.

### **Fabric hueing agents**

The detergent compositions may also include fabric hueing agents such as dyes or pigments which when formulated in detergent compositions can deposit onto a fabric when said fabric is contacted with a wash liquor comprising said detergent compositions thus altering the tint of said fabric through absorption/reflection of visible light. Fluorescent whitening agents emit at least some visible light. In contrast, fabric hueing agents alter the tint of a surface as they absorb at least a portion of the visible light spectrum. Suitable fabric hueing agents include dyes and dye-clay conjugates, and may also include pigments. Suitable dyes include small molecule dyes and polymeric dyes. Suitable small molecule dyes include small molecule dyes selected from the group consisting of dyes falling into the Colour Index (C.I.) classifications of Direct Blue, Direct Red, Direct Violet, Acid Blue, Acid Red, Acid Violet, Basic Blue, Basic Violet and Basic Red, or mixtures thereof,



for example as described in WO2005/03274, WO2005/03275, WO2005/03276 and EP1876226 (hereby incorporated by reference). A detergent composition preferably comprises from about 0.00003 wt% to about 0.2 wt%, from about 0.00008 wt% to about 0.05 wt%, or even from about 0.0001 wt% to about 0.04 wt% fabric hueing agent. The composition may comprise from 0.0001 wt% to 0.2 wt% fabric hueing agent, this may be especially preferred when the composition is in the form of a unit dose pouch. Suitable hueing agents are also disclosed in, e.g., WO 2007/087257, WO2007/087243.

### **(Additional) Enzymes**

In one embodiment, the variants according to the invention are combined with one or more enzymes, such as at least two enzymes, more preferred at least three, four or five enzymes. Preferably, the enzymes have different substrate specificity, e.g., proteolytic activity, amylolytic activity, lipolytic activity, hemicellulytic activity or pectolytic activity.

The detergent additive as well as the detergent composition may comprise one or more additional enzymes such as carbohydrate-active enzymes like carbohydrase, pectinase, mannanase, amylase, cellulase, arabinase, galactanase, xylanase, or protease, lipase, a, cutinase, oxidase, e.g., a laccase, and/or peroxidase.

In general the properties of the selected enzyme(s) should be compatible with the selected detergent, (i.e., pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.), and the enzyme(s) should be present in effective amounts.

#### Cellulases:

Suitable cellulases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Suitable cellulases include cellulases from the genera *Bacillus*, *Pseudomonas*, *Humicola*, *Fusarium*, *Thielavia*, *Acremonium*, e.g., the fungal cellulases produced from *Humicola insolens*, *Myceliophthora thermophila* and *Fusarium oxysporum* disclosed in US 4,435,307, US 5,648,263, US 5,691,178, US 5,776,757 and WO 89/09259.

Especially suitable cellulases are the alkaline or neutral cellulases having colour care benefits. Examples of such cellulases are cellulases described in EP 0 495 257, EP 0 531 372, WO 96/11262, WO 96/29397, WO 98/08940. Other examples are cellulase variants such as those described in WO 94/07998, EP 0 531 315, US 5,457,046, US 5,686,593, US 5,763,254, WO 95/24471, WO 98/12307 and WO99/001544.

Other cellulases are endo-beta-1,4-glucanase enzyme having a sequence of at least 97% identity to the amino acid sequence of position 1 to position 773 of SEQ ID NO:2 of WO 2002/099091 or a family 44 xyloglucanase, which a xyloglucanase enzyme having a sequence of at least 60% identity to positions 40-559 of SEQ ID NO: 2 of WO 2001/062903.

Commercially available cellulases include Celluzyme™, and Carezyme™ (Novozymes A/S) Carezyme Premium™ (Novozymes A/S), Celluclean™ (Novozymes A/S), Celluclean Classic™

(Novozymes A/S), Cellusoft™ (Novozymes A/S), Whitezyme™ (Novozymes A/S), Clazinase™, and Puradax HA™ (Genencor International Inc.), and KAC-500(B)™ (Kao Corporation).

#### Mannanases

Suitable mannanases include those of bacterial or fungal origin. Chemically or genetically modified mutants are included. The mannanase may be an alkaline mannanase of Family 5 or 26. It may be a wild-type from *Bacillus* or *Humicola*, particularly *B. agaradhaerens*, *B. licheniformis*, *B. halodurans*, *B. clausii*, or *H. insolens*. Suitable mannanases are described in WO 1999/064619. A commercially available mannanase is Mannaway (Novozymes A/S).

#### Proteases

Suitable proteases include those of bacterial, fungal, plant, viral or animal origin e.g. vegetable or microbial origin. Microbial origin is preferred. Chemically modified or protein engineered mutants are included. It may be an alkaline protease, such as a serine protease or a metalloprotease. A serine protease may for example be of the S1 family, such as trypsin, or the S8 family such as subtilisin. A metalloproteases protease may for example be a thermolysin from e.g. family M4 or other metalloprotease such as those from M5, M7 or M8 families.

The term "subtilases" refers to a sub-group of serine protease according to Siezen et al., Protein Engng. 4 (1991) 719-737 and Siezen et al. Protein Science 6 (1997) 501-523. Serine proteases are a subgroup of proteases characterized by having a serine in the active site, which forms a covalent adduct with the substrate. The subtilases may be divided into 6 sub-divisions, i.e. the Subtilisin family, the Thermitase family, the Proteinase K family, the Lantibiotic peptidase family, the Kexin family and the Pyrolysin family.

Examples of subtilases are those derived from *Bacillus* such as *Bacillus lentus*, *B. alkalophilus*, *B. subtilis*, *B. amyloliquefaciens*, *Bacillus pumilus* and *Bacillus gibsonii* described in; US7262042 and WO09/021867, and *subtilisin lentus*, *subtilisin Novo*, *subtilisin Carlsberg*, *Bacillus licheniformis*, *subtilisin BPN'*, *subtilisin 309*, *subtilisin 147* and *subtilisin 168* described in WO89/06279 and protease PD138 described in (WO93/18140). Other useful proteases may be those described in WO92/175177, WO01/016285, WO02/026024 and WO02/016547. Examples of trypsin-like proteases are trypsin (e.g. of porcine or bovine origin) and the *Fusarium* protease described in WO89/06270, WO94/25583 and WO05/040372, and the chymotrypsin proteases derived from *Cellulomonas* described in WO05/052161 and WO05/052146.

A further preferred protease is the alkaline protease from *Bacillus lentus* DSM 5483, as described for example in WO95/23221, and variants thereof which are described in WO92/21760, WO95/23221, EP1921147 and EP1921148.

Examples of metalloproteases are the neutral metalloprotease as described in WO07/044993 (Genencor Int.) such as those derived from *Bacillus amyloliquefaciens*.

Examples of useful proteases are the variants described in: WO92/19729, WO96/034946, WO98/20115, WO98/20116, WO99/011768, WO01/44452, WO03/006602, WO04/03186, WO04/041979, WO07/006305, WO11/036263, WO11/036264, especially the variants with

substitutions in one or more of the following positions: 3, 4, 9, 15, 27, 36, 57, 68, 76, 87, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 106, 118, 120, 123, 128, 129, 130, 160, 167, 170, 194, 195, 199, 205, 206, 217, 218, 222, 224, 232, 235, 236, 245, 248, 252 and 274 using the BPN' numbering. More preferred the protease variants may comprise the mutations: S3T, V4I, S9R, A15T, K27R, \*36D, V68A, N76D, N87S,R, \*97E, A98S, S99G,D,A, S99AD, S101G,M,R S103A, V104I,Y,N, S106A, G118V,R, H120D,N, N123S, S128L, P129Q, S130A, G160D, Y167A, R170S, A194P, G195E, V199M, V205I, L217D, N218D, M222S, A232V, K235L, Q236H, Q245R, N252K, T274A (using BPN' numbering).

Suitable commercially available protease enzymes include those sold under the trade names Alcalase®, Duralase™, Durazym™, Release®, Release® Ultra, Savinase®, Savinase® Ultra, Primase®, Polarzyme®, Kannase®, Liquanase®, Liquanase® Ultra, Ovozyme®, Coronase®, Coronase® Ultra, Neutrase®, Everlase® and Esperase® (Novozymes A/S), those sold under the tradename Maxatase®, Maxacal®, Maxapem®, Purafect®, Purafect Prime®, Preferenz™, Purafect MA®, Purafect Ox®, Purafect OxP®, Puramax®, Properase®, Effectenz™, FN2®, FN3®, FN4®, Excellase®, Eraser®, Opticlean® and Optimase® (Danisco/DuPont), Axapem™ (Gist-Brocades N.V.), BLAP (sequence shown in Figure 29 of US5352604) and variants hereof (Henkel AG) and KAP (*Bacillus alkalophilus subtilisin*) from Kao.

#### Lipases and Cutinases:

Suitable lipases and cutinases include those of bacterial or fungal origin. Chemically modified or protein engineered mutant enzymes are included. Examples include lipase from *Thermomyces*, e.g. from *T. lanuginosus* (previously named *Humicola lanuginosa*) as described in EP258068 and EP305216, cutinase from *Humicola*, e.g. *H. insolens* (WO96/13580), lipase from strains of *Pseudomonas* (some of these now renamed to *Burkholderia*), e.g. *P. alcaligenes* or *P. pseudoalcaligenes* (EP218272), *P. cepacia* (EP331376), *P. sp.* strain SD705 (WO95/06720 & WO96/27002), *P. wisconsinensis* (WO96/12012), GDSL-type *Streptomyces* lipases (WO10/065455), cutinase from *Magnaporthe grisea* (WO10/107560), cutinase from *Pseudomonas mendocina* (US5,389,536), lipase from *Thermobifida fusca* (WO11/084412), *Geobacillus stearothermophilus* lipase (WO11/084417), lipase from *Bacillus subtilis* (WO11/084599), and lipase from *Streptomyces griseus* (WO11/150157) and *S. pristinaespiralis* (WO12/137147).

Other examples are lipase variants such as those described in EP407225, WO92/05249, WO94/01541, WO94/25578, WO95/14783, WO95/30744, WO95/35381, WO95/22615, WO96/00292, WO97/04079, WO97/07202, WO00/34450, WO00/60063, WO01/92502, WO07/87508 and WO09/109500.

Preferred commercial lipase products include include Lipolase™, Lipex™; Lipolex™ and Lipoclean™ (Novozymes A/S), Lumafast (originally from Genencor) and Lipomax (originally from Gist-Brocades).

Still other examples are lipases sometimes referred to as acyltransferases or perhydrolases, e.g. acyltransferases with homology to *Candida antarctica* lipase A (WO10/111143), acyltransferase from *Mycobacterium smegmatis* (WO05/56782), perhydrolases from the CE 7 family (WO09/67279), and variants of the *M. smegmatis* perhydrolase in particular the S54V variant used in the commercial product Gentle Power Bleach from Huntsman Textile Effects Pte Ltd (WO10/100028).

Amylases: Suitable amylases which can be used together with the variants of the invention may be an alpha-amylase or a glucoamylase and may be of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Amylases include, for example, alpha-amylases obtained from *Bacillus*, e.g., a special strain of *Bacillus licheniformis*, described in more detail in GB 1,296,839.

Suitable amylases include amylases having SEQ ID NO: 2 in WO 95/10603 or variants having 90% sequence identity to SEQ ID NO: 3 thereof. Preferred variants are described in WO 94/02597, WO 94/18314, WO 97/43424 and SEQ ID NO: 4 of WO 99/019467, such as variants with substitutions in one or more of the following positions: 15, 23, 105, 106, 124, 128, 133, 154, 156, 178, 179, 181, 188, 190, 197, 201, 202, 207, 208, 209, 211, 243, 264, 304, 305, 391, 408, and 444.

Different suitable amylases include amylases having SEQ ID NO: 6 in WO 02/010355 or variants thereof having 90% sequence identity to SEQ ID NO: 6. Preferred variants of SEQ ID NO: 6 are those having a deletion in positions 181 and 182 and a substitution in position 193.

Other amylases which are suitable are hybrid alpha-amylase comprising residues 1-33 of the alpha-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 6 of WO 2006/066594 and residues 36-483 of the *B. licheniformis* alpha-amylase shown in SEQ ID NO: 4 of WO 2006/066594 or variants having 90% sequence identity thereof. Preferred variants of this hybrid alpha-amylase are those having a substitution, a deletion or an insertion in one or more of the following positions: G48, T49, G107, H156, A181, N190, M197, I201, A209 and Q264. Most preferred variants of the hybrid alpha-amylase comprising residues 1-33 of the alpha-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 6 of WO 2006/066594 and residues 36-483 of SEQ ID NO: 4 are those having the substitutions:

M197T;

H156Y+A181T+N190F+A209V+Q264S; or

G48A+T49I+G107A+H156Y+A181T+N190F+I201F+A209V+Q264S.

Further amylases which are suitable are amylases having SEQ ID NO: 6 in WO 99/019467 or variants thereof having 90% sequence identity to SEQ ID NO: 6. Preferred variants of SEQ ID NO: 6 are those having a substitution, a deletion or an insertion in one or more of the following positions: R181, G182, H183, G184, N195, I206, E212, E216 and K269. Particularly preferred amylases are those having deletion in positions R181 and G182, or positions H183 and G184.

Additional amylases which can be used are those having SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 2 or SEQ ID NO: 7 of WO 96/023873 or variants thereof having 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 7. Preferred variants of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 7 are those having a substitution, a deletion or an insertion in one or more of the following positions: 140, 181, 182, 183, 184, 195, 206, 212, 243, 260, 269, 304 and 476, using SEQ ID 2 of WO 96/023873 for numbering. More preferred variants are those having a deletion in two positions selected from 181, 182, 183 and 184, such as 181 and 182, 182 and 183, or positions 183 and 184. Most preferred amylase variants of SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 7 are those having a deletion in positions 183 and 184 and a substitution in one or more of positions 140, 195, 206, 243, 260, 304 and 476.

Other amylases which can be used are amylases having SEQ ID NO: 2 of WO 08/153815, SEQ ID NO: 10 in WO 01/66712 or variants thereof having 90% sequence identity to SEQ ID NO: 2 of WO 08/153815 or 90% sequence identity to SEQ ID NO: 10 in WO 01/66712. Preferred variants of SEQ ID NO: 10 in WO 01/66712 are those having a substitution, a deletion or an insertion in one or more of the following positions: 176, 177, 178, 179, 190, 201, 207, 211 and 264.

Further suitable amylases are amylases having SEQ ID NO: 2 of WO 09/061380 or variants having 90% sequence identity to SEQ ID NO: 2 thereof. Preferred variants of SEQ ID NO: 2 are those having a truncation of the C-terminus and/or a substitution, a deletion or an insertion in one or more of the following positions: Q87, Q98, S125, N128, T131, T165, K178, R180, S181, T182, G183, M201, F202, N225, S243, N272, N282, Y305, R309, D319, Q320, Q359, K444 and G475. More preferred variants of SEQ ID NO: 2 are those having the substitution in one or more of the following positions: Q87E,R, Q98R, S125A, N128C, T131I, T165I, K178L, T182G, M201L, F202Y, N225E,R, N272E,R, S243Q,A,E,D, Y305R, R309A, Q320R, Q359E, K444E and G475K and/or deletion in position R180 and/or S181 or of T182 and/or G183. Most preferred amylase variants of SEQ ID NO: 2 are those having the substitutions:

N128C+K178L+T182G+Y305R+G475K;

N128C+K178L+T182G+F202Y+Y305R+D319T+G475K;

S125A+N128C+K178L+T182G+Y305R+G475K; or

S125A+N128C+T131I+T165I+K178L+T182G+Y305R+G475K wherein the variants are C-terminally truncated and optionally further comprises a substitution at position 243 and/or a deletion at position 180 and/or position 181.

Further suitable amylases are amylases having SEQ ID NO: 1 of WO13184577 or variants having 90% sequence identity to SEQ ID NO: 1 thereof. Preferred variants of SEQ ID NO: 1 are those having a substitution, a deletion or an insertion in one or more of the following positions: K176, R178, G179, T180, G181, E187, N192, M199, I203, S241, R458, T459, D460, G476 and G477. More preferred variants of SEQ ID NO: 1 are those having the substitution in one or more of the following positions: K176L, E187P, N192FYH, M199L, I203YF, S241QADN, R458N, T459S, D460T, G476K

and G477K and/or deletion in position R178 and/or S179 or of T180 and/or G181. Most preferred amylase variants of SEQ ID NO: 1 are those having the substitutions:

E187P+I203Y+G476K

E187P+I203Y+R458N+T459S+D460T+G476K

wherein the variants optionally further comprises a substitution at position 241 and/or a deletion at position 178 and/or position 179.

Further suitable amylases are amylases having SEQ ID NO: 1 of WO10104675 or variants having 90% sequence identity to SEQ ID NO: 1 thereof. Preferred variants of SEQ ID NO: 1 are those having a substitution, a deletion or an insertion in one of more of the following positions: N21, D97, V128 K177, R179, S180, I181, G182, M200, L204, E242, G477 and G478. More preferred variants of SEQ ID NO: 1 are those having the substitution in one of more of the following positions: N21D, D97N, V128I K177L, M200L, L204YF, E242QA, G477K and G478K and/or deletion in position R179 and/or S180 or of I181 and/or G182. Most preferred amylase variants of SEQ ID NO: 1 are those having the substitutions:

N21D+D97N+V128I

wherein the variants optionally further comprises a substitution at position 200 and/or a deletion at position 180 and/or position 181.

Other suitable amylases are the alpha-amylase having SEQ ID NO: 12 in WO01/66712 or a variant having at least 90% sequence identity to SEQ ID NO: 12. Preferred amylase variants are those having a substitution, a deletion or an insertion in one of more of the following positions of SEQ ID NO: 12 in WO01/66712: R28, R118, N174; R181, G182, D183, G184, G186, W189, N195, M202, Y298, N299, K302, S303, N306, R310, N314; R320, H324, E345, Y396, R400, W439, R444, N445, K446, Q449, R458, N471, N484. Particular preferred amylases include variants having a deletion of D183 and G184 and having the substitutions R118K, N195F, R320K and R458K, and a variant additionally having substitutions in one or more position selected from the group: M9, G149, G182, G186, M202, T257, Y295, N299, M323, E345 and A339, most preferred a variant that additionally has substitutions in all these positions.

Other examples are amylase variants such as those described in WO2011/098531, WO2013/001078 and WO2013/001087.

Commercially available amylases are Duramyl™, Termamyl™, Fungamyl™, Stainzyme™, Stainzyme Plus™, Natalase™, Liquozyme X and BAN™ (from Novozymes A/S), and Rapidase™, Purastar™/Effectenz™, Powerase, Preferenz S1000, Preferenz S100 and Preferenz S110 (from Genencor International Inc./DuPont).

Peroxidases/Oxidases: Suitable peroxidases/oxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from *Coprinus*, e.g., from *C. cinereus*, and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257.

Commercially available peroxidases include Guardzyme™ (Novozymes A/S).

Other enzymes: A protease variant according to the invention may also be combined with additional enzymes such as pectate lyases e.g. Pectawash™, chlorophyllases etc. The protease variant of the invention may be mixed with any additional enzyme.

The detergent enzyme(s) may be included in a detergent composition by adding separate additives containing one or more enzymes, or by adding a combined additive comprising all of these enzymes. A detergent additive, *i.e.*, a separate additive or a combined additive, can be formulated, for example, as a granulate, liquid, slurry, etc. Preferred detergent additive formulations are granulates, in particular non-dusting granulates, liquids, in particular stabilized liquids, or slurries.

Non-dusting granulates may be produced, *e.g.*, as disclosed in US 4,106,991 and 4,661,452 and may optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molar weights of 1000 to 20000; ethoxylated nonylphenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty acids; and mono- and di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in GB 1483591. Liquid enzyme preparations may, for instance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lactic acid or boric acid according to established methods. Protected enzymes may be prepared according to the method disclosed in EP 238,216.

### **Adjunct materials**

Any detergent components known in the art for use in laundry detergents may also be utilized. Other optional detergent components include anti-corrosion agents, anti-shrink agents, anti-soil redeposition agents, anti-wrinkling agents, bactericides, binders, corrosion inhibitors, disintegrants/disintegration agents, dyes, enzyme stabilizers (including boric acid, borates, CMC, and/or polyols such as propylene glycol), fabric conditioners including clays, fillers/processing aids, fluorescent whitening agents/optical brighteners, foam boosters, foam (suds) regulators, perfumes, soil-suspending agents, softeners, suds suppressors, tarnish inhibitors, and wicking agents, either alone or in combination. Any ingredient known in the art for use in laundry detergents may be utilized. The choice of such ingredients is well within the skill of the artisan.

Dispersants - The detergent compositions can also contain dispersants. In particular powdered detergents may comprise dispersants. Suitable water-soluble organic materials include the homo- or co-polymeric acids or their salts, in which the polycarboxylic acid comprises at least two carboxyl radicals separated from each other by not more than two carbon atoms. Suitable dispersants are for example described in Powdered Detergents, Surfactant science series volume 71, Marcel Dekker, Inc.

Dye Transfer Inhibiting Agents - The detergent compositions may also include one or more dye transfer inhibiting agents. Suitable polymeric dye transfer inhibiting agents include, but are not limited to, polyvinylpyrrolidone polymers, polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinylloxazolones and polyvinylimidazoles or mixtures thereof. When present in a subject composition, the dye transfer inhibiting agents may be present at levels from about 0.0001 % to about 10%, from about 0.01% to about 5% or even from about 0.1% to about 3% by weight of the composition.

Fluorescent whitening agent - A detergent compositions will preferably also contain additional components that may tint articles being cleaned, such as fluorescent whitening agent or optical brighteners. Where present the brightener is preferably at a level of about 0,01% to about 0,5%.. Any fluorescent whitening agent suitable for use in a laundry detergent composition may be used in the composition. The most commonly used fluorescent whitening agents are those belonging to the classes of diaminostilbene-sulphonic acid derivatives, diarylpyrazoline derivatives and bisphenyl-distyryl derivatives. Examples of the diaminostilbene-sulphonic acid derivative type of fluorescent whitening agents include the sodium salts of: 4,4'-bis-(2-diethanolamino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulphonate; 4,4'-bis-(2,4-dianilino-s-triazin-6-ylamino) stilbene-2,2'-disulphonate; 4,4'-bis-(2-anilino-4(N-methyl-N-2-hydroxy-ethylamino)-s-triazin-6-ylamino) stilbene-2,2'-disulphonate, 4,4'-bis-(4-phenyl-2,1,3-triazol-2-yl)stilbene-2,2'-disulphonate; 4,4'-bis-(2-anilino-4(1-methyl-2-hydroxy-ethylamino)-s-triazin-6-ylamino) stilbene-2,2'-disulphonate and 2-(stilbyl-4"-naphtho-1.,2':4,5)-1,2,3-triazole-2"-sulphonate. Preferred fluorescent whitening agents are Tinopal DMS and Tinopal CBS available from Ciba-Geigy AG, Basel, Switzerland. Tinopal DMS is the disodium salt of 4,4'-bis-(2-morpholino-4 anilino-s-triazin-6-ylamino) stilbene disulphonate. Tinopal CBS is the disodium salt of 2,2'-bis-(phenyl-styryl) disulphonate. Also preferred are fluorescent whitening agents is the commercially available Parawhite KX, supplied by Paramount Minerals and Chemicals, Mumbai, India. Other fluorescers suitable for use include the 1-3-diaryl pyrazolines and the 7-alkylaminocoumarins.

Suitable fluorescent brightener levels include lower levels of from about 0.01, from 0.05, from about 0.1 or even from about 0.2 wt % to upper levels of 0.5 or even 0.75 wt%.

Soil release polymers - The detergent composition may also include one or more soil release polymers which aid the removal of soils from fabrics such as cotton and polyester based fabrics, in particular the removal of hydrophobic soils from polyester based fabrics. The soil release polymers may for example be nonionic or anionic terephthalate based polymers, polyvinyl caprolactam and related copolymers, vinyl graft copolymers, polyester polyamides see for example Chapter 7 in Powdered Detergents, Surfactant science series volume 71, Marcel Dekker, Inc. Another type of soil release polymers are amphiphilic alkoxyated grease cleaning polymers comprising a core structure and a plurality of alkoxyate groups attached to that core structure. The core structure may comprise



a polyalkylenimine structure or a polyalkanolamine structure as described in detail in WO 2009/087523 (hereby incorporated by reference). Furthermore random graft co-polymers are suitable soil release polymers. Suitable graft co-polymers are described in more detail in WO 2007/138054, WO 2006/108856 and WO 2006/113314 (hereby incorporated by reference). Other soil release polymers are substituted polysaccharide structures especially substituted cellulosic structures such as modified cellulose derivatives such as those described in EP 1867808 or WO 2003/040279 (both are hereby incorporated by reference). Suitable cellulosic polymers include cellulose, cellulose ethers, cellulose esters, cellulose amides and mixtures thereof. Suitable cellulosic polymers include anionically modified cellulose, nonionically modified cellulose, cationically modified cellulose, zwitterionically modified cellulose, and mixtures thereof. Suitable cellulosic polymers include methyl cellulose, carboxy methyl cellulose, ethyl cellulose, hydroxyl ethyl cellulose, hydroxyl propyl methyl cellulose, ester carboxy methyl cellulose, and mixtures thereof.

Anti-redeposition agents - The detergent compositions may also include one or more anti-redeposition agents such as carboxymethylcellulose (CMC), polyvinyl alcohol (PVA), polyvinylpyrrolidone (PVP), polyoxyethylene and/or polyethyleneglycol (PEG), homopolymers of acrylic acid, copolymers of acrylic acid and maleic acid, and ethoxylated polyethyleneimines. The cellulose based polymers described under soil release polymers above may also function as anti-redeposition agents.

Other suitable adjunct materials include, but are not limited to, anti-shrink agents, anti-wrinkling agents, bactericides, binders, carriers, dyes, enzyme stabilizers, fabric softeners, fillers, foam regulators, hydrotropes, perfumes, pigments, sod suppressors, solvents, structurants for liquid detergents and/or structure elasticizing agents.

### **Formulation of detergent products**

The detergent composition may be in any convenient form, e.g., a bar, a homogenous tablet, a tablet having two or more layers, a regular or compact powder, a granule, a paste, a gel, or a regular, compact or concentrated liquid.

Detergent formulation forms: Layers (same or different phases), Pouches, versus forms for Machine dosing unit.

Pouches can be configured as single or multicompartments. It can be of any form, shape and material which is suitable for hold the composition, e.g. without allowing the release of the composition to release of the composition from the pouch prior to water contact. The pouch is made from water soluble film which encloses an inner volume. Said inner volume can be divided into compartments of the pouch. Preferred films are polymeric materials preferably polymers which are formed into a film or sheet. Preferred polymers, copolymers or derivatives thereof are selected polyacrylates, and water soluble acrylate copolymers, methyl cellulose, carboxy methyl cellulose, sodium dextrin, ethyl cellulose,

hydroxyethyl cellulose, hydroxypropyl methyl cellulose, malto dextrin, poly methacrylates, most preferably polyvinyl alcohol copolymers and, hydroxypropyl methyl cellulose (HPMC). Preferably the level of polymer in the film for example PVA is at least about 60%. Preferred average molecular weight will typically be about 20,000 to about 150,000. Films can also be of blend compositions comprising hydrolytically degradable and water soluble polymer blends such as polyactide and polyvinyl alcohol (known under the Trade reference M8630 as sold by Chris Craft In. Prod. Of Gary, Ind., US) plus plasticisers like glycerol, ethylene glycerol, Propylene glycol, sorbitol and mixtures thereof. The pouches can comprise a solid laundry cleaning composition or part components and/or a liquid cleaning composition or part components separated by the water soluble film. The compartment for liquid components can be different in composition than compartments containing solids. Ref: (US2009/0011970 A1)

Detergent ingredients can be separated physically from each other by compartments in water dissolvable pouches or in different layers of tablets. Thereby negative storage interaction between components can be avoided. Different dissolution profiles of each of the compartments can also give rise to delayed dissolution of selected components in the wash solution.

Definition/characteristics of the forms:

A liquid or gel detergent, which is not unit dosed, may be aqueous, typically containing at least 20% by weight and up to 95% water, such as up to about 70% water, up to about 65% water, up to about 55% water, up to about 45% water, up to about 35% water. Other types of liquids, including without limitation, alkanols, amines, diols, ethers and polyols may be included in an aqueous liquid or gel. An aqueous liquid or gel detergent may contain from 0-30% organic solvent.

A liquid or gel detergent may be non-aqueous.

### **Granular detergent formulations**

A granular detergent may be formulated as described in WO09/092699, EP1705241, EP1382668, WO07/001262, US6472364, WO04/074419 or WO09/102854. Other useful detergent formulations are described in WO09/124162, WO09/124163, WO09/117340, WO09/117341, WO09/117342, WO09/072069, WO09/063355, WO09/132870, WO09/121757, WO09/112296, WO09/112298, WO09/103822, WO09/087033, WO09/050026, WO09/047125, WO09/047126, WO09/047127, WO09/047128, WO09/021784, WO09/010375, WO09/000605, WO09/122125, WO09/095645, WO09/040544, WO09/040545, WO09/024780, WO09/004295, WO09/004294, WO09/121725, WO09/115391, WO09/115392, WO09/074398, WO09/074403, WO09/068501, WO09/065770, WO09/021813, WO09/030632, and WO09/015951.

WO2011025615, WO2011016958, WO2011005803, WO2011005623, WO2011005730, WO2011005844, WO2011005904, WO2011005630, WO2011005830, WO2011005912, WO2011005905, WO2011005910, WO2011005813, WO2010135238, WO2010120863, WO2010108002, WO2010111365, WO2010108000, WO2010107635, WO2010090915,

WO2010033976, WO2010033746, WO2010033747, WO2010033897, WO2010033979,  
 WO2010030540, WO2010030541, WO2010030539, WO2010024467, WO2010024469,  
 WO2010024470, WO2010025161, WO2010014395, WO2010044905,  
 WO2010145887, WO2010142503, WO2010122051, WO2010102861, WO2010099997,  
 WO2010084039, WO2010076292, WO2010069742, WO2010069718, WO2010069957,  
 WO2010057784, WO2010054986, WO2010018043, WO2010003783, WO2010003792,  
 WO2011023716, WO2010142539, WO2010118959, WO2010115813, WO2010105942,  
 WO2010105961, WO2010105962, WO2010094356, WO2010084203, WO2010078979,  
 WO2010072456, WO2010069905, WO2010076165, WO2010072603, WO2010066486,  
 WO2010066631, WO2010066632, WO2010063689, WO2010060821, WO2010049187,  
 WO2010031607, WO2010000636,

### Methods and uses

The protease variants of the present invention may be added to and thus become a component of a detergent composition, wherein said variant comprises a substitution of one or more amino acids in the loop corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3 and wherein the variant has at least 70%, such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76% at least 77% at least 78% at least 79% at least 80%, at least 81% at least 82% at least 83% at least 84% at least 85%, at least 86% at least 87% at least 88% at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5% or at least 99.6% sequence identity to SEQ ID NO: 3. Detergent compositions is generally used in cleaning processes such as laundry and/or hard surface cleaning e.g. dish wash. A detergent compositions may comprise at least one a variant wherein said variant comprises one or more of the following substitutions S171 {W, K, E, N}, S173 {P}, S175 {A, V, P} or G179 {C, V, Q, S, T, E, H, K, M, N, A, Y} of SEQ ID NO: 3, wherein the variant has a sequence identity to SEQ ID NO: 3 of at least 70% such as at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76% at least 77% at least 78% at least 79% at least 80%, at least 81% at least 82% at least 83% at least 84% at least 85%, at least 86% at least 87% at least 88% at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5% or at least 99.6 sequence identity to SEQ ID NO: 3 and the variant has protease activity. The at least one protease variant preferably has increased detergent stability relative to the parent or relative to a protease parent having the identical amino acid sequence of said variant but not having the substitutions at one or more of said positions when tested in the Example 2, as described under "Material and Methods".

Additionally, any of the protease variants described above may also contain a substitution at position F180Y.

A detergent composition may be formulated, for example, as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dishwashing operations.

A cleaning process or the textile care process may for example be a laundry process, a dishwashing process or cleaning of hard surfaces such as bathroom tiles, floors, table tops, drains, sinks and washbasins. Laundry processes can for example be household laundering, but it may also be industrial laundering. A process for laundering of fabrics and/or garments may be a process comprises treating fabrics with a washing solution containing a detergent composition, and at least one protease variant. A cleaning process or a textile care process can for example be carried out in a machine washing process or in a manual washing process. The washing solution can for example be an aqueous washing solution containing a detergent composition.

The fabrics and/or garments subjected to a washing, cleaning or textile care process may be conventional washable laundry, for example household laundry. Preferably, the major part of the laundry is garments and fabrics, including knits, woven, denims, non-woven, felts, yarns, and towelling. The fabrics may be cellulose based such as natural cellulose, including cotton, flax, linen, jute, ramie, sisal or coir or manmade cellulose (e.g., originating from wood pulp) including viscose/rayon, ramie, cellulose acetate fibers (tricell), lyocell or blends thereof. The fabrics may also be non-cellulose based such as natural polyamides including wool, camel, cashmere, mohair, rabbit and silk or synthetic polymer such as nylon, aramid, polyester, acrylic, polypropylene and spandex/elastane, or blends thereof as well as blend of cellulose based and non-cellulose based fibers. Examples of blends are blends of cotton and/or rayon/viscose with one or more companion material such as wool, synthetic fibers (e.g., polyamide fibers, acrylic fibers, polyester fibers, polyvinyl alcohol fibers, polyvinyl chloride fibers, polyurethane fibers, polyurea fibers, aramid fibers), and cellulose-containing fibers (e.g., rayon/viscose, ramie, flax, linen, jute, cellulose acetate fibers, lyocell).

The last few years there has been an increasing interest in replacing components in detergents, which is derived from petrochemicals with renewable biological components such as enzymes and polypeptides without compromising the wash performance. When the components of detergent compositions change new enzyme activities or new enzymes having alternative and/or improved properties compared to the common used detergent enzymes such as proteases, lipases and amylases is needed to achieve a similar or improved wash performance when compared to the traditional detergent compositions.

Proteases and variants hereof are usable in proteinaceous stain removing processes. The proteinaceous stains may be stains such as food stains, e.g., baby food, sebum, cocoa, egg, blood, milk, ink, grass, or a combination hereof.

Typical detergent compositions include various components in addition to the enzymes, these components have different effects, some components like the surfactants lower the surface tension in the detergent, which allows the stain being cleaned to be lifted and dispersed and then washed away, other components like bleach systems remove discolor often by oxidation and many bleaches also have strong bactericidal properties, and are used for disinfecting and sterilizing. Yet other components like builder and chelator softens, e.g., the wash water by removing the metal ions form the liquid.

The enzyme compositions may further comprise at least one or more of the following: a surfactant, a builder, a chelator or chelating agent, bleach system or bleach component in laundry or dish wash.

The amount of a surfactant, a builder, a chelator or chelating agent, bleach system and/or bleach component may be reduced compared to amount of surfactant, builder, chelator or chelating agent, bleach system and/or bleach component used without the added protease variant of the invention. Preferably the at least one component which is a surfactant, a builder, a chelator or chelating agent, bleach system and/or bleach component is present in an amount that is 1% less, such as 2% less, such as 3% less, such as 4% less, such as 5% less, such as 6% less, such as 7% less, such as 8% less, such as 9% less, such as 10% less, such as 15% less, such as 20% less, such as 25% less, such as 30% less, such as 35% less, such as 40% less, such as 45% less, such as 50% less than the amount of the component in the system without the addition of protease variants of the invention, such as a conventional amount of such component. Detergent compositions may also be composition which is free of at least one component which is a surfactant, a builder, a chelator or chelating agent, bleach system or bleach component and/or polymer.

### **Washing Method**

Detergent compositions are ideally suited for use in laundry applications. These methods include a method for laundering a fabric. The method comprises the steps of contacting a fabric to be laundered with a cleaning laundry solution comprising a detergent composition. The fabric may comprise any fabric capable of being laundered in normal consumer use conditions. The solution preferably has a pH from about 5.5 to about 11.5. The compositions may be employed at concentrations from about 100 ppm, preferably 500 ppm to about 15,000 ppm in solution. The water temperatures typically range from about 5°C to about 95°C, including about 10°C, about 15°C, about 20°C, about 25°C, about 30°C, about 35°C, about 40°C, about 45°C, about 50°C, about 55°C, about 60°C, about 65°C, about 70°C, about 75°C, about 80°C, about 85°C and about 90°C. The water to fabric ratio is typically from about 1:1 to about 30:1.

In particular embodiments, the washing method is conducted at a pH from about 5.0 to about 11.5, or from about 6 to about 10.5, about 5 to about 11, about 5 to about 10, about 5 to about 9, about 5 to about 8, about 5 to about 7, about 5.5 to about 11, about 5.5 to about 10, about 5.5 to about 9, about 5.5 to about 8, about 5.5. to about 7, about 6 to about 11, about 6 to about 10, about

6 to about 9, about 6 to about 8, about 6 to about 7, about 6.5 to about 11, about 6.5 to about 10, about 6.5 to about 9, about 6.5 to about 8, about 6.5 to about 7, about 7 to about 11, about 7 to about 10, about 7 to about 9, or about 7 to about 8, about 8 to about 11, about 8 to about 10, about 8 to about 9, about 9 to about 11, about 9 to about 10, about 10 to about 11, preferably about 5.5 to about 11.5.

In particular embodiments, the washing method is conducted at a degree of hardness of from about 0°dH to about 30°dH, such as about 1°dH, about 2°dH, about 3°dH, about 4°dH, about 5°dH, about 6°dH, about 7°dH, about 8°dH, about 9°dH, about 10°dH, about 11°dH, about 12°dH, about 13°dH, about 14°dH, about 15°dH, about 16°dH, about 17°dH, about 18°dH, about 19°dH, about 20°dH, about 21°dH, about 22°dH, about 23°dH, about 24°dH, about 25°dH, about 26°dH, about 27°dH, about 28°dH, about 29°dH, about 30°dH. Under typical European wash conditions, the degree of hardness is about 16°dH, under typical US wash conditions about 6°dH, and under typical Asian wash conditions, about 3°dH.

The compositions for use in the methods described above may further comprises at least one additional enzyme as set forth in the "other enzymes" section above, such as an enzyme selected from the group of hydrolases such as proteases, lipases and cutinases, carbohydrases such as amylases, cellulases, hemicellulases, xylanases, and pectinase or a combination hereof.

The present invention is further described by the following examples that should not be construed as limiting the scope of the invention.

## Examples

### Materials and Methods

#### Automatic Mechanical Stress Assay (AMSA) for laundry

In order to assess the wash performance in laundry washing experiments are performed, using the Automatic Mechanical Stress Assay (AMSA). With the AMSA, the wash performance of a large quantity of small volume enzyme-detergent solutions can be examined. The AMSA plate has a number of slots for test solutions and a lid firmly squeezing the laundry sample, the textile to be washed against all the slot openings. During the washing time, the plate, test solutions, textile and lid are vigorously shaken to bring the test solution in contact with the textile and apply mechanical stress in a regular, periodic oscillating manner. For further description see WO02/42740 especially the paragraph "Special method embodiments" at page 23-24.

The wash performance is measured as the brightness of the colour of the textile washed. Brightness can also be expressed as the intensity of the light reflected from the sample when illuminated with white light. When the sample is stained the intensity of the reflected light is lower, than that of a clean sample. Therefore the intensity of the reflected light can be used to measure wash performance.

Colour measurements are made with a professional flatbed scanner (Kodak iQsmart, Kodak, Midtager 29, DK-2605 Brøndby, Denmark), which is used to capture an image of the washed textile.

To extract a value for the light intensity from the scanned images, 24-bit pixel values from the image are converted into values for red, green and blue (RGB). The intensity value (Int) is calculated by adding the RGB values together as vectors and then taking the length of the resulting vector:

$$Int = \sqrt{r^2 + g^2 + b^2}$$

Table 1: Composition of model detergents and test materials

Model detergent and test materials were as follows:

Laundry liquid model detergent	0.3 to 0.5% xanthan gum, 0.2 to 0.4% antifoaming agent, 6 to 7% glycerol, 0.3 to 0.5% ethanol, 4 to 7% FAEOS (fatty alcohol ether sulfate), 24 to 28% nonionic surfactants, 1% boric acid, 1 to 2% sodium citrate (dihydrate), 2 to 4% soda, 14 to 16% coconut fatty acid, 0.5% HEDP (1-hydroxyethane-(1,1-diphosphonic acid)), 0 to 0.4% PVP (polyvinylpyrrolidone), 0 to 0.05% optical brighteners, 0 to 0.001% dye, remainder deionized water.
Test material	PC-03 (Chocolate-milk/ink on cotton/polyester) C-05 (Blood/milk/ink on cotton)

General molecular biology methods:

Unless otherwise mentioned the DNA manipulations and transformations were performed using standard methods of molecular biology (Sambrook et al. (1989); Ausubel et al. (1995); Harwood and Cutting (1990).

Protease activity assays:

1) Suc-AAPF-pNA activity assay:

The proteolytic activity can be determined by a method employing the Suc-AAPF-PNA substrate. Suc-AAPF-PNA is an abbreviation for N-Succinyl-Alanine-Alanine-Proline-Phenylalanine-p-Nitroanilide, and it is a blocked peptide which can be cleaved by endo-proteases. Following cleavage a free PNA molecule is liberated and it has a yellow colour and thus can be measured by visible spectrophotometry at wavelength 405nm. The Suc-AAPF-PNA substrate is manufactured by

Bachem (cat. no. L1400, dissolved in DMSO).

The protease sample to be analyzed was diluted in residual activity buffer (100mM Tris pH8.6). The assay was performed by transferring 60µl of diluted enzyme samples to 96 well microtiter plate and adding 140µl substrate working solution (0.72mg/ml in 100mM Tris pH8.6). The solution was mixed at room temperature and absorption is measured every 20 sec. over 5 minutes at OD 405 nm.

The slope (absorbance per minute) of the time dependent absorption-curve is directly proportional to the specific activity (activity per mg enzyme) of the protease in question under the given set of conditions. The protease sample should be diluted to a level where the slope is linear.

### **Example 1: Preparation and testing of protease variants**

#### Preparation and Expression of variants

Site-directed variants were constructed of the TY145 protease (SEQ ID NO: 3) comprising specific insertions/deletions/substitutions in the 170 to 180 region on the *N*-terminal side according to the invention. The variants were made by traditional cloning of DNA fragments (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989) using PCR together with properly designed mutagenic oligonucleotides that introduced the desired mutations in the resulting sequence. Mutagenic oligos were synthesized corresponding to the DNA sequence flanking the desired site(s) of mutation, separated by the DNA base pairs defining the insertions/deletions/substitutions. In this manner, the variants listed in table 2a below were constructed and produced.

#### Fermentation of variants

Fermentation may be performed by methods well known in the art or as follows. A *B. subtilis* strain harboring the relevant expression plasmid was streaked on a LB-agar plate with a relevant antibiotic (6µg/ml chloramphenicol), and grown overnight at 37°C.

The colonies were transferred to 100 ml PS-1 media supplemented with the relevant antibiotic in a 500 ml shaking flask containing a rich media (e.g. PS-1: 100 g/L Sucrose (Danisco cat.no. 109-0429), 40 g/L crust soy (soy bean flour), 10g/L Na<sub>2</sub>HPO<sub>4</sub>.12H<sub>2</sub>O (Merck cat.no. 6579), 0.1ml/L Pluronic PE 6100 (BASF 102-3098)). Cultivation typically takes 4 days at 30°C shaking with 220rpm. Cells and other undissolved material were removed from the fermentation broth by centrifugation at 4500 rpm for 20-25 minutes. Afterwards the supernatant was filtered to obtain a clear solution.

### **Example 2:**

In this example, the above-described PNA-Suc-AAPF assay is used to determine the residual protease activity after incubation in the presence of liquid detergent. In general the residual



protease activity was determined after incubation in liquid detergent (final concentration of 90%) at the indicated temperatures and incubation times and the activity is then compared to the activity of a unstressed incubated at 4°C. For the determination of protease stability in detergent the enzymes to be tested were adjusted to a concentration of 0.15mg/ml of enzyme protein by dilution in enzyme dilution buffer (100mM Tris pH 8.6, 0.0225% (w/V) Brij-35, 2mM CaCl<sub>2</sub>). 30µl of the protease solution and 270µl liquid detergent (Model liquid detergent) were transferred to a 96 well microtiter plate (Nunc 96U PP) in 4 replicates. One small magnet (5 x 2 mm) was placed in each well, and the blend was mixed for 30 minutes at room temperature on a magnetic stirrer. After mixing 20µl is transferred to new 96 well microtiter plate and incubated at 4°C for 24 hours (unstressed sample). Heat seal with alu-foil carefully microtiter plate and incubate at indicated temperature for 24 hours (stressed samples). After incubation, the samples on the plates were analyzed for protease activity as described in the PNA-Suc-AAPF Assay for determination of residual protease activity. It should be noted, that in order to reduce interference from other detergent ingredients than the enzyme on the assay, both unstressed and stressed samples were diluted to the same protein concentration.

After incubation, withdraw 20µl of stressed samples and add 150µl residual activity buffer (100mM Tris pH8.6), and mix using magnetic stirrer for 5 minutes. Transfer 60µl of diluted sample to new 96 well microtiter plate. Before use prepare PNA-Suc-AAPF substrate working solution in residual activity buffer (0.72mg/ml in 100mM Tris pH8.6). Add 140µl substrate working solution to diluted sample, mix and measure immediately absorbance at 405nm for 5-10 minutes every 20 seconds at room temperature. Use V<sub>max</sub> only from linear range of kinetic curves. Repeat residual activity measurement for unstressed sample by adding 150µl residual activity buffer (100mM Tris pH8.6) to microtiter plate with 20µl unstressed sample (incubated at 4°C), and mix using magnetic stirrer for 5 minutes. Transfer 60µl of diluted sample to new 96 well microtiter plate. Add 140µl substrate working solution to diluted sample, mix and measure immediately absorbance at 405nm for 5-10 minutes every 20 seconds at room temperature. Use V<sub>max</sub> only from linear range of kinetic curves.

It was ensured in all experiments that the reference protease was included at least once on all test microtiter plates.

The residual activity (%RA) was calculated as  $\%RA = 100 * V_{max} (\text{stressed sample}) / V_{max} (\text{unstressed sample})$ .

The half-life (T<sub>1/2</sub>(h)) is calculated:  $T_{1/2} (\text{hours}) = T (\text{hours}) * \text{LN}(0.5) / \text{LN}(\%RA/100)$  with T being incubation time (hours) and %RA is residual activity.

Table 3a: stability of variants measured at 35°C

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 35°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	18
G179C	36
G179V	56

G179Q	65
G179S	29
G179Y	67
G179T	31
G179E	28
G179H	79
G179K	47
G179M	29
G179A	82
G179N	37
S171W	28
S171K	23
S171E	23
S175A	44
S175V	30
S175P	108

Table 3b: stability of variants measured at 35°C

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 35°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	18
I121V S175P	96
S175A G179S	78
L81V S175A	90
A102T S175A	86
S144R G179Q	96
S144R S171N	96
S144R F180Y	70
S171N	40
G179S F180Y G183A A187V	95

Table 4a: Stability of variants measured at 42°C.

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 42°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	0
S173P	96

S171N S175P	10
I121V S175P	7
L81V S175P	6
A102T S175P	6
I137E S175P	7
I121V S175A	3
L81F S175A	3
I137E S175A	4
S144Q S175P	6
S144Q S175A	3
I121T S175P	8

Table 4b: Stability of variants measured at 42°C.

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 42°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	0
S173Y G174S S175A F180Y	96
I137E S173Y G174S S175A F180Y	11
S144Q S173Y G174S S175A F180Y	9
S173Y G174S S175A F180Y S274I	10
S173Y G174S S175A F180Y V286Q	10
T40D S173Y G174S S175A F180Y	9
S173P G174K S175P N176G T177S F180Y	30
D155N G159S S173Y G174S S175A F180Y	6
I121V S173P G174K S175P N176G T177S F180Y	52
L81V S173P G174K S175P N176G T177S F180Y	41
A102T S173P G174K S175P N176G T177S F180Y	37
S173P G174K S175P N176G T177S F180Y T241P	48
I137E S173P G174K S175P N176G T177S F180Y	41
S144Q S173P G174K S175P N176G T177S F180Y	41
Q70N S173P G174K S175P N176G T177S F180Y	59
S173P G174K S175P N176G T177S F180Y V286Q	45
T40D S173P G174K S175P N176G T177S F180Y	32
S171N S173P G174K S175P N176G T177S F180Y	52
S173P G174K S175P N176G T177S F180Y S274I	44

Table 5a: Stability of variants measured at 47°C.

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 47°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	0
S173P	26
S171N S175P	6
I121V S175P	6
L81V S175P	6
A102T S175P	6
I137E S175P	6
I121V S175A	6
L81F S175A	6
I137E S175A	6
S144Q S175P	6
S144Q S175A	6
I121T S175P	6
S173P S274I	29
I137M S173P	30
S171N S173P	38
L81F S173P	28
A102T S173P	26
S144Q S173P	29
I137E S173P	35
S173P T241P	32
S173P S175A	34
L81G S173P	39

Table 5b: Stability of variants measured at 47°C.

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 47°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	0
S173P S175P F180Y	96
T74M I137E S173P	26

T79I I137E S173P	27
L34I I137E S173P	36
Y39D I137E S173P	39
T40P I137E S173P	46
I137E S173P I247M	41
I137E S173P H256F	31
S173Y G174S S175A F180Y	22
I137E S173Y S175A F180Y	6
S173Y G174S S175P F180Y	6
I137E S173P S175P F180Y	96
V162R S173P S175P F180Y	96
S173P S175P F180Y S274I	96
S173P G174T S175V T177S F180Y	39
S173Y G174S S175A F180Y T241P	6
I137E S173Y G174S S175A F180Y	6
S144Q S173Y G174S S175A F180Y	6
Q70N S173Y G174S S175A F180Y	6
S173Y G174S S175A F180Y S274I	6
S173Y G174S S175A F180Y V286Q	6
T40D S173Y G174S S175A F180Y	6
V162R S173Y G174S S175A F180Y	6
I121V S173Y G174S S175A F180Y	6
L81V S173Y G174S S175A F180Y	6
A102T S173Y G174S S175A F180Y	6
S173P G174T S175A T177S F180Y	39
I137E S173P S175V T177S F180Y	34
S171N S173Y G174S S175A F180Y	6
I137E S173Y G174S S175P F180Y	7
S173P G174T S175P T177S F180Y	61
S173P G174K S175P N176G T177S F180Y	6
V162R S173P G174T S175V T177S F180Y	68
I121V S173P G174T S175V T177S F180Y	49
L81V S173P G174T S175V T177S F180Y	41
A102T S173P G174T S175V T177S F180Y	42
S173P G174T S175V T177S F180Y T241P	61
I137E S173P G174T S175V T177S F180Y	79
S144Q S173P G174T S175V T177S F180Y	65

Q70N S173P G174T S175V T177S F180Y	80
S173P G174T S175V T177S F180Y S274I	56
S173P G174T S175V T177S F180Y V286Q	56
T40D S173P G174T S175V T177S F180Y	37
S171N S173P G174T S175V T177S F180Y	58
I121V I137E S173Y G174S S175A F180Y	6
L81V I137E S173Y G174S S175A F180Y	6
I137E S173Y G174S S175A F180Y T241P	6
Q70N I137E S173Y G174S S175A F180Y	6
I137E S173Y G174S S175A F180Y S274I	6
I137E S173Y G174S S175A F180Y T297P	8
G132I S173P G174T S175V T177S F180Y	45
S173P G174T S175V T177S F180Y T297P	72
I137E S144Q S173Y G174S S175A F180Y	6
T40L I137E S173Y G174S S175A F180Y	6
I137E S173P S175P N176G T177S F180Y	6
S173P G174K S175A N176G T177S F180Y	6
I137E S173Y G174S S175A F180Y V286Q	6
I137E S173P G174T S175P T177S F180Y	88
D155N G159S S173P G174T S175V T177S F180Y	17
V162R S173P G174K S175P N176G T177S F180Y	11
I121V S173P G174K S175P N176G T177S F180Y	8
L81V S173P G174K S175P N176G T177S F180Y	7
A102T S173P G174K S175P N176G T177S F180Y	7
S173P G174K S175P N176G T177S F180Y T241P	9
I137E S173P G174K S175P N176G T177S F180Y	9
S144Q S173P G174K S175P N176G T177S F180Y	7
Q70N S173P G174K S175P N176G T177S F180Y	8
S173P G174K S175P N176G T177S F180Y V286Q	9
T40D S173P G174K S175P N176G T177S F180Y	7
S171N S173P G174K S175P N176G T177S F180Y	9
I121V I137E S173P G174T S175V T177S F180Y	73
I137E S173P G174T S175V T177S F180Y T241P	90
I137E S173P G174T S175V T177S F180Y V286Q	75
I137E S173P G174T S175V T177S F180Y T297P	96
I137E S171N S173P G174T S175V T177S F180Y	74
I137E S173P G174K S175A N176G T177S F180Y	6

G132I S173P G174K S175P N176G T177S F180Y	6
S173P G174K S175P N176G T177S F180Y T297P	16
I137E S173P G174T S175V T177S F180Y S274I	64
I137E S144Q S173P G174T S175V T177S F180Y	56
S173P G174K S175P N176G T177S F180Y S274I	7
I121V I137E S173P G174K S175P N176G T177S F180Y	13
Q70N I137E S173P G174K S175P N176G T177S F180Y	13
I137E S173P G174K S175P N176G T177S F180Y S274I	12
I137E S173P G174K S175P N176G T177S F180Y V286Q	12
I137E S173P G174K S175P N176G T177S F180Y T297P	23
I137E S171N S173P G174K S175P N176G T177S F180Y	15
I137E S144Q S173P G174K S175P N176G T177S F180Y	11
V162R S171N S173P G174K S175P N176G T177S F180Y	16
I137E S171N S173P G174K S175P N176G T177S F180Y T241P	22
I137E S171N S173P G174K S175P N176G T177S F180Y T297P	41

Table 6: Stability of variants measured at 52°C.

Mutations	Half-life T <sub>1/2</sub> (hours) (incubation at 52°C for 24h in 90% detergent)
TY-145 (SEQ ID NO 3)	0
I137E S173P	6
S173P S175P F180Y	27
T40P I137E S173P	7
I137E S173P S175P F180Y	39
V162R S173P S175P F180Y	45
S173P S175P F180Y S274I	30
S173P S175P F180Y T241P	31
S173P S175P F180Y V286Q	30
S173P S175P F180Y T297P	46
S173P G174T S175V T177S F180Y	11
V162R S173P G174T S175V T177S F180Y	16
I137E S173P G174T S175V T177S F180Y	15
Q70N S173P G174T S175V T177S F180Y	16
S173P G174T S175V T177S F180Y V286Q	14
S171N S173P G174T S175V T177S F180Y	15

I137E S173P G174T S175A T177S F180Y	14
S173P G174T S175V T177S F180Y T297P	20
I137E S173P G174T S175P T177S F180Y	37
L81V I137E S173P G174T S175V T177S F180Y	17
Q70N I137E S173P G174T S175V T177S F180Y	26
I137E S173P G174T S175V T177S F180Y V286Q	16
I137E S171N S173P G174T S175V T177S F180Y	23
I137E S144Q S173P G174T S175V T177S F180Y	15
I137E S173P G174T S175P T177S F180Y T297P	96

### Example 3

The wash performance of protease variants were tested using a liquid detergent on 3 different technical stains using the Automatic Mechanical Stress Assay.

The experiments were conducted as described in the AMSA for laundry method using a single cycle wash procedure, with the detergent composition and swatches described in table 1 and the experimental conditions as specified in table 7 below.

Table 7: Experimental conditions for AMSA for tables 7a to 7f

Test solution	4.66 g/L liquid model detergent
Test solution volume	160 micro L
pH	As is
Wash time	20 minutes
Temperature	20°C
Water hardness	16°dH
Protease concentration	0 (blank), 10 nM or 30 nM
Swatch	PC-03, C-05

Water hardness was adjusted to 16°dH by addition of CaCl<sub>2</sub>, MgCl<sub>2</sub>, and NaHCO<sub>3</sub> (Ca<sup>2+</sup>:Mg<sup>2+</sup>:CO<sub>3</sub><sup>2-</sup>) = 5:1:6 for PC-03 and 5:1:11 for C-05 to the test system. After washing the textiles were flushed in tap water and dried.

Table 7a Wash performance of single and double protease variants on a Chocolate, Milk, Soot stain, reference enzyme is TY-145 (SEQ ID NO 3)

Mutations	Wash performance relative to SEQ ID NO 3, at 20 C on PC-03
G179S	96
S173P	108



I121V S175A	106
L81V S175A	97
S144Q S175P	112
S144Q S175A	97
S173P S274I	102
L81F S173P	103
S144Q S173P	101
I137E S173P	97
S173P T241P	111
S173P S175A	106

Table 7b Wash performance of protease variants on a Chocolate, Milk, Soot stain, reference enzyme is TY-145 (SEQ ID NO 3)

Mutations	Wash performance relative to SEQ ID NO 3, at 20 C on PC-03
S173P S175P F180Y	91
S173Y G174S S175A F180Y	101
S173P G174T S175V T177S F180Y	98
I137E S173Y G174S S175A F180Y	108
S144Q S173Y G174S S175A F180Y	101
S173Y G174S S175A F180Y S274I	117
S173Y G174S S175A F180Y V286Q	94
V162R S173Y G174S S175A F180Y	121
I121V S173Y G174S S175A F180Y	110
S173P G174T S175A T177S F180Y	106
S173P G174K S175P N176G T177S F180Y	98
D155N G159S S173Y G174S S175A F180Y	118
V162R S173P G174T S175V T177S F180Y	125
I121V S173P G174T S175V T177S F180Y	99
L81V S173P G174T S175V T177S F180Y	98
I137E S173P G174T S175V T177S F180Y	112
S173P G174T S175V T177S F180Y V286Q	94
S173P G174T S175V T177S F180Y T297P	94
S173P G174K S175A N176G T177S F180Y	107
D155N G159S S173P G174T S175V T177S F180Y	116
V162R S173P G174K S175P N176G T177S F180Y	135
I121V S173P G174K S175P N176G T177S F180Y	117

L81V S173P G174K S175P N176G T177S F180Y	104
A102T S173P G174K S175P N176G T177S F180Y	110
I137E S173P G174K S175P N176G T177S F180Y	122
S144Q S173P G174K S175P N176G T177S F180Y	107
S173P G174K S175P N176G T177S F180Y V286Q	112
S171N S173P G174K S175P N176G T177S F180Y	125
I137E S173P G174T S175V T177S F180Y V286Q	100
I137E S173P G174K S175A N176G T177S F180Y	106
S173P G174K S175P N176G T177S F180Y T297P	117
D155N G159S S173P G174K S175P N176G T177S F180Y	99
S173P G174K S175P N176G T177S F180Y S274I	125
I121V I137E S173P G174K S175P N176G T177S F180Y	189
I137E S173P G174K S175P N176G T177S F180Y S274I	97
I137E S173P G174K S175P N176G T177S F180Y V286Q	96
I137E S173P G174K S175P N176G T177S F180Y T297P	128
I137E S171N S173P G174K S175P N176G T177S F180Y	121

Table 7c Wash performance of single and double protease variants on a Blood, Milk, Ink stain, reference enzyme is TY-145 (SEQ ID NO 3)

Mutations	Wash performance relative to SEQ ID NO 3, at 20 C on C-05
S173P	110
I121V S175P	113
L81V S175P	105
A102T S175P	100
S175A G179S	95
I121V S175A	111
L81V S175A	101
I137E S175A	95
S144Q S175P	116
S144Q S175A	104
I121T S175P	98
S144R S171N	103
S173P S274I	96
I137M S173P	105

S171N S173P	115
L81F S173P	111
L81H S173P	103
A102T S173P	117
S144Q S173P	108
I137E S173P	120
S173P T241P	129
S173P S175A	100

Table 7d Wash performance of protease variants on a Blood, Milk, Ink stain, reference enzyme is TY-145 (SEQ ID NO 3)

Mutations	Wash performance relative to SEQ ID NO 3, at 20 C on C-05
S173P S175P F180Y	98
S173Y G174S S175A F180Y	120
I137E S173Y S175A F180Y	103
S173P G174T S175V T177S F180Y	106
I137E S173Y G174S S175A F180Y	108
S144Q S173Y G174S S175A F180Y	98
Q70N S173Y G174S S175A F180Y	105
S173Y G174S S175A F180Y S274I	95
S173Y G174S S175A F180Y V286Q	112
V162R S173Y G174S S175A F180Y	116
I121V S173Y G174S S175A F180Y	123
L81V S173Y G174S S175A F180Y	116
A102T S173Y G174S S175A F180Y	101
S173P G174T S175A T177S F180Y	111
S171N S173Y G174S S175A F180Y	103
S173P G174K S175P N176G T177S F180Y	107
D155N G159S S173Y G174S S175A F180Y	97
V162R S173P G174T S175V T177S F180Y	124
I121V S173P G174T S175V T177S F180Y	109
L81V S173P G174T S175V T177S F180Y	102
I137E S173P G174T S175V T177S F180Y	104
S144Q S173P G174T S175V T177S F180Y	95
Q70N S173P G174T S175V T177S F180Y	98

S173P G174T S175V T177S F180Y S274I	116
S173P G174T S175V T177S F180Y V286Q	98
S171N S173P G174T S175V T177S F180Y	101
L81V I137E S173Y G174S S175A F180Y	97
I137E S173Y G174S S175A F180Y S274I	109
I137E S173Y G174S S175A F180Y T297P	100
I137E S173P G174T S175A T177S F180Y	104
S173P G174T S175V T177S F180Y T297P	113
T40L I137E S173Y G174S S175A F180Y	96
S173P G174K S175A N176G T177S F180Y	112
I137E S173Y G174S S175A F180Y V286Q	98
D155N G159S S173P G174T S175V T177S F180Y	107
V162R S173P G174K S175P N176G T177S F180Y	113
I121V S173P G174K S175P N176G T177S F180Y	116
L81V S173P G174K S175P N176G T177S F180Y	114
A102T S173P G174K S175P N176G T177S F180Y	106
S173P G174K S175P N176G T177S F180Y T241P	94
I137E S173P G174K S175P N176G T177S F180Y	122
S144Q S173P G174K S175P N176G T177S F180Y	109
S173P G174K S175P N176G T177S F180Y V286Q	99
T40D S173P G174K S175P N176G T177S F180Y	105
S171N S173P G174K S175P N176G T177S F180Y	116
L81V I137E S173P G174T S175V T177S F180Y	100
Q70N I137E S173P G174T S175V T177S F180Y	113
I137E S173P G174T S175V T177S F180Y V286Q	109
I137E S171N S173P G174T S175V T177S F180Y	102
I137E S173P G174K S175A N176G T177S F180Y	119
G132I S173P G174K S175P N176G T177S F180Y	107
S173P G174K S175P N176G T177S F180Y T297P	109
I137E S173P G174T S175V T177S F180Y S274I	99
D155N G159S S173P G174K S175P N176G T177S F180Y	115
S173P G174K S175P N176G T177S F180Y S274I	106
I121V I137E S173P G174K S175P N176G T177S F180Y	153
I137E S173P G174K S175P N176G T177S F180Y S274I	100
I137E S173P G174K S175P N176G T177S F180Y V286Q	113
I137E S173P G174K S175P N176G T177S F180Y T297P	126
I137E S171N S173P G174K S175P N176G T177S F180Y	122

**Example 4**

The wash performance of variants in detergents was determined by using the following standardized stains:

A: blood, milk, ink on cotton: product no. C-05 obtainable from CFT (Center for Testmaterials) B.V., Vlaardingen, Netherlands,

B: groundnut oil, pigment, high milk on cotton: product no. C-10 obtainable from CFT (Center for Testmaterials) B.V., Vlaardingen, Netherlands,

C: grass on cotton: product no. E164 obtainable from Eidgenössische Material- und Prüfanstalt (EMPA) Testmaterialien AG [Federal materials and testing agency, Testmaterials], St. Gallen, Switzerland.

A liquid washing agent with the following composition was used as base formulation (all values in weight percent): 0 to 0.5% xanthan gum, 0.2 to 0.4% antifoaming agent, 6 to 7% glycerol, 0.3 to 0.5% ethanol, 0 to 7% FAEOS (fatty alcohol ether sulfate), 10 to 28% nonionic surfactants, 0.5-1% boric acid, 1 to 2% sodium citrate (dihydrate), 2 to 4% soda, 0 to 16% coconut fatty acid, 0.5% HEDP (1-hydroxyethane-(1,1-diphosphonic acid)), 0 to 0.4% PVP (polyvinylpyrrolidone), 0 to 0.05% optical brighteners, 0 to 0.001% dye, remainder deionized water.

Based on this base formulation, various detergents were prepared by adding respective proteases as indicated in tables 8a & b. Reference is the protease that has the amino acid sequence described in fig. 2 and SEQ ID NO.3 of WO 03/055713, the reference protease already showing a good wash performance, especially in liquid detergents. The proteases were added in the same amounts based on total protein content (5 mg/l wash liquor).

The dosing ratio of the liquid washing agent was 4.7 grams per liter of washing liquor and the washing procedure was performed for 60 minutes at a temperature of 20°C and 40°C, the water having a water hardness between 15.5 and 16.5° (German degrees of hardness).

The whiteness, i.e. the brightening of the stains, was determined photometrically as an indication of wash performance. A Minolta CM508d spectrometer device was used, which was calibrated beforehand using a white standard provided with the unit.

The results obtained are the difference values between the remission units obtained with the detergents and the remission units obtained with the detergent containing the reference protease. A positive value therefore indicates an improved wash performance of the variants in the detergent. It is evident from tables 8a (results at 40°C) and 8b (results at 20°C) that variants according to the invention show improved wash performance.

Table 8a: Wash performance of protease variants that have the same amino acid sequence as TY-145 (SEQ ID NO: 3) except for the substitutions as per the table below on a blood, milk, ink stain on cotton (A); reference is the protease that has the amino acid sequence described in fig. 2 and SEQ ID NO.3 of WO 03/055713.

Protease variant	A
I137E + S173P	2.9
S173P + S175P + F180Y (variant 2)	3.2
I137E + S173P + G174T + S175V + T177S + F180Y	3.5
S173P + G174T + S175V + T177S + F180Y + S274I	2.6
S173P + G174T + S175V + T177S + F180Y + T297P	3.6
S173P + S175P + F180Y + V286Q	2.5

Table 8b: Wash performance of protease variants on a blood, milk, ink stain on cotton (A), groundnut oil, pigment, high milk on cotton (B); grass on cotton (C); reference is the protease that has the amino acid sequence described in fig. 2 and SEQ ID NO.3 of WO 03/055713.

Protease variant	A	B	C
I137E + S173P	2.5	1.9	0.7
S173P + S175P + F180Y (variant 2)	1.6	0.8	0.9
I137E + S173P + G174T + S175V + T177S + F180Y	2.0	2.1	0.6
S173P + G174T + S175V + T177S + F180Y + S274I	1.5	2.0	1.6
S173P + G174T + S175V + T177S + F180Y + T297P	3.1	1.6	1.2
S173P + S175P + F180Y + V286Q	2.0	0.6	1.0

### Example 5

The stability of variant 2 as defined in example 4 and a non-protease enzyme (Mannanase) was tested in the liquid detergent composition as described above in Example 4 and according to the following protocol:

1. Enzyme Preparation: The correct % of the enzyme preparation is added to the formulation and the formulation is then stored for 8 Weeks at 30°C.
2. Protease activity: The enzyme activity can be measured according to methods known in the art. Enzyme activity assays are well known to the person skilled in the art and are routinely used. Protease activity assays are for example disclosed in Tenside, volume 7 (1970), pages 125-132. The protease activity can further be determined using the Suc-AAPF-pNA activity assay which measures the release of para-nitroanilin (pNA) from the substrate suc-L-Ala-L-Ala-L-Pro-L-Phe-p-nitroanilide (suc-AAPF-pNA. The release of the pNA causes an increase in extinction at 410 nm, of which the curve over time is a measure of enzymatic activity (cf. Del Mar *et al.*, 1979). The measurement is conducted at temperatures of 25°C, at pH 8.6 and a wavelength of 410 nm. The measuring period is 5 min. with a measuring interval of 20 s to 60 s. The protease activity is preferably expressed in PU (protease units).

3. Mannanase activity: After storage the remaining mannanase activity was measured as described in „Assay of endo-1,4-beta-Mannanase using Beat Annanase Tablets“ (Fa. Megazyme). Enzyme samples were incubated in with Azurine-crosslinked cardo Galactomannan in 0.2 M Tris HCl pH 8.2. The reaction was followed spectroscopically at 590 nm.

4. Calculations: all activities are expressed as relative activities, either relative to the start value or relative to the normed activity of the control non-“diluted” granulate mix.

The stability of variant 2 was tested in the liquid detergent composition as described above in Example 4. To assess the effect of borate and 4-formylphenyl boronic acid (4-FPBA) on the stability of variant 2, these two components were added to the liquid detergent composition separately or in combination in varying concentrations as per table 9a below.

Table 9a: Stability of variant 2 in liquid detergent composition containing varying concentrations of Borate and 4-formylphenyl boronic acid (4-FPBA).

Protease variant stability	Without Borate	With 1% w/w Borate
0.9% w/w variant 2 (2% (w/w) 4-FPBA)	65%	79%
0.9% w/w variant 2 (0% (w/w) 4-FPBA)	11%	80%
0.9% w/w variant 2 (1% (w/w) 4-FPBA)	57%	84%

The stability of a non-protease enzyme in the liquid detergent preparation containing variant 2 was tested by adding 0.00001% of active Mannanase (Mannaway™ by Novozymes) to the composition.

Table 9b: Stability of Mannanase in a liquid detergent composition containing variant 2 and varying concentrations of Borate and 4-formylphenyl boronic acid (4-FPBA).

Mannanase stability	Without Borate	With 1% w/w Borate
0.9% w/w variant 2 (2% (w/w) 4-FPBA)	30%	85%
0.9% w/w variant 2 (0% (w/w) 4-FPBA)	0%	81%
0.9% w/w variant 2 (1% (w/w) 4-FPBA)	15%	85%

**Claims**

1. A protease variant, comprising a substitution at one or more positions corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has a sequence identity to SEQ ID NO: 3 of at least 75% and less than 100%, and the variant has protease activity.
2. The protease variant of claim 1, wherein
  - a) the amino acid at the position corresponding to position 171 of SEQ ID NO: 3 is selected from the group consisting of Trp, Lys, Glu, Asn and/or
  - b) the amino acid at the position corresponding to position 173 of SEQ ID NO: 3 is Pro, and/or
  - c) the amino acid at the position corresponding to position 175 of SEQ ID NO: 3 is Ala, Val, Pro, and/or
  - d) the amino acid at the position corresponding to position 179 of SEQ ID NO: 3 is selected from the group consisting of Cys, Val, Gln, Ser, Thr, Glu, His, Lys, Met, Asn, Tyr and Ala.
3. The variant of any of claims 1-2, which comprises an alteration at two positions corresponding to any of positions 171, 173, 175, 179, and 180.
4. The variant according to any one of claims 1-3, wherein the amino acid at the position corresponding to position 180 of SEQ ID NO: 3 is Tyr.
5. The variant according to any one of claims 1-4, wherein the amino acid at the position corresponding to position 175 of SEQ ID NO: 3 is Pro.
6. The variant of any of claims 1-5, which further comprises one or more substitutions selected from the group consisting of Y39D; T40{D,P}; Q70N; T74M; L81{F,H,V}; A102T; I121{V,T}; G132 {I,E}; I137{M,E}; S144{Q,R}; D155N; G159S; V162R; G174{S,T}; N176G; T177S; T241P; I247M; H256F;S274I; V286Q; T297P.
7. A protease variant, comprising any of the following substitutions compared to of SEQ ID NO: 3:

S171N S175P
I121V S175P



L81V S175P
A102T S175P
I137E S175P
S175A G179S
I121V S175A
L81F S175A
L81H S175A
L81V S175A
A102T S175A
I137E S175A
S144Q S175P
S144Q S175A
S144R G179Q
I121T S175P
S144R S171N
S173P S274I
I137M S173P
S171N S173P
L81F S173P
L81H S173P
A102T S173P
S144Q S173P
S144R F180Y
I137E S173P
S173P S175P F180Y
S173Y G174S S175A F180Y
S173P G174T S175V T177S F180Y
S173P G174K S175P N176G T177S F180Y
S173P T241P
G179S F180Y G183A A187V
S173Y G174S S175A F180Y T241P
D155N G159S S173Y G174S S175A F180Y
S173Y G174S S175A F180Y S274I
S173Y G174S S175A F180Y V286Q
T40D S173Y G174S S175A F180Y

V162R S173P G174T S175V T177S F180Y
I121V S173P G174T S175V T177S F180Y
L81V S173P G174T S175V T177S F180Y
A102T S173P G174T S175V T177S F180Y
S173P G174T S175V T177S F180Y T241P
I137E S173P G174T S175V T177S F180Y
S144Q S173P G174T S175V T177S F180Y
Q70N S173P G174T S175V T177S F180Y
D155N G159S S173P G174T S175V T177S F180Y
S173P G174T S175V T177S F180Y S274I
S173P G174T S175V T177S F180Y V286Q
T40D S173P G174T S175V T177S F180Y
S171N S173P G174T S175V T177S F180Y
V162R S173P G174K S175P N176G T177S F180Y
I121V S173P G174K S175P N176G T177S F180Y
L81V S173P G174K S175P N176G T177S F180Y
A102T S173P G174K S175P N176G T177S F180Y
S173P G174K S175P N176G T177S F180Y T241P
I137E S173P G174K S175P N176G T177S F180Y
S144Q S173P G174K S175P N176G T177S F180Y
Q70N S173P G174K S175P N176G T177S F180Y
D155N G159S S173P G174K S175P N176G T177S F180Y
S173P G174K S175P N176G T177S F180Y S274I
S173P G174K S175P N176G T177S F180Y V286Q
T40D S173P G174K S175P N176G T177S F180Y
S171N S173P G174K S175P N176G T177S F180Y
I121V I137E S173Y G174S S175A F180Y
L81V I137E S173Y G174S S175A F180Y
I137E S173Y G174S S175A F180Y T241P
Q70N I137E S173Y G174S S175A F180Y
I137E S173Y G174S S175A F180Y S274I
I137E S173Y G174S S175A F180Y T297P
I121V I137E S173P G174T S175V T177S F180Y
L81V I137E S173P G174T S175V T177S F180Y
I137E S173P G174T S175V T177S F180Y T241P

Q70N I137E S173P G174T S175V T177S F180Y
I137E S173P G174T S175V T177S F180Y V286Q
I137E S173P G174T S175V T177S F180Y T297P
I137E S171N S173P G174T S175V T177S F180Y
I137E S173P G174T S175A T177S F180Y
I121V I137E S173P G174K S175P N176G T177S F180Y
Q70N I137E S173P G174K S175P N176G T177S F180Y
I137E S173P G174K S175P N176G T177S F180Y S274I
I137E S173P G174K S175P N176G T177S F180Y V286Q
I137E S173P G174K S175P N176G T177S F180Y T297P
I137E S171N S173P G174K S175P N176G T177S F180Y
I137E S173P G174K S175A N176G T177S F180Y
V162R S173Y G174S S175A F180Y
A102T S173Y G174S S175A F180Y
G132I S173P G174T S175V T177S F180Y
S173P G174T S175V T177S F180Y T297P
S173P G174T S175A T177S F180Y
S173P S175A
I137E S144Q S173Y G174S S175A F180Y
T40L I137E S173Y G174S S175A F180Y
I137E S173Y S175A F180Y
I137E S173P S175V T177S F180Y
I137E S173P S175P N176G T177S F180Y
S171N S173Y G174S S175A F180Y
S173P G174K S175A N176G T177S F180Y
I137E S173Y G174S S175A F180Y V286Q
I137E S173P G174T S175V T177S F180Y S274I
T74M I137E S173P
T79I I137E S173P
L81G S173P
L34I I137E S173P
Y39D I137E S173P
T40P I137E S173P
I137E S173P I247M
I137E S173P H256F

I137E S144Q S173P G174T S175V T177S F180Y
I137E S144Q S173P G174K S175P N176G T177S F180Y
S173Y G174S S175P F180Y
I137E S173Y G174S S175P F180Y
S173P G174T S175P T177S F180Y
I137E S173P G174T S175P T177S F180Y
I137E S173P G174T S175P T177S F180Y T297P
V162R S171N S173P G174K S175P N176G T177S F180Y
I137E S171N S173P G174K S175P N176G T177S F180Y T241P
I137E S171N S173P G174K S175P N176G T177S F180Y T297P
I137E S173P S175P F180Y
V162R S173P S175P F180Y
S173P S175P F180Y S274I
S173P S175P F180Y T241P
S173P S175P F180Y T297P
S173P S175P F180Y V286Q
I137E S173Y G174S S175A F180Y
S144Q S173Y G174S S175A F180Y
Q70N S173Y G174S S175A F180Y
I121V S173Y G174S S175A F180Y
L81V S173Y G174S S175A F180Y
G132I S173P G174K S175P N176G T177S F180Y
S173P G174K S175P N176G T177S F180Y T297P

8. The variant of any of claims 1-7, which has an improved detergent stability compared to the parent or compared to the protease with SEQ ID NO: 3.
  
9. The variant of any of claims 1-8, wherein the variant is selected from the group consisting of:
  - a) a polypeptide having at least 75% sequence identity to the mature polypeptide of SEQ ID NO: 2;
  - b) a polypeptide encoded by a polynucleotide that hybridizes under medium, or high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 1, (ii) a sequence encoding the mature polypeptide of SEQ ID NO: 2, or (iii) the full-length complement of (i) or (ii);

- c) a polypeptide encoded by a polynucleotide having at least 75% identity to the mature polypeptide coding sequence of SEQ ID NO: 1 or a sequence encoding the mature polypeptide of SEQ ID NO: 2; and
  - d) a fragment of the mature polypeptide of SEQ ID NO: 2, which has protease activity.
10. The variant of any of claims 1-9, wherein the variant has at least at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, e. g. at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to the mature polypeptide of SEQ ID NO: 3.
11. The variant of any of claims 1-10, wherein the total number of alterations compared to SEQ ID NO 3 is 1-20, e.g. 1-10 and 1-5, such as 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 alterations.
12. A method for obtaining a protease variant, comprising introducing into a parent protease a substitution at one or more positions corresponding to positions 171, 173, 175 or 179 of SEQ ID NO: 3, wherein the variant has an amino acid sequence which is at least 70% identical to SEQ ID NO: 3, and recovering the variant.
13. The method of claim 11, wherein the variant comprises two, three, four or five substitutions corresponding to positions 171, 173, 175, 179 or 180 of the mature polypeptide of SEQ ID NO: 3.
14. The method according to any of claims 11-12, wherein the protease variant was obtained by a method comprising substitution of one amino acid selected from the group consisting of Trp, Lys, Glu, Asn at a position corresponding to position 171 of the mature polypeptide of SEQ ID NO: 3.
15. The method according to any of the preceding claims, wherein the protease variant was obtained by a method comprising substitution of Pro at a position corresponding to position 173 of the mature polypeptide of SEQ ID NO: 3.
16. The method according to any of the preceding claims, wherein the protease variant was obtained by a method comprising substitution of one amino acid selected from the group consisting of Ala, Val, Pro at a position corresponding to position 175 of the mature polypeptide of SEQ ID NO: 3.

17. The method according to any of the preceding claims, wherein the protease variant was obtained by a method comprising substitution of one amino acid selected from the group consisting of Cys, Val, Gln, Ser, Thr, Glu, His, Lys, Met, Asn, Ala, Tyr at a position corresponding to position 179 of the mature polypeptide of SEQ ID NO: 3.
18. The method according to claim 12, wherein the protease variant was obtained by a method comprising substitution of Tyr at a position corresponding to position 180 of the mature polypeptide of SEQ ID NO: 3.
19. The method according to any of claims 11-17, wherein the protease variant has at least 75%, *e.g.* at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, *e. g.* at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, but less than 100%, sequence identity to the mature polypeptide of SEQ ID NO: 3.
20. The method according to any of claims 11-18, wherein the parent protease selected from the group consists of:
  - a) a polypeptide having at least 75% sequence identity to the mature polypeptide of SEQ ID NO: 2;
  - b) a polypeptide encoded by a polynucleotide that hybridizes under medium or high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 1, (ii) a sequence encoding the mature polypeptide of SEQ ID NO: 2, or (iii) the full-length complement of (i) or (ii);
  - c) a polypeptide encoded by a polynucleotide having at least 75% identity to the mature polypeptide coding sequence of SEQ ID NO: 1 or a sequence encoding the mature polypeptide of SEQ ID NO: 2; and
  - d) a fragment of the mature polypeptide of SEQ ID NO: 2, which has protease activity.
21. The method according to any of claims 11-19, wherein the parent protease has at least 75%, *e.g.*, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, *e. g.* at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6, or 100% sequence identity to SEQ ID NO: 3.

Figure 1

